SEQUENCE LISTING

<110> AGENSYS, INC.
SEATTLE GENETICS INC.
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AN, Zili
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SNYDER, Josh
JIA, Xiao-chi

<120> ANTIBODY DRUG CONJUGATES (ADC) THAT BIND TO 158P1D7 PROTEINS

<130> 511582005088

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 61/692,448
<151> 2012-08-23

<160> 10

<170> FastSEQ for Windows Version 4.0

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<213> Homo sapiens

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<223> 158P1D7

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tct ctc ctt gcc tgt ata tct tta cac tcc caa act cca gtg ctc tca 100
Ser Leu Leu Ala Cys Ile Ser Leu His Ser Gln Thr Pro Val Leu Ser
15 20 25

tcc aga ggc tct tgt gat tct ctt tgc aat tgt gag gaa aaa gat ggc 148
Ser Arg Gly Ser Cys Asp Ser Leu Cys Asn Cys Glu Glu Lys Asp Gly
30 35 40

aca atg cta ata aat tgt gaa gca aaa ggt atc aag atg gta tct gaa 196
Thr Met Leu Ile Asn Cys Glu Ala Lys Gly Ile Lys Met Val Ser Glu
45 50 55

ata agt gtg cca cca tca cga cct ttc caa cta agc tta tta aat aac 244
Ile Ser Val Pro Pro Ser Arg Pro Phe Gln Leu Ser Leu Leu Asn Asn
60 65 70

ggc ttg acg atg ctt cac aca aat gac ttt tct ggg ctt acc aat gct 292
Gly Leu Thr Met Leu His Thr Asn Asp Phe Ser Gly Leu Thr Asn Ala
75 80 85 90

att tca ata cac ctt gga ttt aac aat att gca gat att gag ata ggt 340
Ile Ser Ile His Leu Gly Phe Asn Asn Ile Ala Asp Ile Glu Ile Gly
95 100 105

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gca ttt aat ggc ctt ggc ctc ctg aaa caa ctt cat atc aat cac aat   388
Ala Phe Asn Gly Leu Gly Leu Leu Lys Gln Leu His Ile Asn His Asn
            110                 115                 120

tct tta gaa att ctt aaa gag gat act ttc cat gga ctg gaa aac ctg   436
Ser Leu Glu Ile Leu Lys Glu Asp Thr Phe His Gly Leu Glu Asn Leu
        125                 130                 135

gaa ttc ctg caa gca gat aac aat ttt atc aca gtg att gaa cca agt   484
Glu Phe Leu Gln Ala Asp Asn Asn Phe Ile Thr Val Ile Glu Pro Ser
    140                 145                 150

gcc ttt agc aag ctc aac aga ctc aaa gtg tta att tta aat gac aat   532
Ala Phe Ser Lys Leu Asn Arg Leu Lys Val Leu Ile Leu Asn Asp Asn
155                 160                 165                 170

gct att gag agt ctt cct cca aac atc ttc cga ttt gtt cct tta acc   580
Ala Ile Glu Ser Leu Pro Pro Asn Ile Phe Arg Phe Val Pro Leu Thr
                175                 180                 185

cat cta gat ctt cgt gga aat caa tta caa aca ttg cct tat gtt ggt   628
His Leu Asp Leu Arg Gly Asn Gln Leu Gln Thr Leu Pro Tyr Val Gly
            190                 195                 200

ttt ctc gaa cac att ggc cga ata ttg gat ctt cag ttg gag gac aac   676
Phe Leu Glu His Ile Gly Arg Ile Leu Asp Leu Gln Leu Glu Asp Asn
        205                 210                 215

aaa tgg gcc tgc aat tgt gac tta ttg cag tta aaa act tgg ttg gag   724
Lys Trp Ala Cys Asn Cys Asp Leu Leu Gln Leu Lys Thr Trp Leu Glu
    220                 225                 230

aac atg cct cca cag tct ata att ggt gat gtt gtc tgc aac agc cct   772
Asn Met Pro Pro Gln Ser Ile Ile Gly Asp Val Val Cys Asn Ser Pro
235                 240                 245                 250

cca ttt ttt aaa gga agt ata ctc agt aga cta aag aag gaa tct att   820
Pro Phe Phe Lys Gly Ser Ile Leu Ser Arg Leu Lys Lys Glu Ser Ile
                255                 260                 265

tgc cct act cca cca gtg tat gaa gaa cat gag gat cct tca gga tca   868
Cys Pro Thr Pro Pro Val Tyr Glu Glu His Glu Asp Pro Ser Gly Ser
            270                 275                 280

tta cat ctg gca gca aca tct tca ata aat gat agt cgc atg tca act   916
Leu His Leu Ala Ala Thr Ser Ser Ile Asn Asp Ser Arg Met Ser Thr
        285                 290                 295

aag acc acg tcc att cta aaa cta ccc acc aaa gca cca ggt ttg ata   964
Lys Thr Thr Ser Ile Leu Lys Leu Pro Thr Lys Ala Pro Gly Leu Ile
    300                 305                 310

cct tat att aca aag cca tcc act caa ctt cca gga cct tac tgc cct   1012
Pro Tyr Ile Thr Lys Pro Ser Thr Gln Leu Pro Gly Pro Tyr Cys Pro
315                 320                 325                 330

att cct tgt aac tgc aaa gtc cta tcc cca tca gga ctt cta ata cat   1060
Ile Pro Cys Asn Cys Lys Val Leu Ser Pro Ser Gly Leu Leu Ile His
                335                 340                 345

tgt cag gag cgc aac att gaa agc tta tca gat ctg aga cct cct ccg   1108
Cys Gln Glu Arg Asn Ile Glu Ser Leu Ser Asp Leu Arg Pro Pro Pro
            350                 355                 360

caa aat cct aga aag ctc att cta gcg gga aat att att cac agt tta   1156
Gln Asn Pro Arg Lys Leu Ile Leu Ala Gly Asn Ile Ile His Ser Leu
        365                 370                 375
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atg aag tct gat cta gtg gaa tat ttc act ttg gaa atg ctt cac ttg   1204
Met Lys Ser Asp Leu Val Glu Tyr Phe Thr Leu Glu Met Leu His Leu
    380                 385                 390

gga aac aat cgt att gaa gtt ctt gaa gaa gga tcg ttt atg aac cta   1252
Gly Asn Asn Arg Ile Glu Val Leu Glu Glu Gly Ser Phe Met Asn Leu
395                 400                 405                 410

acg aga tta caa aaa ctc tat cta aat ggt aac cac ctg acc aaa tta   1300
Thr Arg Leu Gln Lys Leu Tyr Leu Asn Gly Asn His Leu Thr Lys Leu
                415                 420                 425

agt aaa ggc atg ttc ctt ggt ctc cat aat ctt gaa tac tta tat ctt   1348
Ser Lys Gly Met Phe Leu Gly Leu His Asn Leu Glu Tyr Leu Tyr Leu
            430                 435                 440

gaa tac aat gcc att aag gaa ata ctg cca gga acc ttt aat cca atg   1396
Glu Tyr Asn Ala Ile Lys Glu Ile Leu Pro Gly Thr Phe Asn Pro Met
        445                 450                 455

cct aaa ctt aaa gtc ctg tat tta aat aac aac ctc ctc caa gtt tta   1444
Pro Lys Leu Lys Val Leu Tyr Leu Asn Asn Asn Leu Leu Gln Val Leu
    460                 465                 470

cca cca cat att ttt tca ggg gtt cct cta act aag gta aat ctt aaa   1492
Pro Pro His Ile Phe Ser Gly Val Pro Leu Thr Lys Val Asn Leu Lys
475                 480                 485                 490

aca aac cag ttt acc cat cta cct gta agt aat att ttg gat gat ctt   1540
Thr Asn Gln Phe Thr His Leu Pro Val Ser Asn Ile Leu Asp Asp Leu
                495                 500                 505

gat tta cta acc cag att gac ctt gag gat aac ccc tgg gac tgc tcc   1588
Asp Leu Leu Thr Gln Ile Asp Leu Glu Asp Asn Pro Trp Asp Cys Ser
            510                 515                 520

tgt gac ctg gtt gga ctg cag caa tgg ata caa aag tta agc aag aac   1636
Cys Asp Leu Val Gly Leu Gln Gln Trp Ile Gln Lys Leu Ser Lys Asn
        525                 530                 535

aca gtg aca gat gac atc ctc tgc act tcc ccc ggg cat ctc gac aaa   1684
Thr Val Thr Asp Asp Ile Leu Cys Thr Ser Pro Gly His Leu Asp Lys
    540                 545                 550

aag gaa ttg aaa gcc cta aat agt gaa att ctc tgt cca ggt tta gta   1732
Lys Glu Leu Lys Ala Leu Asn Ser Glu Ile Leu Cys Pro Gly Leu Val
555                 560                 565                 570

aat aac cca tcc atg cca aca cag act agt tac ctt atg gtc acc act   1780
Asn Asn Pro Ser Met Pro Thr Gln Thr Ser Tyr Leu Met Val Thr Thr
                575                 580                 585

cct gca aca aca aca aat acg gct gat act att tta cga tct ctt acg   1828
Pro Ala Thr Thr Thr Asn Thr Ala Asp Thr Ile Leu Arg Ser Leu Thr
            590                 595                 600

gac gct gtg cca ctg tct gtt cta ata ttg gga ctt ctg att atg ttc   1876
Asp Ala Val Pro Leu Ser Val Leu Ile Leu Gly Leu Leu Ile Met Phe
        605                 610                 615

atc act att gtt ttc tgt gct gca ggg ata gtg gtt ctt gtt ctt cac   1924
Ile Thr Ile Val Phe Cys Ala Ala Gly Ile Val Val Leu Val Leu His
    620                 625                 630

cgc agg aga aga tac aaa aag aaa caa gta gat gag caa atg aga gac   1972
Arg Arg Arg Arg Tyr Lys Lys Lys Gln Val Asp Glu Gln Met Arg Asp
635                 640                 645                 650
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aac agt cct gtg cat ctt cag tac agc atg tat ggc cat aaa acc act   2020
Asn Ser Pro Val His Leu Gln Tyr Ser Met Tyr Gly His Lys Thr Thr
               655                 660                 665

cat cac act act gaa aga ccc tct gcc tca ctc tat gaa cag cac atg   2068
His His Thr Thr Glu Arg Pro Ser Ala Ser Leu Tyr Glu Gln His Met
           670                 675                 680

gtg agc ccc atg gtt cat gtc tat aga agt cca tcc ttt ggt cca aag   2116
Val Ser Pro Met Val His Val Tyr Arg Ser Pro Ser Phe Gly Pro Lys
       685                 690                 695

cat ctg gaa gag gaa gaa gag agg aat gag aaa gaa gga agt gat gca   2164
His Leu Glu Glu Glu Glu Glu Arg Asn Glu Lys Glu Gly Ser Asp Ala
   700                 705                 710

aaa cat ctc caa aga agt ctt ttg gaa cag gaa aat cat tca cca ctc   2212
Lys His Leu Gln Arg Ser Leu Leu Glu Gln Glu Asn His Ser Pro Leu
715                 720                 725                 730

aca ggg tca aat atg aaa tac aaa acc acg aac caa tca aca gaa ttt   2260
Thr Gly Ser Asn Met Lys Tyr Lys Thr Thr Asn Gln Ser Thr Glu Phe
               735                 740                 745

tta tcc ttc caa gat gcc agc tca ttg tac aga aac att tta gaa aaa   2308
Leu Ser Phe Gln Asp Ala Ser Ser Leu Tyr Arg Asn Ile Leu Glu Lys
           750                 755                 760

gaa agg gaa ctt cag caa ctg gga atc aca gaa tac cta agg aaa aac   2356
Glu Arg Glu Leu Gln Gln Leu Gly Ile Thr Glu Tyr Leu Arg Lys Asn
       765                 770                 775

att gct cag ctc cag cct gat atg gag gca cat tat cct gga gcc cac   2404
Ile Ala Gln Leu Gln Pro Asp Met Glu Ala His Tyr Pro Gly Ala His
   780                 785                 790

gaa gag ctg aag tta atg gaa aca tta atg tac tca cgt cca agg aag   2452
Glu Glu Leu Lys Leu Met Glu Thr Leu Met Tyr Ser Arg Pro Arg Lys
795                 800                 805                 810

gta tta gtg gaa cag aca aaa aat gag tat ttt gaa ctt aaa gct aat   2500
Val Leu Val Glu Gln Thr Lys Asn Glu Tyr Phe Glu Leu Lys Ala Asn
               815                 820                 825

tta cat gct gaa cct gac tat tta gaa gtc ctg gag cag caa aca tag   2548
Leu His Ala Glu Pro Asp Tyr Leu Glu Val Leu Glu Gln Gln Thr  *
           830                 835                 840

atggaga                                                          2555

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<213> Homo sapiens

<220>
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<223> 158P1D7

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 1               5                  10                  15
Ser Leu His Ser Gln Thr Pro Val Leu Ser Ser Arg Gly Ser Cys Asp
            20                  25                  30
Ser Leu Cys Asn Cys Glu Glu Lys Asp Gly Thr Met Leu Ile Asn Cys
        35                  40                  45
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Glu Ala Lys Gly Ile Lys Met Val Ser Glu Ile Ser Val Pro Pro Ser
    50                  55                  60
Arg Pro Phe Gln Leu Ser Leu Leu Asn Asn Gly Leu Thr Met Leu His
65                  70                  75                  80
Thr Asn Asp Phe Ser Gly Leu Thr Asn Ala Ile Ser Ile His Leu Gly
                85                  90                  95
Phe Asn Asn Ile Ala Asp Ile Glu Ile Gly Ala Phe Asn Gly Leu Gly
            100                 105                 110
Leu Leu Lys Gln Leu His Ile Asn His Asn Ser Leu Glu Ile Leu Lys
        115                 120                 125
Glu Asp Thr Phe His Gly Leu Glu Asn Leu Glu Phe Leu Gln Ala Asp
    130                 135                 140
Asn Asn Phe Ile Thr Val Ile Glu Pro Ser Ala Phe Ser Lys Leu Asn
145                 150                 155                 160
Arg Leu Lys Val Leu Ile Leu Asn Asp Asn Ala Ile Glu Ser Leu Pro
                165                 170                 175
Pro Asn Ile Phe Arg Phe Val Pro Leu Thr His Leu Asp Leu Arg Gly
            180                 185                 190
Asn Gln Leu Gln Thr Leu Pro Tyr Val Gly Phe Leu Glu His Ile Gly
        195                 200                 205
Arg Ile Leu Asp Leu Gln Leu Glu Asp Asn Lys Trp Ala Cys Asn Cys
    210                 215                 220
Asp Leu Leu Gln Leu Lys Thr Trp Leu Glu Asn Met Pro Pro Gln Ser
225                 230                 235                 240
Ile Ile Gly Asp Val Val Cys Asn Ser Pro Pro Phe Phe Lys Gly Ser
                245                 250                 255
Ile Leu Ser Arg Leu Lys Lys Glu Ser Ile Cys Pro Thr Pro Pro Val
            260                 265                 270
Tyr Glu Glu His Glu Asp Pro Ser Gly Ser Leu His Leu Ala Ala Thr
        275                 280                 285
Ser Ser Ile Asn Asp Ser Arg Met Ser Thr Lys Thr Thr Ser Ile Leu
    290                 295                 300
Lys Leu Pro Thr Lys Ala Pro Gly Leu Ile Pro Tyr Ile Thr Lys Pro
305                 310                 315                 320
Ser Thr Gln Leu Pro Gly Pro Tyr Cys Pro Ile Pro Cys Asn Cys Lys
                325                 330                 335
Val Leu Ser Pro Ser Gly Leu Leu Ile His Cys Gln Glu Arg Asn Ile
            340                 345                 350
Glu Ser Leu Ser Asp Leu Arg Pro Pro Pro Gln Asn Pro Arg Lys Leu
        355                 360                 365
Ile Leu Ala Gly Asn Ile Ile His Ser Leu Met Lys Ser Asp Leu Val
    370                 375                 380
Glu Tyr Phe Thr Leu Glu Met Leu His Leu Gly Asn Asn Arg Ile Glu
385                 390                 395                 400
Val Leu Glu Glu Gly Ser Phe Met Asn Leu Thr Arg Leu Gln Lys Leu
                405                 410                 415
Tyr Leu Asn Gly Asn His Leu Thr Lys Leu Ser Lys Gly Met Phe Leu
            420                 425                 430
Gly Leu His Asn Leu Glu Tyr Leu Tyr Leu Glu Tyr Asn Ala Ile Lys
        435                 440                 445
Glu Ile Leu Pro Gly Thr Phe Asn Pro Met Pro Lys Leu Lys Val Leu
    450                 455                 460
Tyr Leu Asn Asn Asn Leu Leu Gln Val Leu Pro Pro His Ile Phe Ser
465                 470                 475                 480
Gly Val Pro Leu Thr Lys Val Asn Leu Lys Thr Asn Gln Phe Thr His
                485                 490                 495
Leu Pro Val Ser Asn Ile Leu Asp Asp Leu Asp Leu Leu Thr Gln Ile
            500                 505                 510
Asp Leu Glu Asp Asn Pro Trp Asp Cys Ser Cys Asp Leu Val Gly Leu
        515                 520                 525
Gln Gln Trp Ile Gln Lys Leu Ser Lys Asn Thr Val Thr Asp Asp Ile
    530                 535                 540
Leu Cys Thr Ser Pro Gly His Leu Asp Lys Lys Glu Leu Lys Ala Leu
545                 550                 555                 560
Asn Ser Glu Ile Leu Cys Pro Gly Leu Val Asn Asn Pro Ser Met Pro
                565                 570                 575
Thr Gln Thr Ser Tyr Leu Met Val Thr Thr Pro Ala Thr Thr Thr Asn
            580                 585                 590
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Thr Ala Asp Thr Ile Leu Arg Ser Leu Thr Asp Ala Val Pro Leu Ser
        595                 600                 605
Val Leu Ile Leu Gly Leu Leu Ile Met Phe Ile Thr Ile Val Phe Cys
    610                 615                 620
Ala Ala Gly Ile Val Val Leu Val Leu His Arg Arg Arg Arg Tyr Lys
625                 630                 635                 640
Lys Lys Gln Val Asp Glu Gln Met Arg Asp Asn Ser Pro Val His Leu
                645                 650                 655
Gln Tyr Ser Met Tyr Gly His Lys Thr Thr His His Thr Thr Glu Arg
            660                 665                 670
Pro Ser Ala Ser Leu Tyr Glu Gln His Met Val Ser Pro Met Val His
        675                 680                 685
Val Tyr Arg Ser Pro Ser Phe Gly Pro Lys His Leu Glu Glu Glu Glu
    690                 695                 700
Glu Arg Asn Glu Lys Glu Gly Ser Asp Ala Lys His Leu Gln Arg Ser
705                 710                 715                 720
Leu Leu Glu Gln Glu Asn His Ser Pro Leu Thr Gly Ser Asn Met Lys
                725                 730                 735
Tyr Lys Thr Thr Asn Gln Ser Thr Glu Phe Leu Ser Phe Gln Asp Ala
            740                 745                 750
Ser Ser Leu Tyr Arg Asn Ile Leu Glu Lys Glu Arg Glu Leu Gln Gln
        755                 760                 765
Leu Gly Ile Thr Glu Tyr Leu Arg Lys Asn Ile Ala Gln Leu Gln Pro
    770                 775                 780
Asp Met Glu Ala His Tyr Pro Gly Ala His Glu Glu Leu Lys Leu Met
785                 790                 795                 800
Glu Thr Leu Met Tyr Ser Arg Pro Arg Lys Val Leu Val Glu Gln Thr
                805                 810                 815
Lys Asn Glu Tyr Phe Glu Leu Lys Ala Asn Leu His Ala Glu Pro Asp
            820                 825                 830
Tyr Leu Glu Val Leu Glu Gln Gln Thr
        835                 840
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<213> Homo sapiens

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<223> heavy chain variable region

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cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg   48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat   96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gaa tgg gtg   144
```

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

gca gtt ata tgg tat gat gga agt aat caa tat tat gca gac tcc gtg   192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val
     50                  55                  60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg ttt   240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65                  70                  75                  80

ctg caa atg cac agc ctg aga gcc gag gac acg gct gtg tat tac tgt   288
Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                 85                  90                  95

gcg aga ggt ctg act tct gga cgg tac ggt atg gac gtc tgg ggc caa   336
Ala Arg Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110

ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc   384
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca gcg gcc   432
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg   480
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct gtc   528
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc   576
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac aag   624
Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt gtc   672
Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc ttc   720
Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct   768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc   816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca   864
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc agc gtc   912
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag tgc   960
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```
Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc   1008
Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca   1056
Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc   1104
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat ggg   1152
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc gac   1200
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

ggc tcc ttc ttc ctt tac agc aag ctc acc gtg gac aag agc agg tgg   1248
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac   1296
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taa       1341
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  *
        435                 440                 445



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

<220>
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<223> Ha15-10ac12 heavy chain

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65                  70                  75                  80
Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val 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 Cys Ser Arg Ser Thr Ser Glu Ser 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
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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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220
Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300
Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320
Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 5
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(660)

<220>
<221> misc_feature
<222> (1)...(660)
<223> Ha15-10ac12 light chain

<220>
<221> misc_feature
<222> (1)...(339)
<223> light chain variable region

<220>
<221> misc_feature
<222> (340)...(660)
<223> human kappa constant region

<400> 5
gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga   48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1               5                  10                  15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctg ctt agt   96
```

```
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Leu Ser
            20                  25                  30

cat gga ttc aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct   144
His Gly Phe Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
         35                  40                  45

cca caa ctc ctg atc tat ttg ggt tct agt cgg gcc tcc ggg gtc cct   192
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Ser Arg Ala Ser Gly Val Pro
     50                  55                  60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc   240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65                  70                  75                  80

agc aga gtg gag gct gag gat gtt ggg ctt tat tac tgc atg caa ccc   288
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Pro
                85                  90                  95

cta caa att ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa   336
Leu Gln Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag   384
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc   432
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa   480
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc   528
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag   576
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg   624
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                   660
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  *
    210                 215


<210> 6
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> CHAIN
<222> (1)...(219)
<223> Ha15-10ac12 light chain

<400> 6
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1               5                  10                  15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Leu Ser
            20                  25                  30
His Gly Phe Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
```

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


<210> 7
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<221> CHAIN
<222> (1)...(446)
<223> Ha15-10ac12 lheavy chain

<220>
<221> SITE
<222> (1)...(120)
<223> heavy chain variable region

<220>
<221> SITE
<222> (121)...(446)
<223> human IgG2 constant region

<400> 7
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Gln Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65                  70                  75                  80
Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Leu Thr Ser Gly Arg Tyr Gly Met Asp Val 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 Cys Ser Arg Ser Thr Ser Glu Ser 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
```

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Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220
Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300
Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320
Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 8
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> CHAIN
<222> (1)...(219)
<223> Ha15-10ac12 light chain

<220>
<221> SITE
<222> (1)...(113)
<223> light chain variable region

<220>
<221> SITE
<222> (114)...(219)
<223> human kappa constant region

<400> 8
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1               5                  10                  15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Leu Ser
            20                  25                  30
His Gly Phe Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Ser Arg Ala Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Pro
```

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

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(4)
<223> peptidyl linker

<400> 9
Gly Phe Leu Gly
1

<210> 10
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (1)...(100)
<223> IGKV2D-28*01

<400> 10
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Leu Gln Thr Pro
100