

SEQUENCE LISTING

<110> Hummingbird Bioscience Holdings Pte. Ltd. (All States)
Clegg, Richard (LS only)

<120> HER3 Antigen-Binding Molecules

<130> 007450844

<150> PCT/EP2018/058259

<151> 2018-03-29

<150> US 16/170,370

<151> 2018-10-25

<160> 231

<170> PatentIn version 3.5

<210> 1

<211> 1342

<212> PRT

<213> Homo sapiens HER3 isoform 1

<400> 1

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

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

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

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180 185 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225 230 235 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320

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

Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
340 345 350

Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355 360 365

Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
370 375 380

Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385 390 395 400

Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
405 410 415

Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
420 425 430

Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
435 440 445

Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
450 455 460

His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
465 470 475 480

Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
485 490 495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
500 505 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
515 520 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
530 535 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545 550 555 560

Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
565 570 575

Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
580 585 590

Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
595 600 605

Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
610 615 620

Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
625 630 635 640

His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
645 650 655

Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
660 665 670

Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
675 680 685

Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
690 695 700

Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705 710 715 720

Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
725 730 735

Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740 745 750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755 760 765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770 775 780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785 790 795 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805 810 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820 825 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835 840 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850 855 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865 870 875 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885 890 895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
900 905 910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
915 920 925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
930 935 940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945 950 955 960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
965 970 975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
980 985 990

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
995 1000 1005

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala
1010 1015 1020

Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu
1025 1030 1035

Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly
1040 1045 1050

Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu
1055 1060 1065

Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser
1070 1075 1080

Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu
1085 1090 1095

Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser
1100 1105 1110

Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
1115 1120 1125

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val
1130 1135 1140

Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
1145 1150 1155

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg
1160 1165 1170

Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr
1175 1180 1185

Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
1190 1195 1200

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu
1205 1210 1215

Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala
1220 1225 1230

Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
1235 1240 1245

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met
1250 1255 1260

Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala
1265 1270 1275

Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg
1280 1285 1290

Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala
1295 1300 1305

Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe
1310 1315 1320

Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn
1325 1330 1335

Ala Gln Arg Thr
1340

<210> 2
<211> 183
<212> PRT
<213> Homo sapiens HER3 isoform 2

<400> 2

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu

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

<210> 3
 <211> 331
 <212> PRT
 <213> Homo sapiens HER3 isoform 3
 <400> 3

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1 5 10 15

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

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

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

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180 185 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225 230 235 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320

Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Phe
325 330

<210> 4
<211> 1283
<212> PRT
<213> Homo sapiens HER3 isoform 4

<400> 4

Met Gly Asn Leu Glu Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser
1 5 10 15

Phe Leu Gln Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met
20 25 30

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

Thr Gln Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr
50 55 60

Asn Thr Asn Ser Ser His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu

65

70

75

80

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

Cys His Met Asp Thr Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp
 100 105 110

Ala Glu Ile Val Val Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His
 115 120 125

Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln
 130 135 140

Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe
 145 150 155 160

Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys
 165 170 175

Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp
 180 185 190

Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys
 195 200 205

Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly
 210 215 220

Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln Thr
 225 230 235 240

Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
 245 250 255

Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
 260 265 270

Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
 275 280 285

Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
290 295 300

Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
305 310 315 320

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
325 330 335

Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe Ser Val
340 345 350

Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly
355 360 365

Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe
370 375 380

Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn
385 390 395 400

Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val Leu Arg
405 410 415

Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg
420 425 430

Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly
435 440 445

Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
450 455 460

Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu
465 470 475 480

Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu
485 490 495

Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp

500

505

510

Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser
 515 520 525

Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr
 530 535 540

Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln
 545 550 555 560

Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val
 565 570 575

Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr Val Ile Ala Gly
 580 585 590

Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg
 595 600 605

Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg
 610 615 620

Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val
 625 630 635 640

Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu
 645 650 655

Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp Ile Pro Glu
 660 665 670

Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys
 675 680 685

Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met Leu Ala Ile
 690 695 700

Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro
 705 710 715 720

Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu
725 730 735

Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu
740 745 750

Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu
755 760 765

His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys
770 775 780

Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu
785 790 795 800

Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile
805 810 815

Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln
820 825 830

Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe
835 840 845

Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu
850 855 860

Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp
865 870 875 880

Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg
885 890 895

Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp
900 905 910

Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala
915 920 925

Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val

930

935

940

Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu
 945 950 955 960

Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val
 965 970 975

Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser
 980 985 990

Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln
 995 1000 1005

Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val
 1010 1015 1020

Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser
 1025 1030 1035

Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val
 1040 1045 1050

Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg
 1055 1060 1065

Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro
 1070 1075 1080

Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn
 1085 1090 1095

Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser
 1100 1105 1110

Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly
 1115 1120 1125

Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg
 1130 1135 1140

Arg Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu
1145 1150 1155

Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
1160 1165 1170

Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro
1175 1180 1185

Ile Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr
1190 1195 1200

Met Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala
1205 1210 1215

Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met
1220 1225 1230

Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr
1235 1240 1245

Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala
1250 1255 1260

Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala
1265 1270 1275

Asn Ala Gln Arg Thr
1280

<210> 5
<211> 699
<212> PRT
<213> Homo sapiens HER3 isoform 5

<400> 5

Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu
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Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg
20 25 30

Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp
35 40 45

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

Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val
65 70 75 80

His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val
85 90 95

Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala
100 105 110

Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile
115 120 125

Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr
130 135 140

Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg
145 150 155 160

Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala
165 170 175

Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu
180 185 190

Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala
195 200 205

Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu
210 215 220

Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
225 230 235 240

His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
245 250 255

Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu
260 265 270

Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala
275 280 285

Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys
290 295 300

Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn
305 310 315 320

Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys
325 330 335

Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu
340 345 350

Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu
355 360 365

Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu
370 375 380

Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly
385 390 395 400

Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln
405 410 415

Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser
420 425 430

Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro Arg Gly Cys
435 440 445

Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu
450 455 460

Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser
465 470 475 480

Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu
485 490 495

Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp
500 505 510

Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser
515 520 525

Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly
530 535 540

Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
545 550 555 560

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu
565 570 575

Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu
580 585 590

Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr
595 600 605

Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg
610 615 620

Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro
625 630 635 640

Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly
645 650 655

His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser
660 665 670

Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser
675 680 685

Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr
690 695

<210> 6
<211> 1323
<212> PRT
<213> Homo sapiens HER3 isoform 1

<400> 6

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

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

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
115 120 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145 150 155 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
165 170 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
180 185 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
195 200 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
210 215 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225 230 235 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
245 250 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
260 265 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
275 280 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
290 295 300

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

Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val Asn Cys Thr
325 330 335

Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp
340 345 350

Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe
355 360 365

Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro

370

375

380

Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
 385 390 395 400

Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
 405 410 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
 420 425 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
 435 440 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
 450 455 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
 465 470 475 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
 485 490 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
 500 505 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
 515 520 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
 530 535 540

Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
 545 550 555 560

Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
 565 570 575

Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
 580 585 590

Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
595 600 605

Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr
610 615 620

Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu
625 630 635 640

Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg
645 650 655

Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp
660 665 670

Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr
675 680 685

Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val
690 695 700

His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val
705 710 715 720

Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala
725 730 735

Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile
740 745 750

Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr
755 760 765

Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg
770 775 780

Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala
785 790 795 800

Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu

805

810

815

Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala
 820 825 830

Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu
 835 840 845

Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
 850 855 860

His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
 865 870 875 880

Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu
 885 890 895

Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala
 900 905 910

Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys
 915 920 925

Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn
 930 935 940

Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys
 945 950 955 960

Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu
 965 970 975

Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu
 980 985 990

Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu
 995 1000 1005

Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg Pro Arg
 1010 1015 1020

Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro Met
1025 1030 1035

Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser
1040 1045 1050

Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met
1055 1060 1065

Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr
1070 1075 1080

Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser
1085 1090 1095

Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr
1100 1105 1110

His Ser Gln Arg His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser
1115 1120 1125

Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly Tyr Val Met Pro
1130 1135 1140

Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg Glu Gly Thr Leu
1145 1150 1155

Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu Glu Glu Asp
1160 1165 1170

Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg His Ser
1175 1180 1185

Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly Tyr
1190 1195 1200

Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser
1205 1210 1215

Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala

1220

1225

1230

Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg
 1235 1240 1245

Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys
 1250 1255 1260

Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly
 1265 1270 1275

Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr
 1280 1285 1290

Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp
 1295 1300 1305

Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr
 1310 1315 1320

<210> 7

<211> 164

<212> PRT

<213> Homo sapiens HER3 isoform 2

<400> 7

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

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

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
 35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
 50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
 65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Gly Gln Phe Pro Met Val Pro
115 120 125

Ser Gly Leu Thr Pro Gln Pro Ala Gln Asp Trp Tyr Leu Leu Asp Asp
130 135 140

Asp Pro Arg Leu Leu Thr Leu Ser Ala Ser Ser Lys Val Pro Val Thr
145 150 155 160

Leu Ala Ala Val

<210> 8
<211> 312
<212> PRT
<213> Homo sapiens HER3 isoform 3

<400> 8

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

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

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
115 120 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145 150 155 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
165 170 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
180 185 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
195 200 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
210 215 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225 230 235 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
245 250 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
260 265 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
275 280 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
290 295 300

Gly Gly Leu Cys Pro Lys Ala Phe

305

310

<210> 9

<211> 624

<212> PRT

<213> Homo sapiens HER3 isoform 1 extracellular region

<400> 9

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

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

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
115 120 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145 150 155 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
165 170 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
180 185 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
195 200 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
210 215 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225 230 235 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
245 250 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
260 265 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
275 280 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
290 295 300

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

Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val Asn Cys Thr
325 330 335

Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp
340 345 350

Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe
355 360 365

Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro
370 375 380

Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
385 390 395 400

Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
405 410 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
420 425 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
435 440 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
450 455 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
465 470 475 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
485 490 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
500 505 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
515 520 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
530 535 540

Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
545 550 555 560

Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
565 570 575

Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
580 585 590

Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
595 600 605

Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr
610 615 620

<210> 10

<211> 21

<212> PRT

<213> Homo sapiens HER3 isoform 1 transmembrane domain

<400> 10

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

Gly Gly Thr Phe Leu
20

<210> 11

<211> 678

<212> PRT

<213> Homo sapiens Human HER3 isoform 1 cytoplasmic domain

<400> 11

Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr
1 5 10 15

Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala
20 25 30

Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu
35 40 45

Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp
50 55 60

Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile
65 70 75 80

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

Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly
100 105 110

Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu
115 120 125

Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro
130 135 140

Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr
145 150 155 160

Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val
165 170 175

Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala
180 185 190

Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys
195 200 205

Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr
210 215 220

Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
225 230 235 240

Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val
245 250 255

Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys
260 265 270

Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu
275 280 285

Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met
290 295 300

Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro
305 310 315 320

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

Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu
340 345 350

Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser
355 360 365

Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu
370 375 380

Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu
385 390 395 400

Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg
405 410 415

Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser
420 425 430

Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val
435 440 445

Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
450 455 460

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val Thr
465 470 475 480

Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly Tyr Val
485 490 495

Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg Glu Gly Thr
500 505 510

Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu Glu Glu Asp
515 520 525

Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg His Ser Pro
530 535 540

Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly Tyr Glu Tyr
545 550 555 560

Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser Thr Gln Ser
565 570 575

Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala Gly Thr Thr Pro
580 585 590

Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly Gly Pro
595 600 605

Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly
610 615 620

Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His
625 630 635 640

Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp
645 650 655

Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys
660 665 670

Ala Asn Ala Gln Arg Thr
675

<210> 12
<211> 44
<212> PRT
<213> Homo sapiens HER3 isoform 1 juxtamembrane segment

<400> 12

Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr
1 5 10 15

Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala
20 25 30

Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu
35 40

<210> 13
<211> 258
<212> PRT
<213> Homo sapiensHER3 isoform 1 protein kinase domain

<400> 13

Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His
1 5 10 15

Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys
20 25 30

Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val
35 40 45

Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val
50 55 60

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

Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly
85 90 95

Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys
100 105 110

Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala
115 120 125

Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp
130 135 140

Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr
145 150 155 160

Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His
165 170 175

Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
180 185 190

Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg
195 200 205

Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln
210 215 220

Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp
225 230 235 240

Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu
245 250 255

Phe Thr

<210> 14

<211> 376

<212> PRT

<213> Homo sapiens HER3 isoform 1 C terminal segment

<400> 14

Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser
1 5 10 15

Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys
20 25 30

Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp
35 40 45

Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala
50 55 60

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

Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu
85 90 95

Gly Glu Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys

100

105

110

Pro Arg Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser
 115 120 125

Glu Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu
 130 135 140

Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro
 145 150 155 160

Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro
 165 170 175

Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
 180 185 190

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg Glu
 195 200 205

Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu Glu
 210 215 220

Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg His
 225 230 235 240

Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly Tyr
 245 250 255

Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser Thr
 260 265 270

Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala Gly Thr
 275 280 285

Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly
 290 295 300

Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu
 305 310 315 320

Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala
325 330 335

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

Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe
355 360 365

Pro Lys Ala Asn Ala Gln Arg Thr
370 375

<210> 15

<211> 164

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain I

<400> 15

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

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

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
35 40 45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
50 55 60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65 70 75 80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
115 120 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145 150 155 160

Gly Arg Ser Cys

<210> 16

<211> 146

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain II

<400> 16

Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Ser
1 5 10 15

Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn
20 25 30

Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys
35 40 45

Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg
50 55 60

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

Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys
85 90 95

Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val
100 105 110

Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu
115 120 125

Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys

130

135

140

Pro Lys
145

<210> 17

<211> 166

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain III

<400> 17

Ala Cys Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser
1 5 10 15

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

Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro
35 40 45

Ala Leu Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile
50 55 60

Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe
65 70 75 80

Ser Val Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn
85 90 95

Arg Gly Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu
100 105 110

Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser
115 120 125

Ala Asn Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val
130 135 140

Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro
145 150 155 160

Arg Arg Asp Cys Val Ala
165

<210> 18

<211> 148

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain IV

<400> 18

Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly
1 5 10 15

Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly
20 25 30

Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe
35 40 45

Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met
50 55 60

Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln
65 70 75 80

Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His
85 90 95

Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln
100 105 110

Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly
115 120 125

Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys
130 135 140

Thr His Leu Thr
145

<210> 19

<211> 17

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain II dimerisation loop

<400> 19

Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro
1 5 10 15

His

<210> 20

<211> 1283

<212> PRT

<213> Homo macaque HER3

<400> 20

Met Gly Asn Leu Glu Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser
1 5 10 15

Phe Leu Gln Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met
20 25 30

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

Thr Gln Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr
50 55 60

Asn Thr Asn Ser Ser His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu
65 70 75 80

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

Cys His Met Asp Thr Ile Asp Trp Lys Asp Ile Val Arg Asp Gln Asp
100 105 110

Ala Glu Ile Val Val Lys Asp Asn Gly Arg Ser Cys Pro Leu Cys His
115 120 125

Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Pro Glu Asp Cys Gln
130 135 140

Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe
145 150 155 160

Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys
165 170 175

Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp
180 185 190

Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys
195 200 205

Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly
210 215 220

Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln Thr
225 230 235 240

Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
245 250 255

Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
260 265 270

Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
275 280 285

Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
290 295 300

Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
305 310 315 320

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
325 330 335

Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met Tyr Asn Phe Ser Val
340 345 350

Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly

355

360

365

Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe
 370 375 380

Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn
 385 390 395 400

Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val Leu Arg
 405 410 415

Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg
 420 425 430

Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly
 435 440 445

Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
 450 455 460

Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu
 465 470 475 480

Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu
 485 490 495

Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp
 500 505 510

Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser
 515 520 525

Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr
 530 535 540

Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln
 545 550 555 560

Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val
 565 570 575

Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr Val Ile Ala Gly
580 585 590

Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg
595 600 605

Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg
610 615 620

Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val
625 630 635 640

Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu
645 650 655

Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp Ile Pro Glu
660 665 670

Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Ile Ile Glu Asp Lys
675 680 685

Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met Leu Ala Ile
690 695 700

Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro
705 710 715 720

Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu
725 730 735

Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu
740 745 750

Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu
755 760 765

His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys
770 775 780

Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu

785		790		795		800									
Pro	Pro	Asp	Asp	Lys	Gln	Leu	Leu	Tyr	Ser	Glu	Ala	Lys	Thr	Pro	Ile
				805					810					815	
Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	His	Phe	Gly	Lys	Tyr	Thr	His	Gln
			820					825					830		
Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe
		835					840					845			
Gly	Ala	Glu	Pro	Tyr	Ala	Gly	Leu	Arg	Leu	Ala	Glu	Val	Pro	Asp	Leu
	850					855					860				
Leu	Glu	Lys	Gly	Glu	Arg	Leu	Ala	Gln	Pro	Gln	Ile	Cys	Thr	Ile	Asp
865					870					875					880
Val	Tyr	Met	Val	Met	Val	Lys	Cys	Trp	Met	Ile	Asp	Glu	Asn	Ile	Arg
			885						890					895	
Pro	Thr	Phe	Lys	Glu	Leu	Ala	Asn	Glu	Phe	Thr	Arg	Met	Ala	Arg	Asp
			900					905					910		
Pro	Pro	Arg	Tyr	Leu	Val	Ile	Lys	Arg	Glu	Ser	Gly	Pro	Gly	Ile	Ala
		915					920					925			
Pro	Gly	Pro	Glu	Pro	His	Gly	Leu	Thr	Asn	Lys	Lys	Leu	Glu	Glu	Val
	930					935					940				
Glu	Leu	Glu	Pro	Glu	Leu	Asp	Leu	Asp	Leu	Asp	Leu	Glu	Ala	Glu	Glu
945					950				955						960
Asp	Asn	Leu	Ala	Thr	Thr	Thr	Leu	Gly	Ser	Ala	Leu	Ser	Leu	Pro	Val
			965						970					975	
Gly	Thr	Leu	Asn	Arg	Pro	Arg	Gly	Ser	Gln	Ser	Leu	Leu	Ser	Pro	Ser
			980					985					990		
Ser	Gly	Tyr	Met	Pro	Met	Asn	Gln	Gly	Asn	Leu	Gly	Glu	Ala	Phe	Gln
		995					1000					1005			

Glu Ser Ala Val Ser Gly Ser Ser Glu Trp Cys Pro Arg Pro Val
1010 1015 1020

Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser
1025 1030 1035

Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val
1040 1045 1050

Ser Thr Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg
1055 1060 1065

Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro
1070 1075 1080

Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn
1085 1090 1095

Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser
1100 1105 1110

Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly
1115 1120 1125

Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg
1130 1135 1140

Arg Arg Arg His Ser Pro Pro Arg Pro Pro Arg Pro Ser Ser Leu
1145 1150 1155

Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
1160 1165 1170

Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro
1175 1180 1185

Val Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr
1190 1195 1200

Met Asn Arg Gln Arg Gly Gly Ser Gly Pro Gly Gly Asp Tyr Ala

1205

1210

1215

Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met
1220 1225 1230

Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr
1235 1240 1245

Ala His Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala
1250 1255 1260

Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala
1265 1270 1275

Asn Ala Gln Arg Thr
1280

<210> 21
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognised by anti-HER3 antibody clone 10A6

<400> 21

Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro His
1 5 10

<210> 22
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognised by anti-HER3 antibody clone 4-35-B2 and
4-35-B4

<400> 22

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe
1 5 10

<210> 23
<211> 21

<212> PRT
<213> Artificial Sequence

<220>
<223> Composite sequence of epitopes recognised by anti-HER3 antibody clones 4-35-B2, 4-35-B4 and 10A6

<400> 23

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
1 5 10 15

Glu Pro Asn Pro His
20

<210> 24
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 heavy chain variable region

<400> 24

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 25
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 heavy chain variable region

<400> 25

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 26
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 heavy chain variable region

<400> 26

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 27

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 heavy chain variable region

<400> 27

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp

35

40

45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 28

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1 heavy chain variable region

<400> 28

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
 35 40 45

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

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

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

85

90

95

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 29

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v2 heavy chain variable region

<400> 29

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

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

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

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 30

<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_11B heavy chain variable region

<400> 30

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 31
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85v1 heavy chain variable region

<400> 31

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85v2 heavy chain variable region

<400> 32

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

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

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

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 33
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o1 heavy chain variable region

<400> 33

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

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

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

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 34
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o2 heavy chain variable region

<400> 34

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

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

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

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 35
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c87 heavy chain variable region

<400> 35

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 heavy chain variable region

<400> 36

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

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

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp

35

40

45

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 37

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 heavy chain variable region

<400> 37

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

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

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

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain variable region

<400> 38

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

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

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

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

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

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

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

Gly Thr Ala Val Thr Val Ser Ser
 115 120

<210> 39

<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 heavy chain variable region

<400> 39

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 40
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c93 heavy chain variable region

<400> 40

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1,10D1_c75,0D1_c76,0D1_c77,10D1_c78v1,10D1_c78v2,10D1_11B,10D1_c85v1,10D1_c85v2,10D1_c85o1,0D1_c85o2,10D1_c87, 10D1_c89, 0D1_c90,10D1_c92, 10D1_c93 heavy chain CDR1

<400> 41

Gly Tyr Ser Ile Thr Ser Gly Tyr Ser
1 5

<210> 42

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain CDR1

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X = S or Y

<400> 42

Gly Tyr Tyr Ile Thr Ser Gly Tyr Ser
1 5

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus heavy chain CDR1

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X = S or Y

<400> 43

Gly Tyr Xaa Ile Thr Ser Gly Tyr Ser
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1,10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1,10D1_c78v2,
10D1_11B, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR2

<400> 44

Ile His Tyr Ser Gly Gly Thr
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85v1,10D1_c85v2,10D1_c85o1,10D1_c85o2,
10D1_c89,10D1_c90,10D1_c91 heavy chain CDR2

<400> 45

Ile Arg Tyr Ser Gly Gly Thr
1 5

<210> 46

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus heavy chain CDR2

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X = H or R

<400> 46

Ile Xaa Tyr Ser Gly Gly Thr
1 5

<210> 47

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1,10D1_c75,10D1_c76,10D1_c77,10D1_c78v1,10D1_c78v2,10D1_11B,10D1_c85v1,10D1_c85v2,10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR3

<400> 47

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr
1 5 10

<210> 48

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c90,10D1_c91 heavy chain CDR3

<400> 48

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr
1 5 10

<210> 49
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o1 heavy chain CDR3

<400> 49

Ala	Arg	Glu	Thr	Thr	Ala	Pro	Arg	Tyr	Pro	Phe	Asp	Tyr
1				5					10			

<210> 50
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o2 heavy chain CDR3

<400> 50

Ala	Arg	Gly	Thr	Thr	Ala	Pro	Arg	Tyr	Pro	Phe	Asp	Tyr
1				5					10			

<210> 51
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus heavy chain CDR3

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X = M, E or G

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X = R or W

<400> 51

Ala	Arg	Xaa	Thr	Thr	Ala	Pro	Xaa	Tyr	Pro	Phe	Asp	Tyr
1				5					10			

<210> 52
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2,10D1_c85v1,
10D1_c85v2, 10D1_c85o1, 10D1_c85o2,10D1_c87, 10D1_c92, 10D1_c93
heavy chain FR1

<400> 52

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

Thr Leu Ser Leu Thr Cys Ala Val Thr
20 25

<210> 53
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 110D1_c89, 10D1_c91 heavy chain FR1

<400> 53

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 54
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 heavy chain FR1

<400> 54

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

Thr Leu Phe Leu Thr Cys Thr Val Ser

20

25

<210> 55
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 heavy chain FR1

<400> 55

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

Ser Leu Ser Leu Thr Cys Thr Val Thr
20 25

<210> 56
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c85v1, 10D1_c87,
10D1_c92, 10D1_c93 heavy chain FR2

<400> 56

Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v2, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2 heavy chain FR2

<400> 57

Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 58
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 heavy chain FR2

<400> 58

Trp	His	Trp	Ile	Arg	Gln	Phe	Pro	Gly	Asn	Lys	Leu	Glu	Trp	Met	Gly
1				5					10					15	

Ser

<210> 59
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c90, 10D1_c91 heavy chain FR2

<400> 59

Trp	His	Trp	Ile	Arg	Gln	His	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly
1				5					10					15	

Ser

<210> 60
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_11B heavy chain FR2

<400> 60

Trp	His	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly
1				5					10					15	

Ser

<210> 61
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c92 heavy chain FR3

<400> 61

Asn Tyr Asn Pro Thr Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1 5 10 15

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

Thr Ala Val Tyr Phe Cys
35

<210> 62
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2 heavy chain FR3

<400> 62

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1 5 10 15

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

Thr Ala Val Tyr Phe Cys
35

<210> 63
<211> 38
<212> PRT
<213> Artificial Sequence

<220>

<223> 10D1_11B heavy chain FR3

<400> 63

Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Arg	Asp	Thr
1				5					10					15	

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

Thr	Ala	Val	Tyr	Tyr	Cys
					35

<210> 64

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1,10D1_c85v2, 10D1_c85o1, 10D1_c85o2 heavy chain FR3

<400> 64

Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Ile	Thr	Ile	Ser	Arg	Asp	Thr
1				5					10					15	

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

Thr	Ala	Val	Tyr	Phe	Cys
					35

<210> 65

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87, 10D1_c93 heavy chain FR3

<400> 65

Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Ile	Thr	Ile	Ser	Arg	Asp	Thr
1				5					10					15	

Ser	Lys	Asn	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp
			20					25					30		

Thr Ala Val Tyr Phe Cys
35

<210> 66
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89 heavy chain FR3

<400> 66

Asp Tyr Asn Pro Ser Leu Lys Ser Leu Val Thr Ile Ser Ala Asp Thr
1 5 10 15

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

Thr Ala Val Tyr Tyr Cys
35

<210> 67
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 heavy chain FR3

<400> 67

Asp Tyr Asn Pro Ser Leu Lys Ser Leu Val Thr Ile Ser Val Asp Thr
1 5 10 15

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

Thr Ala Val Tyr Tyr Cys
35

<210> 68
<211> 38
<212> PRT
<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain FR3

<400> 68

Asp Tyr Asn Pro Ser Leu Lys Ser Leu Ala Thr Ile Ser Ala Asp Thr
1 5 10 15

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

Thr Ala Val Tyr Tyr Cys
35

<210> 69

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain FR3

<400> 69

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Glu Asp
20 25 30

Thr Ala Thr Tyr Phe Cys
35

<210> 70

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75,10D1_c76,10D1_c77,10D1_c78v1,10D1_c78v2,10D1_11B,10D1_c8
5v1,10D1_c85v2,10D1_c85o1,10D1_c85o2,10D1_c87,10D1_c92, 10D1_c93
heavy chain FR4

<400> 70

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 71
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c90 heavy chain FR4

<400> 71

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 72
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c91 heavy chain FR4

<400> 72

Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 73
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1, 4-35-B4, 10A6 heavy chain FR4

<400> 73

Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser
1				5					10	

<210> 74
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 light chain variable region

<400> 74

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 75

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 light chain variable region

<400> 75

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr Phe 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 Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 76
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 light chain variable region

<400> 76

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

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

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

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

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

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> 10D1_c77 light chain variable region

<400> 77

Val Ile Val 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 Ile Val Gly Pro Asn
20 25 30

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

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

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

<210> 78

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1, 10D1_c78v2, 10D1_11B light chain variable region

<400> 78

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

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

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

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

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

<210> 79

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2 light chain variable region

<400> 79

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 80
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o1 light chain variable region

<400> 80

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 81
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o2 light chain variable region

<400> 81

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 82

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 light chain variable region

<400> 82

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

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

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

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

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

<210> 83
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89 light chain variable region

<400> 83

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr 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 Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 84
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 light chain variable region

<400> 84

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

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

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

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

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

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

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

<210> 85

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 light chain variable region

<400> 85

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

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

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

Tyr Ser Ala Ser Tyr Gly Tyr 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 Tyr Ser Ser His Pro Leu
85 90 95

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

<210> 86
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 light chain variable region

<400> 86

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr Phe 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 Val Ala Glu Tyr Phe Cys Gln Gln Tyr Phe Ser His Pro Leu
85 90 95

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

<210> 87
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c93 light chain variable region

<400> 87

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

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

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

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

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

<210> 88
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1,10D1_c75,10D1_c78v1,10D1_c78v2,10D1_11B,10D1_c85v1,10D1_c85v
2,10D1_c85o1,10D1_c85o2,10D1_c87,10D1_c89,10D1_c90,10D1_c91,10D1_
c92,10D1_c93 light chain CDR1

<400> 88

Gln Ile Val Gly Ser Asn
1 5

<210> 89
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 light chain CDR1

<400> 89

Gln Ile Val Gly Tyr Asn
1 5

<210> 90
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain CDR1

<400> 90

Gln Ile Val Gly Pro Asn
1 5

<210> 91
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus light chain CDR1

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X = S, Y or P

<400> 91

Gln Ile Val Gly Xaa Asn
1 5

<210> 92
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1,10D1_c75,10D1_c76,10D1_c77,10D1_c78v1, 10D1_c78v2, 10D1_11B,
10D1_c87, 10D1_c89, 10D1_c90,10D1_c91, 10D1_c92, 10D1_c93 light

chain CDR2

<400> 92

Ser Ala Ser
1

<210> 93

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1,10D1_c85v2, 10D1_c85o1, 10D1_c85o2 light chain CDR2

<400> 93

Ser Ala Arg
1

<210> 94

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus light chain CDR2

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X = S or R

<400> 94

Ser Ala Xaa
1

<210> 95

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1, 10D1_c75, 10D1_c76, 0D1_c78v1, 10D1_c78v2, 0D1_11B,
10D1_c85v1,10D1_c85v2, 10D1_c85o1, 0D1_c85o2, 10D1_c87, 10D1_c89,
10D1_c91, 10D1_c93 light chain CDR3

<400> 95

Gln Gln Tyr Ser Ser His Pro Leu Thr
1 5

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain CDR3

<400> 96

Gln Gln Tyr Ser Thr His Pro Leu Thr
1 5

<210> 97
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 light chain CDR3

<400> 97

Gln Gln Tyr Thr Thr His Pro Leu Thr
1 5

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 light chain CDR3

<400> 98

Gln Gln Tyr Phe Ser His Pro Leu Thr
1 5

<210> 99
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus light chain CDR3

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X = S, T or F

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X = S or T

<400> 99

Gln Gln Tyr Xaa Xaa His Pro Leu Thr
1 5

<210> 100
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75,10D1_c92 light chain FR1

<400> 100

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

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 101
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 light chain FR1

<400> 101

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 102

<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain FR1

<400> 102

Val	Ile	Val	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
		20						25	

<210> 103
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v1, 10D1_c78v2,10D1_11B,10D1_c85v1, 10D1_c85v2,
10D1_c85o1,10D1_c85o2,10D1_c87,10D1_c93 light chain FR1

<400> 103

Asp	Ile	Val	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
		20						25	

<210> 104
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c91 light chain FR1

<400> 104

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser
		20						25	

<210> 105
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 light chain FR1

<400> 105

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

Asp	Arg	Val	Thr	Phe	Thr	Cys	Lys	Ala	Ser
		20						25	

<210> 106
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 light chain FR1

<400> 106

Asp	Ile	Val	Met	Thr	Gln	Ser	Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Ser	Val	Thr	Cys	Lys	Ala	Ser
		20						25	

<210> 107
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 light chain FR2

<400> 107

Val	Ala	Trp	Tyr	Gln	Met	Lys	Pro	Gly	Lys	Ser	Pro	Lys	Pro	Leu	Ile
1				5				10						15	

Tyr

<210> 108
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B,
10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c93 light
chain FR2

<400> 108

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
1 5 10 15

Tyr

<210> 109
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c87 light chain FR2

<400> 109

Val Ala Trp Tyr Gln Gln Met Pro Gly Lys Ser Pro Glu Pro Leu Ile
1 5 10 15

Tyr

<210> 110
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c90 light chain FR2

<400> 110

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
1 5 10 15

Tyr

<210> 111
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c91 light chain FR2

<400> 111

Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Met	Pro	Leu	Ile
1				5					10					15	

Tyr

<210> 112
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 light chain FR2

<400> 112

Val	Ala	Trp	Tyr	Gln	Met	Lys	Leu	Gly	Lys	Ser	Pro	Lys	Pro	Leu	Ile
1				5					10					15	

Tyr

<210> 113
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 light chain FR2

<400> 113

Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Pro	Leu	Ile
1				5					10					15	

Tyr

<210> 114
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c92 light chain FR3

<400> 114

Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

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

Glu Tyr Phe Cys
35

<210> 115
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 light chain FR3

<400> 115

Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Ala Ser Gly Ser Gly
1 5 10 15

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

Glu Tyr Phe Cys
35

<210> 116
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain FR3

<400> 116

Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

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

Glu Tyr Phe Cys
35

<210> 117

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1, 10D1_c78v2, 10D1_11B light chain FR3

<400> 117

Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 118

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2 light chain FR3

<400> 118

Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

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

Thr Tyr Tyr Cys
35

<210> 119
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c87, 10D1_c93 light chain FR3

<400> 119

Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 120
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89 light chain FR3

<400> 120

Tyr Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 121
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<223> 10D1_c90 light chain FR3

<400> 121

Tyr Leu Tyr Ser Ser Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Glu Phe Thr Met Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 122

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 light chain FR3

<400> 122

Tyr Gly Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 123

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain FR3

<400> 123

Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Ala Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Glu Asp Leu Ala
20 25 30

Glu Tyr Phe Cys
35

<210> 124
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B,
10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87,
10D1_c90, 10D1_c92, 10D1_c93 light chain FR4

<400> 124

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c91 light chain FR4

<400> 125

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 light chain FR4

<400> 126

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1 5 10

<210> 127
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain variable region

<400> 127

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

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

Asn Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65 70 75 80

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

Val Ser Leu Arg Trp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 128

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain CDR1

<400> 128

Gly Tyr Ser Phe Thr Asp Tyr Asn
1 5

<210> 129

<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain CDR2

<400> 129

Ile Asn Pro Tyr Asn Gly Gly Thr
1 5

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain CDR3

<400> 130

Val Ser Leu Arg Trp Gly Ala Met Asp Tyr
1 5 10

<210> 131
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR1

<400> 131

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 132
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR2

<400> 132

Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly
1 5 10 15

His

<210> 133
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR3

<400> 133

Thr Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
1 5 10 15

Ser Ser Ser Thr Ala Phe Met His Leu Asn Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Val Tyr Phe Cys
35

<210> 134
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR4

<400> 134

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1 5 10

<210> 135
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain variable region

<400> 135

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Tyr Thr
85 90 95

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

<210> 136
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain CDR1

<400> 136

Ser Ser Val Ser Tyr
1 5

<210> 137
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain CDR2

<400> 137

Leu Thr Ser
1

<210> 138
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain CDR3

<400> 138

Gln Gln Trp Asn Ser Asn Pro Tyr Thr
1 5

<210> 139
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR1

<400> 139

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser
20 25

<210> 140
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR2

<400> 140

Met Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile
1 5 10 15

Tyr

<210> 141
<211> 36

<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR3

<400> 141

Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2, 4-35-B4, 10A6 light chain FR4

<400> 142

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 143
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain variable region

<400> 143

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

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

Tyr Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
35 40 45

Gly Lys Ile Ile Asp Pro Ala Asn Gly Asn Thr Asn Tyr Asp Pro Lys
50 55 60

Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala
65 70 75 80

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

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

Ser

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain CDR1

<400> 144

Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain CDR2

<400> 145

Ile Asp Pro Ala Asn Gly Asn Thr
1 5

<210> 146
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain CDR3

<400> 146

Ala Arg Gly Leu His
1 5

<210> 147

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain FR1

<400> 147

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

Ser Val Lys Leu Ser Cys Thr Ala Ser
20 25

<210> 148

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain FR2

<400> 148

Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly
1 5 10 15

Lys

<210> 149

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain FR3

<400> 149

Asn Tyr Asp Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr
1 5 10 15

Ser Ser Asn Thr Ala Tyr Leu Gln Leu Ser Ser Leu Ser Ser Glu Asp
20 25 30

Thr Ala Val Tyr Phe Cys
35

<210> 150

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain variable region

<400> 150

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

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

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

<210> 151

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain CDR1

<400> 151

Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
1 5 10

<210> 152
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain CDR2

<400> 152

Leu Ala Ser
1

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain CDR3

<400> 153

Gln His Ser Arg Glu Leu Pro Tyr Thr
1 5

<210> 154
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain FR1

<400> 154

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

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

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain FR2

<400> 155

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 156
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain FR3

<400> 156

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 157
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 heavy chain variable region

<400> 157

Asp 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 Asn Phe Ile Thr Ser Gly
20 25 30

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

Met Gly Phe Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Lys Pro Ser Leu
50 55 60

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 158
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 heavy chain CDR1

<400> 158

Gly Asn Phe Ile Thr Ser Gly Tyr Phe
1 5

<210> 159
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 heavy chain CDR2

<400> 159

Ile Ser Tyr Asp Gly Ser Asn
1 5

<210> 160

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain CDR3

<400> 160

Ala Arg Glu Asn Tyr Gly Phe Gly Phe Asp Tyr
1 5 10

<210> 161

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain FR1

<400> 161

Asp 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
20 25

<210> 162

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain FR2

<400> 162

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
1 5 10 15

Phe

<210> 163
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 heavy chain FR3

<400> 163

Asn Tyr Lys Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp
20 25 30

Thr Ala Thr Tyr Tyr Cys
35

<210> 164
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain variable region

<400> 164

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

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

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

Tyr Phe Thr Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 165
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain CDR1

<400> 165

Gln Ser Leu Leu Tyr Ser Asp Asn Gln Lys Asn Tyr
1 5 10

<210> 166
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain CDR2

<400> 166

Trp Ala Ser
1

<210> 167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain CDR3

<400> 167

Gln Gln Tyr Phe Thr Phe Pro Trp Thr
1 5

<210> 168
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain FR1

<400> 168

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

Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser
			20					25	

<210> 169
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain FR2

<400> 169

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
1				5					10					15	

Tyr

<210> 170
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 light chain FR3

<400> 170

Thr	Trp	Lys	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly
1				5					10					15	

Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Lys	Ala	Glu	Asp	Leu	Ala
			20					25					30		

Val Tyr Tyr Cys
35

<210> 171

<211> 330

<212> PRT

<213> Homo sapiens IgG1 constant region (IGHG1; UniProt:P01857-1, v1)

<400> 171

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> 172
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1 IgG1 (positions 1-98 of P01857-1, v1)

<400> 172

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

<210> 173
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge IgG1 (positions 99-110 of P01857-1, v1)

<400> 173

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1 5 10

<210> 174
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2 IgG1 (positions 111-223 of P01857-1, v1)

<400> 174

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

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

20

25

30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 100 105 110

Lys

<210> 175

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> CH3 IgG1 (positions 224-330 of P01857-1, v1)

<400> 175

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

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

65		70		75		80									
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85					90					95	

Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
			100					105		

<210> 176
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH3 (D356E, L358M; positions numbered according to EU numbering)

<400> 176

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

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

Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		35					40					45			

Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	50					55					60				

Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
65					70					75					80

Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85					90					95	

Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
			100					105		

<210> 177
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Ckappa CL (IGCK; UniProt: P01834-1, v2)

<400> 177

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

<210> 178

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain SignalP

<400> 178

Met Lys Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Ile Pro Gly Ile
1 5 10 15

Leu Ser

<210> 179

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain SignalP

<400> 179

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

Leu Ser

<210> 180

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain SignalP

<400> 180

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

Gly	Val	Asp	Gly
			20

<210> 181

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain SignalP

<400> 181

Met	Glu	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Thr	Gly
1				5					10					15	

Val His Ser

<210> 182

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 light chain SignalP

<400> 182

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Met	Ser	Ala	Ser
1				5					10					15	

Val	Met	Met	Ser	Arg	Gly
			20		

<210> 183

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain SignalP

<400> 183

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

Val	Asn	Ser
-----	-----	-----

<210> 184

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain SignalP

<400> 184

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

Gly	Ser	Thr	Gly
			20

<210> 185

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B,
10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87,
10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 heavy chain
SignalP

<400> 185

Met	Glu	Leu	Gly	Leu	Arg	Trp	Val	Phe	Leu	Ile	Ala	Thr	Leu	Ala	Gly
1				5					10					15	

Ala Arg Cys

<210> 186

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B,
10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87,
10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 light chain
SignalP

<400> 186

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

Leu	Arg	Gly	Ala	Arg	Cys
				20	

<210> 187

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 VH-CH1-CH2-CH3

<400> 187

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

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly

20

25

30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
 35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

450

<210> 188
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 VL-Ckappa

<400> 188

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr Phe 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 Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro 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 Cys
 210

<210> 189

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 VH-CH1-CH2-CH3

<400> 189

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
 35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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

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

115

120

125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 190
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 VL-Ckappa

<400> 190

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

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

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

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

Thr Phe Gly Pro 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 Cys
210

<210> 191
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 VH-CH1-CH2-CH3

<400> 191

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

210

215

220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 192
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 VL-Ckappa

<400> 192

Val Ile Val 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 Ile Val Gly Pro Asn
20 25 30

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

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

Thr Phe Gly Pro 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 Cys
210

<210> 193
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v1 VH-CH1-CH2-CH3

<400> 193

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

305		310		315		320
Glu Tyr Lys Cys	Lys Val Ser Asn Lys	Ala Leu Pro Ala	Pro Ile Glu			
	325	330	335			
Lys Thr Ile Ser	Lys Ala Lys Gly	Gln Pro Arg Glu	Pro Gln Val Tyr			
	340	345	350			
Thr Leu Pro Pro	Ser Arg Asp Glu	Leu Thr Lys Asn	Gln Val Ser Leu			
	355	360	365			
Thr Cys Leu Val	Lys Gly Phe Tyr	Pro Ser Asp Ile	Ala Val Glu Trp			
	370	375	380			
Glu Ser Asn Gly	Gln Pro Glu Asn	Asn Tyr Lys Thr	Thr Pro Pro Val			
385	390	395	400			
Leu Asp Ser Asp	Gly Ser Phe Phe	Leu Tyr Ser Lys	Leu Thr Val Asp			
	405	410	415			
Lys Ser Arg Trp	Gln Gln Gly Asn	Val Phe Ser Cys	Ser Val Met His			
	420	425	430			
Glu Ala Leu His	Asn His Tyr Thr	Gln Lys Ser Leu	Ser Leu Ser Pro			
	435	440	445			
Gly Lys						
450						
<210>	194					
<211>	450					
<212>	PRT					
<213>	Artificial Sequence					
<220>						
<223>	10D1_c78v2	VH-CH1-CH2-CH3				
<400>	194					
Asp Val Gln Leu	Gln Glu Trp Gly	Ala Gly Leu Leu	Lys Pro Ser Glu			
1	5	10	15			
Thr Leu Ser Leu	Thr Cys Ala Val	Thr Gly Tyr Ser	Ile Thr Ser Gly			

20

25

30

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

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

450

<210> 195
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v1, 10D1_c78v2, 10D1_11B VL-Ckappa

<400> 195

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

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

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

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

Thr Phe Gly Pro 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 Cys
 210

<210> 196

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B VH-CH1-CH2-CH3

<400> 196

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

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

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

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

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

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

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

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

115

120

125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 197
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85v1 VH-CH1-CH2-CH3

<400> 197

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

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

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

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

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

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

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

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

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

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

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

260

265

270

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
 450

<210> 198

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v2 VH-CH1-CH2-CH3

<400> 198

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

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

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

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

405

410

415

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

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

Gly Lys
 450

<210> 199

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2 VL-Ckappa

<400> 199

Asp Ile Val 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 Ile Val Gly Ser Asn
 20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
 85 90 95

Thr Phe Gly Pro 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 Cys
 210

<210> 200

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 VH-CH1-CH2-CH3

<400> 200

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

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

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

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

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser

80

95

110

125

140

160

175

190

205

220

240

255

270

285

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 201
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o1 VL-Ckappa

<400> 201

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro 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 Cys

210

<210> 202
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o2 VH-CH1-CH2-CH3

<400> 202

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

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

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

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

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

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

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

165

170

175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 203
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c85o2 VL-Ckappa

<400> 203

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro 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 Cys
210

<210> 204
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c87 VH-CH1-CH2-CH3

<400> 204

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

260

265

270

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
 450

<210> 205

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 VL-Ckappa

<400> 205

Asp Ile Val 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 Ile Val Gly Ser Asn
20 25 30

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

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

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

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

Thr Phe Gly Pro 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 Cys
210

<210> 206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89 VH-CH1-CH2-CH3

<400> 206

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

355

360

365

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

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

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

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

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

Gly Lys
 450

<210> 207
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10D1_c89 VL-Ckappa

<400> 207

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr 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 Tyr Ser Ser His Pro Leu						
		85		90		95
Thr Phe Gly Gln Gly Thr Lys Leu 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 Cys						
		210				

<210> 208
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10D1_c90 VH-CH1-CH2-CH3

<400> 208

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

Thr Leu Phe Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly

20

25

30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

450

<210> 209
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 VL-Ckappa

<400> 209

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

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

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

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

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

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

Thr Phe Gly Pro 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 Cys
 210

<210> 210

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 VH-CH1-CH2-CH3

<400> 210

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

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

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

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

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

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

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

Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115

120

125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 211
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c91 VL-Ckappa

<400> 211

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

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

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

Tyr Ser Ala Ser Tyr Gly Tyr 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 Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu 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 Cys
210

<210> 212
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 VH-CH1-CH2-CH3

<400> 212

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

210

215

220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 213
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 VL-Ckappa

<400> 213

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

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

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

Tyr Ser Ala Ser Tyr Leu Tyr Phe 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 Val Ala Glu Tyr Phe Cys Gln Gln Tyr Phe Ser His Pro Leu
85 90 95

Thr Phe Gly Pro 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 Cys
210

<210> 214
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c93 VH-CH1-CH2-CH3

<400> 214

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 215
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10D1_c93 VL-Ckappa

<400> 215

Asp Ile Val 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 Ile Val Gly Ser Asn

20

25

30

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

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

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

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

Thr Phe Gly Pro 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 Cys
 210

<210> 216

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VH-CH1-CH2-CH3

<400> 216

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

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

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

405

410

415

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

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

Gly Lys
 450

<210> 217
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10D1 VL-Ckappa

<400> 217

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

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

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

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu 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 Cys
 210

<210> 218

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 VH-CH1-CH2-CH3

<400> 218

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

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

Asn Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

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

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe

65		70		75		80									
Met	His	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			85						90					95	
Val	Ser	Leu	Arg	Trp	Gly	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser
			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	Gly	Gly	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	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn
		195					200					205			
Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His
	210					215					220				
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu
			260					265					270		
Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			

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

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

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

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

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

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

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

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

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

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 219
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 VL-Ckappa

<400> 219

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu 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 Cys
210

<210> 220

<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 VH-CH1-CH2-CH3

<400> 220

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

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

Tyr Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
35 40 45

Gly Lys Ile Ile Asp Pro Ala Asn Gly Asn Thr Asn Tyr Asp Pro Lys
50 55 60

Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala
65 70 75 80

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

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

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

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln

180

185

190

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

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

Cys Pro Ala Pro Glu Leu Leu 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 His Glu Asp Pro Glu Val Lys Phe Asn
 260 265 270

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

Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp
 340 345 350

Glu Leu 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 Gln Gly
405 410 415

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

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

<210> 221
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 VL-Ckappa

<400> 221

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

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 222
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> 10A6 VH-CH1-CH2-CH3

<400> 222

Asp 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 Asn Phe Ile Thr Ser Gly
20 25 30

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

Met Gly Phe Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Lys Pro Ser Leu
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

290

295

300

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

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

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

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

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

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

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 223

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 VL-Ckappa

<400> 223

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser

20

25

30

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

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

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

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

Tyr Phe Thr Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140

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

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

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

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

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

<210> 224

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B heavy chain FR1

<400> 224

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr
20 25

<210> 225

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1F.FcA VH-CH1-CH2-CH3 (GASDALIE; LCKC) (10D1F.FcB)

<400> 225

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115

120

125

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

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

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

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

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

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

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

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

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

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

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

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

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

Cys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1F.FcA VH-CH1-CH2-CH3 (N297Q)

<400> 226

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

260

265

270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 227

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VH-CH1-CH2-CH3 (GASDALIE; LCKC)

<400> 227

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Ala Gly
225 230 235 240

Pro Asp Val Phe Cys Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Leu Pro Glu Glu
325 330 335

Cys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

405

410

415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 228
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10D1 VH-CH1-CH2-CH3 (GASD)

<400> 228

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
 1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
 20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115

120

125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Ala Gly
 225 230 235 240

Pro Asp Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 229
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> HER3 binding site for 10D1-derived clones

<400> 229

Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly
1 5 10 15

Gly Cys

<210> 230
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 binding site motif 1

<400> 230

Pro Asn Pro Asn Gln
1 5

<210> 231

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 binding site motif 2

<400> 231

Asp Glu Cys Ala Gly
1 5