SEQUENCE LISTING

<110> MacroGenics, Inc.
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Moore, Paul
Liu, Liqin
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<120> Bi-Specific Monovalent Diabodies That Are Capable of Binding CD19 and CD3, and Uses Thereof

<130> 1301.0116PCT

<150> US 62/0255,695
<151> 2014-09-26

<160> 48

<170> PatentIn version 3.5

<210> 1
<211> 8
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<223> Intervening Spacer Peptide (Linker 1)

<400> 1

Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 2
<211> 5
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<220>
<223> Linker 2

<400> 2

Ala Ser Thr Lys Gly
1 5

<210> 3
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<220>
<223> Cysteine-Containing Linker

<400> 3

Gly Gly Cys Gly Gly Gly
1 5

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<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(10)
<223> IgG1 Hinge Domain

<400> 4

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

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<220>
<223> Spacer-Linker 3

<400> 5

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

<210> 6
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<220>
<223> Heterodimer-Promoting Domain

<400> 6

Gly Val Glu Pro Lys Ser Cys
1 5

<210> 7
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<400> 7

Val Glu Pro Lys Ser Cys
1 5

<210> 8
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<220>
<223> Heterodimer-Promoting Domain

<400> 8

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 9
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<220>
<223> Heterodimer-Promoting Domain

<400> 9

Phe Asn Arg Gly Glu Cys
1 5

<210> 10
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> E-coil Heterodimer-Promoting Domain

<400> 10

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

<210> 11
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> K-coil Heterodimer-Promoting Domain

<400> 11

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

<210> 12
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<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing E-coil Heterodimer-Promoting Domain

<400> 12

Glu Val Ala Ala Cys 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

<210> 13
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<223> Cysteine-Containing K-coil Heterodimer-Promoting Domain

<400> 13

Lys Val Ala Ala Cys 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

<210> 14
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
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<223> CH2-CH3 Domain of Human IgG1

<400> 14

Ala Pro Glu Leu Leu 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 Thr 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> 15
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> "Knob-Bearing" CH2-CH3 Domain

<400> 15

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> 16
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> "Hole-Bearing" CH2-CH3 Domain

<400> 16

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> 17
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Light Chain of Anti-CD19 Antibody

<400> 17

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

Glu Lys Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

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

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

Gly Ser Gly Thr Asp His Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Val Tyr Pro Phe Thr
85 90 95

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

<210> 18
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of Variable Light Chain of Anti-CD19 Antibody

<400> 18

Arg Ala Ser Gln Ser Val Ser Tyr Met His
1 5 10

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of Variable Light Chain of Anti-CD19 Antibody

<400> 19

Asp Ala Ser Asn Arg Ala Ser
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of Variable Light Chain of Anti-CD19 Antibody

<400> 20

Phe Gln Gly Ser Val Tyr Pro Phe Thr
1 5

<210> 21
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Chain of Anti-CD19 Antibody

<400> 21

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

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

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

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

Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 22
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of Variable Heavy Chain of Anti-CD19 Antibody

<400> 22

Thr Ser Gly Met Gly Val Gly
1 5

<210> 23
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of Variable Heavy Chain of Anti-CD19 Antibody

<400> 23

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

<210> 24
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of Variable Heavy Chain of Anti-CD19 Antibody

<400> 24

Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 25
<211> 110
<212> PRT
<213> Artificial Sequence

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

<400> 25

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

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of Variable Light Chain of Anti-CD3 Antibody

<400> 26

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of Variable Light Chain of Anti-CD3 Antibody

<400> 27

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 28

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 29
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Chain of Anti-CD3 Antibody

<400> 29

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 Gly 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

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of Variable Heavy Chain of Anti-CD3 Antibody

<400> 30

Thr Tyr Ala Met Asn
1 5

<210> 31
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of Variable Heavy Chain of Anti-CD3 Antibody

<400> 31

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

Val Lys Gly

<210> 32
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR3 of Variable Heavy Chain of Anti-CD3 Antibody

<400> 32

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

<210> 33
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 4

<400> 33

Gly Gly Gly Ser
1

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

<220>
<223> Albumin-Binding Domain (ABD)

<400> 34

Leu Ala Glu Ala Lys Val Leu Ala Asn 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> 502
<212> PRT
<213> Artificial Sequence

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

<400> 35

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

Glu Lys Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

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

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

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Gly Ser Gly Thr Asp His Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65                  70                  75                  80

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

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

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

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

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

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

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335
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Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
340 345 350

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
500

<210> 36
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding DART-A (SEQ ID NO:35)

<400> 36
gagaatgtgc tcacacagtc ccctgcaact ctgagcgtaa ctccagggga gaaggccacc 60

atcacgtgta gagcctccca gagtgtgagc tacatgcact ggtatcagca gaaacctgga 120

caagctccca ggttgctgat ctatgacgcg agcaaccggg ctagtggcgt tccatcccgg 180

ttttctggct caggatctgg cactgaccac accctcacca tatccagcct tgaagccgaa 240

gatgccgcaa cctactactg ctttcagggg agtgtgtatc ccttcacatt cggtcagggt 300

acaaagctgg agattaaggg 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

aagggtagat tcaccatctc aagagatgat tcaaagaact cactgtatct gcaaatgaac 600

agcctgaaaa ccgaggacac ggccgtgtat tactgtgtga gacacggtaa cttcggcaat 660

tcttacgtgt cttggtttgc ttattgggga caggggacac tggtgactgt gtcttccgcc 720

tccaccaagg gcgaagtggc cgcatgtgag aaagaggttg ctgctttgga gaaggaggtc 780

gctgcacttg aaaaggaggt cgcagccctg gagaaaggcg gcggggacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg gggggaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gaggagatga ccaagaacca ggtcagcctg 1260

tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggtaaa 1506

<210> 37
<211> 271
<212> PRT
<213> Artificial Sequence

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

<400> 37

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 Thr Leu Arg Glu Ser Gly Pro Ala
115 120 125

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

Phe Ser Leu Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro
145 150 155 160

Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp
165 170 175

Lys Arg Tyr Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp
180 185 190

Thr Ser Lys Asn Gln Val Phe Leu Thr Met Thr Asn Met Asp Pro Val
195 200 205

Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr
210 215 220

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

Thr Lys Gly Lys Val Ala Ala Cys 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> 38
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Second Polypeptide Chain of DART-A (SEQ ID NO:37)

<400> 38
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 tggacaggtg 360

acactgaggg aatctggtcc agctctggtg aaacccactc agacgctcac tctcacttgc 420

acctttagtg ggttctcact gtccacatct ggcatgggag taggctggat tcgacagcca 480

cctgggaaag ccttggagtg gcttgcccac atctggtggg atgacgacaa gcggtataat 540

cccgcactga agagcagact gaccatcagc aaggatacat ccaagaacca ggtgtttctg 600

accatgacca acatggaccc tgtcgataca gccacctact attgtgctcg catggagttg 660

tggtcctact acttcgacta ttggggacaa ggcacaaccg tgactgtctc atccgcctcc 720

accaagggca aagtggccgc atgtaaggag aaagttgctg ctttgaaaga gaaggtcgcc 780

gcacttaagg aaaaggtcgc agccctgaaa gag 813

<210> 39
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART-A

<400> 39

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> 40
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Third Polypeptide Chain of DART-A

<400> 40
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> 41
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Light Chain Domain of Anti-Fluorescein Antibody 4-4-20

<400> 41

Asp Val Val Met Thr Gln Thr Pro Phe Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 42
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Chain Domain Of Anti-Fluorescein Antibody 4-4-20

<400> 42

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

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

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

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

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

Val Tyr Leu Gln Met Asn Asn Leu Arg Val Glu Asp Met Gly Ile Tyr
85 90 95

Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 43
<211> 508
<212> PRT
<213> Artificial Sequence

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

<400> 43

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

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

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

Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
165 170 175

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

Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
195 200 205

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
210 215 220

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu

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225                 230                 235                 240

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu Val Ala Ala Cys Glu
                245                 250                 255

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

Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys Thr His Thr Cys Pro
        275                 280                 285

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

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                325                 330                 335

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            340                 345                 350

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    370                 375                 380

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
385                 390                 395                 400

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
            420                 425                 430

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    450                 455                 460

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                485                 490                 495

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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500 505

<210> 44
<211> 269
<212> PRT
<213> Artificial Sequence

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

<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 Glu Val Lys Leu Asp Glu Thr Gly Gly Gly
115 120 125

Leu Val Gln Pro Gly Arg Pro Met Lys Leu Ser Cys Val Ala Ser Gly
130 135 140

Phe Thr Phe Ser Asp Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu
145 150 155 160

Lys Gly Leu Glu Trp Val Ala Gln Ile Arg Asn Lys Pro Tyr Asn Tyr
165 170 175

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

Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Val
195 200 205

Glu Asp Met Gly Ile Tyr Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp
210 215 220

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

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

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

<210> 45
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Frst Polypeptide Chain of Control DART 2

<400> 45

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

Glu Lys Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

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

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

Gly Ser Gly Thr Asp His Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Val Tyr Pro Phe 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 Lys Leu Asp Glu Thr Gly Gly Gly Leu Val Gln Pro
115 120 125

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

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

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

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys

180 185 190

Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Val Glu Asp Met Gly
195 200 205

Ile Tyr Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
210 215 220

Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu Val Ala
225 230 235 240

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

Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys Thr His
260 265 270

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
275 280 285

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
290 295 300

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
305 310 315 320

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
325 330 335

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
340 345 350

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
355 360 365

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
370 375 380

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
385 390 395 400

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
405 410 415

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
420 425 430

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
435 440 445

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg

450 455 460

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
465 470 475 480

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490 495

<210> 46
<211> 269
<212> PRT
<213> Artificial Sequence

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

<400> 46

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 Glu Val Lys Leu Asp Glu Thr Gly Gly Gly
115 120 125

Leu Val Gln Pro Gly Arg Pro Met Lys Leu Ser Cys Val Ala Ser Gly
130 135 140

Phe Thr Phe Ser Asp Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu
145 150 155 160

Lys Gly Leu Glu Trp Val Ala Gln Ile Arg Asn Lys Pro Tyr Asn Tyr
165 170 175

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

Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Val
195 200 205

Glu Asp Met Gly Ile Tyr Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp
210 215 220

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

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

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

<210> 47
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Intervening Spacer Peptide (Linker 4)

<400> 47

Ala Pro Ser Ser Ser
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Intervening Spacer Peptide (Linker 4)

<400> 48

Ala Pro Ser Ser Ser Pro Met Glu
1 5