SEQUENCE LISTING

<110> Agensys, Inc.
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SNYDER, Josh
BUTTERWORTH, Leslie Renee
HSU, Ssucheng Jeff
YANG, Peng
GUEVARA, Claudia Isabel

<120> ANTIBODY DRUG CONJUGATES (ADC) THAT BIND TO CD37 PROTEINS

<130> 511582008940

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 61/861,321
<151> 2013-08-01

<160> 12

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Homo sapiens

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g atg tca gcc cag gag agc tgc ctc agc ctc atc aag tac ttc ctc ttc 169
  Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
   1               5                  10                  15

gtt ttc aac ctc ttc ttc ttc gtc ctc ggc agc ctg atc ttc tgc ttc   217
Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
             20                  25                  30

ggc atc tgg atc ctc att gac aag acc agc ttc gtg tcc ttt gtg ggc   265
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
         35                  40                  45

ttg gcc ttc gtg cct ctg cag atc tgg tcc aaa gtc ctg gcc atc tca   313
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
     50                  55                  60

gga atc ttc acc atg ggc atc gcc ctc ctg ggt tgt gtg ggg gcc ctc   361
Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
 65                  70                  75                  80

aag gag ctc cgc tgc ctc ctg ggc ctg tat ttt ggg atg ctg ctg ctc   409
Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                 85                  90                  95

ctg ttt gcc aca cag atc acc ctg gga atc ctc atc tcc act cag cgg   457
Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

gcc cag ctg gag cga agc ttg cgg gac gtc gta gag aaa acc atc caa   505
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Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
        115                 120                 125

aag tac ggc acc aac ccc gag gag acc gcg gcc gag gag agc tgg gac   553
Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

tat gtg cag ttc cag ctg cgc tgc tgc ggc tgg cac tac ccg cag gac   601
Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145                 150                 155                 160

tgg ttc caa gtc ctc atc ctg aga ggt aac ggg tcg gag gcg cac cgc   649
Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
                165                 170                 175

gtg ccc tgc tcc tgc tac aac ttg tcg gcg acc aac gac tcc aca atc   697
Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
            180                 185                 190

cta gat aag gtg atc ttg ccc cag ctc agc agg ctt gga cac ctg gcg   745
Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205

cgg tcc aga cac agt gca gac atc tgc gct gtc cct gca gag agc cac   793
Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220

atc tac cgc gag ggc tgc gcg cag ggc ctc cag aag tgg ctg cac aac   841
Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

aac ctt att tcc ata gtg ggc att tgc ctg ggc gtc ggc cta ctc gag   889
Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

ctc ggg ttc atg acg ctc tcg ata ttc ctg tgc aga aac ctg gac cac   937
Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

gtc tac aac cgg ctc gct cga tac cgt tag gccccgccct ccccaaagtc     987
Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280

ccgccccgcc cccgtcacgt gcgctgggca cttccctgct gcctgtaaat atttgtttaa 1047
tccccagttc gcctggagcc ctccgccttc acattcccct ggggacccac gtggctgcgt 1107
gcccctgctg ctgtcacctc tcccacggga cctggggctt tcgtccacag cttcctgtcc 1167
ccatctgtcg gcctaccacc acccacaaga ttatttttca cccaaacctc aaataaatcc 1227
cctgcgtttt tggtaaaaaa aaaaaaaaaa aaaaaa                           1263

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            20                  25                  30
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60
Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80
Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95
Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
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            100                 105                 110
Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
        115                 120                 125
Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140
Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145                 150                 155                 160
Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
                165                 170                 175
Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
            180                 185                 190
Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205
Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220
Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240
Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255
Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270
Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280


<210> 3
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<220>
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<220>
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<222> (1)...(1326)
<223> HvCD37-6b15.1.1 heavy chain

<220>
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<222> (1)...(345)
<223> heavy chain variable region

<220>
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<222> (346)...(1326)
<223> heavy chain human IgG2 constant region

<400> 3
cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct tcg gag   48
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1               5                  10                  15

acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc agt cct tac   96
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Pro Tyr
            20                  25                  30

tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ttg gag tgg att   144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

ggg gaa atc aat cat agt gga agc acc aac tac aac ccg tcc ctc aag   192
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

agt cga gtc acc att tca gta gac acg tcc aag aac cag ttc tcc ctg   240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
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 65                  70                  75                  80

aag ctg agc tct gtg acc gcc gcg gac acg gct gtc tat tac tgt gcg   288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                 85                  90                  95

agg aga gct ggg gac ttt gac tac tgg ggc cag gga acc ctg gtc acc   336
Arg Arg Ala Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

gtc tcc tca gca tcc acc aag ggc cca tcg gtc ttc ccc ctg gcg ccc   384
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

tgc tcc agg agc acc tcc gag agc aca gcg gcc ctg ggc tgc ctg gtc   432
Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gct   480
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

ctg acc agc ggc gtg cac acc ttc cca gct gtc cta cag tcc tca gga   528
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc aac ttc ggc   576
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190

acc cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc aag   624
Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

gtg gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc   672
Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220

cca gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa   720
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg   768
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac   816
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag gag   864
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

cag ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac   912
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
    290                 295                 300

cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa   960
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320

ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag   1008
Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
                325                 330                 335

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg   1056
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
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            340                 345                 350

acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc   1104
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365

agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac   1152
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380

tac aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc   1200
Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400

tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc   1248
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
                405                 410                 415

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

aag agc ctc tcc ctg tct ccg ggt aaa taa                           1326
Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440


<210> 4
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<213> Homo sapiens

<400> 4
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Pro Tyr
            20                  25                  30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Arg Ala Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125
Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190
Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205
Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
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        275                 280                 285
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
    290                 295                 300
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320
Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
                325                 330                 335
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
            340                 345                 350
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380
Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
                405                 410                 415
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            420                 425                 430
Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440


<210> 5
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<213> Homo sapiens

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<222> (1)...(318)
<223> light chain variable region

<220>
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<223> human kappa constant region

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gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gtt gga   48
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15

gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt agc tgg   96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
             20                  25                  30

ttg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc   144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

tat aag gcg tct agt tta gaa agt ggg gtc cca tca agg ttt agc ggc   192
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
     50                  55                  60

agt gga tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct   240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80
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gat gat ttt gca act tat tac tgc caa cag tat aat agt tac att ttt   288
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ile Phe
                 85                  90                  95

ggc cag ggg acc aag ctg gag atc aaa cgg act gtg gct gca cca tct   336
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
            100                 105                 110

gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc   384
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        115                 120                 125

tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta   432
Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130                 135                 140

cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt   480
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145                 150                 155                 160

gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc   528
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                165                 170                 175

ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc   576
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            180                 185                 190

gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac   624
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        195                 200                 205

agg gga gag tgt tag                                               639
Arg Gly Glu Cys
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<210> 6
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<213> Homo sapiens

<400> 6

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Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ile Phe
                85                  90                  95
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
            100                 105                 110
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        115                 120                 125
Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130                 135                 140
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145                 150                 155                 160
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                165                 170                 175
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            180                 185                 190
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
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195 200 205
Arg Gly Glu Cys
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<210> 7
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<220>
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<223> human IgG2 constant region

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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Pro Tyr
20 25 30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Arg Ala Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125
Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
130 135 140
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
180 185 190
Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
195 200 205
Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
210 215 220
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
260 265 270
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
290 295 300
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320
Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
325 330 335

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


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

<220>
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<223> HvCD37-6b15.1.1 light chain

<220>
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<220>
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<223> human kappa constant region

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Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ile Phe
                85                  90                  95
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
            100                 105                 110
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        115                 120                 125
Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130                 135                 140
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145                 150                 155                 160
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                165                 170                 175
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            180                 185                 190
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        195                 200                 205
Arg Gly Glu Cys
    210


<210> 9
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<211> 346
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(346)

<400> 9
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cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct tcg gag   48
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1               5                  10                  15

acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc agt cct tac   96
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Pro Tyr
             20                  25                  30

tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ttg gag tgg att   144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
         35                  40                  45

ggg gaa atc aat cat agt gga agc acc aac tac aac ccg tcc ctc aag   192
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
     50                  55                  60

agt cga gtc acc att tca gta gac acg tcc aag aac cag ttc tcc ctg   240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65                  70                  75                  80

aag ctg agc tct gtg acc gcc gcg gac acg gct gtc tat tac tgt gcg   288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                 85                  90                  95

agg aga gct ggg gac ttt gac tac tgg ggc cag gga acc ctg gtc acc   336
Arg Arg Ala Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

gtc tcc tca g                                                    346
Val Ser Ser
        115
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<213> Homo sapiens

<400> 10
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 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Pro Tyr
            20                  25                  30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Arg Ala Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser
        115
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 1               5                  10                  15

gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt agc tgg   96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
             20                  25                  30

ttg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc   144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

tat aag gcg tct agt tta gaa agt ggg gtc cca tca agg ttt agc ggc   192
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
     50                  55                  60

agt gga tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct   240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

gat gat ttt gca act tat tac tgc caa cag tat aat agt tac att ttt   288
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ile Phe
                 85                  90                  95

ggc cag ggg acc aag ctg gag atc aaa cgg                           318
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ile Phe
                85                  90                  95
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```