

SEQUENCE LISTING

<110> MacroGenics, Inc.
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<120> Bi-Specific Monovalent Diabodies That Are Capable Of Binding
 CD123, And CD3 And Uses Thereof

<130> 1301.0109PCT

<150> US 61/869,510
 <151> 2013-08-23

<150> US 61/907,749
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<150> EP 13198784
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<150> US 61/990,475
 <151> 2014-05-08

<160> 59

<170> PatentIn version 3.5

<210> 1
 <211> 272
 <212> PRT
 <213> Artificial Sequence

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

<400> 1

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 Gln Leu Val Gln Ser Gly Ala Glu
115 120 125

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

Tyr Thr Phe Thr Asp Tyr Tyr Met Lys Trp Val Arg Gln Ala Pro Gly
145 150 155 160

Gln Gly Leu Glu Trp Ile Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr
165 170 175

Phe Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val 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 Ser His Leu Leu Arg Ala Ser Trp
210 215 220

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

Cys Gly Gly Gly Glu Val Ala Ala Leu 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

<210> 2

<211> 816

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 2

caggctgtgg tgactcagga gccttactg accgtgtccc caggcggaac tgtgaccctg 60

acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag 120

aagccaggac aggcaccaag gggcctgata ggggggtacaa acaaaagggc tccctggacc 180

cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca 240
 caggccgagg acgaagccga ttactattgt gctctgtggg atagcaatct gtgggtgttc 300
 ggggggtggca caaaactgac tgtgctggga ggggggtggat ccggcggcgg aggcgaggtg 360
 cagctgggtgc agtccggggc tgagctgaag aaaccggag cttccgtgaa ggtgtcttgc 420
 aaagccagtg gctacacctt cacagactac tatatgaagt gggtcaggca ggctccagga 480
 cagggactgg aatggatcgg cgatatcatt ccttccaacg gggccacttt ctacaatcag 540
 aagtttaaag gcaggggtgac tattaccgtg gacaaatcaa caagcactgc ttatatggag 600
 ctgagctccc tgcgctctga agatacagcc gtgtactatt gtgctcggtc acacctgctg 660
 agagccagct ggtttgctta ttggggacag ggcaccctgg tgacagtgtc ttccggagga 720
 tgtggcgggtg gagaagtggc cgcactggag aaagaggttg ctgctttgga gaaggaggtc 780
 gctgcacttg aaaaggaggt cgcagccctg gagaaa 816

<210> 3

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> Second Polypeptide Chain of DART-A

<400> 3

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

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

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

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

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly 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 Lys Val Ala Ala Leu Lys Glu
275 280

<210> 4
<211> 840
<212> DNA
<213> Artificial Sequence

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

<400> 4
gacttcgtga tgacacagtc tctgatagt ctggccgtga gtctggggga gcggtgact 60
atgtcttgca agagctocca gtcactgctg aacagcggaa atcagaaaaa ctatctgacc 120
tggtaccagc agaagccagg ccagccccct aaactgctga tctattgggc ttccaccagg 180
gaatctggcg tgcccagacag attcagcggc agcggcagcg gcacagattt taccctgaca 240
atttctagtc tgcaggccga ggacgtggct gtgtactatt gtcagaatga ttacagctat 300

ccctacactt tcggccaggg gaccaagctg gaaattaaag gaggcggatc cggcggcggg 360
ggcgaggtgc agctggtgga gtctggggga ggcttggtcc agcctggagg gtccctgaga 420
ctctcctgtg cagcctctgg attcaccttc agcacatacg ctatgaattg ggtccgccag 480
gctccagggg aggggctgga gtgggttgga aggatcaggt ccaagtacaa caattatgca 540
acctactatg ccgactctgt gaaggataga ttcaccatct caagagatga ttcaaagaac 600
tcaactgtatc tgcaaatgaa cagcctgaaa accgaggaca cggccgtgta ttactgtgtg 660
agacacggta acttcggcaa ttcttacgtg tcttggtttg cttattgggg acaggggaca 720
ctggtgactg tgtcttccgg aggatgtggc ggtggaaaag tggccgcact gaaggagaaa 780
gttgctgctt tgaaagagaa ggtcgccgca cttaaggaaa aggtcgcagc cctgaaagag 840

<210> 5

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> First Polypeptide Chain of DART-B

<400> 5

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

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

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

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
50 55 60

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

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

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

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

Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

130		135		140
Asp Tyr Tyr Met Lys Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu				
145		150		155
Trp Ile Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr Phe Tyr Asn Gln				
	165		170	175
Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser Thr				
	180		185	190
Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr				
	195		200	205
Tyr Cys Ala Arg Ser His Leu Leu Arg Ala Ser Trp Phe Ala Tyr Trp				
	210		215	220
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly				
225		230		235
				240
Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val				
	245		250	255
Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys				
	260		265	

<210> 6
 <211> 804
 <212> DNA
 <213> Artificial Sequence

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

<400> 6	
gacattcagc tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
atgacctgca gagccagttc aagtgtgaagt tacatgaact ggtaccagca gaagtcaggc	120
acctccccc aaagatggat ttatgacaca tccaaagtgg cttctggagt cccttatcgc	180
ttcagtggca gtgggtctgg gacctcatc tctctcaca tcagcagcat ggaggctgaa	240
gatgctgcc cttattactg ccaacagtgg agtagtaacc cgtcacgtt cgggtgctggg	300
accaagctgg agctgaaagg aggcggatcc ggcggcggag gccaggtgca gctgggtgcag	360
tccggggctg agctgaagaa acccggagct tccgtgaagg tgtcttgcaa agccagtggc	420
tacaccttca cagactacta tatgaagtgg gtcaggcagg ctccaggaca gggactggaa	480
tggatcggcg atatcattcc ttccaacggg gccactttct acaatcagaa gtttaaaggc	540

agggtgacta ttaccgtgga caaatcaaca agcactgctt atatggagct gagctccctg 600
cgctctgaag atacagccgt gtactattgt gctcggtcac acctgctgag agccagctgg 660
tttgcttatt ggggacaggg caccctggtg acagtgtctt ccggaggatg tggcgggtgga 720
gaagtggccg cactggagaa agaggttgct gctttggaga aggaggtcgc tgcacttgaa 780
aaggaggtcg cagccctgga gaaa 804

<210> 7

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> Second Polypeptide Chain of DART-B

<400> 7

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

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

Lys Gly Gly Gly Ser Gly Gly Gly Gly Asp Ile Lys Leu Gln Gln Ser
115 120 125

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

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

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

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

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

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
210 215 220

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu 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

<210> 8

<211> 822

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 8

gacttcgtga tgacacagtc tctgatagt ctggccgtga gtctggggga gcggtgact 60
atgtcttgca agagctccca gtcactgctg aacagcggaa atcagaaaaa ctatctgacc 120
tggtaccagc agaagccagg ccagccccct aaactgctga tctattgggc ttccaccagg 180
gaatctggcg tgcccagacag attcagcggc agcggcagcg gcacagattt taccctgaca 240
atttctagtc tgcaggccga ggacgtggct gtgtactatt gtcagaatga ttacagctat 300
ccctacactt tcggccaggg gaccaagctg gaaattaaag gaggcggatc cggcggcgga 360
ggcgatatca aactgcagca gtcaggggct gaactggcaa gacctggggc ctcagtgaag 420
atgtcctgca agacttctgg ctacacctt actaggtaca cgatgcactg ggtaaaacag 480
aggcctggac agggctctgga atggattgga tacattaatc ctagccgtgg ttataactaat 540
tacaatcaga agttcaagga caaggccaca ttgactacag acaaatcctc cagcacagcc 600
tacatgcaac tgagcagcct gacatctgag gactctgcag tctattactg tgcaagatat 660
tatgatgata attactgcct tgactactgg ggccaaggca ccactctcac agtctcctcc 720

ggaggatgtg gcggtggaaa agtggccgca ctgaaggaga aagttgctgc tttgaaagag 780

aaggtcgccg cacttaagga aaaggtcgca gccctgaaag ag 822

<210> 9

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> CD123 x CD3 Diabody Polypeptide Chain Having Albumin Binding Site

<400> 9

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 Gln Leu Val Gln Ser Gly Ala Glu
115 120 125

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

Tyr Thr Phe Thr Asp Tyr Tyr Met Lys Trp Val Arg Gln Ala Pro Gly
145 150 155 160

Gln Gly Leu Glu Trp Ile Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr
165 170 175

Phe Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val 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 Ser His Leu Leu Arg Ala Ser Trp
 210 215 220
 Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 225 230 235 240
 Cys Gly Gly Gly Glu Val Ala Ala Leu 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 Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu
 275 280 285
 Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asp Asn Ala
 290 295 300
 Lys Ser Ala Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala
 305 310 315 320
 Leu Pro

<210> 10

<211> 966

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding CD123 x CD3 Diabody Polypeptide Chain
Having Albumin Binding Site

<400> 10

caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg	60
acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag	120
aagccaggac aggcaccaag gggcctgata ggggggtacaa acaaaaagggc tccctggacc	180
cctgcacggt tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca	240
caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc	300
gggggtggca caaaactgac tgtgctggga ggggggtggat ccggcggcgg aggcgaggtg	360
cagctggtgc agtccggggc tgagctgaag aaaccgggag cttccgtgaa ggtgtcttgc	420
aaagccagtg gctacacctt cacagactac tatatgaagt gggtcaggca ggctccagga	480
cagggactgg aatggatcgg cgatatcatt ccttccaacg gggccacttt ctacaatcag	540

aagtttaaag gcaggggtgac tattaccgtg gacaaatcaa caagcactgc ttatatggag 600
ctgagctccc tgcgctctga agatacagcc gtgtactatt gtgctcggtc acacctgctg 660
agagccagct ggtttgctta ttggggacag ggcaccctgg tgacagtgtc ttccggagga 720
tgtggcgggtg gagaagtggc cgcactggag aaagaggttg ctgctttgga gaaggaggtc 780
gctgcacttg aaaaggaggt cgcagccctg gagaaaggcg gcgggtctct ggccgaagca 840
aaagtgctgg ccaaccgcga actggataaa tatggcgtga gcgattatta taagaacctg 900
attgacaacg caaaatccgc ggaaggcgtg aaagcactga ttgatgaaat tctggccgcc 960
ctgcct 966

<210> 11

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> CH2-CH3 Domains of a Modified Human Antibody Fc Region

<400> 11

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> 12

<211> 681

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic Acid Molecule Encoding Peptide 1 and the CH2 and CH3
 Domains of an IgG Fc region

<400> 12

gacaaaactc acacatgccc accgtgcccga gcacctgaag ccgcgggggg accgtcagtc 60
 ttctctttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120
 tgcgtggttg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180
 ggcgtggagg tgcataatgc caagacaaaag ccgcggggagg agcagtacaa cagcacgtac 240
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300
 tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 420
 aaccagggtca gctgagttg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 540
 gacggctcct tcttctcgt cagcaagctc accgtggaca agagcaggtg gcagcagggg 600
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accgctacac gcagaagagc 660
 ctctccctgt ctccgggtaa a 681

<210> 13

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 13

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly 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 Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys Thr His Thr
 275 280 285
 Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 290 295 300
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 305 310 315 320
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 325 330 335
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 340 345 350
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 355 360 365
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 370 375 380
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 385 390 395 400
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 405 410 415
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 420 425 430
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 435 440 445
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 450 455 460
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 465 470 475 480
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 485 490 495
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505 510

<210> 14

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 14

gacttcgtga tgacacagtc tctgatagt ctggccgtga gtctggggga gcggtgact	60
atgtcttgca agagctccca gtcactgctg aacagcggaa atcagaaaaa ctatctgacc	120
tggtaccagc agaagccagg ccagccccct aaactgctga tctattgggc ttccaccagg	180
gaatctggcg tgcccagacag attcagcggc agcggcagcg gcacagattt taccctgaca	240
atttctagtc tgcaggccga ggacgtggct gtgtactatt gtcagaatga ttacagctat	300
ccctacactt tcggccaggg gaccaagctg gaaattaaag gaggcggatc cggcggcgga	360
ggcgaggtgc agctgggtga gtctggggga ggcttgggtcc agcctggagg gtccctgaga	420
ctctcctgtg cagcctctgg attcaccttc agcacatacg ctatgaattg ggtccgccag	480
gtccaggga aggggctgga gtgggttga aggatcagggt ccaagtacaa caattatgca	540
acctactatg ccgactctgt gaaggataga ttcacatct caagagatga ttcaaagaac	600
tcactgtatc tgcaaatgaa cagcctgaaa accgaggaca cgcccggtga ttactgtgtg	660
agacacggta acttcggcaa ttcttacgtg tcttggtttg cttattgggg acaggggaca	720
ctggtgactg tgtcttccgg aggatgtggc ggtggagaag tggccgcact ggagaaagag	780
gttgctgctt tggagaagga ggctcgtgca cttgaaaagg aggtcgcagc cctggagaaa	840
ggcggcgggg acaaaactca cacatgcca ccgtgcccag cacctgaagc cgcgggggga	900
ccgtcagtct tctcttccc cccaaaaccc aaggacacc tcatgatctc ccggaccct	960
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	1080
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1140
gagtacaagt gcaagggtct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1200
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag	1260
atgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc	1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1380
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg	1440

cagcagggga acgttttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500

cagaagagcc tctccctgtc tccgggtaaa 1530

<210> 15

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 15

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 Gln Leu Val Gln Ser Gly Ala Glu
115 120 125

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

Tyr Thr Phe Thr Asp Tyr Tyr Met Lys Trp Val Arg Gln Ala Pro Gly
145 150 155 160

Gln Gly Leu Glu Trp Ile Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr
165 170 175

Phe Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val 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 Ser His Leu Leu Arg Ala Ser Trp
 210 215 220

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

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

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

<210> 16

<211> 816

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 16

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caggctgtgg tgactcagga gccttcactg accgtgtccc caggcggaac tgtgaccctg      60
acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag      120
aagccaggac aggcaccaag gggcctgacg ggggggtacaa acaaaagggc tccctggacc      180
cctgcacggg tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca      240
caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc      300
gggggtggca caaaactgac tgtgctggga ggggggtggat ccggcggcgg aggcgaggtg      360
cagctgggtgc agtccggggc tgagctgaag aaaccgggag cttccgtgaa ggtgtcttgc      420
aaagccagtg gctacacctt cacagactac tatatgaagt gggtcaggca ggctccagga      480
cagggactgg aatggatcgg cgatatcatt ccttccaacg gggccacttt ctacaatcag      540
aagtttaaag gcaggggtgac tattaccgtg gacaaatcaa caagcactgc ttatatggag      600
ctgagctccc tgcgctctga agatacagcc gtgtactatt gtgctcggtc acacctgctg      660
agagccagct ggtttgctta ttggggacag ggcaccctgg tgacagtgtc ttccggagga      720
tgtggcggtg gaaaagtggc cgcactgaag gagaaagttg ctgctttgaa agagaaggtc      780
gccgcactta aggaaaaggt cgcagccctg aaagag                                816
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<210> 17

<211> 515

<212> PRT
 <213> Artificial Sequence

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

 <400> 17

 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 Phe Val Met Thr
 225 230 235 240

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Val Thr Met
 245 250 255
 Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn
 260 265 270
 Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 275 280 285
 Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
 290 295 300
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
 305 310 315 320
 Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro
 325 330 335
 Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser
 340 345 350
 Gly Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 355 360 365
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 370 375 380
 Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
 385 390 395 400
 Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
 405 410 415
 Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
 420 425 430
 Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
 435 440 445
 Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
 450 455 460
 Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 465 470 475 480
 Ser Gly Gly Cys Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val
 485 490 495
 Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala
 500 505 510
 Leu Lys Glu
 515

<210> 18
 <211> 1545
 <212> DNA
 <213> Artificial Sequence

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

<400> 18
 gacaaaactc acacatgccc accgtgcccga gcacctgaag ccgcgggggg accgtcagtc 60
 ttctctttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120
 tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180
 ggcgtggagg tgcataatgc caagacaaag ccgcggggagg 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 gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 480
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 540
 gacggctcct tcttctctca cagcaagctc accgtggaca agagcagggtg gcagcagggg 600
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660
 ctctccctgt ctccgggtaa agccccctcc agctccccta tggaagactt cgtgatgaca 720
 cagtctcttg atagtctggc cgtgagtctg ggggagcggg tgactatgtc ttgcaagagc 780
 tcccagtcac tgctgaacag cggaaatcag aaaaactatc tgacctggta ccagcagaag 840
 ccaggccagc cccctaaact gctgatctat tgggcttcca ccagggaatc tggcgtgccc 900
 gacagattca gcggcagcgg cagcggcaca gattttaccc tgacaatttc tagtctgcag 960
 gccgaggacg tggctgtgta ctattgtcag aatgattaca gctatcccta cactttcggc 1020
 caggggacca agctggaaat taaaggaggc ggatccggcg gcggaggcga ggtgcagctg 1080
 gtggagtctg ggggaggctt ggtccagcct ggagggtccc tgagactctc ctgtgcagcc 1140
 tctggattca ccttcagcac atacgctatg aattgggtcc gccaggctcc aggggaagggg 1200
 ctggagtggg ttggaaggat caggtccaag tacaacaatt atgcaaccta ctatgccgac 1260

tctgtgaagg atagattcac catctcaaga gatgattcaa agaactcact gtatctgcaa 1320
atgaacagcc tgaaaaccga ggacacggcc gtgtattact gtgtgagaca cggtaacttc 1380
ggcaattctt acgtgtcttg gtttgcttat tggggacagg ggacactggg gactgtgtct 1440
tccggaggat gtggcgggtg aaaagtggcc gcactgaagg agaaagttgc tgctttgaaa 1500
gagaaggctg ccgcacttaa ggaaaaggtc gcagccctga aagag 1545

<210> 19

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<223> First Polypeptide Chain of Control DART

<400> 19

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

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

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp 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
225 230 235 240

Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly 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

Glu Val Ala Ala Leu Glu Lys
275

<210> 20

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Second Polypeptide Chain of Control DART

<400> 20

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 Gly Gly Cys Gly				
	225	230	235	240
Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu				
	245	250	255	
Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu				
	260	265	270	

<210> 21

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain CD3-Binding Domain of DART-A

<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
100 105 110

<210> 22

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain CD3-Binding Domain of DART-A

<400> 22

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

<210> 23

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain CD3-Binding Domain of DART-B

<400> 23

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

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

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

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
 50 55 60

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

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

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 24

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain CD3-Binding Domain of DART-B

<400> 24

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

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

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

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> 25
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light Chain CD123-Binding Domain of DART-A

<400> 25

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

Lys

<210> 26
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy Chain CD123-Binding Domain of DART-A

<400> 26

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Leu	Lys	Lys	Pro	Gly	Ala
1			5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr
			20				25					30			
Tyr	Met	Lys	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35				40					45				

Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr Phe Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Val 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 Ser His Leu Leu Arg Ala Ser Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 27
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CD123-Binding Domain of DART-B

<400> 27

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

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

Lys

<210> 28
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> Heavy Chain CD123-Binding Domain of DART-B

<400> 28

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

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

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

Gly Asp Ile Ile Pro Ser Asn Gly Ala Thr Phe Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Val 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 Ser His Leu Leu Arg Ala Ser Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 29

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 1 Polypeptide

<400> 29

Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 30

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 2 Polypeptide

<400> 30

Gly Gly Cys Gly Gly Gly
1 5

<210> 31
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3 Polypeptide

<400> 31

Gly Gly Gly Ser
1

<210> 32

<400> 32
000

<210> 33
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 4 Polypeptide

<400> 33

Ala Pro Ser Ser Ser Pro Met Glu
1 5

<210> 34
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> E-Coil Domain

<400> 34

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> 35
<211> 28
<212> PRT

<213> Artificial Sequence

<220>

<223> K-Coil Domain

<400> 35

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> 36

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Preferred Albumin Binding Domain

<400> 36

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> 37

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> CH2-CH3 Domains of Human Fc Region

<400> 37

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> 38
 <211> 14
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> CDR1 of Light Chain Variable Domain of Anti-CD3 Antibody

 <400> 38

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

<210> 39
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDR2 of Light Chain Variable Domain of Anti-CD3 Antibody

<400> 39

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 40
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDR3 of Light Chain Variable Domain of Anti-CD3 Antibody

<400> 40

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 41
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDR1 of Heavy Chain Variable Domain of Anti-CD3 Antibody

<400> 41

Thr Tyr Ala Met Asn
1 5

<210> 42
<211> 19
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> CDR2 of Heavy Chain Variable Domain of Anti-CD3 Antibody

<400> 42

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

Val Lys Asp

<210> 43

<211> 14

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(14)

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

<400> 43

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

<210> 44

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDR1 of Light Chain Variable Domain of Anti-CD123 Antibody

<400> 44

Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
 1 5 10 15

Thr

<210> 45

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDR2 of Light Chain Variable Domain of Anti-CD123 Antibody

<400> 45

Trp Ala Ser Thr Arg Glu Ser
 1 5

<210> 46
 <211> 9
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MISC_FEATURE
 <222> (1)..(9)
 <223> CDR3 of Light Chain Variable Domain of Anti-CD123 Antibody

 <400> 46

Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr
 1 5

<210> 47
 <211> 5
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDR1 of Heavy Chain Variable Domain of Anti-CD123 Antibody

 <400> 47

Asp Tyr Tyr Met Lys
 1 5

<210> 48
 <211> 17
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDR2 of Heavy Chain Variable Domain of Anti-CD123 Antibody

 <400> 48

Asp Ile Ile Pro Ser Asn Gly Ala Thr Phe Tyr Asn Gln Lys Phe Lys
 1 5 10 15

Gly

<210> 49
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDR3 of Heavy Chain Variable Domain of Anti-CD123 Antibody

<400> 49

Ser His Leu Leu Arg Ala Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 50

Gly Val Glu Pro Lys Ser Cys
1 5

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 51

Val Glu Pro Lys Ser Cys
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimerization Domain

<400> 52

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 53
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Heterodimerization Domain

<400> 53

Phe Asn Arg Gly Glu Cys

1 5

<210> 54

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 54

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> 55
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide 1

<400> 55

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

<210> 56
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred CH2 and CH3 Domains of Fc Region

<400> 56

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> 57

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 4 Polypeptide

<400> 57

Ala Pro Ser Ser Ser
1 5

<210> 58

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Sequence of First Polypeptide Chain of "Control
DART-2"

<400> 58

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
	35						40					45				
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
	50					55					60					
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
65					70					75					80	
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Asn	
			85						90					95		
Asp	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	
			100					105					110			
Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Glu	Val	Lys	Leu	Asp	Glu	Thr	
	115						120					125				
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg	Pro	Met	Lys	Leu	Ser	Cys	Val	
	130					135					140					
Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr	Trp	Met	Asn	Trp	Val	Arg	Gln	
145					150					155					160	
Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gln	Ile	Arg	Asn	Lys	Pro	
			165					170						175		
Tyr	Asn	Tyr	Glu	Thr	Tyr	Tyr	Ser	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	
			180					185					190			
Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	Val	Tyr	Leu	Gln	Met	Asn	Asn	
		195					200					205				
Leu	Arg	Val	Glu	Asp	Met	Gly	Ile	Tyr	Tyr	Cys	Thr	Gly	Ser	Tyr	Tyr	
	210					215					220					
Gly	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	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

<210> 59
 <211> 274
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino Acid Sequence of Second Polypeptide Chain of "Control
DART-2"

<400> 59

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 Gln Ser Gly
115 120 125

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

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

Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Ile Pro Ser Asn Gly
165 170 175

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

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser His Leu Leu Arg Ala
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