SEQUENCE LISTING

<110> MacroGenics, Inc.
Moore, Paul
Li, Jonathan
Chen, Francine
Johnson, Leslie
Shah, Kalpana
Bonvini, Ezio

<120> Bi-Specific Monovalent Diabodies That Are Capable Of Binding to gpA33 And CD3, And Uses Thereof

<130> 1301.0112PCT

<150> US 61/869,528
<151> 2013-08-23

<150> US 61/907,691
<151> 2013-11-22

<150> EP 13198859
<151> 2013-12-20

<160> 57

<170> PatentIn version 3.5

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Gly Gly Gly Ser Gly Gly Gly Gly
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Gly Gly Cys Gly Gly Gly
1 5

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Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

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Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

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<223> Light Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 5

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

```
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
    50                  55                  60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> CDR1 of Light Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 6

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Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10
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<222> (1)..(7)
<223> CDR2 of Light Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 7

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Gly Thr Asn Lys Arg Ala Pro
1               5
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<213> Mus musculus

<220>
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<223> CDR3 of Light Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 8

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 9
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<223> Heavy Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 9

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

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

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

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<220>
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<222> (1)..(5)
<223> CDR1 of Heavy Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 10

Thr Tyr Ala Met Asn
1 5

<210> 11
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<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(19)
<223> CDR2 of Heavy Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 11

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

Val Lys Asp

<210> 12
<211> 14
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(14)
<223> CDR3 of Heavy Chain Variable Domain of Murine Anti-CD3 Antibody

<400> 12

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 13
<211> 106
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Light Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 13

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

Glu Arg Val Thr Met Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met
20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr
                85                  90                  95

Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
            100                 105
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<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(10)
<223> CDR1 of Light Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 14

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Ser Ala Arg Ser Ser Ile Ser Phe Met Tyr
1               5                   10
```

<210> 15
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(7)
<223> CDR2 of Light Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 15

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Asp Thr Ser Asn Leu Ala Ser
1               5
```

<210> 16
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<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)

<223> CDR3 of Light Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 16

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> 17
<211> 119
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(119)
<223> Heavy Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 17

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

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

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

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

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 18
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> CDR1 of Heavy Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 18

Gly Ser Trp Met Asn
1 5

<210> 19
<211> 17
<212> PRT
<213> Mus musculus

<220>
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<223> CDR2 of Heavy Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 19

Arg Ile Tyr Pro Gly Asp Gly Glu Thr Asn Tyr Asn Gly Lys Phe Lys
1 5 10 15

Asp

<210> 20
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<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> CDR3 of Heavy Chain Variable Domain of Murine Anti-gpA33 Antibody

<400> 20

Ile Tyr Gly Asn Asn Val Tyr Phe Asp Val
1 5 10

<210> 21
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART-1

<400> 21

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

```
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
    50                  55                  60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
        115                 120                 125

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
    130                 135                 140

Tyr Thr Phe Ser Gly Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
145                 150                 155                 160

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Glu Thr
                165                 170                 175

Asn Tyr Asn Gly Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
            180                 185                 190

Ser Ser Thr Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Val Asp
        195                 200                 205

Ser Ala Val Tyr Phe Cys Ala Arg Ile Tyr Gly Asn Asn Val Tyr Phe
    210                 215                 220

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys
225                 230                 235                 240

Gly Gly Gly Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
                245                 250                 255

Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
            260                 265                 270
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<210> 22
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding First Polypeptide Chain of DART-1

<400> 22
caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg 60

acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag 120

aagccaggac aggcaccaag gggcctgatc gggggtacaa acaaaagggc tccctggacc 180

cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca 240

caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc 300

gggggtggca caaaactgac tgtgctggga ggtggtggat ccggcggagg tggacaggtc 360

cagctgcagc agtctggacc tgagctggtg aagcctgggg cctcagtgaa gatttcctgc 420

aaagcttcag gctacacatt cagtggctct tggatgaact gggtgaagca gaggcctgga 480

cagggtcttg agtggattgg acggatctac cctggagatg gagaaactaa ctacaatggg 540

aagtttaagg acaaggccac actgactgca gacaaatcat ccaccacagc ctacatggag 600

ctcagcagcc tgacctctgt ggactctgcg gtctatttct gtgcaagaat ctatggtaat 660

aacgtttact tcgatgtctg gggcgcaggg accacggtca ccgtgtcttc cggaggatgt 720

ggcggtggag aagtggccgc actggagaaa gaggttgctg ctttggagaa ggaggtcgct 780

gcacttgaaa aggaggtcgc agccctggag aaa 813

<210> 23
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of DART-1

<400> 23

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

Glu Arg Val Thr Met Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met
20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80

```
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr
                85                  90                  95

Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly
            100                 105                 110

Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
        115                 120                 125

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    130                 135                 140

Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
145                 150                 155                 160

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
                165                 170                 175

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
            180                 185                 190

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
        195                 200                 205

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val
    210                 215                 220

Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240

Gly Gly Cys Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala
                245                 250                 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu
            260                 265                 270

Lys Glu
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<210> 24
<211> 822
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding Second Polypeptide Chain of DART-1

<400> 24
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gagggtcacc 60

atgacctgca gtgccaggtc aagtataagt ttcatgtact ggtaccagca gaagccagga 120

tcctccccca gactcctgat ttatgacaca tccaacctgg cttctggagt ccctgttcgc 180

ttcagtggca gtgggtctgg gacctcttat tctctcacaa tcagccgaat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg agtagttacc cactcacgtt cggttctggg 300

accaagctgg agctgaaacg gggtggagga tccggcggag gcggagaggt gcagctggtg 360

gagtctgggg gaggcttggt ccagcctgga gggtccctga gactctcctg tgcagcctct 420

ggattcacct tcaacacata cgctatgaat tgggtccgcc aggctccagg gaaggggctg 480

gagtgggttg caaggatcag gtccaagtac aacaattatg caacctacta tgccgactct 540

gtgaaggata gattcaccat ctcaagagat gattcaaaga actcactgta tctgcaaatg 600

aacagcctga aaaccgagga cacggccgtg tattactgtg tgagacacgg taacttcggc 660

aattcttacg tgtcttggtt tgcttattgg ggacagggga cactggtgac tgtgtcttcc 720

ggaggatgtg gcggtggaaa agtggccgca ctgaaggaga aagttgctgc tttgaaagag 780

aaggtcgccg cacttaagga aaaggtcgca gccctgaaag ag 822

<210> 25
<211> 125
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(125)
<223> Heavy Chain Variable Domain of Anti-CD3 Antibody

<400> 25

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

```
Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 26
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain Variable Domain of Humanized Anti-gpA33 Antibody

<400> 26

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

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met
            20                  25                  30

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

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

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 27
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain Variable Domain of Humanized Anti-gpA33 Antibody

<400> 27

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

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

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

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

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

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

Ala Arg Ile Tyr Gly Asn Asn Val Tyr Phe Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser
        115
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<210> 28
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART-2

<400> 28

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
    50                  55                  60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu
        115                 120                 125
```

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Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
    130                 135                 140

Tyr Thr Phe Thr Gly Ser Trp Met Asn Trp Val Arg Gln Ala Pro Gly
145                 150                 155                 160

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Glu Thr
                165                 170                 175

Asn Tyr Asn Gly Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
            180                 185                 190

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
        195                 200                 205

Thr Ala Val Tyr Tyr Cys Ala Arg Ile Tyr Gly Asn Asn Val Tyr Phe
    210                 215                 220

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys
225                 230                 235                 240

Gly Gly Gly Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
                245                 250                 255

Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
            260                 265                 270
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<210> 29
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding First Polypeptide Chain of DART-2

<400> 29
caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg 60

acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag 120

aagccaggac aggcaccaag gggcctgatc gggggtacaa acaaaagggc tccctggacc 180

cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca 240

caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc 300

gggggtggca caaaactgac tgtgctggga ggtggtggat ccggcggagg tggacaggtc 360

cagctggtcc agagcggggc cgaagtcaaa aaacccggag caagcgtgaa ggtctcctgc 420

aaagcatcag gctatacatt tacaggcagc tggatgaact gggtgaggca ggctccagga 480

cagggactgg agtggatcgg gcgcatctac cctggagacg gcgaaactaa ctataatgga 540

aagttcaaag accgagtgac catcacagcc gataagtcta ctagtaccgc ctacatggag 600

ctgagctccc tgcggtctga agataccgcc gtctactatt gcgctagaat ttacggaaac 660

aatgtctatt ttgacgtgtg ggggcaggga acaactgtga ctgtctcctc cggaggatgt 720

ggcggtggag aagtggccgc actggagaaa gaggttgctg ctttggagaa ggaggtcgct 780

gcacttgaaa aggaggtcgc agccctggag aaa 813

<210> 30
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of DART-2

<400> 30

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

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met
20 25 30

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

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

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr
85 90 95

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

Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
130 135 140

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145 150 155 160

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
165 170 175

```
Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
            180                 185                 190

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
        195                 200                 205

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
    210                 215                 220

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
225                 230                 235                 240

Gly Cys Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala
                245                 250                 255

Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys
            260                 265                 270

Glu
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<210> 31
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding Second Polypeptide Chain of DART-2

<400> 31
gacattcagc tgactcagtc cccctctttt ctgtccgcat ccgtcggaga tcgagtgact 60

attacttgct ctgctaggtc ctcaatcagc ttcatgtact ggtatcagca gaagcccggc 120

aaagcaccta agctgctgat ctacgacaca agcaacctgg cctccggggt gccatctcgg 180

ttctctggca gtgggtcagg aactgagttt accctgacaa ttagctccct ggaggctgaa 240

gatgccgcta cctactattg ccagcagtgg agcagctatc ctctgacctt cggacagggg 300

actaaactgg aaatcaaggg tggaggatcc ggcggcggag gcgaggtgca gctggtggag 360

tctgggggag gcttggtcca gcctggaggg tccctgagac tctcctgtgc agcctctgga 420

ttcaccttca gcacatacgc tatgaattgg gtccgccagg ctccagggaa ggggctggag 480

tgggttggaa ggatcaggtc caagtacaac aattatgcaa cctactatgc cgactctgtg 540

aaggatagat tcaccatctc aagagatgat tcaaagaact cactgtatct gcaaatgaac 600

agcctgaaaa ccgaggacac ggccgtgtat tactgtgtga gacacggtaa cttcggcaat 660

tcttacgtgt cttggtttgc ttattgggga caggggacac tggtgactgt gtcttccgga 720

ggatgtggcg gtggaaaagt ggccgcactg aaggagaaag ttgctgcttt gaaagagaag 780

gtcgccgcac ttaaggaaaa ggtcgcagcc ctgaaagag 819

<210> 32
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3 Polypeptide

<400> 32

Gly Gly Gly Ser
1

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

<220>
<223> Linker 3 Polypeptide

<400> 33

Gly Gly Gly Asn Ser
1 5

<210> 34
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Albumin Binding Domain

<400> 34

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

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asp Asn Ala Lys Ser Ala Glu
20 25 30

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 35
<211> 321

<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART-2 w/ABD

<400> 35

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu
115 120 125

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
130 135 140

Tyr Thr Phe Thr Gly Ser Trp Met Asn Trp Val Arg Gln Ala Pro Gly
145 150 155 160

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Glu Thr
165 170 175

Asn Tyr Asn Gly Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
180 185 190

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
195 200 205

Thr Ala Val Tyr Tyr Cys Ala Arg Ile Tyr Gly Asn Asn Val Tyr Phe
210 215 220

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys
225 230 235 240

```
Gly Gly Gly Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
                245                 250                 255

Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly
            260                 265                 270

Gly Gly Ser Leu Ala Gln Ala Lys Glu Ala Ala Ile Arg Glu Leu Asp
        275                 280                 285

Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asp Asn Ala Lys
    290                 295                 300

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

Pro
```

<210> 36
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding First Polypeptide Chain of DART-2 w/ABD

<400> 36

```
caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg       60

acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag      120

aagccaggac aggcaccaag gggcctgatc gggggtacaa acaaaagggc tccctggacc      180

cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca      240

caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc      300

gggggtggca caaaactgac tgtgctggga gggggtggat ccggcggagg tggacaggtc      360

cagctggtcc agagcggggc cgaagtcaaa aaacccggag caagcgtgaa ggtctcctgc      420

aaagcatcag gctatacatt tacaggcagc tggatgaact gggtgaggca ggctccagga      480

cagggactgg agtggatcgg gcgcatctac cctggagacg gcgaaactaa ctataatgga      540

aagttcaaag accgagtgac catcacagcc gataagtcta ctagtaccgc ctacatggag      600

ctgagctccc tgcggtctga agataccgcc gtctactatt gcgctagaat ttacggaaac      660

aatgtctatt ttgacgtgtg ggggcaggga acaactgtga ctgtctcctc cggaggatgt      720

ggcggtggag aagtggccgc actggagaaa gaggttgctg ctttggagaa ggaggtcgct      780
```

gcacttgaaa aggaggtcgc agccctggag aaaggcggcg ggtctctggc ccaggcaaaa 840

gaggcagcca tccgcgaact ggataaatat ggcgtgagcg attattataa gaacctgatt 900

gacaacgcaa aatccgcgga aggcgtgaaa gcactgattg atgaaattct ggccgccctg 960

cct 963

<210> 37
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 4 Polypeptide

<400> 37

Ala Pro Ser Ser Ser
1 5

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 4 Polypeptide

<400> 38

Ala Pro Ser Ser Ser Pro Met Glu
1 5

<210> 39
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide 1

<400> 39

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 40
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2 and CH3 Domains of Modified Fc Domain of First DART Polypeptide Chain

<400> 40

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 41
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2 and CH3 Domains of Modified Fc Domain of Third DART Polypeptide Chain

<400> 41

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 42
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 42

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

Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met
            20                  25                  30

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

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

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr
                85                  90                  95

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

Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
        115                 120                 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
    130                 135                 140

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145                 150                 155                 160

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
                165                 170                 175

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
            180                 185                 190

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
        195                 200                 205

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
    210                 215                 220

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
225                 230                 235                 240

Gly Cys Gly Gly Gly Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala
                245                 250                 255
```

```
Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
            260                 265                 270

Lys Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
        275                 280                 285

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
    290                 295                 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
305                 310                 315                 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                325                 330                 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            340                 345                 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
        355                 360                 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
    370                 375                 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
385                 390                 395                 400

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
                405                 410                 415

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
            420                 425                 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
        435                 440                 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
    450                 455                 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465                 470                 475                 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                485                 490                 495

Leu Ser Leu Ser Pro Gly Lys
            500
```

<210> 43
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding First Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 43

gacattcagc tgactcagtc cccctctttt ctgtccgcat ccgtcggaga tcgagtgact 60

attacttgct ctgctaggtc ctcaatcagc ttcatgtact ggtatcagca gaagcccggc 120

aaagcaccta agctgctgat ctacgacaca agcaacctgg cctccggggt gccatctcgg 180

ttctctggca gtgggtcagg aactgagttt accctgacaa ttagctccct ggaggctgaa 240

gatgccgcta cctactattg ccagcagtgg agcagctatc ctctgacctt cggacagggg 300

actaaactgg aaatcaaggg tggaggatcc ggcggcggag gcgaggtgca gctggtggag 360

tctgggggag gcttggtcca gcctggaggg tccctgagac tctcctgtgc agcctctgga 420

ttcaccttca gcacatacgc tatgaattgg gtccgccagg ctccagggaa ggggctggag 480

tgggttggaa ggatcaggtc caagtacaac aattatgcaa cctactatgc cgactctgtg 540

aaggatagat tcaccatctc aagagatgat tcaaagaact cactgtatct gcaaatgaac 600

agcctgaaaa ccgaggacac ggccgtgtat tactgtgtga gacacggtaa cttcggcaat 660

tcttacgtgt cttggtttgc ttattgggga caggggacac tggtgactgt gtcttccgga 720

ggatgtggcg gtggagaagt ggccgcactg gagaaagagg ttgctgcttt ggagaaggag 780

gtcgctgcac ttgaaaagga ggtcgcagcc ctggagaaag gcggcgggga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggggggac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1260

ctgtggtgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtaaa 1509

<210> 44
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 44

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu
115 120 125

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
130 135 140

Tyr Thr Phe Thr Gly Ser Trp Met Asn Trp Val Arg Gln Ala Pro Gly
145 150 155 160

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Glu Thr
165 170 175

Asn Tyr Asn Gly Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
180 185 190

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
195 200 205

```
Thr Ala Val Tyr Tyr Cys Ala Arg Ile Tyr Gly Asn Asn Val Tyr Phe
    210                 215                 220

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys
225                 230                 235                 240

Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys
                245                 250                 255

Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
            260                 265                 270
```

<210> 45
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Molecule Encoding Second Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 45

```
caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg       60

acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag      120

aagccaggac aggcaccaag gggcctgatc gggggtacaa acaaaagggc tccctggacc      180

cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca      240

caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc      300

gggggtggca caaaactgac tgtgctggga gggggtggat ccggcggagg tggacaggtc      360

cagctggtcc agagcggggc cgaagtcaaa aaacccggag caagcgtgaa ggtctcctgc      420

aaagcatcag gctatacatt tacaggcagc tggatgaact gggtgaggca ggctccagga      480

cagggactgg agtggatcgg gcgcatctac cctggagacg gcgaaactaa ctataatgga      540

aagttcaaag accgagtgac catcacagcc gataagtcta ctagtaccgc ctacatggag      600

ctgagctccc tgcggtctga agataccgcc gtctactatt gcgctagaat ttacggaaac      660

aatgtctatt ttgacgtgtg ggggcaggga acaactgtga ctgtctcctc cggaggatgt      720

ggcggtggaa aagtggccgc actgaaggag aaagttgctg ctttgaaaga gaaggtcgcc      780

gcacttaagg aaaaggtcgc agccctgaaa gag                                   813
```

<210> 46
<211> 227
<212> PRT

<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 46

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 47

<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid Molecule Encoding Third Polypeptide Chain of DART-2 w/Fc Version 1 Construct

<400> 47
gacaaaactc acacatgccc accgtgccca gcacctgaag ccgcgggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 420

aaccaggtca gcctgagttg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcgt cagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accgctacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 48
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART-2 w/Fc Version 2 Construct

<400> 48

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Ala Pro Ser Ser Ser Pro Met Glu Asp Ile Gln Leu Thr
225                 230                 235                 240

Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
                245                 250                 255

Thr Cys Ser Ala Arg Ser Ser Ile Ser Phe Met Tyr Trp Tyr Gln Gln
            260                 265                 270

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Thr Ser Asn Leu
        275                 280                 285

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
    290                 295                 300

Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr
305                 310                 315                 320

Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr
                325                 330                 335
```

```
Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Gln
            340                 345                 350

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
        355                 360                 365

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn
    370                 375                 380

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile
385                 390                 395                 400

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
                405                 410                 415

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu
            420                 425                 430

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
        435                 440                 445

Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
    450                 455                 460

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
465                 470                 475                 480

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
                485                 490                 495

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
            500                 505

<210>  49
<211>  198
<212>  PRT
<213>  Macaca fascicularis

<220>
<221>  MISC_FEATURE
<222>  (1)..(198)
<223>  V35 allele (FN18+) of CD3 epsilon

<400>  49

Met Gln Ser Gly Thr Arg Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1               5                   10                  15

Ile Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr
            20                  25                  30
```

```
Gln Thr Pro Tyr Gln Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
        35                  40                  45

Cys Ser Gln His Leu Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys
    50                  55                  60

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

Met Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly Ser Asn Pro
                85                  90                  95

Glu Asp Ala Ser His His Leu Tyr Leu Lys Ala Arg Val Cys Glu Asn
            100                 105                 110

Cys Met Glu Met Asp Val Met Ala Val Ala Thr Ile Val Ile Val Asp
        115                 120                 125

Ile Cys Ile Thr Leu Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys
    130                 135                 140

Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly
145                 150                 155                 160

Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn
                165                 170                 175

Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Gln Asp Leu Tyr Ser Gly
            180                 185                 190

Leu Asn Gln Arg Arg Ile
        195

<210>  50
<211>  171
<212>  PRT
<213>  Macaca fascicularis

<220>
<221>  MISC_FEATURE
<222>  (1)..(171)
<223>  CD3 delta

<400>  50

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

Ser Gln Val Ser Pro Phe Lys Ile Pro Val Glu Glu Leu Glu Asp Arg
            20                  25                  30

Val Phe Val Lys Cys Asn Thr Ser Val Thr Trp Val Glu Gly Thr Val
        35                  40                  45
```

```
Gly Thr Leu Leu Thr Asn Asn Thr Arg Leu Asp Leu Gly Lys Arg Ile
    50                  55                  60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
65                  70                  75                  80

Asp Lys Glu Ser Ala Val Gln Val His Tyr Arg Met Cys Gln Asn Cys
                85                  90                  95

Val Glu Leu Asp Pro Ala Thr Leu Ala Gly Ile Ile Val Thr Asp Val
            100                 105                 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
        115                 120                 125

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
    130                 135                 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
145                 150                 155                 160

Ser Arg Leu Gly Gly Asn Trp Ala Arg Asn Lys
                165                 170
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<210> 51
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(207)
<223> CD3 epsilon

<400> 51

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Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1               5                   10                  15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
            20                  25                  30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
    50                  55                  60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65                  70                  75                  80
```

```
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
                85                  90                  95

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

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
        115                 120                 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
    130                 135                 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145                 150                 155                 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
                165                 170                 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
            180                 185                 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
        195                 200                 205
```

<210> 52
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(150)
<223> CD3 delta

<400> 52

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Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1               5                   10                  15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
            20                  25                  30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
        35                  40                  45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
    50                  55                  60

Val Gln Val His Tyr Arg Met Cys Gln Ser Cys Val Glu Leu Asp Pro
65                  70                  75                  80

Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val Ile Ala Thr Leu Leu
                85                  90                  95
```

```
Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His Glu Thr Gly Arg Leu
            100                 105                 110

Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg Asn Asp Gln Val Tyr
        115                 120                 125

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

Asn Trp Ala Arg Asn Lys
145                 150
```

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6His Peptide

<400> 53

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His His His His His His
1               5
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<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 54

```
Gly Val Glu Pro Lys Ser Cys
1               5
```

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 55

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Val Glu Pro Lys Ser Cys
1               5
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<210> 56

<211> 7
<212> PRT
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<220>
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<400> 56

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 57
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 57

Phe Asn Arg Gly Glu Cys
1 5