SEQUENCE LISTING

<110> Adicet Bio Inc.
JAKOBOVITS, Aya
FOORD, Orit
SATPAYEV, Daulet Kadyl
PELED KAMAR, Mira
DENKBERG, Galit
REITER, Yoram
BEER, Ilan
SINIK, Keren
TEBOUL (ELBAZ), Yael
SHPERBER (SERY), Yael
EREL SEGAL, Reut
OREN, Ravit
ALISHEKEVITZ, Dror Shmuel

<120> ANTIBODIES CAPABLE OF BINDING HLA-A2/TYRD IN AN HLA RESTRICTED MANNER AND USES THEREOF

<130> 70151

<160> 39

<170> PatentIn version 3.5

<210> 1
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Variable light chain

<400> 1
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca aggcgagtca ggacattcac aactatatag cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccactat acatccactt tgcaaccagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtctacag tatgataatc tctggacgtt cggtcaaggc 300

accaaggtgg aaatcaaacg g 321

<210> 2
<211> 107
<212> PRT
<213> Artificial sequence

<220>

<223> Variable light chain

<400> 2

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


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


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


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


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


Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp Thr
                85                  90                  95


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

<210> 3
<211> 366
<212> DNA
<213> Artificial sequence

<220>
<223> Variable heavy chain

<400> 3

```
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg       60

acctgcacct tctctgggtt ctcactcagc actagtggaa tgggtgtgtc ctggatccgt      120

cagcccccag gaaaggccct ggagtggctt gcacacattt attgggatga tgataagcgc      180

tacaacccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg      240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacgaaag      300

gactacggta gtagcttcta tgctatgcac tactggggtc aaggaaccct agtcaccgtc      360

tcgagt                                                                 366
```

<210> 4
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> Variable heavy chain

<400> 4

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Lys Asp Tyr Gly Ser Ser Phe Tyr Ala Met His Tyr Trp
100 105 110

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

<210> 5
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> CDR1 light chain

<400> 5

Lys Ala Ser Gln Asp Ile His Asn Tyr Ile Ala
1 5 10

<210> 6
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR2 light chain

<400> 6

Tyr Thr Ser Thr Leu Gln Pro
1 5

<210> 7
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> CDR3 light chain

<400> 7

Leu Gln Tyr Asp Asn Leu Trp Thr
1 5

<210> 8
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR1 Heavy chain

<400> 8

Thr Ser Gly Met Gly Val Ser
1 5

<210> 9
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> CDR2 Heavy chain

<400> 9

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

<210> 10
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> CDR3 Heavy chain

<400> 10

Lys Asp Tyr Gly Ser Ser Phe Tyr Ala Met His Tyr
1 5 10

<210> 11
<211> 639
<212> DNA
<213> Mus musculus

<400> 11
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcctgggcgg caaagtgacc 60

atcacatgca aggccagcca ggacatccac aactatatcg cctggtatca gcacaagccc 120

gtgaagggcc ccagactgct gatccactac accagcaccc tgcagcccgg cacccccctcc 180

agattttctg gcagcggctc cggcagagac tacagcttca gcatcagcaa cctggaaccc 240

gaggatatcg ccacctacta ctgcctgcag tacgacaacc tgtggacctt cggcggaggc 300

accaagctgg aaatcaagcg ggccgatgcc gcccctaccg tgtccatctt cccacccagc 360

tccgagcagc tgaccagcgg cggagccagc gtcgtgtgct tcctgaacaa cttctacccc 420

aaggacatca acgtgaagtg gaagatcgac ggcagcgagc ggcagaacgg cgtgctgaac 480

agctggaccg accaggacag caaggactcc acctacagca tgtccagcac actgaccctg 540

accaaggacg agtacgagag acacaactcc tatacctgcg aggccaccca caagacctcc 600

accagcccca tcgtgaagtc cttcaaccgg aacgagtgc 639

<210> 12
<211> 213
<212> PRT
<213> Mus musculus

<400> 12

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp Thr
                85                  90                  95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro
            100                 105                 110

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

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

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205
```

Asn Arg Asn Glu Cys
210

<210> 13
<211> 1341
<212> DNA
<213> Mus musculus

<400> 13
caagtcacac tgaaagagag cggccctggc atcctgcagc ccagccagac cctgagcctg 60

acctgcagct tcagcggctt ctccctgacc acctccggca tgggcgtgtc ctggatcaga 120

cagcctagcg gcaagggcct ggaatggctg gcccacatct actgggacga cgacaagcgg 180

tacaacccca gcctgaagtc ccggctgacc atcagcaagg acaccagccg gaaccaggtg 240

ttcctgaaga tcaccagcgt ggacgccgcc gacaccgcca cctactactg cgccagaaag 300

gactacggca gcagcttcta cgccatgcac tactggggcc agggcacctc cgtgaccgtg 360

tccagcgcca agaccacccc ccccagcgtg taccctctgg cccctggaag cgccgctcag 420

accaacagca tggtcaccct gggctgcctg gtcaagggct acttccccga gcccgtgaca 480

gtgacctgga acagcggcag cctgagcagc ggcgtgcaca cctttccagc cgtgctgcag 540

agcgacctgt acaccctgtc cagcagcgtc accgtgccca gcagcacctg gcccagcgaa 600

accgtgacct gtaacgtggc ccaccccgcc agctccacca aggtggacaa gaaaatcgtg 660

ccccgggact gcggctgcaa gccctgcatc tgcacagtgc ccgaggtgtc ctccgtgttc 720

atcttcccac ccaagcccaa ggacgtgctg acaatcaccc tgaccccaa agtgacatgc 780

gtggtggtgg acatctccaa ggatgaccca gaggtgcagt tcagttggtt cgtggacgac 840

gtggaagtgc acacagccca gacccagcct agagaggaac agttcaacag caccttcaga 900

agcgtgtccg agctgcccat catgcaccag gactggctga acggcaaaga attcaagtgc 960

agagtgaaca gcgccgcctt ccctgccccc atcgagaaaa ccatctctaa gaccaagggc 1020

agacccaagg cccctcaggt ctacaccatc ccccccaccta aagaacagat ggccaaggac 1080

aaggtgtccc tcacctgtat gatcaccgat ttcttcccag aggacatcac cgtcgagtgg 1140

cagtggaacg gccagcccgc cgagaactac aagaacaccc agccaatcat ggacaccgac 1200

ggcagctact tcgtgtacag caagctgaac gtgcagaagt ccaactggga ggccggcaac 1260

accttcacct gttctgtgct gcacgagggc ctgcacaacc accacaccga gaagtccctg 1320

tcccacagcc ccggcaagta a 1341

<210> 14
<211> 446
<212> PRT
<213> Mus musculus

<400> 14

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Lys Asp Tyr Gly Ser Ser Phe Tyr Ala Met His Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
115 120 125

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
130 135 140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
165 170 175

```
Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
            180                 185                 190

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
        195                 200                 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
    210                 215                 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
225                 230                 235                 240

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
                245                 250                 255

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
            260                 265                 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
        275                 280                 285

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
    290                 295                 300

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
305                 310                 315                 320

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
            340                 345                 350

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
        355                 360                 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
    370                 375                 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
385                 390                 395                 400
```

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
405 410 415

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

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> 15
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> TyrD 369-377 amino acid sequence

<400> 15

Tyr Met Asp Gly Thr Met Ser Gln Val
1 5

<210> 16
<211> 759
<212> PRT
<213> Artificial sequence

<220>
<223> ScFv CD3 nucleic acid sequence

<400> 16

Gly Ala Cys Ala Thr Cys Cys Ala Gly Ala Thr Gly Ala Cys Cys Cys
1 5 10 15

Ala Gly Ala Gly Cys Cys Cys Cys Ala Gly Cys Ala Gly Cys Cys Thr
20 25 30

Gly Ala Gly Cys Gly Cys Cys Ala Gly Cys Gly Thr Gly Gly Gly Cys
35 40 45

Gly Ala Cys Ala Gly Ala Gly Thr Gly Ala Cys Cys Ala Thr Cys Ala
50 55 60

```
Cys Cys Thr Gly Thr Cys Gly Gly Gly Cys Cys Ala Gly Cys Cys Ala
65                  70                  75                  80


Gly Gly Ala Cys Ala Thr Cys Cys Gly Gly Ala Ala Cys Thr Ala Cys
                85                  90                  95


Cys Thr Gly Ala Ala Cys Thr Gly Gly Thr Ala Thr Cys Ala Gly Cys
            100                 105                 110


Ala Gly Ala Ala Gly Cys Cys Cys Gly Gly Cys Ala Ala Gly Gly Cys
        115                 120                 125


Cys Cys Cys Cys Ala Ala Gly Cys Thr Gly Cys Thr Gly Ala Thr Cys
    130                 135                 140


Thr Ala Cys Thr Ala Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Cys
145                 150                 155                 160


Thr Gly Gly Ala Ala Ala Gly Cys Gly Gly Cys Gly Thr Gly Cys Cys
                165                 170                 175


Cys Ala Gly Cys Ala Gly Ala Thr Thr Cys Ala Gly Cys Gly Gly Cys
            180                 185                 190


Ala Gly Cys Gly Gly Cys Thr Cys Cys Gly Gly Cys Ala Cys Cys Gly
        195                 200                 205


Ala Cys Thr Ala Cys Ala Cys Cys Cys Thr Gly Ala Cys Cys Ala Thr
    210                 215                 220


Cys Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala Gly Cys Cys Cys
225                 230                 235                 240


Gly Ala Gly Gly Ala Cys Thr Thr Cys Gly Cys Cys Ala Cys Cys Thr
                245                 250                 255


Ala Cys Thr Ala Cys Thr Gly Cys Cys Ala Gly Cys Ala Gly Gly Gly
            260                 265                 270


Cys Ala Ala Cys Ala Cys Cys Cys Thr Gly Cys Cys Cys Thr Gly Gly
        275                 280                 285
```

```
Ala Cys Cys Thr Thr Cys Gly Gly Cys Cys Ala Ala Gly Gly Cys Ala
    290                 295                 300

Cys Cys Ala Ala Gly Gly Thr Gly Gly Ala Ala Ala Thr Cys Ala Ala
305                 310                 315                 320

Gly Gly Gly Cys Gly Gly Ala Gly Gly Cys Gly Gly Cys Thr Cys Thr
                325                 330                 335

Gly Gly Ala Gly Gly Cys Gly Gly Ala Gly Gly Ala Ala Gly Cys Gly
            340                 345                 350

Gly Ala Gly Gly Cys Gly Gly Ala Gly Gly Ala Thr Cys Thr Gly Gly
        355                 360                 365

Gly Gly Gly Ala Gly Gly Gly Gly Gly Ala Thr Cys Thr Gly Gly Cys
    370                 375                 380

Gly Gly Ala Gly Gly Cys Thr Cys Thr Gly Ala Gly Gly Thr Gly Cys
385                 390                 395                 400

Ala Gly Cys Thr Gly Gly Thr Gly Gly Ala Ala Thr Cys Cys Gly Gly
                405                 410                 415

Cys Gly Gly Ala Gly Gly Cys Cys Thr Gly Gly Thr Gly Cys Ala Gly
            420                 425                 430

Cys Cys Thr Gly Gly Cys Gly Gly Cys Ala Gly Cys Cys Thr Gly Ala
        435                 440                 445

Gly Ala Cys Thr Gly Thr Cys Thr Thr Gly Thr Gly Cys Cys Gly Cys
    450                 455                 460

Cys Ala Gly Cys Gly Gly Cys Thr Ala Cys Ala Gly Cys Thr Thr Cys
465                 470                 475                 480

Ala Cys Cys Gly Gly Cys Thr Ala Cys Ala Cys Cys Ala Thr Gly Ala
                485                 490                 495
```

```
Ala Cys Thr Gly Gly Gly Thr Cys Cys Gly Ala Cys Ala Ala Gly Cys
            500                 505                 510

Cys Cys Cys Thr Gly Gly Cys Ala Ala Gly Gly Gly Cys Cys Thr Gly
        515                 520                 525

Gly Ala Ala Thr Gly Gly Gly Thr Gly Gly Cys Cys Cys Thr Gly Ala
    530                 535                 540

Thr Cys Ala Ala Cys Cys Cys Cys Thr Ala Cys Ala Ala Gly Gly Gly
545                 550                 555                 560

Cys Gly Thr Gly Thr Cys Cys Ala Cys Cys Thr Ala Cys Ala Ala Cys
                565                 570                 575

Cys Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Gly Ala Cys Cys
            580                 585                 590

Gly Gly Thr Thr Cys Ala Cys Cys Ala Thr Cys Ala Gly Cys Gly Thr
        595                 600                 605

Gly Gly Ala Cys Ala Ala Gly Ala Gly Cys Ala Ala Gly Ala Ala Cys
    610                 615                 620

Ala Cys Cys Gly Cys Cys Thr Ala Cys Cys Thr Gly Cys Ala Gly Ala
625                 630                 635                 640

Thr Gly Ala Ala Cys Ala Gly Cys Cys Thr Gly Ala Gly Ala Gly Cys
                645                 650                 655

Cys Gly Ala Gly Gly Ala Cys Ala Cys Cys Gly Cys Cys Gly Thr Gly
            660                 665                 670

Thr Ala Cys Thr Ala Cys Thr Gly Cys Gly Cys Cys Ala Gly Ala Ala
        675                 680                 685

Gly Cys Gly Gly Cys Thr Ala Cys Thr Ala Cys Gly Gly Cys Gly Ala
    690                 695                 700

Cys Ala Gly Cys Gly Ala Cys Thr Gly Gly Thr Ala Cys Thr Thr Cys
705                 710                 715                 720
```

```
Gly Ala Cys Gly Thr Gly Thr Gly Gly Gly Gly Cys Cys Ala Gly Gly
                725                 730                 735


Gly Ala Ala Cys Cys Cys Thr Gly Gly Thr Cys Ala Cys Cys Gly Thr
            740                 745                 750


Gly Thr Cys Thr Ala Gly Cys
        755


<210>  17
<211>  253
<212>  PRT
<213>  Artificial sequence

<220>
<223>  ScFv CD3 amino acid sequence

<400>  17

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


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


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


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


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


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


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
```

```
Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
    130                 135                 140

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe
145                 150                 155                 160

Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn
            180                 185                 190

Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn
        195                 200                 205

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    210                 215                 220

Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe
225                 230                 235                 240

Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                245                 250
```

<210> 18
<211> 639
<212> DNA
<213> Artificial sequence

<220>
<223> Light chain D11 in BS nucleic acid sequence

<400> 18

```
gatattcaga tgacccagtc tcctagctct ctgtctgcca gcctcggcgg caaagtgaca       60

atcacatgca aggcctctca ggatatccac aactatatcg cctggtatca acacaaaccc      120

gtgaagggac ccagactgct gattcactat acaagcaccc tgcagccagg cacacctagc      180

agattcagcg gaagcggcag cggaagagac tactccttca gcatcagcaa cctggaacca      240

gaggacattg ccacatatta ctgcctgcag tacgacaacc tgtggacctt cggaggcgga      300

acaaagctcg agatcaagag aacagtggcc gctcctagcg tgttcatctt cccaccaagc      360
```

gacgagcagc tgaagtctgg cacagcctct gtcgtgtgcc tgctgaacaa cttctacccc 420

agagaagcca aggtgcagtg gaaggtggac aatgccctgc agagcggcaa tagccaagag 480

agcgtgaccg agcaggacag caaggatagc acctatagcc tgagcagcac actgaccctg 540

agcaaggccg actacgagaa gcacaaagtg tacgcctgcg aagtgacaca ccagggactg 600

agcagccctg tgaccaagag cttcaacaga ggcgagtgc 639

<210> 19
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain D11 in BS amino acid sequence

<400> 19

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp 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> 20
<211> 675
<212> DNA
<213> Artificial sequence

<220>
<223> VHCH1 in BS nucleic acis sequence

<400> 20
cagatcaccc tgaaagaatc tggccctaca ctggtcaagc ccacacagac cctgacactg 60

acctgcacct ttagcggctt tagcctgagc acaagcggca tgggagtgtc ctggattaga 120

cagcctcctg gaaaggccct cgaatggctg gcccacatct actgggacga cgacaagaga 180

tacaacccca gcctgaagtc ccggctgaca atcaccaagg acaccagcaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccctgtg gacaccgcta cctactattg cgcccggaag 300

gattacggca gcagcttcta cgccatgcac tactggggac agggcacact cgtgacagtg 360

tctagcgcct ctacaaaggg ccctagcgtt ttcccactgg ctcctagcag caagtctaca 420

agcggaggaa cagccgctct gggctgcctg gtcaaggatt actttcctga gcctgtgacc 480

gtgtcttgga actctggtgc tctgacctcc ggcgtgcaca catttccagc cgtgctgcag 540

tctagcggcc tgtactctct gagcagcgtt gtgacagtgc caagctctag cctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag cctagcaaca ccaaggtcga caagaaggtg 660

gaacccaaga gctgc 675

<210> 21
<211> 225
<212> PRT
<213> Artificial sequence

<220>
<223> VHCH1 in BS amino acid sequence

<400> 21

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Lys Asp Tyr Gly Ser Ser Phe Tyr Ala Met His Tyr Trp
100 105 110

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

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

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

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

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys
225

<210> 22
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> CDR1 light chain nucleic acid sequence

<400> 22
aaggcgagtc aggacattca caactatata gct 33

<210> 23
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> CDR2 light chain nucleic acid sequence

<400> 23
tatacatcca ctttgcaacc a 21

<210> 24
<211> 639
<212> DNA
<213> Artificial sequence

<220>
<223> hD11-5 Full length light chain nucleic acid sequence

<400> 24
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca aggcgagtca ggacattcac aactatatag cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccactat acatccactt tgcaaccagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtctacag tatgataatc tctggacgtt cggtcaaggc 300

accaaggtgg aaatcaaacg gaccgtggcc gcacctagtg tgttcatctt ccctccctcc 360

gacgagcagc tgaagtctgg caccgcctcc gtggtctgcc tgctgaacaa cttctaccct 420

cgggaggcca aggtgcagtg gaaggtggac aacgccctgc agtccggcaa ctcccaggaa 480

tccgtcaccg agcaggactc caaggactct acctactccc tgtcctccac cctgaccctg 540

tccaaggccg actacgagaa gcacaaggta tacgcctgcg aggtcaccca ccagggcctg 600

tcctctcccg tcaccaagtc cttcaaccgg ggcgagtgc 639

<210> 25
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> hD11-5 Full length light chain amino acid sequence

<400> 25

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp Thr
85 90 95

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


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


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


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


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


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


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


Asn Arg Gly Glu Cys
    210
```

<210> 26
<211> 1353
<212> DNA
<213> Artificial sequence

<220>
<223> hD11-5 Full length heavy chain nucleic acid sequence

<400> 26

```
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg       60

acctgcacct tctctgggtt ctcactcagc actagtggaa tgggtgtgtc ctggatccgt      120

cagcccccag gaaaggccct ggagtggctt gcacacattt attgggatga tgataagcgc      180

tacaacccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg      240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacgaaag      300

gactacggta gtagcttcta tgctatgcac tactggggtc aaggaaccct agtcaccgtc      360
```

tcgagtgcct ctaccaaggg cccttccgtg ttccctctgg cccccagctc gaagtccacc 420

tccggcggca ccgccgctct gggctgcctg gtcaaggact acttccctga gcctgtgaca 480

gtgtcctgga actctggcgc tctgacctct ggcgtgcata ccttccctgc cgtgctgcag 540

tcctccggcc tgtactccct gtcctctgtg gtcacagtgc cttcctcctc cctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag ccttccaaca ccaaggtgga caagaaggtg 660

gagcctaagt cctgcgacaa gacccacacc tgtcctccct gccctgctcc tgagctgctg 720

ggcggaccct ccgtgttcct gttccctcct aagcctaagg acaccctgat gatctcccgg 780

acccctgagg tcacctgtgt ggtggtggat gtgtcccacg aggatcctga ggtcaagttc 840

aattggtacg tggacggcgt ggaggtgcac aacgccaaga caaagccacg cgaggaacag 900

tacaactcca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960

ggcaaagagt acaagtgcaa ggtctccaac aaggccctgc ctgccccat cgagaaaacc 1020

atctccaagg ccaagggaca gcctcgcgag cctcaggtgt acaccctgcc tccctctcgg 1080

gatgaactga ccaagaatca ggtgtccctg acatgtctgg tcaagggctt ctacccttcc 1140

gatatcgccg tggagtggga gtccaacggc cagcctgaga acaactacaa gaccacccct 1200

cctgtgctgg actccgacgg ctctttcttc ctgtactcca agctgaccgt ggacaagtcc 1260

cggtggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaaccac 1320

tacacccaga agtctctgtc cctctctccc ggc 1353

<210> 27
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> hD11-5 Full length heavy chain amino acid sequence

<400> 27

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
    50                  55                  60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Lys Asp Tyr Gly Ser Ser Phe Tyr Ala Met His Tyr Trp
            100                 105                 110

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

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

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

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

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly
    450
```

<210> 28
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> CDR3 light chain nucleic acid sequence

<400> 28
ctacagtatg ataatctctg gacg 24

<210> 29
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> CDR1 Heavy chain nucleic acid sequence

<400> 29
actagtggaa tgggtgtgtc c 21

<210> 30
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> CDR2 Heavy chain nucleic acid sequence

<400> 30
cacatttatt gggatgatga taagcgctac aacccatctc tgaagagc 48

<210> 31
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> CDR3 Heavy chain nucleic acid sequence

<400> 31
aaggactacg gtagtagctt ctatgctatg cactac 36

<210> 32
<211> 15
<212> DNA
<213> Artificial sequence

<220>

<223> Connector between anti CD3 to D11 VL nucleic acid sequence

<400> 32
ggcggtggcg gaagc 15

<210> 33
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Connector between anti CD3 to D11 VL amino acid sequence

<400> 33

Gly Gly Gly Gly Ser
1 5

<210> 34
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Mouse IgH signal sequence - leader sequence for expression in pCDNA3.4

<400> 34
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactcc 57

<210> 35
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Mouse IgH signal sequence - leader sequence for expression in pCDNA3.4

<400> 35

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

Val His Ser

<210> 36
<211> 60

<212> DNA
<213> Artificial sequence

<220>
<223> Leader sequence for expression in pCI Light chain

<400> 36
atggagacag acacactcct gctatgggta ctgctgctct gggtcccggg atccactggt 60

<210> 37
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Leader sequence for expression in pCI Light chain

<400> 37

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> 38
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Leader sequence for expression in pCI Heavy chain

<400> 38
atggaatggt cctgggtgtt cctgttcttc ctgtccgtga ccaccggtgt gcactcc 57

<210> 39
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Leader sequence for expression in pCI Heavy chain

<400> 39

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

Val His Ser