

2921075PC02SEQLIST
SEQUENCE LISTING

<110> IMMUNOGEN, INC.

<120> ANTIBODIES AND ASSAYS FOR DETECTION OF CD37

<130> 2921.075PC02

<150> 62/212,183

<151> 2015-08-31

<150> 62/211,455

<151> 2015-08-28

<160> 34

<170> PatentIn version 3.5

<210> 1

<211> 281

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1 5 10 15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

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Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
115 120 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
165 170 175

Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
180 185 190

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
195 200 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
210 215 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225 230 235 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
245 250 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
260 265 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
275 280

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<210> 2
 <211> 843
 <212> DNA
 <213> Homo sapiens

<400> 2
 atgtcagccc aggagagctg cctcagcctc atcaagtact tcctcttcgt tttcaacctc 60
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 aaccttattt ccatagtggg catttgcttg ggcgtcggcc tactcgagct cgggttcattg 780
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 cgt 843

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<220>
 <223> muCD37-1B11-2 VH-CDR1
 <400> 3

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Gly Tyr Phe Met Asn
1 5

<210> 4
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<213> Artificial Sequence

<220>
<223> muCD37-1B11-2 VH-CDR2 (Kabat)

<400> 4

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

Gly

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-1B11-2 VH -CDR3

<400> 5

Arg Gly Ile Val Ala Ser Ser Arg Phe Phe Asp Val
1 5 10

<210> 6
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-1B11-2 VL-CDR1

<400> 6

Lys Ala Ser Gln Gly Val Ser Asn Asp Val Asp
1 5 10

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

<220>
 <223> muCD37-1B11-2 VL-CDR2

<400> 7

Tyr Ala Ser Asn Arg Tyr Thr
 1 5

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

<220>
 <223> muCD37-1B11-2 VL-CDR3

<400> 8

Cys His Gln Asp Tyr Thr Ser Pro Thr
 1 5

<210> 9
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-1B11-2 heavy chain variable region (VH)

<400> 9

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

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

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Phe Met Asn Trp Val Ile Gln Ser His Gly Lys Gly Leu Glu Trp Ile
 35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala His
 65 70 75 80

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

Gly Ser Arg Gly Ile Val Ala Ser Ser Arg Phe Phe Asp Val Trp Gly
 100 105 110

Ala Gly Thr Ser Val Ile Val Ser Ser
 115 120

<210> 10

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> muCD37-1B11-2 light chain variable region

<400> 10

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

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

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

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

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Ser Gly Tyr Gly Thr Asp Phe Thr Phe Ser Ile Ser Thr Val Gln Ala
65 70 75 80

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

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

<210> 11
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-1B11-2 full length heavy chain

<400> 11

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

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

Phe Met Asn Trp Val Ile Gln Ser His Gly Lys Gly Leu Glu Trp Ile
35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala His
65 70 75 80

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

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Gly Ser Arg Gly Ile Val Ala Ser Ser Arg Phe Phe Asp Val Trp Gly
 100 105 110

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

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

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

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

Val Leu Glu Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
 180 185 190

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

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

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

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

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

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

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

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

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

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

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

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

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser
 385 390 395 400

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

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

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

<210> 12
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-1B11-2 full length light chain

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<400> 12

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

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

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

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

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Ser Ile Ser Thr Val Gln Ala
 65 70 75 80

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

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

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

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

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

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

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

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

Asn Arg Asn Glu Cys
 210

<210> 13
 <211> 376
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muCD37-1B11-2 VH

<400> 13
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 tcctgcaagg cttctgggta ctcatcttact ggctacttta tgaactgggt gatacagagc 120
 catggaaaagg gccttgagtg gattggacgt attaatacctt acaatgggtga taccttctac 180
 aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctctac cacagcccac 240
 atggagctcc tgagcctgac atctgaggac tctgccgtct attattgtgg atcccggggg 300
 atagtggctt cctctagggt cttcgatgtc tggggcgcag ggacctcgtt catcgtctcc 360
 tcagccaaaa cgacac 376

<210> 14
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muCD37-1B11-2 VL

<400> 14
 agtattgtga tgaccagac tcccaaattc ctgcttgat cagcaggaga cagggttacc 60
 ataacctgca aggcagtc ggggtgtgagt aatgatgtag attggtacca acagaagcca 120
 gggcagtcctc ctaaactgct gatatactat gcatccaatc gctacactgg agtccctgat 180

2921075PC02SEQLIST

cgcttcactg gcagtggata tgggacggat ttcactttca gcatcagcac tgtgcaggct 240
gaagacctgg cagtttattt ctgtcaccag gattatacct ctccgacgtt cgggtggaggc 300
accaagctgg aaatcaaacg ggctgat 327

<210> 15
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37-LEL

<400> 15

Thr Met Glu Leu Leu Ile Ser Thr Gln Arg Ala Gln Leu Glu Arg Ser
1 5 10 15

Leu Arg Asp Val Val Glu Lys Thr Ile Gln Lys Tyr Gly Thr Asn Pro
20 25 30

Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu
35 40 45

Arg Cys Cys Gly Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile
50 55 60

Leu Arg Gly Asn Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr
65 70 75 80

Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu
85 90 95

Pro Gln Leu Ser Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala
100 105 110

Asp Ile Cys Ala Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys
115 120 125

2921075PC02SEQLIST

Ala Gln Gly Leu Gln Lys Trp Leu His Asn Asn Leu Ser Phe Leu Glu
130 135 140

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His
145 150 155 160

His His His His

<210> 16
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37-ECD-Fc

<400> 16

Gly Pro Glu Phe Leu Ile Ser Thr Gln Arg Ala Gln Leu Glu Arg Ser
1 5 10 15

Leu Arg Asp Val Val Glu Lys Thr Ile Gln Lys Tyr Gly Thr Asn Pro
20 25 30

Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu
35 40 45

Arg Cys Cys Gly Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile
50 55 60

Leu Arg Gly Asn Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr
65 70 75 80

Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu
85 90 95

2921075PC02SEQLIST

Pro Gln Leu Ser Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala
 100 105 110

Asp Ile Cys Ala Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys
 115 120 125

Ala Gln Gly Leu Gln Gly Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro
 130 135 140

Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser
 145 150 155 160

Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu
 165 170 175

Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro
 180 185 190

Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
 195 200 205

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

Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe
 225 230 235 240

Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr
 245 250 255

Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu
 260 265 270

Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys
 275 280 285

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Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn
 290 295 300

Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp
 305 310 315 320

Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys
 325 330 335

Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly
 340 345 350

Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 355 360 365

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 <223> hCD37-Fc-LAGA

<400> 17

Gly Pro Glu Phe Leu Ile Ser Thr Gln Arg Ala Gln Leu Glu Arg Ser
 1 5 10 15

Leu Arg Asp Val Val Glu Lys Thr Ile Gln Lys Tyr Gly Thr Asn Pro
 20 25 30

Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu
 35 40 45

Arg Cys Cys Gly Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile
 50 55 60

Leu Arg Gly Asn Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr
 65 70 75 80

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Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu
85 90 95

Pro Gln Leu Ser Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala
100 105 110

Asp Ile Cys Ala Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys
115 120 125

Ala Gln Gly Leu Gln Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
130 135 140

Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
145 150 155 160

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
165 170 175

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
180 185 190

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
195 200 205

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
225 230 235 240

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
245 250 255

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
260 265 270

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Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 275 280 285

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 290 295 300

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 305 310 315 320

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 325 330 335

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 340 345 350

Gln Lys Ser Leu Ser Leu Ser Pro Gly
 355 360

<210> 18
 <211> 340
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD37-ECD-S2-Fc

<400> 18

Gly Pro Glu Phe Leu Ile Ser Ala Ala Glu Glu Ser Trp Asp Tyr Val
 1 5 10 15

Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp Trp Phe
 20 25 30

Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg Val Pro
 35 40 45

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Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile Leu Asp
 50 55 60

Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala Arg Ser
 65 70 75 80

Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His Ile Tyr
 85 90 95

Arg Glu Gly Cys Ala Gln Gly Leu Gln Gly Ser Glu Pro Arg Gly Pro
 100 105 110

Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
 115 120 125

Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
 130 135 140

Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
 145 150 155 160

Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
 165 170 175

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

Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
 195 200 205

Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
 210 215 220

Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
 225 230 235 240

2921075PC02SEQLIST

Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
245 250 255

Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
260 265 270

Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
275 280 285

Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
290 295 300

Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
305 310 315 320

Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
325 330 335

Thr Pro Gly Lys
340

<210> 19
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37

<400> 19

Leu Ile Ser Thr Gln Arg Ala Gln Leu Glu Arg Ser Leu Arg Asp Val
1 5 10 15

Val Glu Lys Thr Ile Gln Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala
20 25 30

Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly
35 40 45

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Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile Leu Arg Gly Asn
50 55 60

Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala
65 70 75 80

Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu Pro Gln Leu Ser
85 90 95

Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala Asp Ile Cys Ala
100 105 110

Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu
115 120 125

Gln

<210> 20
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37

<400> 20

Leu Ile Ser Thr Gln Arg Ala Gln Leu Glu Arg Ser Leu Arg Asp Val
1 5 10 15

Val Glu Lys Thr Ile Gln Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala
20 25 30

Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly
35 40 45

2921075PC02SEQLIST

Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile Leu Arg Gly Asn
50 55 60

Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala
65 70 75 80

Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu Pro Gln Leu Ser
85 90 95

Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala Asp Ile Cys Ala
100 105 110

Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu
115 120 125

Gln Lys Trp Leu His Asn Asn Leu
130 135

<210> 21
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37

<400> 21

Leu Ile Ser Ala Ala Glu Glu Ser Trp Asp Tyr Val Gln Phe Gln Leu
1 5 10 15

Arg Cys Cys Gly Trp His Tyr Pro Gln Asp Trp Phe Gln Val Leu Ile
20 25 30

Leu Arg Gly Asn Gly Ser Glu Ala His Arg Val Pro Cys Ser Cys Tyr
35 40 45

Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile Leu Asp Lys Val Ile Leu
50 55 60

2921075PC02SEQLIST

Pro Gln Leu Ser Arg Leu Gly His Leu Ala Arg Ser Arg His Ser Ala
65 70 75 80

Asp Ile Cys Ala Val Pro Ala Glu Ser His Ile Tyr Arg Glu Gly Cys
85 90 95

Ala Gln Gly Leu Gln
100

<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3 VH-CDR1

<400> 22

Thr Ser Gly Val Ser
1 5

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3 VH-CDR2

<400> 23

Val Ile Trp Gly Asp Gly Ser Thr Asn
1 5

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

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<223> huCD37-3 VH-CDR3

<400> 24

Gly Gly Tyr Ser Leu Ala His
1 5

<210> 25

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 VL-CDR1

<400> 25

Arg Ala Ser Glu Asn Ile Arg Ser Asn Leu Ala
1 5 10

<210> 26

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 VL-CDR2

<400> 26

Val Ala Thr Asn Leu Ala Asp
1 5

<210> 27

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 VL-CDR3

<400> 27

Gln His Tyr Trp Gly Thr Thr Trp Thr
1 5

2921075PC02SEQLIST

<210> 28
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huCD37-3 VH v. 1.0

<400> 28

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

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

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

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Pro Ser Leu Lys
 50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
 65 70 75 80

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

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

Val Ser Ser
 115

<210> 29
 <211> 108
 <212> PRT
 <213> Artificial Sequence

2921075PC02SEQLIST

<220>

<223> huCD37-3 VL

<400> 29

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

Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Val
35 40 45

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

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

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

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

<210> 30

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 Heavy Chain (HC) v. 1.0

<400> 30

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

2921075PC02SEQLIST

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

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

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Pro Ser Leu Lys
 50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
 65 70 75 80

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

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

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

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

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

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

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

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

2921075PC02SEQLIST

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

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

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

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

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

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

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

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

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

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

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

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

2921075PC02SEQLIST

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

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

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

<210> 31
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huCD37-3 Light Chain

<400> 31

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

Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Val
 35 40 45

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

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

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
 85 90 95

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

2921075PC02SEQLIST

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 32
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3 VH v. 1.1

<400> 32

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

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

2921075PC02SEQLIST

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

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

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

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

Val Ser Ser
115

<210> 33

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 Heavy Chain (HC) v. 1.1

<400> 33

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

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

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

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ser Leu Lys
50 55 60

2921075PC02SEQLIST

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

2921075PC02SEQLIST

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

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

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

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

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

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

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

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

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

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

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

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

2921075PC02SEQLIST

<210> 34
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-1B11-2 VH-CDR2 (AbM)

<400> 34

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