

SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> Anti CDH6 antibodies and anti CDH6 antibody drug conjugates

<130> DSPCT-FP1814

<150> JP2017-096749

<151> 2017-05-15

<160> 86

<170> PatentIn version 3.5

<210> 1

<211> 790

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro
1 5 10 15

Tyr Pro Thr Leu Ser Thr Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro
20 25 30

Ala Lys Lys Arg Ala Leu Glu Leu Ser Gly Asn Ser Lys Asn Glu Leu
35 40 45

Asn Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu
50 55 60

Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp
65 70 75 80

Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly
85 90 95

Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala
100 105 110

Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala
115 120 125

Gln Ala Ile Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu
130 135 140

Phe Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe Thr
145 150 155 160

Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly Thr
165 170 175

Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr Gly
180 185 190

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

Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met
210 215 220

Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys Asp
225 230 235 240

Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile
245 250 255

Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Ser Thr
260 265 270

Tyr Gln Phe Lys Thr Pro Glu Ser Ser Pro Pro Gly Thr Pro Ile Gly
275 280 285

Arg Ile Lys Ala Ser Asp Ala Asp Val Gly Glu Asn Ala Glu Ile Glu
290 295 300

Tyr Ser Ile Thr Asp Gly Glu Gly Leu Asp Met Phe Asp Val Ile Thr
305 310 315 320

Asp Gln Glu Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Leu Leu Asp
325 330 335

Phe Glu Lys Lys Lys Val Tyr Thr Leu Lys Val Glu Ala Ser Asn Pro
340 345 350

Tyr Val Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe Lys Asp Ser Ala
 355 360 365

Thr Val Arg Ile Val Val Glu Asp Val Asp Glu Pro Pro Val Phe Ser
 370 375 380

Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn Thr
 385 390 395 400

Thr Ile Gly Ser Val Thr Ala Gln Asp Pro Asp Ala Ala Arg Asn Pro
 405 410 415

Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe Asn
 420 425 430

Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp Arg
 435 440 445

Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile Asn
 450 455 460

Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu Asp
 465 470 475 480

Val Asn Asp Asn Ala Pro Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val
 485 490 495

Cys Glu Lys Ala Lys Ala Asp Gln Leu Ile Gln Thr Leu His Ala Val
 500 505 510

Asp Lys Asp Asp Pro Tyr Ser Gly His Gln Phe Ser Phe Ser Leu Ala
 515 520 525

Pro Glu Ala Ala Ser Gly Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp
 530 535 540

Asn Thr Ala Gly Ile Leu Thr Arg Lys Asn Gly Tyr Asn Arg His Glu
 545 550 555 560

Met Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro
565 570 575

Val Gln Ser Ser Thr Gly Thr Val Thr Val Arg Val Cys Ala Cys Asp
580 585 590

His His Gly Asn Met Gln Ser Cys His Ala Glu Ala Leu Ile His Pro
595 600 605

Thr Gly Leu Ser Thr Gly Ala Leu Val Ala Ile Leu Leu Cys Ile Val
610 615 620

Ile Leu Leu Val Thr Val Val Leu Phe Ala Ala Leu Arg Arg Gln Arg
625 630 635 640

Lys Lys Glu Pro Leu Ile Ile Ser Lys Glu Asp Ile Arg Asp Asn Ile
645 650 655

Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe
660 665 670

Asp Ile Gly Thr Leu Arg Asn Pro Glu Ala Ile Glu Asp Asn Lys Leu
675 680 685

Arg Arg Asp Ile Val Pro Glu Ala Leu Phe Leu Pro Arg Arg Thr Pro
690 695 700

Thr Ala Arg Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Gln Arg Leu
705 710 715 720

Lys Glu Asn Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala
725 730 735

Thr Tyr Ala Tyr Glu Gly Thr Gly Ser Val Ala Asp Ser Leu Ser Ser
740 745 750

Leu Glu Ser Val Thr Thr Asp Ala Asp Gln Asp Tyr Asp Tyr Leu Ser
755 760 765

Asp Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Val
770 775 780

Asp Ser Asp Lys Asp Ser
785 790

<210> 2
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2

Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu Glu Tyr Thr Gly Ser
1 5 10 15

Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp Gln Asp Arg Gly Asp
20 25 30

Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly Ala Gly Asp Leu Phe
35 40 45

Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala Thr Lys Arg Leu Asp
50 55 60

Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala Gln Ala Ile Asn Arg
65 70 75 80

Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu Phe Ile Ile Lys Ile
85 90 95

His Asp Ile Asn Asp Asn Glu Pro Ile Phe
100 105

<210> 3
<211> 109
<212> PRT
<213> Homo sapiens

<400> 3

Thr Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly
1 5 10 15

Thr Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr
20 25 30

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

Phe Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn
50 55 60

Met Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys
65 70 75 80

Asp Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn
85 90 95

Ile Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe
100 105

<210> 4
<211> 115
<212> PRT
<213> Homo sapiens

<400> 4

Pro Gln Ser Thr Tyr Gln Phe Lys Thr Pro Glu Ser Ser Pro Pro Gly
1 5 10 15

Thr Pro Ile Gly Arg Ile Lys Ala Ser Asp Ala Asp Val Gly Glu Asn
20 25 30

Ala Glu Ile Glu Tyr Ser Ile Thr Asp Gly Glu Gly Leu Asp Met Phe
35 40 45

Asp Val Ile Thr Asp Gln Glu Thr Gln Glu Gly Ile Ile Thr Val Lys
50 55 60

Lys Leu Leu Asp Phe Glu Lys Lys Lys Val Tyr Thr Leu Lys Val Glu
65 70 75 80

Ala Ser Asn Pro Tyr Val Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe
85 90 95

Lys Asp Ser Ala Thr Val Arg Ile Val Val Glu Asp Val Asp Glu Pro

100

105

110

Pro Val Phe
115

<210> 5
<211> 103
<212> PRT
<213> Homo sapiens

<400> 5

Ser Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn
1 5 10 15

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

Pro Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe
35 40 45

Asn Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp
50 55 60

Arg Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile
65 70 75 80

Asn Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu
85 90 95

Asp Val Asn Asp Asn Ala Pro
100

<210> 6
<211> 122
<212> PRT
<213> Homo sapiens

<400> 6

Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val Cys Glu Lys Ala Lys Ala
1 5 10 15

Asp Gln Leu Ile Gln Thr Leu His Ala Val Asp Lys Asp Asp Pro Tyr

	20		25		30
Ser Gly His Gln Phe Ser Phe Ser Leu Ala Pro Glu Ala Ala Ser Gly	35		40		45
Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp Asn Thr Ala Gly Ile Leu	50		55		60
Thr Arg Lys Asn Gly Tyr Asn Arg His Glu Met Ser Thr Tyr Leu Leu	65		70		75
Pro Val Val Ile Ser Asp Asn Asp Tyr Pro Val Gln Ser Ser Thr Gly		85		90	95
Thr Val Thr Val Arg Val Cys Ala Cys Asp His His Gly Asn Met Gln		100		105	110
Ser Cys His Ala Glu Ala Leu Ile His Pro	115		120		
<210> 7					
<211> 790					
<212> PRT					
<213> Mus musculus					
<400> 7					
Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro	1		5		10
Tyr Pro Thr Phe Ser Asn Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro		20		25	30
Ala Lys Arg Lys Ala Leu Glu Leu Ser Ala Asn Ser Arg Asn Glu Leu		35		40	45
Ser Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu		50		55	60
Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp	65		70		75
					80

Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly
85 90 95

Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala
100 105 110

Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala
115 120 125

Gln Ala Val Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu
130 135 140

Phe Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe Thr
145 150 155 160

Lys Asp Val Tyr Thr Ala Thr Val Pro Glu Met Ala Asp Val Gly Thr
165 170 175

Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr Gly
180 185 190

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

Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met
210 215 220

Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys Asp
225 230 235 240

Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile
245 250 255

Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Ser Thr
260 265 270

Tyr Gln Phe Lys Thr Pro Glu Ser Ser Pro Pro Gly Thr Pro Ile Gly
275 280 285

Arg Ile Lys Ala Ser Asp Ala Asp Val Gly Glu Asn Ala Glu Ile Glu
290 295 300

Tyr Ser Ile Thr Asp Gly Glu Gly His Glu Met Phe Asp Val Ile Thr
 305 310 315 320

Asp Gln Glu Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Leu Leu Asp
 325 330 335

Phe Glu Lys Lys Lys Val Tyr Thr Leu Lys Val Glu Ala Ser Asn Pro
 340 345 350

His Val Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe Lys Asp Ser Ala
 355 360 365

Thr Val Arg Ile Val Val Asp Asp Val Asp Glu Pro Pro Val Phe Ser
 370 375 380

Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Arg Ile Asn Thr
 385 390 395 400

Thr Ile Gly Ser Val Ala Ala Gln Asp Pro Asp Ala Ala Arg Asn Pro
 405 410 415

Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe Asn
 420 425 430

Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp Arg
 435 440 445

Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile Asn
 450 455 460

Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu Asp
 465 470 475 480

Val Asn Asp Asn Ala Pro Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val
 485 490 495

Cys Glu Lys Ala Lys Ala Asp Gln Leu Ile Gln Thr Leu Arg Ala Val
 500 505 510

Asp Lys Asp Asp Pro Tyr Ser Gly His Gln Phe Ser Phe Ser Leu Ala
515 520 525

Pro Glu Ala Ala Ser Ser Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp
530 535 540

Asn Thr Ala Gly Ile Leu Thr Arg Lys Asn Gly Tyr Asn Arg His Glu
545 550 555 560

Met Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro
565 570 575

Val Gln Ser Ser Thr Gly Thr Val Thr Val Arg Val Cys Ala Cys Asp
580 585 590

His His Gly Asn Met Gln Ser Cys His Ala Glu Ala Leu Ile His Pro
595 600 605

Thr Gly Leu Ser Thr Gly Ala Leu Val Ala Ile Leu Leu Cys Ile Val
610 615 620

Ile Leu Leu Val Thr Val Val Leu Phe Ala Ala Leu Arg Arg Gln Arg
625 630 635 640

Lys Lys Glu Pro Leu Ile Ile Ser Lys Glu Asp Ile Arg Asp Asn Ile
645 650 655

Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe
660 665 670

Asp Ile Gly Thr Leu Arg Asn Pro Glu Ala Met Glu Asp Ser Lys Ser
675 680 685

Arg Arg Asp Ile Val Pro Glu Ala Leu Phe Leu Pro Arg Arg Thr Pro
690 695 700

Thr Ala Arg Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Gln Arg Leu
705 710 715 720

Lys Glu Asn Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala
725 730 735

Thr Tyr Ala Tyr Glu Gly Thr Gly Ser Val Ala Asp Ser Leu Ser Ser
740 745 750

Leu Glu Ser Val Thr Thr Asp Gly Asp Gln Asp Tyr Asp Tyr Leu Ser
755 760 765

Asp Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Met
770 775 780

Asp Ser Asp Lys Asp Ser
785 790

<210> 8
<211> 789
<212> PRT
<213> Rattus norvegicus

<400> 8

Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro
1 5 10 15

Tyr Pro Thr Phe Ser Asn Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro
20 25 30

Ala Lys Arg Arg Ala Leu Glu Leu Ser Ala Asn Ser Arg Asn Glu Leu
35 40 45

Ser Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu
50 55 60

Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp
65 70 75 80

Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly
85 90 95

Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala
100 105 110

Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala

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

Phe Glu Lys Lys Arg Val Tyr Thr Leu Lys Val Glu Ala Ser Asn Pro
340 345 350

His Ile Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe Lys Asp Ser Ala
355 360 365

Thr Val Arg Ile Val Val Asp Asp Val Asp Glu Pro Pro Val Phe Ser
370 375 380

Lys Pro Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn Thr
385 390 395 400

Thr Ile Gly Ser Val Ala Ala Gln Asp Pro Asp Ala Ala Arg Asn Pro
405 410 415

Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe Asn
420 425 430

Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp Arg
435 440 445

Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile Asn
450 455 460

Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu Asp
465 470 475 480

Val Asn Asp Asn Ala Pro Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val
485 490 495

Cys Glu Lys Ala Lys Ala Asp Gln Leu Ile Gln Thr Leu His Ala Val
500 505 510

Asp Lys Asp Asp Pro Tyr Ser Gly His Gln Phe Ser Phe Ser Leu Ala
515 520 525

Pro Glu Ala Ala Ser Gly Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp
530 535 540

Asn Thr Ala Gly Ile Leu Thr Arg Lys Asn Gly Tyr Asn Arg His Glu

545		550		555		560									
Met	Ser	Thr	Tyr	Leu	Leu	Pro	Val	Val	Ile	Ser	Asp	Asn	Asp	Tyr	Pro
				565					570					575	
Val	Gln	Ser	Ser	Thr	Gly	Thr	Val	Thr	Val	Arg	Val	Cys	Ala	Cys	Asp
			580					585					590		
His	His	Gly	Asn	Met	Gln	Ser	Cys	His	Ala	Glu	Ala	Leu	Ile	His	Pro
		595					600					605			
Thr	Gly	Leu	Ser	Thr	Gly	Ala	Leu	Val	Ala	Ile	Leu	Leu	Cys	Ile	Val
	610					615					620				
Ile	Leu	Leu	Val	Thr	Val	Val	Leu	Phe	Ala	Ala	Leu	Arg	Arg	Gln	Arg
625					630					635					640
Lys	Lys	Glu	Pro	Leu	Ile	Ile	Ser	Lys	Glu	Asp	Ile	Arg	Asp	Asn	Ile
				645					650					655	
Val	Ser	Tyr	Asn	Asp	Glu	Gly	Gly	Gly	Glu	Glu	Asp	Thr	Gln	Ala	Phe
			660					665					670		
Asp	Ile	Gly	Thr	Leu	Arg	Asn	Pro	Lys	Pro	Trp	Arg	Gln	Gln	Ser	Arg
		675					680					685			
Arg	Asp	Met	Val	Pro	Glu	Ala	Leu	Phe	Leu	Pro	Arg	Arg	Thr	Pro	Thr
		690				695					700				
Ala	Arg	Asp	Asn	Thr	Asp	Val	Arg	Asp	Phe	Ile	Ser	Gln	Arg	Leu	Arg
705					710					715				720	
Lys	Met	Asn	Thr	Asp	Pro	Thr	Ala	Pro	Pro	Tyr	Asp	Ser	Leu	Ala	Thr
				725				730					735		
Tyr	Ala	Tyr	Glu	Gly	Thr	Gly	Ser	Val	Ala	Asp	Ser	Leu	Ser	Ser	Leu
			740					745					750		
Glu	Ser	Val	Thr	Thr	Asp	Gly	Asp	Gln	Asp	Tyr	Gly	Tyr	Leu	Ser	Asp
		755				760						765			

Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Met Asp
770 775 780

Ser Asp Lys Asp Ser
785

<210> 9
<211> 790
<212> PRT
<213> *Macaca fascicularis*

<400> 9

Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro
1 5 10 15

Tyr Pro Thr Leu Ser Thr Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro
20 25 30

Ala Lys Lys Arg Ala Leu Glu Leu Ser Gly Asn Ser Lys Asn Glu Leu
35 40 45

Asn Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu
50 55 60

Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp
65 70 75 80

Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly
85 90 95

Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala
100 105 110

Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala
115 120 125

Gln Ala Ile Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu
130 135 140

Phe Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe Thr
145 150 155 160

Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly Thr
165 170 175

Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr Gly
180 185 190

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

Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met
210 215 220

Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys Asp
225 230 235 240

Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile
245 250 255

Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Ser Thr
260 265 270

Tyr Gln Phe Lys Thr Pro Glu Ser Ser Pro Pro Gly Thr Pro Ile Gly
275 280 285

Arg Ile Lys Ala Ser Asp Ala Asp Val Gly Glu Asn Ala Glu Ile Glu
290 295 300

Tyr Ser Ile Thr Asp Gly Glu Gly Leu Asp Met Phe Asp Val Ile Thr
305 310 315 320

Asp Gln Glu Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Leu Leu Asp
325 330 335

Phe Glu Lys Lys Lys Val Tyr Thr Leu Lys Val Glu Ala Ser Asn Pro
340 345 350

His Val Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe Lys Asp Ser Ala
355 360 365

Thr Val Arg Ile Val Val Glu Asp Val Asp Glu Pro Pro Val Phe Ser
370 375 380

Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn Thr
385 390 395 400

Thr Ile Gly Ser Val Thr Ala Gln Asp Pro Asp Ala Ala Arg Asn Pro
405 410 415

Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe Asn
420 425 430

Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp Arg
435 440 445

Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile Asn
450 455 460

Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu Asp
465 470 475 480

Val Asn Asp Asn Ala Pro Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val
485 490 495

Cys Glu Lys Ala Lys Ala Asp Gln Leu Ile Gln Thr Leu Arg Ala Val
500 505 510

Asp Lys Asp Asp Pro Tyr Ser Gly His Gln Phe Ser Phe Ser Leu Ala
515 520 525

Pro Glu Ala Ala Ser Gly Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp
530 535 540

Asn Thr Ala Gly Ile Leu Thr Arg Lys Asn Gly Tyr Asn Arg His Glu
545 550 555 560

Met Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro
565 570 575

Val Gln Ser Ser Thr Gly Thr Val Thr Val Arg Val Cys Ala Cys Asp
580 585 590

His His Gly Asn Met Gln Ser Cys His Ala Glu Ala Leu Ile His Pro
595 600 605

Thr Gly Leu Ser Thr Gly Ala Leu Val Ala Ile Leu Leu Cys Ile Val
610 615 620

Ile Leu Leu Val Thr Val Val Leu Phe Ala Ala Leu Arg Arg Gln Arg
625 630 635 640

Lys Lys Glu Pro Leu Ile Ile Ser Lys Glu Asp Ile Arg Asp Asn Ile
645 650 655

Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe
660 665 670

Asp Ile Gly Thr Leu Arg Asn Pro Glu Ala Ile Glu Asp Asn Lys Leu
675 680 685

Arg Arg Asp Ile Val Pro Glu Ala Leu Phe Leu Pro Arg Arg Thr Pro
690 695 700

Thr Ala Arg Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Gln Arg Leu
705 710 715 720

Lys Glu Asn Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala
725 730 735

Thr Tyr Ala Tyr Glu Gly Thr Gly Ser Val Ala Asp Ser Leu Ser Ser
740 745 750

Leu Glu Ser Val Thr Thr Asp Gly Asp Gln Asp Tyr Asp Tyr Leu Ser
755 760 765

Asp Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Val
770 775 780

Asp Ser Asp Lys Asp Ser
785 790

<210> 10
 <211> 108
 <212> PRT
 <213> Rattus norvegicus

<400> 10

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

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

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

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

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

Phe Gly Gly Val Thr Asn Leu Glu Leu Lys Arg Ala
 100 105

<210> 11
 <211> 324
 <212> DNA
 <213> Rattus norvegicus

<400> 11

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ggagaaggtc ccaaactcct gatttatgat gcaaacactt tgcaaacggg catcccatca	180
aggttcagtg gcagtggatc tggttcagat ttcacactca ccatcagcag cctgcagcct	240
gaagatgttg ccacatattt ctgccagcag tactatagcg ggtgggcgtt cgggtggagtc	300
accaacctgg aattgaaacg ggct	324

<210> 12
<211> 11
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<213> Rattus norvegicus

<400> 12

Lys Ala Ser Gln Asn Ile Tyr Lys Asn Leu Ala
1 5 10

<210> 13
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<400> 13

Asp Ala Asn Thr Leu Gln Thr
1 5

<210> 14
<211> 8
<212> PRT
<213> Rattus norvegicus

<400> 14

Gln Gln Tyr Tyr Ser Gly Trp Ala
1 5

<210> 15
<211> 122
<212> PRT
<213> Rattus norvegicus

<400> 15

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

Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Cys Gly Asp Gly Glu Thr Glu Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe Trp
100 105 110

Gly Gln Gly Val Met Val Thr Val Ser Ser
115 120

<210> 16
<211> 366
<212> DNA
<213> Rattus norvegicus

<400> 16
caggtacagc tgcagcaatc tggggctgaa ctggtgaagc ctgggtcctc agtgaaaatt 60
tcctgcaagg cttctggcta caccttcacc aggaacttta tgcactggat aaaacagcag 120
cctggaaaatg gccttgagtg gattgggtgg atttattgtg gagatgggtga gacagagtac 180
aatcaaaaagt tcaatgggaa ggcaacactc actgcggaca gatcctccag cacagcctat 240
atggagctca gcagactgac atctgaggac tctgcagtct atttctgtgc aagaggggtt 300
tacggagggt ttgccggggg ctactttgat ttctggggcc aaggagtcac ggtcacagtc 360
tcctca 366

<210> 17
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 17

Gly Tyr Thr Phe Thr Arg Asn Phe Met His
1 5 10

<210> 18
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 18

Trp Ile Tyr Cys Gly Asp Gly Glu Thr Glu
1 5 10

<210> 19

<211> 13

<212> PRT

<213> Rattus norvegicus

<400> 19

Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe
1 5 10

<210> 20

<211> 109

<212> PRT

<213> Rattus norvegicus

<400> 20

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

Glu Ser Val Ser Ile Ser Cys Lys Thr Ser Lys Asn Ile Ser Asn Tyr
20 25 30

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

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Gly Leu Tyr Phe Cys Gln Gln Tyr Tyr Glu Lys Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
100 105

<210> 21

<211> 327
 <212> DNA
 <213> Rattus norvegicus

<400> 21
 gatgtccaga tgaccactc tccgtcttat cttgctgcgt ctcctggaga aagtgtttcc 60
 atcagttgca agacaagtaa gaacattagt aattatttag tctggtatca acagaaacct 120
 ggggaagcat ataagcttct tatctattct ggggtcaactt tgcaatctgg aactccatca 180
 aggttcagtg gcagtggatc tggtagagat ttcactctca ctatcagaag cctggagcct 240
 gaagattttg gactctattt ctgtcaacag tattatgaaa aaccattcac gttcgggtca 300
 gggacgaagt tggaaataaa acggggct 327

<210> 22
 <211> 11
 <212> PRT
 <213> Rattus norvegicus

<400> 22
 Lys Thr Ser Lys Asn Ile Ser Asn Tyr Leu Val
 1 5 10

<210> 23
 <211> 7
 <212> PRT
 <213> Rattus norvegicus

<400> 23
 Ser Gly Ser Thr Leu Gln Ser
 1 5

<210> 24
 <211> 9
 <212> PRT
 <213> Rattus norvegicus

<400> 24
 Gln Gln Tyr Tyr Glu Lys Pro Phe Thr
 1 5

<210> 25
 <211> 121
 <212> PRT

<213> Rattus norvegicus

<400> 25

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

Ser Leu Ser Leu Ser Cys Ser Val Thr Asp Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Arg Phe Pro Gly Asn Lys Met Glu Trp Met
35 40 45

Gly Tyr Ile Thr Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu Gln
50 55 60

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

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

Arg Ser Ile Asn His Gly Gly Tyr Ser Tyr Val Val Asp Ala Trp Gly
100 105 110

Pro Gly Ala Ser Val Thr Val Ser Ser
115 120

<210> 26

<211> 363

<212> DNA

<213> Rattus norvegicus

<400> 26

gaggtgcaac ttcaggagtc aggacctggc cttgtgagac cctcacagtc actctccctc 60

tcctgttctg tctactgatta ctccatcact agtaattact ggggctggat ccggagggttc 120

ccaggaaata aaatggagtg gatgggatac ataacctata gtggttacac tagctacaac 180

ccatctctcc aaagtcgaat ctccattact agagacacat cgaagaatca gttcttcctg 240

cagttgaact ctgtaactgc tgaggacaca gccacatatt actgtgcaag atcgattaac 300

cacggaggat atagttatgt tgtggatgcc tgggggccgg gagcttcagt cactgtctcc 360

<210> 27
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 27

Asp Tyr Ser Ile Thr Ser Asn Tyr Trp Gly
1 5 10

<210> 28
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 28

Tyr Ile Thr Tyr Ser Gly Tyr Thr Ser
1 5

<210> 29
<211> 13
<212> PRT
<213> Rattus norvegicus

<400> 29

Ser Ile Asn His Gly Gly Tyr Ser Tyr Val Val Asp Ala
1 5 10

<210> 30
<211> 109
<212> PRT
<213> Rattus norvegicus

<400> 30

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

Glu Ser Val Ser Ile Ser Cys Arg Ala Thr Lys Ser Ile Gly Ile Tyr
20 25 30

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

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Arg Arg Ala
100 105

<210> 31
<211> 327
<212> DNA
<213> Rattus norvegicus

<400> 31
gatgtccaga tgacccagtc tccgtcttct cttgctgctg ctcctggaga aagtgtttcc 60
atcagttgca gggcaactaa gagcattggt atttatttag cctggatatca acagaaacct 120
gggaaaacat ttaagcttct tatctactct ggggtcaactt tgcaatctgg aactccatca 180
aggttcagtg gcagtgggtc tggtacagat ttcactctca ccatcagaag cctggagcct 240
gaagattttg gactctatct ctgtcaacag ttttatgaaa acccattcac gttcggctca 300
gggacgaagt tggaaataag acgggct 327

<210> 32
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 32

Arg Ala Thr Lys Ser Ile Gly Ile Tyr Leu Ala
1 5 10

<210> 33
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 33

Ser Gly Ser Thr Leu Gln Ser
1 5

<210> 34
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 34

Gln Gln Phe Tyr Glu Asn Pro Phe Thr
1 5

<210> 35
<211> 121
<212> PRT
<213> Rattus norvegicus

<400> 35

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

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

Phe Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Met
35 40 45

Gly Tyr Met Ser Tyr Arg Gly Gly Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Cys Pro Asn Tyr Gly Gly His Ser Leu Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Val Met Val Thr Val Ser Ser
115 120

<210> 36
 <211> 363
 <212> DNA
 <213> Rattus norvegicus

<400> 36
 gaggtgcagc ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60
 acctgttctg tcactgatta ctccatcact acttatttct ggggctggat ccggaagttc 120
 ccaggaaata aaatggagtg gatgggatac atgagctacc gtggtggcac ttcctacaac 180
 ccatctctca agagtcgaat ctccattact agagacacat cgaagaatca gttcttcctg 240
 cagttgaact ctgtaactac tgaggacaca gccacatatt actgtgcaag atgccctaac 300
 tacggagggc attcccttgt ttttgattac tggggccaag gagtcatggt cacagtgtcc 360
 tca 363

<210> 37
 <211> 10
 <212> PRT
 <213> Rattus norvegicus

<400> 37

Asp Tyr Ser Ile Thr Thr Tyr Phe Trp Gly
 1 5 10

<210> 38
 <211> 9
 <212> PRT
 <213> Rattus norvegicus

<400> 38

Tyr Met Ser Tyr Arg Gly Gly Thr Ser
 1 5

<210> 39
 <211> 13
 <212> PRT
 <213> Rattus norvegicus

<400> 39

Cys Pro Asn Tyr Gly Gly His Ser Leu Val Phe Asp Tyr
 1 5 10

<210> 40
 <211> 109
 <212> PRT
 <213> Rattus norvegicus

<400> 40

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

Glu Ser Val Ser Ile Ser Cys Lys Ala Thr Lys Ser Ile Ser Asn Tyr
 20 25 30

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

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Phe Gly Leu Tyr Ser Cys Gln Gln Tyr Tyr Glu Lys Pro Leu
 85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
 100 105

<210> 41
 <211> 327
 <212> DNA
 <213> Rattus norvegicus

<400> 41

gatgtccaga tgaccagtc tccgtcttat cttgctgcgt ctcctggaga aagtgtttcc	60
atcagttgca aggcaactaa gagcattagt aattatttag cctggatatca acagaaacct	120
ggggaagcat ataaggttct tatctattct ggggtcaactt tgcaatctgg aactccatca	180
aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagaag cctggagcct	240
gaagattttg gactctattc ctgtcaacag tattatgaaa aaccgctcac gttcggttct	300
gggaccaagc tggagatcaa acgggct	327

<210> 42
 <211> 11
 <212> PRT
 <213> Rattus norvegicus

<400> 42

Lys Ala Thr Lys Ser Ile Ser Asn Tyr Leu Ala
 1 5 10

<210> 43
 <211> 7
 <212> PRT
 <213> Rattus norvegicus

<400> 43

Ser Gly Ser Thr Leu Gln Ser
 1 5

<210> 44
 <211> 9
 <212> PRT
 <213> Rattus norvegicus

<400> 44

Gln Gln Tyr Tyr Glu Lys Pro Leu Thr
 1 5

<210> 45
 <211> 121
 <212> PRT
 <213> Rattus norvegicus

<400> 45

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

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

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Met
 35 40 45

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

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

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

Arg Ser Pro Ile Asn His Gly Gly Tyr Trp Tyr Phe Asp Phe Trp Gly
100 105 110

Pro Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 46
<211> 363
<212> DNA
<213> Rattus norvegicus

<400> 46
gaggtgcagc ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60
acctgttctg tcaactggta ctccatcact acttattact ggggctggat ccggaagtcc 120
ccaggaaata aaatggagtg gatggggtac ataagctaca gtggtcgcac tagttataac 180
ccatctctca aaagtcgaat gtccattact agagacgcat cgaagaatca gttcttccta 240
cagttgaact ctgtaactac tgacgacaca gccacatatt actgtgcaag atccccaatt 300
aaccacggag ggtactggta ctttgacttc tggggcccag gaaccatggt caccgtgtcc 360
tca 363

<210> 47
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 47

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

<210> 48
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 48

Tyr Ile Ser Tyr Ser Gly Arg Thr Ser
1 5

<210> 49

<211> 13

<212> PRT

<213> Rattus norvegicus

<400> 49

Ser Pro Ile Asn His Gly Gly Tyr Trp Tyr Phe Asp Phe
1 5 10

<210> 50

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for human light chain signal
sequence and kappa chain constant region

<400> 50

gcctccggac tctagagcca ccatgggtgct gcagacccag gtgttcatct ccctgctgct 60
gtggatctcc ggcgcgtagc gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120
cgtgttcatc ttccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtgggtgtg 180
cctgctgaat aacttctacc ccagagaggc caagggtgcag tggaagggtgg acaacgccct 240
gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300
cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360
cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420
ttaggggccc gtttaaacgg gggaggcta 449

<210> 51

<211> 1132

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA comprising DNA sequence coding for human heavy chain signal
sequence and IgG1 constant region

<400> 51
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tgggtggcagc 60
tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120
ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180
ctgggctgcc tgggtcaagga ctacttcccc gaaccctga ccgtgagctg gaactcaggc 240
gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300
ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360
gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420
aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 540
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600
gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720
aaggctctca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc 780
cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 840
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900
gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc 1080
tccctgtctc ccggcaaatg agatatcggg cccgtttaa cgggggaggc ta 1132

<210> 52
<211> 749
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA comprising DNA sequence coding for chG019 light chain

<400> 52
ccagcctccg gactctagag ccaccatggg gctgcagacc caggtgttca tcagcctgct 60
gctgtggatc agcggcgcct acggcgacat ccagatgacc cagagcccta gcctgctgag 120
cgccagcgtg ggcatagag tgaccctgaa ctgcaaggcc agccagaaca tctacaagaa 180

cctggcctgg tatcagcaga agctgggcca gggccccaag ctgctgatct acgacgcaa	240
caccctgcag accggcatcc ccagcagatt ttctggcagc ggcagcggct ccgacttcac	300
cctgacaatc agcagcctgc agcccagga cgtggccacc tacttttgcc agcagtacta	360
cagcggctgg gccttcggcg gcgtgaccaa cctggaactg aagagagccg tggccgctcc	420
ctccgtgttc atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt	480
gtgcctgctg aacaacttct acccccgca ggccaagggt cagtggaagg tggacaatgc	540
cctgcagtct ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta	600
cagcctgagc agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc	660
ctgcgaagtg acccaccagg gcctgtctag ccccgtagcc aagagcttca accggggcga	720
gtgttgagtt taaacggggg aggctaact	749

<210> 53
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequeance of chG019 light chain full-length

<400> 53

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

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

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

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

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

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

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

Ser Gly Trp Ala Phe Gly Gly Val Thr Asn Leu Glu Leu Lys Arg Ala
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 54
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequesnce of chG019 light chain full-length

<400> 54	
atggtgctgc agaccaggt gttcatcagc ctgctgctgt ggatcagcgg cgcctacggc	60
gacatccaga tgaccagag ccctagcctg ctgagcgcca gcgtgggcga tagagtgacc	120
ctgaactgca aggcagcca gaacatctac aagaacctgg cctggtatca gcagaagctg	180
ggcgagggcc ccaagctgct gatctacgac gccaacaccc tgcagaccgg catccccagc	240

agattttctg gcagcggcag cggctccgac ttcaccctga caatcagcag cctgcagccc	300
gaggacgtgg ccacctactt ttgccagcag tactacagcg gctgggcctt cggcggcgtg	360
accaacctgg aactgaagag agccgtggcc gctccctccg tgttcacttt cccacctagc	420
gacgagcagc tgaagtccgg cacagcctct gtcgtgtgcc tgctgaacaa cttctacccc	480
cgcgaggcca aggtgcagtg gaaggtggac aatgccctgc agtctggcaa cagccaggaa	540
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg	600
agcaaggccg actacgagaa gcacaagggtg tacgcctgcg aagtgaccca ccagggcctg	660
tctagccccg tgaccaagag cttcaaccgg ggcgagtgt	699

<210> 55
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of chG019 light chain variable region

<400> 55	
gacatccaga tgaccagag ccctagcctg ctgagcgcca gcgtgggcga tagagtgacc	60
ctgaactgca aggccagcca gaacatctac aagaacctgg cctggtatca gcagaagctg	120
ggcgagggcc ccaagctgct gatctacgac gccaacaccc tgcagaccgg catccccagc	180
agattttctg gcagcggcag cggctccgac ttcaccctga caatcagcag cctgcagccc	240
gaggacgtgg ccacctactt ttgccagcag tactacagcg gctgggcctt cggcggcgtg	300
accaacctgg aactgaagag agcc	324

<210> 56
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of chG019 heavy chain full-length

<400> 56

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

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

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

Thr Arg Asn Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Asn
65 70 75 80

Gln Lys Phe Asn Gly Lys Ala Thr Leu Thr Ala Asp Arg Ser Ser Ser
85 90 95

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

Tyr Phe Cys Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe
115 120 125

Asp Phe Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 465 470

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

<220>
 <223> nucleotide sequesnce of chG019 heavy chain full-length

<400> 57
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60
 gtgcagctgc agcagtctgg cgccgagctc gtgaagcctg gcagcagcgt gaagatcagc 120
 tgcaaggcca gcggtacac cttcaccgg aacttcatgc actggatcaa gcagcagccc 180
 ggcaacggcc tggaatggat cggctggatc tatcccggcg acggcgagac agagtacaac 240
 cagaagttca acggcaaggc caccctgacc gccgacagaa gcagctccac cgcctacatg 300
 gaactgagcc ggctgaccag cgaggacagc gccgtgtact ttgcgccag aggcgtgtac 360
 ggcggtctcg ctggcggtta cttcgatttt tggggccagg gcgtgatggt caccgtcagc 420
 tcagcctcca ccaaggggcc aagcgtcttc cccctggcac cctcctcaa gagcacctct 480
 ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540
 agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600
 tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720
 cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780
 ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900
 tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccccggga ggagcagtag 960
 aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020
 aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080
 tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgcccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1200
atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac caccctccc 1260
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320
tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380
accagaaga gcctctccct gtctcccggc aaa 1413

<210> 58
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of chG019 heavy chain variable region

<400> 58

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

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

Phe Met His Trp Ile Lys Gln Gln Pro Gly Asn Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe Trp
100 105 110

Gly Gln Gly Val Met Val Thr Val Ser Ser
115 120

<210> 59
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of chG019 heavy chain variable region

<400> 59
 cagggtgcagc tgcagcagtc tggcgccgag ctctgaagc ctggcagcag cgtgaagatc 60
 agctgcaagg ccagcggcta caccttcacc cggaacttca tgacttgat caagcagcag 120
 cccggcaacg gcctggaatg gatcggctgg atctatcccg gcgacggcga gacagagtac 180
 aaccagaagt tcaacggcaa ggccaccctg accgccgaca gaagcagctc caccgcctac 240
 atggaactga gccggctgac cagcaggagc agcgccgtgt acttttgcgc cagaggcgtg 300
 tacggcggct tcgctggcgg ctacttcgat ttttggggcc agggcgtgat ggtcaccgtc 360
 agctca 366

<210> 60
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of chG019 CDRH2

<400> 60

Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu
 1 5 10

<210> 61
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of hL02 light chain full-length

<400> 61

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

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

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

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

Lys Leu Leu Ile Tyr Asp Ala Asn Thr Leu Gln Thr Gly Val Pro Ser
65 70 75 80

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

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

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

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 62
 <211> 699
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of hL02 light chain full-length

<400> 62
 atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60
 gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 120
 atcacatgca aggccagcca gaacatctac aagaacctgg cctgggtatca gcagaagccc 180
 ggcaaggccc ccaagctgct gatctacgac gccaacaccc tgcagaccgg cgtgcccagc 240
 agattttctg gcagcggcag cggctccgac ttcaccctga caatcagcag cctgcagccc 300
 gaggacttcg ccacctactt ttgccagcag tactacagcg gctgggcctt cggccagggc 360
 accaaggtgg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccctcc 420
 gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480
 agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540
 agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600
 agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660
 agtcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 63
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of hL02 light chain variable region

<400> 63

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Ser Gly Trp Ala
 85 90 95

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

<210> 64
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of hL02 light chain variable region

<400> 64
 gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
 atcacatgca aggccagcca gaacatctac aagaacctgg cctggtatca gcagaagccc 120
 ggcaaggccc ccaagctgct gatctacgac gccaacaccc tgcagaccgg cgtgcccagc 180
 agattttctg gcagcggcag cggctccgac ttcaccctga caatcagcag cctgcagccc 240
 gaggacttcg ccacctactt ttgccagcag tactacagcg gctgggcctt cggccagggc 300
 accaaggtgg aaatcaagcg tacg 324

<210> 65
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of hL03 light chain full-length

<400> 65

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

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

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

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

Lys Leu Leu Ile Tyr Asp Ala Asn Thr Leu Gln Thr Gly Val Pro Ser
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 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
100 105 110

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

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 66
 <211> 699
 <212> DNA
 <213> Artificial Sequence

<220>

<223> nucleotide sequence of hL03 light chain full-length

<400> 66

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atggtgtgtc agaccaggt gttcatctcc ctgctgtgt ggatctccg cgctacggc      60
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc    120
atcacatgca aggccagcca gaacatctac aagaacctgg cctggatatca gcagaagctg    180
ggcgagggcc ccaagctgct gatctacgac gccaacaccc tgcagaccgg cgtgcccagc    240
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagcag cctgcagccc    300
gaggacttcg ccacctacta ctgccagcag tactacagcg gctgggcctt tggccagggc    360
accaaggtgg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccctcc    420
gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc    480
agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag    540
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg    600
agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgacca ccagggcctg    660
agctcccccg tcaccaagag cttcaacagg ggggagtgt      699
  
```

<210> 67
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>

<223> amino acid sequence of hL03 light chain variable region

<400> 67

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Gly Trp Ala
 85 90 95

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

<210> 68
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of hL03 light chain variable region

<400> 68
 gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
 atcacatgca aggccagcca gaacatctac aagaacctgg cctggtatca gcagaagctg 120
 ggcgagggcc ccaagctgct gatctacgac gccaacaccc tgcagaccgg cgtgcccagc 180
 agatttttctg gcagcggctc cggcaccgac ttcaccctga caatcagcag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag tactacagcg gctgggcctt tggccagggc 300
 accaaggtgg aaatcaagcg tacg 324

<210> 69
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of hH01 heavy chain full-length

<400> 69

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

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

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

Thr Arg Asn Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Ala
65 70 75 80

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

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

Tyr Tyr Cys Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe
115 120 125

Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 70
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of hH01 heavy chain full-length

<400> 70
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgaa 60
 gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120
 tgcaaggcca gcggctacac ctttaccggg aacttcatgc actgggtgcg ccaggctcca 180
 ggccagggac tggaatggat gggctggatc tatccggcg acggcgagac agagtacgcc 240
 cagaaattcc agggcagagt gaccatcacc gccgacacca gcacctccac cgcctacatg 300
 gaactgagca gcctgcggag cgaggacacc gccgtgtact attgtgccag aggcgtgtac 360
 ggcggtcttc ctggcggcta cttcgatttt tggggccagg gcaccctcgt gaccgtcagc 420
 tcagcctcca ccaaggggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480
 ggcgggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540
 agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 660
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720
 cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780
 ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctccgggacc 840
 cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 900
 tgggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccccggga ggagcagtac 960
 aacagcacgt accgggtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020
 aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgcccc atcccgggag 1140
 gagatgacca agaaccaggt cagcctgacc tgccttgtca aaggcttcta tcccagcgac 1200
 atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac caccctccc 1260
 gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg 1320
 tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380
 acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 71
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of hH01 heavy chain variable region

<400> 71

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

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

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

Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe Trp
 100 105 110

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

<210> 72
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of hH01 heavy chain variable region

<400> 72
 gaagtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg 60
 tcctgcaagg ccagcggcta cacctttacc cggaacttca tgcactgggt gcgccaggct 120
 ccaggccagg gactggaatg gatgggctgg atctatcccg gcgacggcga gacagagtac 180
 gccagaaat tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac 240
 atggaactga gcagcctgcg gagcgaggac accgccgtgt actattgtgc cagaggcgtg 300
 tacggcggct tcgctggcgg ctacttcgat ttttggggcc agggcaccct cgtgaccgtc 360
 agctca 366

<210> 73
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of hH02 heavy chain full-length

<400> 73

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

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

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

Thr Arg Asn Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Asn
 65 70 75 80

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

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

Tyr Phe Cys Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe
115 120 125

Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 74

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequesnce of hH02 heavy chain full-length

<400> 74

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gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc      120
tgcaaggcca gcggctacac ctttaccggg aacttcatgc actgggtgcg ccaggctcca      180
ggccagggac tggaatggat gggctggatc tatccggcg acggcgagac agagtacaac      240
cagaaattcc agggcagagt gaccatcacc gccgacagaa gcaccagcac cgcctacatg      300
gaactgagca gcctgcggag cgaggatacc gccgtgtact tctgtgccag aggcgtgtac      360
ggcggcttcg ctggcggcta cttcgatttt tggggccagg gcaccctcgt gaccgtcagc      420
tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctcaa gagcacctct      480
ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg      540
agctggaact caggcgcctt gaccagcggc gtgcacacct tccccgctgt cctgcagtcc      600
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag      660
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cccaaattctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg      780
ggaccctcag tcttcctctt cccccaaaa ccaaggaca ccctcatgat ctcccggacc      840
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      900
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccccggga ggagcagtac      960
aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc     1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1080
tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgcccc atcccgggag     1140
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac     1200
atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac caccctccc     1260
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1320
tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1380
accagaaga gcctctcctt gtctcccggc aaa                                  1413
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<210> 75

<211> 122

<212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of hH02 heavy chain variable region
 <400> 75

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

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

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

Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Asn Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe Trp
 100 105 110

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

<210> 76
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of hH02 heavy chain variable region

<400> 76
 gaagtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggt 60
 tcctgcaagg ccagcggcta cacctttacc cggaacttca tgcactgggt gcgccaggct 120
 ccaggccagg gactggaatg gatgggctgg atctatcccg gcgacggcga gacagagtac 180

aaccagaaat tccagggcag agtgaccatc accgccgaca gaagcaccag caccgcctac 240
 atggaactga gcagcctgcg gagcgaggat accgccgtgt acttctgtgc cagaggcgtg 300
 tacggcggct tcgctggcgg ctacttcgat ttttggggcc agggcaccct cgtgaccgtc 360
 agctca 366

<210> 77
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequesnce of hH04 heavy chain full-length
 <400> 77

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

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

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

Thr Arg Asn Phe Met His Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Ala
 65 70 75 80

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

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

Tyr Tyr Cys Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe
 115 120 125

Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 78
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of hH04 heavy chain full-length

<400> 78
 atgaaacacc tgtgtttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60
 gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120
 tgcaaggcca gcggctacac ctttaccgga aacttcattg actggatccg gcaggcccct 180
 ggacagggcc tggaatggat gggctggatc tatccggcg acggcgagac agagtacgcc 240
 cagaaattcc agggcagagt gaccctgacc gccgacagaa gcaccagcac cgcctacatg 300
 gaactgagca gcctgcggag cgaggacacc gccgtgtact attgtgccag aggcgtgtac 360
 ggcggtctcg ctggcggcta cttcgatttt tggggccagg gcaccctcgt gaccgtcagc 420

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

Gly Trp Ile Tyr Pro Gly Asp Gly Glu Thr Glu Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Leu Thr Ala Asp Arg Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Gly Val Tyr Gly Gly Phe Ala Gly Gly Tyr Phe Asp Phe Trp
 100 105 110

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

<210> 80
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequesnce of hH04 heavy chain variable region

<400> 80
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 60
 tcctgcaagg ccagcggcta cacctttacc cggaacttca tgcaactggat ccggcaggcc 120
 cctggacagg gcctggaatg gatgggctgg atctatcccg gcgacggcga gacagagtac 180
 gcccagaaat tccagggcag agtgaccctg accgccgaca gaagcaccag caccgcctac 240
 atggaactga gcagcctgcg gagcgaggac accgccgtgt actattgtgc cagaggcgtg 300
 tacggcggct tcgctggcgg ctacttcgat ttttggggcc agggcaccct cgtgaccgtc 360
 agctca 366

<210> 81
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>

<223> amino acid sequence of NOV0712 light chain full-length

<400> 81

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 82
 <211> 705
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of sequence number 81

<400> 82
 atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60
 gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 120
 atcacctgta gagccagcca gagcatcagc agctacctga actggtatca gcagaagccc 180
 ggcaaggccc ccaaactgct gatctacgcc gtgtccacac tgcagagcgg cgtgcccagc 240
 agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagcag cctgcagccc 300
 gaggacttcg ccacctacta ctgtcagcag tccggcacct tccccccac cacatttggc 360
 cagggcacca aggtggaaat caagcgtacg gtggccgccc cctccgtgtt catcttcccc 420
 ccctccgacg agcagctgaa gtccggcacc gcctccgtgg tgtgcctgct gaataacttc 480
 taccacagag aggccaaggt gcagtggaag gtggacaacg ccctgcagtc cgggaactcc 540
 caggagagcg tgaccgagca ggacagcaag gacagcacct acagcctgag cagcaccctg 600
 accctgagca aagccgacta cgagaagcac aaggtgtacg cctgcgaggt gaccaccag 660
 ggcttgagct ccccgtcac caagagcttc aacagggggg agtgt 705

<210> 83
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of NOV0712 heavy chain full-length

<400> 83

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

Val Leu Ser Gln 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 Phe
 35 40 45

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

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

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Tyr Cys Ala Arg Gln Trp Gly Ser Tyr Ala Phe Asp Ser Trp Gly
 115 120 125

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

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

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

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

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

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

210		215		220
Lys Pro Ser Asn Thr	Lys Val Asp Lys Arg Val	Glu Pro Lys Ser Cys		
225	230	235	240	
Asp Lys Thr His	Thr Cys Pro Pro Cys Pro Ala Pro	Glu Leu Leu Gly		
	245	250	255	
Gly Pro Ser Val Phe	Leu Phe Pro Pro Lys Pro Lys Asp	Thr Leu Met		
	260	265	270	
Ile Ser Arg Thr Pro	Glu Val Thr Cys Val Val Val Asp	Val Ser His		
	275	280	285	
Glu Asp Pro Glu Val	Lys Phe Asn Trp Tyr Val Asp Gly	Val Glu Val		
	290	295	300	
His Asn Ala Lys Thr	Lys Pro Arg Glu Glu Gln Tyr Asn Ser	Thr Tyr		
	305	310	315	320
Arg Val Val Ser Val	Leu Thr Val Leu His Gln Asp Trp	Leu Asn Gly		
	325	330	335	
Lys Glu Tyr Lys Cys	Lys Val Ser Asn Lys Ala Leu Pro	Ala Pro Ile		
	340	345	350	
Glu Lys Thr Ile Ser	Lys Ala Lys Gly Gln Pro Arg Glu	Pro Gln Val		
	355	360	365	
Tyr Thr Leu Pro Pro	Ser Arg Glu Glu Met Thr Lys Asn	Gln Val Ser		
	370	375	380	
Leu Thr Cys Leu Val	Lys Gly Phe Tyr Pro Ser Asp Ile	Ala Val Glu		
	385	390	395	400
Trp Glu Ser Asn Gly	Gln Pro Glu Asn Asn Tyr Lys Thr	Thr Pro Pro		
	405	410	415	
Val Leu Asp Ser Asp	Gly Ser Phe Phe Leu Tyr Ser Lys	Leu Thr Val		
	420	425	430	

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

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

Pro Gly Lys
 465

<210> 84
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of sequence
 number 83

<400> 84
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60
 gtgcagctgc tggaatctgg cggaggactg gtgcagcctg gcggctctct gagactgtct 120
 tgtgcccca gcggcttcac cttcagcagc cacggaatgc actgggtgcg ccaggcccct 180
 ggaaagggac tggaatgggt gtccgtgatc agcggcagcg gctccaatac cggctacgcc 240
 gatagcgtga agggccggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg 300
 cagatgaaca gcctgcgggc cgaggacacc gccgtgtact attgtgccag acagtggggc 360
 agctacgcct tcgattcttg gggccagggc accctcgtga ccgtcagctc agcctccacc 420
 aaggggccaa gcgtcttccc cctggcaccc tcctccaaga gcacctctgg cggcacagcc 480
 gccctgggct gcctggtcaa ggactacttc cccgaacccg tgaccgtgag ctggaactca 540
 ggcgccctga ccagcggcgt gcacaccttc cccgtgtcc tgcaatcctc aggactctac 600
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
 aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt 720
 gacaaaactc acacatgccc accctgcca gcacctgaac tcctgggggg accctcagtc 780
 ttctcttccc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
 tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 900
 ggcggtggagg tgcataatgc caagacaaag ccccgaggagg agcagtacaa cagcacgtac 960

cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
ggccagcccc gggaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag	1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atggccagcc cgagaacaac tacaagacca cccctccgt gctggactcc	1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggc	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac ccagaagagc	1380
ctctccctgt ctcccggcaa a	1401

<210> 85
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 85	
cacatgaga acttaccgct acttcttgct gctc	34

<210> 86
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 86	
ttaggagtct ttgtcactgt ccactcctcc	30