SEQUENCE LISTING

<110> SANOFI

<120> Peptide or peptide complex binding to alpha 2 integrin and methods and uses involving the same

<130> DE2010/156

<140> EP10305929.1
<141> 2010-08-31

<160> 54

<170> PatentIn version 3.5

<210> 1
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable domain of anti-alpha2-integrin mAb

<400> 1

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

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

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

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

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

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 2
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable domain of anti-alpha2-integrin mAb

<400> 2

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

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

20 25 30

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 3
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of the heavy chain variable domain

<400> 3

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn
1 5 10

<210> 4
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of the heavy chain variable domain

<400> 4

Arg Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of the heavy chain variable domain

<400> 5

Val Gly Arg Gly Tyr Phe Asp Tyr
1 5

<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of the light chain variable domain

<400> 6

Arg Ala Ser Glu Ser Val Glu Ser Tyr Gly Asn Ser Phe Ile Tyr
1 5 10 15

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

<220>
<223> CDR2 of the light chain variable domain

<400> 7

Leu Ala Ser Asn Leu Ala Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of the light chain variable domain

<400> 8

Gln Gln Asn Asn Glu Asp Pro Tyr Thr
1 5

<210> 9
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VL-IGKC-CL) light chain

<400> 9

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

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

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

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

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp

65 70 75 80

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

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

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 10
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VH-IGHG4-CH1) mAb

<400> 10

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

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

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

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

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
```

355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 11
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VH-IGHG1-CH1) heavy chain Fab fragment

<400> 11

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

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

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

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

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

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

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

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

Thr His His His His His His
225 230

<210> 12
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain variable domain of anti-alpha2-integrin mAb"

<400> 12
aacattgtgc tgacccaatc tccagcttct ttggctgtgt ctagggca gagggccacc 60

atatcctgca gagccagtga aagtgttgag agttatggca acagttttat ttactggtac 120

cagcagaaac caggacaggc acccaaactc ctcatctatc ttgcatccaa cctagcatct 180

ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240

cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaa 333

<210> 13
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain variable domain of anti-alpha2-integrin mAb

<400> 13
caggtccaac tgcatcagcc tggggctgaa cttgtgaagc ctggggctcc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120

cctggacgag gcctcgagtg gattggcagg attgatcctt ccgatagtga aactcactac 180

aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac 240

atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga 300

cgggggtact ttgactactg gggccaaggc accactctca cagtctcctc a 351

<210> 14

<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VL-IGKC-CL) light chain

<400> 14
aacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atatcctgca gagccagtga aagtgttgag agttatggca acagttttat ttactggtac 120

cagcagaaac caggacaggc acccaaactc ctcatctatc ttgcatccaa cctagcatct 180

ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240

cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaacgtacgg tggccgctcc ttccgtgttc 360

atcttccctc cctccgacga gcagctgaag tccggcaccg cctccgtggt gtgtctgctg 420

aacaacttct accctcggga ggccaaggtg cagtggaagg tggacaacgc cctgcagtcc 480

ggcaactccc aggagtccgt caccgagcag gactccaagg acagcaccta ctccctgtcc 540

tccaccctga ccctgtccaa ggccgactac gagaagcaca aggtgtacgc ctgtgaggtg 600

acccaccagg gcctgtccag ccctgtgacc aagtccttca accggggcga gtgc 654

<210> 15
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VH-IGHG4-CH1) mAb

<400> 15
caggtccaac tgcatcagcc tggggctgaa cttgtgaagc ctggggctcc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120

cctggacgag gcctcgagtg gattggcagg attgatcctt ccgatagtga aactcactac 180

aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac 240

atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga 300

cgggggtact ttgactactg gggccaaggc accactctca cagtctcctc agccagcacc 360

aagggccctt ccgtgttccc tctggccct tgctcccggt ccacctccga gtccaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tcctccctgg gcaccaagac ctacacctgt 600

aacgtggacc acaagccttc caacaccaag gtggacaagc gggtggagtc caagtacggc 660

cctccttgcc ctccctgccc tgcccctgag ttcgagggcg gacctagcgt gttcctgttc 720

cctcctaagc ctaaggacac cctgatgatc tcccggaccc ctgaggtgac ctgtgtggtg 780

gtggacgtgt cccaggagga ccctgaggtc cagttcaact ggtacgtgga cggcgtggag 840

gtgcacaacg ccaagaccaa gcctcgggag gagcagttca attccaccta ccgggtggtg 900

tctgtgctga ccgtgctgca ccaggactgg ctgaacggca aagaatacaa gtgtaaggtc 960

tccaacaagg gcctgccctc ctccatcgag aaaaccatct ccaaggccaa gggccagcct 1020

agggagcctc aggtgtacac cctgcctcct agccaggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa gggcttctac ccttccgaca tcgccgtgga gtgggagtcc 1140

aacggccagc ctgagaacaa ctacaagacc acccctcctg tgctggactc cgacggctcc 1200

ttcttcctgt actccaggct gaccgtggac aagtcccggt ggcaggaggg caacgtcttt 1260

tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320

tctctgggc 1329

<210> 16
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric (anti-alpha2-VH-IGHG1-CH1) heavy chain Fab fragment

<400> 16
caggtccaac tgcatcagcc tggggctgaa cttgtgaagc ctggggctcc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120

cctggacgag gcctcgagtg gattggcagg attgatcctt ccgatagtga aactcactac 180

aatcaaaagt tcaaggacaa ggccacactg actgtagaca aatcctccag cacagcctac 240

atccaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aaaggtggga 300

cgggggtact ttgactactg gggccaaggc accactctca cagtctcctc agccagcacc 360

aagggcccat ccgtgttccc tctggccccc tcctccaagt ccacctccgg cggcaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga ccagcggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tcctccctgg gcacccagac ctacatctgt 600

aacgtgaacc acaagccctc caacaccaag gtggacaaga aggtggagcc taagtcctgt 660

gacaagaccc acacccatca ccatcaccat cac 693

<210> 17
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGKC protein (Swiss-Prot: Q502W4)

<400> 17

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

```
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
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<210> 18
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHG4 protein (Swiss-Prot: P01861.1 (S108P, L115E))

<400> 18

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
```

```
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 19
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHG1 protein (Swiss-Prot: Q569F4)

<400> 19

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
```

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 20
<211> 1181
<212> PRT
<213> Homo sapiens

<400> 20

Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val
1 5 10 15

Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
20 25 30

Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
35 40 45

Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu
50 55 60

Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val
65 70 75 80

Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn
85 90 95

Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn
100 105 110

Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe
115 120 125

Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr
130 135 140

Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala
145 150 155 160

Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val
165 170 175

Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys
180 185 190

Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
195 200 205

Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe
210 215 220

Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser
225 230 235 240

```
Gln Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile
                245                 250                 255

Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg
            260                 265                 270

Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp
        275                 280                 285

Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile
    290                 295                 300

Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu
305                 310                 315                 320

Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro
                325                 330                 335

Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu
            340                 345                 350

Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
        355                 360                 365

Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
    370                 375                 380

Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
385                 390                 395                 400

Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
                405                 410                 415

Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
            420                 425                 430

His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
        435                 440                 445

Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
    450                 455                 460

Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
465                 470                 475                 480

Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
                485                 490                 495

Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
            500                 505                 510

Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
```

515 520 525

Leu Phe Thr Ile Lys Glu Gly Ile Leu Gly Gln His Gln Phe Leu Glu
530 535 540

Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
545 550 555 560

Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
565 570 575

Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
580 585 590

Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
595 600 605

Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
610 615 620

Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
625 630 635 640

Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
645 650 655

Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
660 665 670

Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
675 680 685

Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
690 695 700

Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
705 710 715 720

Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
725 730 735

Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
740 745 750

Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
755 760 765

Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
770 775 780

Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
785 790 795 800

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Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
                805                 810                 815

Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
            820                 825                 830

Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
        835                 840                 845

Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr
    850                 855                 860

Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
865                 870                 875                 880

Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp
                885                 890                 895

Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala
            900                 905                 910

Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu
        915                 920                 925

Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr
    930                 935                 940

Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile
945                 950                 955                 960

Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys
                965                 970                 975

Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His
            980                 985                 990

Ile Pro Gln Tyr Thr Lys Glu Lys  Asn Pro Leu Met Tyr  Leu Thr Gly
        995                 1000                1005

Val Gln  Thr Asp Lys Ala Gly  Asp Ile Ser Cys Asn  Ala Asp Ile
    1010                1015                1020

Asn Pro  Leu Lys Ile Gly Gln  Thr Ser Ser Ser Val  Ser Phe Lys
    1025                1030                1035

Ser Glu  Asn Phe Arg His Thr  Lys Glu Leu Asn Cys  Arg Thr Ala
    1040                1045                1050

Ser Cys  Ser Asn Val Thr Cys  Trp Leu Lys Asp Val  His Met Lys
    1055                1060                1065
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Gly Glu  Tyr Phe Val Asn Val  Thr Thr Arg Ile Trp  Asn Gly Thr
    1070                1075                1080

Phe Ala  Ser Ser Thr Phe Gln  Thr Val Gln Leu Thr  Ala Ala Ala
    1085                1090                1095

Glu Ile  Asn Thr Tyr Asn Pro  Glu Ile Tyr Val Ile  Glu Asp Asn
    1100                1105                1110

Thr Val  Thr Ile Pro Leu Met  Ile Met Lys Pro Asp  Glu Lys Ala
    1115                1120                1125

Glu Val  Pro Thr Gly Val Ile  Ile Gly Ser Ile Ile  Ala Gly Ile
    1130                1135                1140

Leu Leu  Leu Leu Ala Leu Val  Ala Ile Leu Trp Lys  Leu Gly Phe
    1145                1150                1155

Phe Lys  Arg Lys Tyr Glu Lys  Met Thr Lys Asn Pro  Asp Glu Ile
    1160                1165                1170

Asp Glu  Thr Thr Glu Leu Ser  Ser
    1175                1180
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<210> 21
<211> 3546
<212> DNA
<213> Homo sapiens

<400> 21

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caaggcattt taaattgttg tttggcctac aatgttggtc tcccagaagc aaaaatattt      120

tccggtcctt caagtgaaca gtttggctat gcagtgcagc agtttataaa tccaaaaggc      180

aactggttac tggttggttc accctggagt ggctttcctg agaaccgaat gggagatgtg      240

tataaatgtc ctgttgacct atccactgcc acatgtgaaa aactaaattt gcaaacttca      300

acaagcattc caaatgttac tgagatgaaa accaacatga gcctcggctt gatcctcacc      360

aggaacatgg gaactggagg ttttctcaca tgtggtcctc tgtgggcaca gcaatgtggg      420

aatcagtatt acacaacggg tgtgtgttct gacatcagtc ctgattttca gctctcagcc      480

agcttctcac ctgcaactca gccctgccct tccctcatag atgttgtggt tgtgtgtgat      540

gaatcaaata gtatttatcc ttgggatgca gtaaagaatt ttttggaaaa atttgtacaa      600

ggcctggata taggccccac aaagacacag gtggggttaa ttcagtatgc caataatcca      660

agagttgtgt ttaacttgaa cacatataaa accaaagaag aaatgattgt agcaacatcc      720

cagacatccc aatatggtgg ggacctcaca aacacattcg gagcaattca atatgcaaga      780

aaatatgctt attcagcagc ttctggtggg cgacgaagtg ctacgaaagt aatggtagtt      840

gtaactgacg gtgaatcaca tgatggttca atgttgaaag ctgtgattga tcaatgcaac      900
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catgacaata tactgaggtt tggcatagca gttcttgggt acttaaacag aaacgccctt 960

gatactaaaa atttaataaa agaaataaaa gcaatcgcta gtattccaac agaaagatac 1020

tttttcaatg tgtctgatga agcagctcta ctagaaaagg ctgggacatt aggagaacaa 1080

attttcagca ttgaaggtac tgttcaagga ggagacaact ttcagatgga aatgtcacaa 1140

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gctcaccgag gtgaccagat tggctcctat tttggtagtg tgctgtgttc agttgatgtg 1500

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aagaaagagg aaggaagagt ctacctgttt actatcaaag agggcatttt gggtcagcac 1620

caatttcttg aaggccccga gggcattgaa aacactcgat ttggttcagc aattgcagct 1680

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agtgttccag taagcatggc aactgtaatc atccacatcc ctcagtatac caaagaaaag 3000

aacccactga tgtacctaac tggggtgcaa acagacaagg ctggtgacat cagttgtaat 3060

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<210> 22
<211> 798
<212> PRT
<213> Homo sapiens

<400> 22

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20 25 30

Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
35 40 45

Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
50 55 60

Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
65 70 75 80

Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
85 90 95

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

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

Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
130 135 140

Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
145 150 155 160

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Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
                165                 170                 175

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

Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
        195                 200                 205

Ser Glu Gln Asn Cys Thr Ser Pro Phe Ser Tyr Lys Asn Val Leu Ser
    210                 215                 220

Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
225                 230                 235                 240

Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
                245                 250                 255

Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
            260                 265                 270

Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
        275                 280                 285

Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
    290                 295                 300

Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
305                 310                 315                 320

His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
                325                 330                 335

Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
            340                 345                 350

Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
        355                 360                 365

Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
    370                 375                 380

Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
385                 390                 395                 400

Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
                405                 410                 415

Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
            420                 425                 430

Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu
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435 440 445

Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
450 455 460

Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
465 470 475 480

Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val
485 490 495

Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met
500 505 510

Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn
515 520 525

Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr
530 535 540

Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys
545 550 555 560

Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys
565 570 575

Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
580 585 590

Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn
595 600 605

Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys
610 615 620

Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
625 630 635 640

Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
645 650 655

Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
660 665 670

Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
675 680 685

Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
690 695 700

Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
705 710 715 720

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Pro Glu Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
                725                 730                 735

Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
            740                 745                 750

Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
        755                 760                 765

Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys
    770                 775                 780

Ser Ala Val Thr Thr Val Val Asn Pro Lys Tyr Glu Gly Lys
785                 790                 795
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<210> 23
<211> 3879
<212> DNA
<213> Homo sapiens

<400> 23

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cacccgggag gccccgccag cccgcgggag aggcccagcg ggagtcgcgg aacagcaggc      180

ccgagcccac cgcgccgggc cccggacgcc gcgcggaaaa gatgaattta caaccaattt      240

tctggattgg actgatcagt tcagtttgct gtgtgtttgc tcaaacagat gaaaatagat      300

gtttaaaagc aaatgccaaa tcatgtggag aatgtataca agcagggcca aattgtgggt      360

ggtgcacaaa ttcaacattt ttacaggaag gaatgcctac ttctgcacga tgtgatgatt      420

tagaagcctt aaaaaagaag ggttgccctc cagatgacat agaaaatccc agaggctcca      480

aagatataaa gaaaaataaa aatgtaacca accgtagcaa aggaacagca gagaagctca      540

agccagagga tattactcag atccaaccac agcagttggt tttgcgatta agatcagggg      600

agccacagac atttacatta aaattcaaga gagctgaaga ctatcccatt gacctctact      660

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gcacaagtga acagaactgc accagcccat ttagctacaa aaatgtgctc agtcttacta      900

ataaaggaga agtatttaat gaacttgttg gaaaacagcg catatctgga aatttggatt      960

ctccagaagg tggtttcgat gccatcatgc aagttgcagt ttgtggatca ctgattggct     1020

ggaggaatgt tacacggctg ctggtgtttt ccacagatgc cgggtttcac tttgctggag     1080

atgggaaact tggtggcatt gttttaccaa atgatggaca atgtcacctg gaaaataata     1140

tgtacacaat gagccattat tatgattatc cttctattgc tcaccttgtc cagaaactga     1200

gtgaaaataa tattcagaca atttttgcag ttactgaaga atttcagcct gtttacaagg     1260
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tttatagatt aaagaagttg aggaaaagca aaaaaaaaa 3879

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5`-GeneRacer primer for amplifying variable domains of anti-alpha2-integrin mAb

<400> 24
cgactggagc acgaggacac tga 23

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> RACEMOG2a: 3`-primer internal to murine hinge region for amplifying variable domains of anti-alpha2-integrin mAb

<400> 25
aggacagggc ttgattgtgg g 21

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> CKFOR: 3`-primer internal to murine Ck region for amplifying variable domains of anti-alpha2-integrin mAb

<400> 26
ctcattcctg ttgaagctct tgac 24

<210> 27
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> alpha2mAB-VL FOR: primer for amplifying the light chain of anti-alpha2-integrin mAb

<400> 27
ctggtggcca ccgccaccgg cgtgcacagc aacattgtgc tgacccaatc tc 52

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> alpha2mAB-VL REV: primer for amplifying the light chain of anti-alpha2-integrin mAb

<400> 28
accgtacgtt ttatttccag cttggtcccc 30

<210> 29
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> alpha2mAB mAB-VH FOR: primer for amplifying the heavy chain of anti-alpha2-integrin mAb

<400> 29
ctggtggcca ccgccaccgg cgtgcacagc caggtccaac tgcatcagcc tg 52

<210> 30
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> alpha2mAB mAB-VH REV: primer for amplifying the heavy chain of anti-alpha2-integrin mAb

<400> 30
tagggccctt ggtgctggct gaggagactg tgagagtgg 39

<210> 31
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader FOR1-54: primer for introducing leader sequence into the variable chains of anti-alpha2-integrin mAb

<400> 31
gctagcacca tgggctggtc ctgcatcatc ctgtttctgg tggccaccgc cacc 54

<210> 32
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader FOR1-23: primer for introducing leader sequence into the variable chains of anti-alpha2-integrin mAb

<400> 32
caagctagca ccatgggctg gtcctg 26

<210> 33
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC1: Light chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 33

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

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

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

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

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

Pro Val Gln Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 34
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC2: Light chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 34

Asn Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ser Tyr
20 25 30

Gly Gln Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

Pro Val Gln Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 35
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC3: Light chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 35

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

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

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

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

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

Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 36
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC4: Light chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 36

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

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

Gly Gln Ser Phe Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

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

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

Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 37
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LC5: Light chain variable domain of anti-alpha2-integrin mAb with grafted mutations

<400> 37

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

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

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

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

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

Pro Val Glu Ala Asp Asp Thr Ala Asn Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

<210> 38
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC1: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 38

Gln Val Gln Leu His Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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 Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 39
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC2: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing mutations

<400> 39

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

Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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 Asp Pro Ser Glu Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 40
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC3: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 40

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

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

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 41
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC4: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 41

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

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

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

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

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

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Lys Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 42
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC5: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 42

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

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

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 43
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC6: Heavy chain variable domain of anti-alpha2-integrin mAb with humanizing and stabilizing mutations

<400> 43

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

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

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

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

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

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Lys Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Val Ser
115

<210> 44
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HC7: Heavy chain variable domain of anti-alpha2-integrin mAb with grafted mutations

<400> 44

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 Ser Tyr
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 Asp Pro Ser Asp Ser Glu Thr His Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Ala Thr Leu 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 Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 45
<211> 717
<212> DNA
<213> Mus musculus

<400> 45
atggagacag acacactcct gctatgggtg ctgctgctct gggttccagg ttccacaggt 60

aacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120

atatcctgca gagccagtga aagtgttgag agttatggca acagttttat ttactggtac 180

cagcagaaac caggacaggc acccaaactc ctcatctatc ttgcatccaa cctagcatct 240

ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 300

cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtac 360

acgttcggag gggggaccaa gctggaaata aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgctag 717

<210> 46
<211> 1401
<212> DNA
<213> Mus musculus

<400> 46
atgggatgga gctgtatcat cctcttcttg gtagcaacag ccacaggtgt ccactcccag 60

gtccaactgc atcagcctgg ggctgaactt gtgaagcctg gggctccagt gaagctgtcc 120

tgcaaggctt ctggctacac cttcaccagc tactggatga actgggtgaa gcagaggcct 180

ggacgaggcc tcgagtggat tggcaggatt gatccttccg atagtgaaac tcactacaat 240

caaaagttca aggacaaggc cacactgact gtagacaaat cctccagcac agcctacatc 300

caactcagca gcctgacatc tgaggactct gcggtctatt actgtgcaaa ggtgggacgg 360

gggtactttg actactgggg ccaaggcacc actctcacag tctcctcagc taaaacaaca 420

gccccatcgg tctatccact ggcccctgtg tgtggagata caactggctc ctcggtgact 480

ctaggatgcc tggtcaaggg ttatttccct gagccagtga ccttgacctg gaactctgga 540

tccctgtcca gtggtgtgca caccttccca gctgtcctgc agtctgacct ctacaccctc 600

agcagctcag tgactgtaac ctcgagcacc tggcccagcc agtccatcac ctgcaatgtg 660

gcccacccgg caagcagcac caaggtggac aagaaaattg agcccagagg gcccacaatc 720

aagccctgtc ctccatgcaa atgcccagca cctaacctct tgggtggacc atccgtcttc 780

atcttccctc caaagatcaa ggatgtactc atgatctccc tgagccccat agtcacatgt 840

gtggtggtgg atgtgagcga ggatgaccca gatgtccaga tcagctggtt tgtgaacaac 900

gtggaagtac acacagctca gacacaaacc catagagagg attacaacag tactctccgg 960

gtggtcagtg ccctccccat ccagcaccag gactggatga gtggcaagga gttcaaatgc 1020

aaggtcaaca acaaagacct cccagcgccc atcgagagaa ccatctcaaa acccaaaggg 1080

tcagtaagag ctccacaggt atatgtcttg cctccaccag aagaagagat gactaagaaa 1140

caggtcactc tgacctgcat ggtcacagac ttcatgcctg aagacattta cgtggagtgg 1200

accaacaacg ggaaaacaga gctaaactac aagaacactg aaccagtcct ggactctgat 1260

ggttcttact tcatgtacag caagctgaga gtggaaaaga agaactgggt ggaaagaaat 1320

agctactcct gttcagtggt ccacgagggt ctgcacaatc accacacgac taagagcttc 1380

tcccggactc ccgggaagtg a 1401

<210> 47
<211> 218
<212> PRT
<213> Mus musculus

<400> 47

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

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

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

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

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

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

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

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

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

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

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 48
<211> 447
<212> PRT
<213> Mus musculus

<400> 48

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

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

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

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

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

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

Ala Lys Val Gly Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu
115 120 125

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

Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser
145 150 155 160

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

Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp
            180                 185                 190

Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr
        195                 200                 205

Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
    210                 215                 220

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
                245                 250                 255

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

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

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
    290                 295                 300

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

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
                325                 330                 335

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
            340                 345                 350

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
        355                 360                 365

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
    370                 375                 380

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
                405                 410                 415

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
            420                 425                 430
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His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 49
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> IGLKV79_IGLKJ2

<400> 49

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

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

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

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

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

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

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

<210> 50
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV11_IGHD33_IGHJ8

<400> 50

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 Ser Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Leu Thr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 51
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Vk1LC

<400> 51

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

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

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

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

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

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

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

<210> 52
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Vh1b

<400> 52

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 Ser Tyr

20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Lys Ser Ser 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 Trp Gly Tyr Asp Tyr Asp Val Phe Tyr Tyr Ala Met Asp Tyr
100 105 110

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

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

<220>
<223> light chain variable domain of anti-integrin 2 mAb

<400> 53

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 54
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable domain of anti-integrin 2 mAb

<400> 54

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

Gly Val Ile Trp Ala Arg Gly Phe Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

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

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

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

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

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

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

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

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
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Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
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