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SEQUENCE LISTING

<110> Kyowa Hakko Kirin Co., Ltd.

<120> ANTI-DEATH RECEPTOR 3 (DR3) ANTAGONISTIC ANTIBODIES WITH REDUCED AGONISTIC ACTIVITY

<130> W518296

<150> 61/975,214

<151> 2014-04-04

<160> 83

<170> PatentIn version 3.3

<210> 1

<211> 639

<212> DNA

<213> Artificial

<220>

<223> Description of the artificial sequence: TL1A-flag

<220>

<221> CDS

<222> (1).. (639)

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

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cag gtc aca ttc cgt ggg atg acc tct gag tgc agt gaa atc aga caa	384
Gln Val Thr Phe Arg Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln	
115 120 125	
gca ggc cga cca aac aag cca gac tcc atc act gtg gtc atc acc aag	432
Ala Gly Arg Pro Asn Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys	
130 135 140	
gta aca gac agc tac cct gag cca acc cag ctc ctc atg ggg acc aag	480
Val Thr Asp Ser Tyr Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys	
145 150 155 160	
tct gta tgc gaa gta ggt agc aac tgg ttc cag ccc atc tac ctc gga	528
Ser Val Cys Glu Val Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly	
165 170 175	
gcc atg ttc tcc ttg caa gaa ggg gac aag cta atg gtg aac gtc agt	576
Ala Met Phe Ser Leu Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser	
180 185 190	
gac atc tct ttg gtg gat tac aca aaa gaa gat aaa acc ttc ttt gga	624
Asp Ile Ser Leu Val Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly	
195 200 205	
gcc ttc tta cta tag	639
Ala Phe Leu Leu	
210	

<210> 2
 <211> 212
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

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Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
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Ile Met Phe Ala Ala Ser Gln Ala Asp Tyr Lys Asp Asp Asp Asp Lys
20 25 30

Leu Lys Gly Gln Glu Phe Ala Pro Ser His Gln Gln Val Tyr Ala Pro
35 40 45

Leu Arg Ala Asp Gly Asp Lys Pro Arg Ala His Leu Thr Val Val Arg
50 55 60

Gln Thr Pro Thr Gln His Phe Lys Asn Gln Phe Pro Ala Leu His Trp
65 70 75 80

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Glu His Glu Leu Gly Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr
 85 90 95

Asn Lys Phe Leu Leu Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser
 100 105 110

Gln Val Thr Phe Arg Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln
 115 120 125

Ala Gly Arg Pro Asn Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys
 130 135 140

Val Thr Asp Ser Tyr Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys
 145 150 155 160

Ser Val Cys Glu Val Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly
 165 170 175

Ala Met Phe Ser Leu Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser
 180 185 190

Asp Ile Ser Leu Val Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly
 195 200 205

Ala Phe Leu Leu
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 <213> Homo sapiens

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 <221> CDS
 <222> (1)..(1254)

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 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1 5 10 15

ctg gtg ctg ctg ggg gcc cgg gcc cag ggc ggc act cgt agc ccc agg 96
 Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
 20 25 30

tgt gac tgt gcc ggt gac ttc cac aag aag att ggt ctg ttt tgt tgc 144
 Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys

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35	40	45	
aga ggc tgc cca gcg ggg cac tac ctg aag gcc cct tgc acg gag ccc Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro	50	55	60
192			
tgc ggc aac tcc acc tgc ctt gtg tgt ccc caa gac acc ttc ttg gcc Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala	65	70	75
240			80
tgg gag aac cac cat aat tct gaa tgt gcc cgc tgc cag gcc tgt gat Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp	85	90	95
288			
gag cag gcc tcc cag gtg gcg ctg gag aac tgt tca gca gtg gcc gac Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp	100	105	110
336			
acc cgc tgt ggc tgt aag cca ggc tgg ttt gtg gag tgc cag gtc agc Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser	115	120	125
384			
caa tgt gtc agc agt tca ccc ttc tac tgc caa cca tgc cta gac tgc Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys	130	135	140
432			
ggg gcc ctg cac cgc cac aca cgg cta ctc tgt tcc cgc aga gat act Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr	145	150	155
480			160
gac tgt ggg acc tgc ctg cct ggc ttc tat gaa cat ggc gat ggc tgc Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys	165	170	175
528			
gtg tcc tgc ccc acg agc acc ctg ggg agc tgt cca gag cgc tgt gcc Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala	180	185	190
576			
gct gtc tgt ggc tgg agg cag atg ttc tgg gtc cag gtg ctc ctg gct Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala	195	200	205
624			
ggc ctt gtg gtc ccc ctc ctg ctt ggg gcc acc ctg acc tac aca tac Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr	210	215	220
672			
cgc cac tgc tgg cct cac aag ccc ctg gtt act gca gat gaa gct ggg Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly	225	230	235
720			240
atg gag gct ctg acc cca cca ccg gcc acc cat ctg tca ccc ttg gac Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp	245	250	255
768			
agc gcc cac acc ctt cta gca cct cct gac agc agt gag aag atc tgc Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys	260	265	270
816			

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acc gtc cag ttg gtg ggt aac agc tgg acc cct ggc tac ccc gag acc	864
Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr	
275 280 285	
cag gag gcg ctc tgc ccg cag gtg aca tgg tcc tgg gac cag ttg ccc	912
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro	
290 295 300	
agc aga gct ctt ggc ccc gct gct gcg ccc aca ctc tcg cca gag tcc	960
Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser	
305 310 315 320	
cca gcc ggc tcg cca gcc atg atg ctg cag ccg ggc ccg cag ctc tac	1008
Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr	
325 330 335	
gac gtg atg gac gcg gtc cca gcg cgg cgc tgg aag gag ttc gtg cgc	1056
Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg	
340 345 350	
acg ctg ggg ctg cgc gag gca gag atc gaa gcc gtg gag gtg gag atc	1104
Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile	
355 360 365	
ggc cgc ttc cga gac cag cag tac gag atg ctc aag cgc tgg cgc cag	1152
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln	
370 375 380	
cag cag ccc gcg ggc ctc gga gcc gtt tac gcg gcc ctg gag cgc atg	1200
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met	
385 390 395 400	
ggg ctg gac ggc tgc gtg gaa gac ttg cgc agc cgc ctg cag cgc ggc	1248
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly	
405 410 415	
ccg tga	1254
Pro	

<210> 4
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 4

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

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
 35 40 45

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Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 65 70 75 80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
 85 90 95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
 100 105 110

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

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
 130 135 140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
 145 150 155 160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
 165 170 175

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

Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
 195 200 205

Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
 210 215 220

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

Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
 245 250 255

Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
 260 265 270

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 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
 275 280 285

Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
 290 295 300

Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
 305 310 315 320

Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
 325 330 335

Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
 340 345 350

Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
 355 360 365

Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
 370 375 380

Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
 385 390 395 400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
 405 410 415

Pro

<210> 5
 <211> 1299
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hDR3-Fc

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 <221> CDS
 <222> (1)..(1299)

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 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1 5 10 15

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ctg	gtg	ctg	ctg	ggg	gcc	cgg	gcc	cag	ggc	ggc	act	cgt	agc	ccc	agg	96
Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg	
		20						25					30			
tgt	gac	tgt	gcc	ggt	gac	ttc	cac	aag	aag	att	ggt	ctg	ttt	tgt	tgc	144
Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys	
		35					40					45				
aga	ggc	tgc	cca	gcg	ggg	cac	tac	ctg	aag	gcc	cct	tgc	acg	gag	ccc	192
Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	
	50					55					60					
tgc	ggc	aac	tcc	acc	tgc	ctt	gtg	tgt	ccc	caa	gac	acc	ttc	ttg	gcc	240
Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
65					70				75					80		
tgg	gag	aac	cac	cat	aat	tct	gaa	tgt	gcc	cgc	tgc	cag	gcc	tgt	gat	288
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	
				85					90					95		
gag	cag	gcc	tcc	cag	gtg	gcg	ctg	gag	aac	tgt	tca	gca	gtg	gcc	gac	336
Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	
			100					105					110			
acc	cgc	tgt	ggc	tgt	aag	cca	ggc	tgg	ttt	gtg	gag	tgc	cag	gtc	agc	384
Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	
		115					120					125				
caa	tgt	gtc	agc	agt	tca	ccc	ttc	tac	tgc	caa	cca	tgc	cta	gac	tgc	432
Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	
	130					135					140					
ggg	gcc	ctg	cac	cgc	cac	aca	cgg	cta	ctc	tgt	tcc	cgc	aga	gat	act	480
Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	
145					150					155					160	
gac	tgt	ggg	acc	tgc	ctg	cct	ggc	ttc	tat	gaa	cat	ggc	gat	ggc	tgc	528
Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
				165					170					175		
gtg	tcc	tgc	ccc	acg	agc	acc	ctg	ggg	agc	tgt	cca	gag	cgc	tgt	gcc	576
Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
			180					185					190			
gct	gtc	tgt	ggc	tgg	agg	cag	atg	ttc	ccc	aaa	tct	tgt	gac	aaa	act	624
Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Pro	Lys	Ser	Cys	Asp	Lys	Thr	
		195					200					205				
cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	672
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	
	210					215					220					
gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	720
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
225					230					235					240	
acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	768
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	

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245								250				255				
gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	816
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
			260					265					270			
aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	864
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	
		275					280					285				
agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	912
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
	290					295					300					
aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	960
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
305					310		315								320	
atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	1008
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
				325				330						335		
ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	1056
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
			340					345					350			
ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	1104
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
		355					360					365				
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	1152
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	
	370					375					380					
tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	1200
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	
385					390					395					400	
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	1248
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
				405					410					415		
ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	1296
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
			420					425					430			
tga																1299

<210> 6
 <211> 432
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 6

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

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
 35 40 45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 65 70 75 80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
 85 90 95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
 100 105 110

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

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
 130 135 140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
 145 150 155 160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
 165 170 175

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

Ala Val Cys Gly Trp Arg Gln Met Phe Pro Lys Ser Cys Asp Lys Thr
 195 200 205

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 210 215 220

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

225					230					11/58					235				240
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro			
				245						250					255				
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala			
			260						265					270					
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val				
		275					280					285							
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr				
	290					295					300								
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr				
305					310					315					320				
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu				
				325					330					335					
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys				
			340					345					350						
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser				
		355					360					365							
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp				
	370					375					380								
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser				
385					390					395				400					
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala				
				405					410					415					
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
			420					425					430						

$\langle 210 \rangle$	7
$\langle 211 \rangle$	936
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial

<220>
<223> Description of the artificial sequence: hDR3-mG1Fc

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<220>

<221> CDS

<222> (1)... (936)

<400> 7

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

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gct cca cag gtg tac acc att cca cct ccc aag gag cag atg gcc aag 672
 Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys
 210 215 220

gat aaa gtc agt ctg acc tgc atg ata aca gac ttc ttc cct gaa gac 720
 Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp
 225 230 235 240

att act gtg gag tgg cag tgg aat ggg cag cca gcg gag aac tac aag 768
 Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys
 245 250 255

aac act cag ccc atc atg gac aca gat ggc tct tac ttc gtc tac agc 816
 Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser
 260 265 270

aag ctc aat gtg cag aag agc aac tgg gag gca gga aat act ttc acc 864
 Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
 275 280 285

tgc tct gtg tta cat gag ggc ctg cac aac cac cat act gag aag agc 912
 Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser
 290 295 300

ctc tcc cac tct cct ggt aaa tga 936
 Leu Ser His Ser Pro Gly Lys
 305 310

<210> 8
 <211> 311
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 8

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1 5 10 15

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

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
 35 40 45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Ala Ser Gly Gly Gly Ser Gly Gly Gly
 65 70 75 80

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Ser Gly Gly Gly Ser Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys
85 90 95

Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
100 105 110

Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val
115 120 125

Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp
130 135 140

Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe
145 150 155 160

Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp
165 170 175

Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe
180 185 190

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys
195 200 205

Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys
210 215 220

Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp
225 230 235 240

Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys
245 250 255

Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser
260 265 270

Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
275 280 285

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser
290 295 300

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Leu Ser His Ser Pro Gly Lys
305 310

<210> 9
<211> 1038
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: HDR3-DD

<220>
<221> CDS
<222> (1).. (1038)

<400> 9
atg gag cag cgg ccg cgg ggc tgc gcg gcg gtg gcg gcg ggc ctc ctc 48
Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
1 5 10 15
ctg gtg ctg ctg ggg gcc cgg gcc cag ggc ggc act cgt agc ccc agg 96
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
20 25 30
tgt gac tgt gcc ggt gac ttc cac aag aag att ggt ctg ttt tgt tgc 144
Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
35 40 45
aga ggc tgc cca gcg ggg cac tac ctg aag gcc cct tgc acg gag ccc 192
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
50 55 60
tgc ggc aac tcc acc tgc ctt gtg tgt ccc caa gac acc ttc ttg gcc 240
Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
65 70 75 80
tgg gag aac cac cat aat tct gaa tgt gcc gcg tgc cag gcc tgt gat 288
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
85 90 95
gag cag gcc tcc cag gtg gcg ctg gag aac tgt tca gca gtg gcc gac 336
Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
100 105 110
acc gcg tgt ggc tgt aag cca ggc tgg ttt gtg gag tgc cag gtc agc 384
Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
115 120 125
caa tgt gtc agc agt tca ccc ttc tac tgc caa cca tgc cta gac tgc 432
Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
130 135 140
ggg gcc ctg cac gcg cac aca cgg cta ctc tgt tcc gcg aga gat act 480
Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
145 150 155 160

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gac	tgt	ggg	acc	tgc	ctg	cct	ggc	ttc	tat	gaa	cat	ggc	gat	ggc	tgc	528
Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
				165					170					175		
gtg	tcc	tgc	ccc	acg	agc	acc	ctg	ggg	agc	tgt	cca	gag	cgc	tgt	gcc	576
Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
			180					185					190			
gct	gtc	tgt	ggc	tgg	agg	cag	atg	ttc	tgg	gtc	cag	gtg	ctc	ctg	gct	624
Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	
		195					200					205				
ggc	ctt	gtg	gtc	ccc	ctc	ctg	ctt	ggg	gcc	acc	ctg	acc	tac	aca	tac	672
Gly	Leu	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	
	210					215					220					
cgc	cac	tgc	tgg	cct	cac	aag	ccc	ctg	gtt	act	gca	gat	gaa	gct	ggg	720
Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
225					230					235					240	
atg	gag	gct	ctg	acc	cca	cca	ccg	gcc	acc	cat	ctg	tca	ccc	ttg	gac	768
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	
				245					250					255		
agc	gcc	cac	acc	ctt	cta	gca	cct	cct	gac	agc	agt	gag	aag	atc	tgc	816
Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	
			260					265					270			
acc	gtc	cag	ttg	gtg	ggt	aac	agc	tgg	acc	cct	ggc	tac	ccc	gag	acc	864
Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	
		275					280					285				
cag	gag	gcg	ctc	tgc	ccg	cag	gtg	aca	tgg	tcc	tgg	gac	cag	ttg	ccc	912
Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	
	290					295					300					
agc	aga	gct	ctt	ggc	ccc	gct	gct	gcg	ccc	aca	ctc	tcg	cca	gag	tcc	960
Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	Leu	Ser	Pro	Glu	Ser	
305					310				315						320	
cca	gcc	ggc	tcg	cca	gcc	atg	atg	ctg	cag	ccg	ggc	ccg	cag	ctc	tac	1008
Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	
				325					330					335		
gac	gtg	atg	gac	gcg	gtc	cca	gcg	cgg	tga							1038
Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg								
			340					345								

<210> 10
 <211> 345
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 10

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Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1 5 10 15

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

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
 35 40 45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 65 70 75 80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
 85 90 95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
 100 105 110

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

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
 130 135 140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
 145 150 155 160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
 165 170 175

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

Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
 195 200 205

Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
 210 215 220

Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly

225 230 18/58 235 240

Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
245 250 255

Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
260 265 270

Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
275 280 285

Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
290 295 300

Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
305 310 315 320

Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
325 330 335

Asp Val Met Asp Ala Val Pro Ala Arg
340 345

$\langle 210 \rangle$	11
$\langle 211 \rangle$	975
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial

$\langle 220 \rangle$
 $\langle 223 \rangle$ Description of the artificial sequence: mDR3-DD

<220>
 <221> CDS
 <222> (1).. (975)

<400>	11																
atg	gag	gca	cgg	ctg	ctg	cgg	ggc	tgc	gtg	gtg	gag	cct	ctg	ttc	cta	48	
Met	Glu	Ala	Arg	Leu	Leu	Arg	Gly	Cys	Val	Val	Glu	Pro	Leu	Phe	Leu		
1				5					10					15			
cca	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctt	ggt	ggc	cag	ggc	cag	ggc	96	
Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Gln	Gly	Gln	Gly		
			20					25					30				
ggc	atg	tct	ggc	agg	tgt	gac	tgt	gcc	agt	gag	tcc	cag	aag	agg	tat	144	
Gly	Met	Ser	Gly	Arg	Cys	Asp	Cys	Ala	Ser	Glu	Ser	Gln	Lys	Arg	Tyr		
		35					40					45					
ggc	ccg	ttt	tgt	tgc	agg	ggc	tgc	cca	aag	gga	cac	tac	atg	aag	gcc	192	

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Gly 50	Pro	Phe	Cys	Cys	Arg	Gly 55	Cys	Pro	Lys	Gly	His 60	Tyr	Met	Lys	Ala
ccc Pro 65	tgc Cys	gca Ala	gaa Glu	ccc Pro	tgt Cys 70	ggc Gly	aac Asn	tcc Ser	acc Thr	tgc Cys 75	ctt Leu	ccc Pro	tgt Cys	ccc Pro	tgc Ser 80
gac Asp	acc Thr	ttc Phe	ttg Leu	acc Thr 85	aga Arg	gac Asp	aac Asn	cac His	ttt Phe 90	aag Lys	act Thr	gac Asp	tgt Cys	acc Thr 95	cgc Arg
tgc Cys	caa Gln	gtc Val	tgt Cys 100	gat Asp	gaa Glu	gag Glu	gcc Ala	ctt Leu 105	caa Gln	gtg Val	acc Thr	ctt Leu	gag Glu 110	aac Asn	tgc Cys
tgc Ser	gca Ala	aag Lys 115	tgc Ser	gac Asp	acc Thr	cac His	tgt Cys 120	ggc Gly	tgc Cys	cag Gln	tca Ser	ggc Gly 125	tgg Trp	tgt Cys	gtt Val
gac Asp 130	tgc Cys	tcc Ser	acc Thr	gag Glu	cca Pro	tgt Cys 135	ggg Gly	aaa Lys	agc Ser	tca Ser	cct Pro 140	ttc Phe	tct Ser	tgt Cys	gtc Val
cca Pro 145	tgc Cys	ggg Gly	gct Ala	aca Thr	aca Thr 150	cca Pro	gtc Val	cat His	gag Glu	gct Ala 155	cca Pro	acc Thr	ccc Pro	cgg Arg	ccc Pro 160
tgc Cys	ctg Leu	cct Pro	ggc Gly	ttc Phe 165	tat Tyr	ata Ile	cgt Arg	ggc Gly	aat Asn 170	gac Asp	tgc Cys	acg Thr	tcc Ser	tgc Cys 175	ccc Pro
acg Thr	ggc Gly	ttc Phe 180	agc Ser	agc Ser	gtt Val	tgc Cys	cct Pro	aag Lys 185	gct Ala	tgc Cys	act Thr	gct Ala	gtc Val 190	tgt Cys	ggc Gly
tgg Trp	aag Lys	cag Gln 195	atg Met	ttt Phe	tgg Trp	gtc Val	cag Gln 200	gtg Val	ctt Leu	cta Leu	gga Gly 205	gtc Val	gcg Ala	ttc Phe	ott Leu
ttt Phe 210	ggg Gly	gct Ala	atc Ile	ctg Leu	atc Ile	tgt Cys 215	gca Ala	tat Tyr	tgt Cys	cga Arg	tgg Trp 220	cag Gln	cct Pro	tgt Cys	aag Lys
gcc Ala 225	gtg Val	gtc Val	act Thr	gca Ala	gac Asp 230	aca Thr	gct Ala	ggg Gly	acg Thr	gag Glu 235	acc Thr	ctg Leu	gcc Ala	tca Ser	cca Pro 240
cag Gln	act Thr	gcc Ala	cat His	ctc Leu 245	tca Ser	gcc Ala	tca Ser	gac Asp	agc Ser 250	gcc Ala	cac His	acc Thr	ctc Leu	ctg Leu 255	gca Ala
cct Pro	cca Pro	agc Ser	agt Ser 260	act Thr	ggg Gly	aaa Lys	atc Ile	tgt Cys 265	acc Thr	act Thr	gtc Val	cag Gln	ttg Leu 270	gta Val	ggc Gly
aac Asn	aac Asn	tgg Trp 275	acc Thr	cct Pro	ggc Gly	tta Leu	tcc Ser 280	cag Gln	act Thr	cag Gln	gag Glu	gtg Val 285	gtc Val	tgc Cys	gga Gly

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cag gcc tca caa ccc tgg gat cag ctg cca aac aga act ctt gga act 912
 Gln Ala Ser Gln Pro Trp Asp Gln Leu Pro Asn Arg Thr Leu Gly Thr
 290 295 300

cct ctg gca tct ccg ctc tcg cca gcg ccc cct gcg ggc tct ccg gct 960
 Pro Leu Ala Ser Pro Leu Ser Pro Ala Pro Pro Ala Gly Ser Pro Ala
 305 310 315 320

gct gtg ctc cag tga 975
 Ala Val Leu Gln

<210> 12
 <211> 324
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 12

Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu Phe Leu
 1 5 10 15

Pro Leu Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly Gln Gly
 20 25 30

Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys Arg Tyr
 35 40 45

Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met Lys Ala
 50 55 60

Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys Pro Ser
 65 70 75 80

Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys Thr Arg
 85 90 95

Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu Asn Cys
 100 105 110

Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp Cys Val
 115 120 125

Asp Cys Ser Thr Glu Pro Cys Gly Lys Ser Ser Pro Phe Ser Cys Val
 130 135 140

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Pro Cys Gly Ala Thr Thr Pro Val His Glu Ala Pro Thr Pro Arg Pro
145 150 155 160

Cys Leu Pro Gly Phe Tyr Ile Arg Gly Asn Asp Cys Thr Ser Cys Pro
165 170 175

Thr Gly Phe Ser Ser Val Cys Pro Lys Ala Cys Thr Ala Val Cys Gly
180 185 190

Trp Lys Gln Met Phe Trp Val Gln Val Leu Leu Gly Val Ala Phe Leu
195 200 205

Phe Gly Ala Ile Leu Ile Cys Ala Tyr Cys Arg Trp Gln Pro Cys Lys
210 215 220

Ala Val Val Thr Ala Asp Thr Ala Gly Thr Glu Thr Leu Ala Ser Pro
225 230 235 240

Gln Thr Ala His Leu Ser Ala Ser Asp Ser Ala His Thr Leu Leu Ala
245 250 255

Pro Pro Ser Ser Thr Gly Lys Ile Cys Thr Thr Val Gln Leu Val Gly
260 265 270

Asn Asn Trp Thr Pro Gly Leu Ser Gln Thr Gln Glu Val Val Cys Gly
275 280 285

Gln Ala Ser Gln Pro Trp Asp Gln Leu Pro Asn Arg Thr Leu Gly Thr
290 295 300

Pro Leu Ala Ser Pro Leu Ser Pro Ala Pro Pro Ala Gly Ser Pro Ala
305 310 315 320

Ala Val Leu Gln

<210> 13
<211> 456
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VH full

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<220>

<221> CDS

<222> (1).. (456)

<400> 13

atg	tct	gtc	tcc	ttc	ctc	atc	ttc	ctg	ccc	gtg	ctg	ggc	ctc	cca	tgg	48
Met	Ser	Val	Ser	Phe	Leu	Ile	Phe	Leu	Pro	Val	Leu	Gly	Leu	Pro	Trp	
1				5					10					15		

ggt	gtc	ctg	tca	cag	gta	cag	cta	cag	cag	tca	ggt	cca	gga	ctg	gtg	96
Gly	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	
		20						25					30			

aag	ccc	tcg	cag	acc	ctc	tca	ctc	acc	tgt	gcc	atc	tcc	ggg	gac	agt	144
Lys	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	
		35					40					45				

gtc	tct	ggg	tac	agt	gct	gct	tgg	aac	tgg	atc	agg	cag	tcc	cca	tcg	192
Val	Ser	Gly	Tyr	Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Ser	
	50					55					60					

aga	ggc	ctt	gag	tgg	ctg	gga	agg	aca	tac	tac	agg	tcc	aag	tgg	tat	240
Arg	Gly	Leu	Glu	Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	
65					70					75					80	

aat	gat	tat	gca	gta	tct	gtg	aaa	agt	cga	ata	acc	atc	aac	cca	gac	288
Asn	Asp	Tyr	Ala	Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	
				85					90					95		

aca	tcc	aag	aac	cag	ttc	tcc	ctg	cag	ctg	aac	tct	gtg	act	ccc	gag	336
Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	
			100					105					110			

gac	acg	gct	gtg	tat	tac	tgt	gca	aga	gat	tac	tat	ggt	tcg	gag	agt	384
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Tyr	Tyr	Gly	Ser	Glu	Ser	
		115					120					125				

tat	tat	aac	ggg	ggg	tac	tac	tac	tac	ggt	atg	gac	gtc	tgg	ggc	caa	432
Tyr	Tyr	Asn	Gly	Gly	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	
	130					135					140					

ggg	acc	acg	gtc	acc	gtc	tcc	tca									456
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
145					150											

<210> 14

<211> 152

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 14

Met Ser Val Ser Phe Leu Ile Phe Leu Pro Val Leu Gly Leu Pro Trp

1	5	23/58 10	15
Gly Val Leu Ser 20 Gln Val Gln Leu 25 Gln Gln Ser Gly Pro Gly 30 Leu Val			
Lys Pro Ser 35 Gln Thr Leu Ser 40 Leu Thr Cys Ala Ile Ser 45 Gly Asp Ser			
Val Ser 50 Gly Tyr Ser Ala 55 Ala Trp Asn Trp Ile Arg 60 Gln Ser Pro Ser			
Arg Gly Leu Glu Trp 70 Leu Gly Arg Thr Tyr 75 Tyr Arg Ser Lys Trp 80 Tyr			
Asn Asp Tyr Ala 85 Val Ser Val Lys Ser 90 Arg Ile Thr Ile Asn 95 Pro Asp			
Thr Ser Lys 100 Asn Gln Phe Ser Leu 105 Gln Leu Asn Ser Val 110 Thr Pro Glu			
Asp Thr 115 Ala Val Tyr Tyr Cys 120 Ala Arg Asp Tyr Tyr 125 Gly Ser Glu Ser			
Tyr Tyr 130 Asn Gly Gly Tyr 135 Tyr Tyr Tyr Gly Met 140 Asp Val Trp Gly Gln			
Gly Thr Thr Val Thr Val Ser Ser			
145	150		

$\langle 210 \rangle$	15
$\langle 211 \rangle$	132
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial

 $\langle 220 \rangle$

<223> Description of the artificial sequence: 142A2-VH

<400> 15

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu

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35

40

45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

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

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Glu Ser Tyr Tyr Asn Gly
 100 105 110

Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
 115 120 125

Thr Val Ser Ser
 130

<210> 16
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142A2-HCDR1

<400> 16

Gly Tyr Ser Ala Ala Trp Asn
 1 5

<210> 17
 <211> 18
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142A2-HCDR2

<400> 17

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Val
 1 5 10 15

Lys Ser

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<210> 18
 <211> 20
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-HCDR3

<400> 18

Asp Tyr Tyr Gly Ser Glu Ser Tyr Tyr Asn Gly Gly Tyr Tyr Tyr Tyr
 1 5 10 15

Gly Met Asp Val
 20

<210> 19
 <211> 387
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VL full

<220>

<221> CDS

<222> (1).. (387)

<400> 19

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctt ctg ctg ctc tgg 48
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

ctc cca ggt gcc aga tgt gcc atc cag ttg acc cag tct cca tcc tcc 96
 Leu Pro Gly Ala Arg Cys Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser
 20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45

cgg ggc att agc agt gct tta gcc tgg tat cag cag aaa cca ggg aaa 192
 Pro Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

gct cct aag ctc ctg atg tat gat gcc tcc agt ttg gaa agt ggg gtc 240
 Ala Pro Lys Leu Leu Met Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
 65 70 75 80

cca tca agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc 288
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95

atc agc agc ctg cag cct gaa gat ttt gca act tat tac tgt caa cag 336

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

ttt aat gat tac ccg ctc act ttc ggc gga ggg acc aag gtg gag atc 384
 Phe Asn Asp Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125

aaa 387
 Lys

<210> 20
 <211> 129
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 20

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

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

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

Pro Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60

Ala Pro Lys Leu Leu Met Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
 65 70 75 80

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

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

Phe Asn Asp Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125

Lys

27/58

<210> 21
 <211> 107
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VL

<400> 21

Ala 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 Arg Ala Ser Pro Gly Ile Ser Ser Ala
 20 25 30

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

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

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

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

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

<210> 22
 <211> 11
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-LCDRI

<400> 22

Arg Ala Ser Pro Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 23
 <211> 7
 <212> PRT
 <213> Artificial

<220>

28/58

<223> Description of the artificial sequence: 142A2-LCDR2

<400> 23

Asp Ala Ser Ser Leu Glu Ser
 1 5

<210> 24
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142A2-LCDR3

<400> 24

Gln Gln Phe Asn Asp Tyr Pro Leu Thr
 1 5

<210> 25
 <211> 408
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-VH full

<220>
 <221> CDS
 <222> (1).. (408)

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

	85	29/58 90	95	
acg ctg tat ctc caa atg aac agc ctg aga gcc gag gac acg gcc gta				336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	100	105	110	
tat ttc tgt gcg aaa gag ttc ggt gac tac ctt gac tac tgg ggc cag				384
Tyr Phe Cys Ala Lys Glu Phe Gly Asp Tyr Leu Asp Tyr Trp Gly Gln	115	120	125	
gga acc ctg gtc acc gtc tcc tca				408
Gly Thr Leu Val Thr Val Ser Ser	130	135		

<210> 26
 <211> 136
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 26

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu 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 Thr Val
 35 40 45

Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Val Ser Ala Ile Ser Asp Ser Gly Gly Arg Thr Tyr Tyr Ala
 65 70 75 80

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

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

Tyr Phe Cys Ala Lys Glu Phe Gly Asp Tyr Leu Asp Tyr Trp Gly Gln
 115 120 125

Gly Thr Leu Val Thr Val Ser Ser

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130

135

<210> 27
 <211> 117
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142S38BA-VH

<400> 27

Glu Val Gln Leu Leu 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 Thr Val Ser Arg Tyr
 20 25 30

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

Ser Ala Ile Ser Asp Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Glu Phe Gly Asp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 28
 <211> 5
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142S38BA-HCDR1

<400> 28

Arg Tyr Ala Met Ser
 1 5

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<210> 29
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-HCDR2

<400> 29

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

Gly

<210> 30
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-HCDR3

<400> 30

Glu	Phe	Gly	Asp	Tyr	Leu	Asp	Tyr
1				5			

<210> 31
 <211> 378
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-VL full

<220>
 <221> CDS
 <222> (1).. (378)

<400> 31

atg	gaa	gcc	cca	gct	cag	ctt	ctc	ttc	ctc	ctg	cta	ctc	tgg	ctc	cca	48
Met	Glu	Ala	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5					10					15		
gat	acc	acc	gga	gaa	att	gtg	ttg	aca	cag	tct	cca	gcc	acc	ctg	tct	96
Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	
			20					25					30			
ttg	tct	cca	ggg	gaa	aga	gcc	acc	ctc	tcc	tgc	agg	gcc	agt	cag	agt	144
Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	
		35					40					45				

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gtt agc agc tac tta gcc tgg tac caa cag aaa cct ggc cag gct ccc 192
 Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60

agg ctc ctc atc tat gat gca tcc aac agg gcc act ggc atc cca gcc 240
 Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
 65 70 75 80

agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

agc cta gag cct gaa gat ttt gca gtt tat tac tgt cag cag cgt agc 336
 Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
 100 105 110

aac tgg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 378
 Asn Trp Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 115 120 125

<210> 32
 <211> 126
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 32

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

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

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

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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
 100 105 110

33/58

Asn Trp Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 115 120 125

<210> 33
 <211> 106
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-VL

<400> 33

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Trp Thr
 85 90 95

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

<210> 34
 <211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-LCDR1

<400> 34

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

34/58

<210> 35
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-LCDR2

<400> 35

Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 36
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA-LCDR3

<400> 36

Gln Gln Arg Ser Asn Trp Trp Thr
 1 5

<210> 37
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hCL kappa

<400> 37

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

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

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

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

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

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

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

$\langle 210 \rangle$	38
$\langle 211 \rangle$	330
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial

<220>
<223> Description of the artificial sequence: hIgG1 CH

<400> 38

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

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

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

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

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

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

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

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

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

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

<210> 39

<211> 326

<212> PRT

<213> Artificial

<220>

<223> Description of the artificial sequence: hIgG2 CH

<400> 39

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

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30 37/58

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 65 70 75 80

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 100 105 110

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

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

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

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 180 185 190

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 325

<210> 40

<211> 327

<212> PRT

<213> Artificial

<220>

<223> Description of the artificial sequence: IgG4 variant

<400> 40

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

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

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

39/58

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
 325

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<210> 41
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hTL1A_F

<400> 41
 atggccgagg atctgggact gagctttg 28

<210> 42
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hTL1A-3' _R

<400> 42
 ccgttgtccc tgtggaatgc cccctac 27

<210> 43
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: VCAM-FLAGR-Sall_F

<400> 43
 agagaggctg accaccatgc ctgggaagat ggtcgtgatc c 41

<210> 44
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hTL1A-EC_BamHI-R

<400> 44
 agagagggat ccctatagta agaaggctcc aaagaaggtt ttatc 45

<210> 45
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: VCAM-FLAG_hTL1A_F

<400> 45
 cgacgatgac aagctaaaag gacaggagtt tgcaccttca c 41

41/58

<210> 46
 <211> 43
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: VCAM-FLAG_hTL1A_R

<400> 46
 cctgtccttt tagcttgta tcgtgtcct tgtagtcagc ttg

43

<210> 47
 <211> 23
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: hDR3_F5'

<400> 47
 gaaggcggaa ccacgacggg cag

23

<210> 48
 <211> 23
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: hDR3-EC_R

<400> 48
 tggtaggggc agagcctcca tcc

23

<210> 49
 <211> 40
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: hDR3-SalI_F

<400> 49
 agagaggtcg accaccatgg agcagcggcc gcggggctgc

40

<210> 50
 <211> 40
 <212> DNA
 <213> Artificial

<220>

<223> Description of the artificial sequence: hDR3_hG1Fc_R

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<400> 50
cacaagattt ggggaacatc tgcctccagc cacagacagc 40

<210> 51
<211> 43
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: hDR3_hG1Fc_F

<400> 51
gaggcagatg ttccccaat cttgtgacaa aactcacaca tgc 43

<210> 52
<211> 40
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: hG1Fc_BamHI-R

<400> 52
agagagggat cctcatttac ccggagacag ggagaggctc 40

<210> 53
<211> 42
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: hDR3-pG-NheI_R

<400> 53
ctccagatcc tcctccgcta gcaaggcagg tggagttgcc gc 42

<210> 54
<211> 64
<212> DNA
<213> Artificial

<220>
<223> Description of the artificial sequence: mG1Fc-pG-NheI_F

<400> 54
gctagcggag gaggatctgg aggaggaagt ggaggaggat ctcccaggga ttgtggttgt 60

aagc 64

<210> 55
<211> 43
<212> DNA
<213> Artificial

43/58

<220>

<223> Description of the artificial sequence: mG1Fc_BamHI-R

<400> 55

agagaggggat cctcatttac caggagagtg ggagaggctc ttc

43

<210> 56

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Description of the artificial sequence: hDR3 Δ DD_BamHI_R

<400> 56

agagaggggat cctcaccgcg ctgggaccgc gtccatcac

39

<210> 57

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Description of the artificial sequence: mDR3_Fwd

<400> 57

atggaggcac ggctgctgcg gggctg

26

<210> 58

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of the artificial sequence: mDR3_3' _ R

<400> 58

ctgctacgca ggaccacggc aggggggtag

30

<210> 59

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Description of the artificial sequence: mDR3-SalI_F

<400> 59

agagaggtcg accaccatgg aggcaoggct gctgoggggc tg

42

<210> 60

<211> 38

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<212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: mDR3(1-324)_BamHI

<400> 60
 agagagggat cctcactgga gcacagcagc cggagagc 38

<210> 61
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: IgG1 primer

<400> 61
 tottggtccac cttggtgttg ctgggcttgt g 31

<210> 62
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: hk5 primer

<400> 62
 aggcacacaa cagaggcagt tccagatttc 30

<210> 63
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38BA_VLF_BglI

<400> 63
 atatagatct ccaccatgga agccccagct cag 33

<210> 64
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142P20_VL1_BsiWI_

<400> 64
 tatacgtacg ttgatttcc accttggtcc ct 32

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<210> 65
<211> 36
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2_BglII_F

<400> 65
atatagatct ccaccatgag ggtccccgct cagctc 36

<210> 66
<211> 36
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2_BsiWI_R

<400> 66
atatcgtaag tttgatctcc accttggtcc ctccgc 36

<210> 67
<211> 40
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VH_SalI_F

<400> 67
atatgtcgac ccaccatgtc tgtctccttc ctcatcttcc 40

<210> 68
<211> 30
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VH_NheI_R

<400> 68
atatgctagc tgaggagacg gtgaccgtgg 30

<210> 69
<211> 32
<212> DNA
<213> Artificial

<220>

<223> Description of the artificial sequence: 142S38BA_VHF_SalI

<400> 69
tatagtcgac caccatggag tttgggctga gc 32

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<210> 70
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: F429_VH_R1

<400> 70
 ttgctagctg aggagacggt gacc 24

<210> 71
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> Description of the artificial sequence: IgG2 primer

<400> 71
 gtgcacgccg ctggtcaggg cgccctg 26

<210> 72
 <211> 459
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142A2_mvG4_HC

<400> 72
 Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Gly Tyr
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

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Tyr Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Glu Ser Tyr Tyr Asn Gly
 100 105 110

Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
 115 120 125

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

Pro Ser Ser Lys Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
 210 215 220

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 225 230 235 240

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
 245 250 255

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 275 280 285

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

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 305 310 315 320

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285

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Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300

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

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
 420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 74
 <211> 444
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38B_mvG4_HC

<400> 74

Glu Val Gln Leu Leu 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 Thr Val Ser Arg Tyr
 20 25 30

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

Ser Ala Ile Ser Asp Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Glu Phe Gly Asp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335

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

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 75
 <211> 442
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142S38B_mvG4_LC

<400> 75

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Trp Thr
 85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
 210 215 220

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 225 230 235 240

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Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 245 250 255

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
 260 265 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 275 280 285

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 290 295 300

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

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
 340 345 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
 405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
 420 425 430

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 76
 <211> 132
 <212> PRT
 <213> Artificial

55/58

<220>

<223> Description of the artificial sequence: 142A2-VH_G112R

<400> 76

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

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

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Glu Ser Tyr Tyr Asn Arg
 100 105 110

Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
 115 120 125

Thr Val Ser Ser
 130

<210> 77

<211> 107

<212> PRT

<213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VL_A51E

<400> 77

Ala 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 Arg Ala Ser Pro Gly Ile Ser Ser Ala
 20 25 30

56/58

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

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

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

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

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

<210> 78
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> Description of the artificial sequence: 142A2-VL_ L54Q

<400> 78

Ala 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 Arg Ala Ser Pro Gly Ile Ser Ser Ala
 20 25 30

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

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

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

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

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

57/58

<210> 79
 <211> 107
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-VL_A51E-L54Q

<400> 79

Ala 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 Arg Ala Ser Pro Gly Ile Ser Ser Ala
 20 25 30

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

Tyr Asp Glu Ser Ser Gln Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> 80
 <211> 20
 <212> PRT
 <213> Artificial

<220>

<223> Description of the artificial sequence: 142A2-HCDR_G112R

<400> 80

Asp Tyr Tyr Gly Ser Glu Ser Tyr Tyr Asn Arg Gly Tyr Tyr Tyr Tyr
 1 5 10 15

Gly Met Asp Val
 20

58/58

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

<220>
<223> Description of the artificial sequence: 142A2-LCDR2_A51E

<400> 81

Asp Glu Ser Ser Leu Glu Ser
1 5

<210> 82
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: 142A2-LCDR2_L54Q

<400> 82

Asp Ala Ser Ser Gln Glu Ser
1 5

<210> 83
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Description of the artificial sequence: 142A2-LCDR2_A51E/L54Q

<400> 83

Asp Glu Ser Ser Gln Glu Ser
1 5