SEQUENCE LISTING

<110> Tan, Phillip
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Morales, Cecile

<120> CD37 IMMUNOTHERAPEUTIC AND COMBINATION WITH BIFUNCTIONAL CHEMOTHERAPEUTIC THEREOF

<130> EMER-017/01SG 309814-2369

<140> Singapore Patent Application No. 201007096-9
<141> 2010-09-28

<150> PCT/US2009/040288
<151> 2009-04-11

<150> US 61/190,067
<151> 2008-04-11

<160> 293

<170> PatentIn version 3.3

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tctgtgggag agactgtcac catcacatgt cgaacaagtg aaaatgttta cagttatttg 180

gcttggtatc agcagaaaca gggaaaatct cctcagctcc tggtctcttt tgcaaaaacc 240

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ggtggtgggt cgggtggcgg cggatcgtca gcggtccagc tgcagcagtc tggacctgag 480

tcggaaaagc ctggcgcttc agtgaagatt tcctgcaagg cttctggtta ctcattcact 540

ggctacaata tgaactgggt gaagcagaat aatggaaaga gccttgagtg gattggaaat 600

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tcagtcaccg tctcttcaga tctggagccc aaatcttctg acaaaactca cacatctcca 840

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cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

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Ser Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr
35 40 45

Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly
50 55 60

Lys Ser Pro Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu
85 90 95

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

His His Ser Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

130 135 140

Ser Ser Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro
145 150 155 160

Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr
165 170 175

Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu
180 185 190

Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg
195 200 205

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
210 215 220

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

Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr
245 250 255

Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr
260 265 270

His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
275 280 285

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

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

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

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

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

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

405 410 415

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

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

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

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20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu

130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

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gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggagctctg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

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cggaccccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

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cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

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agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

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cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

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aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Ser Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu

210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

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ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

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gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 12
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 12

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255
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Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                405                 410                 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    450                 455                 460

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 13
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aagtgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 14
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 14

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser

20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Ser
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

290 295 300

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 15
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 15
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gagcaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 16
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 16

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

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Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 17
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 17
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gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga gactgtcacc 120

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ggaaaatctc ctcagctcct ggtctctttt gcaaaaacct tagcagaagg tgtgccatca 240

aggttcagtg gcagtggatc aggcacacag ttttctctga agatcagcag cctgcagcct 300

gaagattctg gaagttattt ctgtcaacat cattccgata atccgtggac gttcggtgga 360

ggcaccgaac tggagatcaa aggtggcggt ggctcgggcg gtggtgggtc gggtggcggc 420

ggagctagcg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaggattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 18
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 18

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
50 55 60

Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser

100 105 110

Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

370 375 380

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 19
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 19
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtagtggatc tggaggaggt 420

ggagctagcg cggtccagct gcagcagtct ggacctgagt cggaaaagcc tggcgcttca 480

gtgaagattt cctgcaaggc ttctggttac tcattcactg gctacaatat gaactgggtg 540

aagcagaata atggaaagag ccttgagtgg attggaaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggcaag gccacattga ctgtagacaa atcctccagc 660

acagcctaca tgcagctcaa gagtctgaca tctgaggact ctgcagtcta ttactgtgca 720

agatcggtcg gccctatgga ctactggggt caaggaacct cagtcaccgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 20
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 20

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1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly Gly Ala Ser Ala
130 135 140

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Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
    210                 215                 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350

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

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

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 21
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 21
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 22
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 22

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly

180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 23
<211> 1503
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 23
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tcctgcaagg cttctggtta ctcattcact ggctacaata tgaactgggt gaagcagaat 180

aatggaaaga gccttgagtg gattggaaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 300

atgcagctca agagtctgac atctgaggac tctgcagtct attactgtgc aagatcggtc 360

ggccctatgg actactgggg tcaaggaacc tcagtcaccg tctcttctgg tggcggtggc 420

tcgggcggtg gtgggtcggg tggcggcgga tcaggaggag gcgggagtgc tagcgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gcgaaagagc caccctctcc 540

tgccgaacaa gtgaaaatgt ttacagctac ttagcctggt accaacagaa acctggccag 600

gctcctaggc tcctcatcta ttttgcaaaa accttagcag aaggaattcc agccaggttc 660

agtggcagtg gatccgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca acatcattcc gataatccgt ggacattcgg ccaagggacc 780

aaggtggaaa tcaaaggctc gagcgagccc aaatcttctg acaaaactca cacatctcca 840

ccgtgcccag cacctgaact cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260

ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

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tga 1503

<210> 24
<211> 500
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 24

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1 5 10 15

Asp Thr Thr Gly Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu
20 25 30

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
35 40 45

Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser
50 55 60

Leu Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr
65 70 75 80

Asn Arg Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85 90 95

Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Glu Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175

Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
180 185 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe
195 200 205

Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly

210 215 220

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225 230 235 240

Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe
245 250 255

Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Ser Glu Pro Lys Ser
260 265 270

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

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

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

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

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

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

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

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430

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

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

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

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

485 490 495

Ser Pro Gly Lys
500

<210> 25
<211> 1488
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 25
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agagccaccc tctcctgccg aacaagtgaa aatgtttaca gctacttagc ctggtaccaa 180

cagaaacctg gccaggctcc taggctcctc atctattttg caaaaacctt agcagaagga 240

attccagcca ggttcagtgg cagtggatcc gggacagact tcactctcac catcagcagc 300

ctagagcctg aagattttgc agtttattac tgtcaacatc attccgataa tccgtggaca 360

ttcggccaag ggaccaaggt ggaaatcaaa ggtggcggtg gctcgggcgg tggtggatct 420

ggaggaggtg gagctagcgc ggtccagctg cagcagtctg gacctgagtc ggaaaagcct 480

ggcgcttcag tgaagatttc ctgcaaggct tctggttact cattcactgg ctacaatatg 540

aactgggtga agcagaataa tggaaagagc cttgagtgga ttggaaatat tgatccttat 600

tatggtggta ctacctacaa ccggaagttc aagggcaagg ccacattgac tgtagacaaa 660

tcctccagca cagcctacat gcagctcaag agtctgacat ctgaggactc tgcagtctat 720

tactgtgcaa gatcggtcgg ccctatggac tactggggtc aaggaacctc agtcaccgtc 780

tcctcgagcg agcccaaatc ttctgacaaa actcacacat ctccaccgtg cccagcacct 840

gaactcctgg gtggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga 1488

<210> 26

<211> 495
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 26

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Ile Ala Arg Gly Val Glu Ile Val Leu Thr Gln Ser Pro Ala
            20                  25                  30

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr
        35                  40                  45

Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly
65                  70                  75                  80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                85                  90                  95

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
            100                 105                 110

His His Ser Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ala Ser Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro
145                 150                 155                 160

Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr
                165                 170                 175

Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu
            180                 185                 190

Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg
        195                 200                 205

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
    210                 215                 220

Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225                 230                 235                 240
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Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr
245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 27
<211> 1503
<212> DNA

<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 27
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tcctgcaagg cttctggtta ctcattcact ggctacaata tgaactgggt gaagcagaat 180

aatggaaaga gccttgagtg gattggaaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 300

atgcagctca agagtctgac atctgaggac tctgcagtct attactgtgc aagatcggtc 360

ggccctatgg actactgggg tcaaggaacc tcagtcaccg tctcttctgg tggcggtggc 420

tcgggcggtg gtgggtcggg tggcggcgga tcaggaggag gcgggagtgc tagcgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gcgaaagagc caccctctcc 540

tgccgaacaa gtgaaaatgt ttacagctac ttagcctggt accaacagaa acctggccag 600

gctcctaggc tcctcatcta ttttgcaaaa accttagcag aaggaattcc agccaggttc 660

agtggcagtg gatccgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca acatcattcc gataatccgt ggacattcgg ccaagggacc 780

aaggtggaaa tcaaaggctc gagcgagccc aaatcttctg acaaaactca cacatgccca 840

ccgtgcccag cacctgaact cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

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ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260

ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

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tga 1503

<210> 28
<211> 500
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 28

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            20                  25                  30

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
        35                  40                  45

Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser
    50                  55                  60

Leu Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr
65                  70                  75                  80

Asn Arg Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
                85                  90                  95

Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Glu Ile
145                 150                 155                 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175

Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe
        195                 200                 205

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

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225                 230                 235                 240

Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe
                245                 250                 255

Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Ser Glu Pro Lys Ser
            260                 265                 270
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Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        275                 280                 285

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

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

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

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

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

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

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430

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

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

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

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

Ser Pro Gly Lys
            500
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<210> 29
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 29
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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccccа aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

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ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

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gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

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aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 30
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 30

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Ala
    130                 135                 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
    210                 215                 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 31
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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gtgaagattt cctgcaaggc ttctggttac tcattcactg gctacaatat gaactgggtg 540

aagcagaata atggaaagag ccttgagtgg attggaaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggcaag gccacattga ctgtagacaa atcctccagc 660

acagcctaca tgcagctcaa gagtctgaca tctgaggact ctgcagtcta ttactgtgca 720

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gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

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gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

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tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 32
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 32

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

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Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Ala
    130                 135                 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
    210                 215                 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

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

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

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    450                 455                 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 33
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 33

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ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc    240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct    300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa    360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt    420

ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc    480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc    540
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cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

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cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

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<210> 34
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 34

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser

100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

370 375 380

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 35
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

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ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc 480

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cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

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ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

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tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 36
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 36

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
130 135 140

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Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350

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

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

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 37
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

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cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

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<210> 38
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 38

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly

180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 39
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 39
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct tggtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 40
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 40

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

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Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    450                 455                 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 41
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 41
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct ctgtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccccа aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 42
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 42

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 43
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 43

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct ctgtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccccа aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 44
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 44

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    290                 295                 300
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Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    450                 455                 460

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 45
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 45
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gagcaagtca aagtgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

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cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 46
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 46

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala

65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu

340 345 350

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 47
<211> 1500
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 47
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gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gcggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gactactggg gccagggcac cctggtcact 780

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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atgatctaga 1500

<210> 48
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 48

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

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Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

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

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

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

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    370                 375                 380
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Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
385 390 395 400

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 49
<400> 49
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<210> 50
<400> 50
000

<210> 51
<211> 1381
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 51
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gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gactcctggg gccagggcac cctggtcact 780

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gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

a 1381

<210> 52
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 52

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

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

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

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

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

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

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

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
385                 390                 395                 400
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Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                405                 410                 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    450                 455                 460

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 53
<400> 53
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<210> 54
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<210> 61
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 61

Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 62
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 62

Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 63
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 63

Gly Tyr Asn Met Asn
1 5

<210> 64
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 64

Phe Ala Lys Thr Leu Ala Glu
1 5

<210> 65
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 65

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

Gly

<210> 66
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 66

Gln His His Ser Asp Asn Pro Trp Thr
1 5

<210> 67
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 67

Ser Val Gly Pro Phe Asp Tyr
1 5

<210> 68
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 68

Ser Val Gly Pro Phe Asp Ser
1 5

<210> 69
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 69

Ser Val Gly Pro Met Asp Tyr
1 5

<210> 70
<400> 70
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<210> 71
<400> 71
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<210> 72
<400> 72

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<210> 73
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<400> 76
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<210> 77
<400> 77
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<210> 78
<400> 78
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<210> 79
<211> 1500
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 79
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gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gacctctggg gcagaggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atgatctaga 1500

<210> 80
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 80

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 81
<211> 1494
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 81
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gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

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caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtggggctag cgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tagctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctggagt ggatgggcaa tattgatcct 600

tattatggtg gtactaacta cgcccagaag ttccagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctatg gactactggg gccgcggcac cctggtcact 780

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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 82
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 82

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

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Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                405                 410                 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    450                 455                 460
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Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
465 470 475 480

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

<210> 83
<211> 1476
<212> DNA
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<220>
<223> CD37 specific binding protein

<400> 83
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caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

gggattccag ccagattcag tggcagtggt tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggagcgg aggaggagct agcgaggtgc agctggtgca gtctggagca 480

gaggtgaaaa agcccggaga gtctctgaag atttcctgta agggatccgg ttactcattc 540

actggctaca atatgaactg ggtgcgccag atgcccggga aaggcctcga atggatgggc 600

aatattgatc cttattatgg tggtactacc tacaaccgga agttcaaggg ccaggtcact 660

atctccgccg acaagtccat cagcaccgcc tacctgcaag gagcagcctg aaggcctcgg 720

acaccgccat gtattactgt gcacgctcag tcggcccttt cgactcctgg ggccagggca 780

ccctggtcac tgtctcgagt tgtccaccgt gcccagcacc tgaactcctg ggtggaccgt 840

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tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc aactggtacg 960

tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag tacaacagca 1020

cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt 1080

acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc atctccaaag 1140

ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg gatgagctga 1200

ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc gacatcgccg 1260

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actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc aggtggcagc 1380

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agagcctctc cctgtctccg ggtaaatgac tctaga 1476

<210> 84
<211> 485
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 84

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
                165                 170                 175

Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn
        195                 200                 205

Arg Lys Phe Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
    210                 215                 220

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
225                 230                 235                 240
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Tyr Tyr Cys Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly
                245                 250                 255

Thr Leu Val Thr Val Ser Ser Cys Pro Pro Cys Pro Ala Pro Glu Leu
            260                 265                 270

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    290                 295                 300

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
305                 310                 315                 320

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                325                 330                 335

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            340                 345                 350

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        355                 360                 365

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    370                 375                 380

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                405                 410                 415

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            420                 425                 430

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        435                 440                 445

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    450                 455                 460

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
465                 470                 475                 480

Leu Ser Pro Gly Lys
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<210> 85
<211> 1494

<212> DNA
<213> Artificial sequence

<220>
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caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctggagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctatg gactactggg gccgcggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

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ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 86
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 86

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270
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Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

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

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

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

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 87
<211> 1494
<212> DNA
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

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caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtggggctag cgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

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tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

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caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

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tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

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gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 88
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> CD37 specific binding protein

<400> 88

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

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Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

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

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320
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Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

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

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

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<211> 45
<212> DNA
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<212> DNA
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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
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<210> 106
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<400> 106

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
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<210> 107
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<210> 108
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<213> Artificial sequence

<220>
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<400> 108

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 109
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<212> DNA
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<220>
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<210> 110
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<212> PRT
<213> Artificial sequence

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<400> 110

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1 5 10 15

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<210> 112
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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 113
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<210> 114
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<210> 115
<211> 19
<212> PRT
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<400> 115

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
1 5 10 15

Ser Pro Ser

<210> 116
<211> 6
<212> PRT
<213> Artificial sequence

<220>
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<400> 116

Val Pro Pro Pro Pro Pro
1 5

<210> 117
<211> 186
<212> DNA
<213> Artificial sequence

<220>
<223> Hinge region

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ccaccgtgtc cccgctgtcc tgaaccaaag tcatgcgata ccccaccacc atgtccaaga 180

tgccca 186

<210> 118
<211> 62
<212> PRT
<213> Artificial sequence

<220>
<223> Hinge region

<400> 118

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

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
50 55 60

<210> 119
<211> 45
<212> DNA
<213> Artificial sequence

<220>
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<400> 119
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<210> 120
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Hinge region

<400> 120

Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
1 5 10 15

<210> 121
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Hinge region

<400> 121
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<220>
<223> Hinge region

<400> 122

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro
1 5 10 15

<210> 123
<211> 45
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<220>
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<400> 123
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<210> 124
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<400> 124

Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro
1 5 10 15

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<400> 125
gagcccaaat cttgtgacac acctcccca tccccacggt gccca 45

<210> 126
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<400> 126

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Ser Pro Arg Cys Pro
1 5 10 15

<210> 127
<211> 58
<212> PRT
<213> Artificial sequence

<220>
<223> Hinge region

<400> 127

Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1 5 10 15

Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
20 25 30

Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu
35 40 45

Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro
50 55

<210> 128
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 128

Arg Thr Ser Gln Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 129
<211> 11
<212> PRT
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<220>
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<400> 129

Arg Thr Ser Glu Ser Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 130
<211> 11
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<213> Artificial sequence

<220>
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<400> 130

Arg Ala Ser Gln Ser Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 131
<211> 11
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<213> Artificial sequence

<220>
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<400> 131

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 132
<211> 11
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<220>
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<400> 132

Arg Ala Ser Gln Ser Val Ser Tyr Tyr Leu Ala
1 5 10

<210> 133
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<400> 133

Ser Tyr Met Asn Met
1 5

<210> 134
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<213> Artificial sequence

<220>
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<400> 134

Ser Tyr Trp Ile Gly
1 5

<210> 135
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<220>
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<400> 135

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 136
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<213> Artificial sequence

<220>
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<400> 136

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 137
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<212> PRT
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<220>
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<400> 137

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 138
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<220>
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<400> 138

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

Gly

<210> 139
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> CDR

<400> 139

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

Gly

<210> 140
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 140

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
20 25 30

<210> 141
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 141

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

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

<210> 142
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 142

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

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

<210> 143
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 143

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

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

<210> 144
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 144

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
20 25 30

<210> 145
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 145

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
20 25 30

<210> 146
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 146

Gln Val Gln Leu Val Gln Ser Gly Ser 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
20 25 30

<210> 147
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 147

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 148
<400> 148
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<210> 149
<400> 149
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<210> 150
<211> 14
<212> PRT
<213> Artificial sequence

<220>
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<400> 150

Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 151
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 151

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 152
<400> 152
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<210> 154
<211> 32
<212> PRT
<213> Artificial sequence

<220>
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<400> 154

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 155
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 155

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Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1               5                   10                  15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30
```

<210> 156
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 156

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Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1               5                   10                  15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30
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<210> 157
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 157

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Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1               5                   10                  15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr
            20                  25                  30
```

<210> 158
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 158

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Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1               5                   10                  15
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```
Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  159
<211>  32
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Framework region

<400>  159

His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1               5                   10                  15


Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  160
<211>  32
<212>  PRT
<213>  Artificial sequence

<220>
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<400>  160

Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln
1               5                   10                  15


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


<210>  161
<211>  11
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Framework region

<400>  161

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1               5                   10


<210>  162
<211>  11
<212>  PRT
<213>  Artificial sequence

<220>
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<400>  162

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1               5                   10
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<210> 163
<211> 11
<212> PRT
<213> Artificial sequence

<220>
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<400> 163

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 164
<400> 164
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<210> 165
<400> 165
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<210> 166
<400> 166
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<400> 167
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<210> 168
<211> 11
<212> PRT
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<220>
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<400> 168

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 169
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 169

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 170
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 170

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 171
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 171

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 172
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 172

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
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<210> 173
<400> 173
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<210> 174
<400> 174
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<210> 175
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 175

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 176
<400> 176
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<210> 177
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<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 177

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 178
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 178

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 179
<211> 23
<212> PRT
<213> Artificial sequence

<220>
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<400> 179

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 180
<211> 23
<212> PRT
<213> Artificial sequence

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<400> 180

Ala 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
20

<210> 181
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 181

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 182
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<400> 182

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 183
<400> 183
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<210> 184
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 184

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 185
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 185

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 186
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 186

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr
1 5 10 15

<210> 187
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 187

Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys His Leu Ile Tyr
1 5 10 15

<210> 188
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 188

Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr
1 5 10 15

<210> 189
<400> 189
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<210> 190
<400> 190
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<210> 191
<211> 15
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<220>
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<400> 191

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1               5                  10                  15


<210>  192
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<210>  193
<400>  193
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<210>  194
<211>  32
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Framework region

<400>  194

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


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


<210>  195
<211>  32
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Framework region

<400>  195

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


Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20                  25                  30


<210>  196
<211>  32
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Framework region

<400>  196

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                  10                  15


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
            20                  25                  30
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<210> 197
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<213> Artificial sequence

<220>
<223> Framework region

<400> 197

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
20 25 30

<210> 198
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 198

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 199
<400> 199
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<210> 201
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<400> 202
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<210> 203
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Framework region

<400> 203

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 204
<400> 204
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<210> 205
<211> 32
<212> PRT
<213> Artificial sequence

<220>
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<400> 205

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 206
<211> 10
<212> PRT
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<220>
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<400> 206

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 207
<211> 10
<212> PRT
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<400> 207

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 208
<211> 10
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<220>
<223> Framework region

<400> 208

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

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<400> 209

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 210
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<220>
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<400> 210

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
1 5 10

<210> 211
<211> 7
<212> PRT
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<220>
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<400> 211

Ser Val Gly Pro Met Asp Tyr
1 5

<210> 212
<211> 7
<212> PRT
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<220>
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<400> 212

Ser Val Gly Pro Phe Asp Tyr
1 5

<210> 213
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<213> Artificial sequence

<220>
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<400> 213

Ser Val Gly Pro Met Asp Val

1 5

<210> 214
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<400> 214

Ser Val Gly Pro Phe Asp Ser
1 5

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<220>
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<400> 215

Ser Val Gly Pro Phe Asp Pro
1 5

<210> 216
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<400> 216

Ser Val Gly Pro Phe Gln His
1 5

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Ser Val Gly Pro Phe Asp Val
1 5

<210> 218
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Ser Val Gly Pro Phe Asp Ile
1 5

<210> 219
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<400> 219

Ser Val Gly Pro Phe Asp Leu
1 5

<210> 220
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<400> 220

Gln His His Ser Asp Asn Pro Trp Thr
1 5

<210> 221
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<220>
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gataccaccg gagaggtgca gctggtgcag tctggagcag aggtgaaaaa gcccggagag 120

tctctgaaga tttcctgtaa gggctccggt tactcattca ctggctacaa tatgaactgg 180

gtgcgccaga tgcccgggaa aggcctcgag tggatgggca tattgatcc ttattatggt 240

ggtactacct acaaccggaa gttcaagggc caggtcacta tctccgccga caagtccatc 300

agcaccgcct acctgcaatg gagcagcctg aaggcctcgg acaccgccat gtattactgt 360

gcacgctcag tcggcccttt cgactcctgg ggccagggca ccctggtcac tgtctcctct 420

gggggtggag gctctggtgg cggtggctct ggcggaggtg gatccggtgg cggcggatct 480

ggcgggggtg gctctgaaat tgtgttgaca cagtctccag ccaccctgtc tttgtctcca 540

ggcgaaagag ccaccctctc ctgccgagca agtgaaaatg tttacagcta cttagcctgg 600

taccaacaga aacctggcca ggctcctagg ctcctcatct attttgcaaa aaccttagca 660

gaaggaattc cagccaggtt cagtggcagt ggctccggga cagacttcac tctcaccatc 720

agcagcctag agcctgaaga ttttgcagtt tattactgtc aacatcattc cgataatccg 780

tggacattcg gccaagggac caaggtggaa atcaaaggtg atcaggagcc caaatcttct 840

gacaaaactc acacatctcc accgtgccca gcacctgaac tcctgggtgg accgtcagtc 900

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 960

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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1140

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gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1260

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc caagcgacat cgccgtggag 1320

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gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1440

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1 5 10 15

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

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
35 40 45

Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly
50 55 60

Leu Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr
65 70 75 80

Asn Arg Lys Phe Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
85 90 95

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln
115 120 125

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Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
                165                 170                 175

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser
            180                 185                 190

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        195                 200                 205

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
225                 230                 235                 240

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro
                245                 250                 255

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Asp Gln Glu
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
            500
```

<210> 223
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 223
```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ala Arg Gly Val
            20
```

<210> 224
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 224
```
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
Asp Thr Thr Gly
            20
```

<210> 225
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 225
```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
```

1 5 10 15

<210> 226
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 226
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser
1 5 10 15

<210> 227
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 227
Gly Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly Gly Ala Ser
1 5 10 15

<210> 228
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 228
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
1 5 10 15

<210> 229
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence

<400> 229
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 230
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 230
Cys Pro Pro Cys Pro
1 5

<210> 231
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 231
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 232
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 232
Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys
 1   5   10   15
Pro

<210> 233
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 233
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys
 1   5   10   15
Pro

<210> 234
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 234
Gly Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 1   5   10   15
Cys Pro

<210> 235
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 235
Gly Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 1   5   10   15
Cys Pro

<210> 236
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain region

<400> 236
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35   40   45
Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser Asp Asn Pro Trp
                85   90   95
Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys
            100   105

<210> 237
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain region

<400> 237
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 238
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain region

<400> 238
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15

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

<210> 239
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain region

<400> 239
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Asn Val Tyr Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 240
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain region

<400> 240
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Ser Val Tyr Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 241
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain region

<400> 241
Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu 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
Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile
        35   40   45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
            100   105   110
Thr Val Ser Ser
        115

<210> 242
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain region

<400> 242
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30
Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50   55   60
Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

<210> 243
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain region

<400> 243
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30
Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50   55   60
Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Ser Val Gly Pro Met Asp Val Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 244
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain region

<400> 244
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
50 55 60
Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Ser Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 245
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain region

<400> 245
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
50 55 60
Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 246
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 CH2 and CH3 regions

<400> 246
```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115                 120                 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 247
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 247
```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45
Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ala Val Gln Leu Gln
        115                 120                 125
Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser Val Lys Ile Ser
    130                 135                 140
Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Lys Ala Thr
            180                 185                 190
Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Lys Ser
```

```
        195                 200                 205
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
225                 230                 235                 240
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 248
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223>  CD37 specific binding protein

<400> 248
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1                5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
```

```
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 249
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 249

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
```

```
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 250
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223>  CD37 specific binding protein

<400> 250
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1                5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
```

```
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 251
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223>  CD37 specific binding protein

<400> 251
Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu 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
Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
```

```
                100                 105                 110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Glu Ile Val Leu Thr Gln
    130                 135                 140
Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
145                 150                 155                 160
Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln
                165                 170                 175
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu
            180                 185                 190
Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205
Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr
    210                 215                 220
Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr
225                 230                 235                 240
Lys Val Glu Ile Lys Gly Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
            260                 265                 270
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        275                 280                 285
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    290                 295                 300
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
305                 310                 315                 320
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                325                 330                 335
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            340                 345                 350
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        355                 360                 365
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    370                 375                 380
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
385                 390                 395                 400
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                405                 410                 415
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            420                 425                 430
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        435                 440                 445
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    450                 455                 460
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475                 480


<210> 252
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223>  CD37 specific binding protein

<400> 252
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Ala Val Gln Leu Gln
        115                 120                 125
Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser Val Lys Ile Ser
    130                 135                 140
Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Lys Ala Thr
            180                 185                 190
Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Lys Ser
        195                 200                 205
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser
225                 230                 235                 240
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 253
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 253

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

```
    50                  55                  60
Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160
Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190
Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220
Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240
Gln Gly Thr Lys Val Glu Ile Lys Gly Asp Gln Glu Pro Lys Ser Ser
                245                 250                 255
Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
            260                 265                 270
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385                 390                 395                 400
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480
Pro Gly Lys
```

<210> 254
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 254

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
                20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
            35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
        50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 255
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 255
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 256
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 256
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Ser
1 5 10 15

<210> 257
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 257
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 258
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 258
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
1 5 10 15

<210> 259
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 259
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Ser Pro
1 5 10 15

<210> 260
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 260
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Ser Pro Arg Cys Pro
1 5 10 15

<210> 261
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region

<400> 261
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Ser Pro
 1   5   10   15

<210> 262
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 262
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20   25   30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
        35   40   45
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50   55   60
Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65   70   75   80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85   90   95
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100   105   110
Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115   120   125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130   135   140
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145   150   155   160
Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr Asn
                165   170   175
Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180   185   190
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Gly Tyr Ala Gln Lys Phe Gln
        195   200   205
Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210   215   220
Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225   230   235   240
Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245   250   255
Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260   265   270
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275   280   285
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290   295   300
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305   310   315   320
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325   330   335
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            340   345   350

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        355                 360                 365
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    370                 375                 380
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
385                 390                 395                 400
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                405                 410                 415
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            420                 425                 430
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    450                 455                 460
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
465                 470                 475                 480
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
```

<210> 263
<211> 10
<212> PRT
<213> Homo sapiens

<400> 263
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 1   5   10

<210> 264
<211> 4
<212> PRT
<213> Homo sapiens

<400> 264
Cys Pro Pro Cys
 1

<210> 265
<211> 4
<212> PRT
<213> Homo sapiens

<400> 265
Gly Thr Cys Tyr
 1

<210> 266
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 266
```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
```

65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
115 120 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
130 135 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145 150 155 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
165 170 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
180 185 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
195 200 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
210 215 220
Pro Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp
225 230 235 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
245 250 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
260 265 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
290 295 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385 390 395 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 267
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 267
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

```
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Met Glu His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 268
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 268

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1                  5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
```

```
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 269
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CD37 specific binding protein

<400> 269

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu Val Gln Leu Val
        115                 120                 125
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
    130                 135                 140
Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn Met Asn Trp Val
145                 150                 155                 160
Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
                165                 170                 175
Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys Gly Gln Val Thr
            180                 185                 190
Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser
        195                 200                 205
Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Val Gly
    210                 215                 220
Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Asp
225                 230                 235                 240
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 270
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus heavy chain sequence

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<220>
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<223> Xaa = Gln or Val

<220>
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<223> Xaa = Pro or Ala

<220>
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<222> 11
<223> Xaa = Ser or Val

<220>
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<223> Xaa = Glu or Lys

<220>
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<222> 18
<223> Xaa = Val or Leu

<220>
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<223> Xaa = Ala or Gly

<220>
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<222> 38
<223> Xaa = Lys or Arg

<220>
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<222> 40
<223> Xaa = Asn or Met

<220>
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<222> 41
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<220>
<221> VARIANT
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<220>
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<220>
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<222> 67
<223> Xaa = Lys or Gln

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<222> 68, 72
<223> Xaa = Ala or Val

<220>
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<220>
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<220>
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<220>
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<223> Xaa = Ser or Ala

<220>
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<222> 89
<223> Xaa = Glu or Ser

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<222> 93
<223> Xaa = Val or Met

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<222> 103
<223> Xaa = Met or Phe

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<222> 105
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<400> 270

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Xaa Val Gln Leu Xaa Gln Ser Gly Xaa Glu Xaa Xaa Lys Pro Gly Xaa
 1               5                  10                  15
Ser Xaa Lys Ile Ser Cys Lys Xaa Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Asn Met Asn Trp Val Xaa Gln Xaa Xaa Gly Lys Xaa Leu Glu Trp Xaa
        35                  40                  45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50                  55                  60
Lys Gly Xaa Xaa Thr Xaa Xaa Xaa Asp Lys Ser Xaa Ser Thr Ala Tyr
65                  70                  75                  80
Xaa Gln Xaa Xaa Ser Leu Xaa Xaa Xaa Asp Xaa Ala Xaa Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Val Gly Pro Xaa Asp Xaa Trp Gly Gln Gly Thr Xaa Val
            100                 105                 110
Thr Val Ser Ser
        115
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<210> 271
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus light chain sequence

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<223> Xaa = Asp or Glu

<220>
<221> VARIANT
<222> 3
<223> Xaa = Gln or Val

<220>
<221> VARIANT
<222> 4
<223> Xaa = Met or Leu

<220>
<221> VARIANT
<222> 13
<223> Xaa = Ala or Leu

<220>
<221> VARIANT
<222> 15
<223> Xaa = Val or Pro

<220>
<221> VARIANT
<222> 18
<223> Xaa = Thr or Arg

<220>
<221> VARIANT
<222> 19
<223> Xaa = Val or Ala

<220>
<221> VARIANT
<222> 21
<223> Xaa = Ile or Leu

<220>

<221> VARIANT
<222> 22, 72
<223> Xaa = Thr or Ser

<220>
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<222> 25
<223> Xaa = Thr or Ala

<220>
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<222> 40
<223> Xaa = Gln or Pro

<220>
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<222> 42
<223> Xaa = Lys or Gln

<220>
<221> VARIANT
<222> 43, 60
<223> Xaa = Ser or Ala

<220>
<221> VARIANT
<222> 45
<223> Xaa = Gln or Arg

<220>
<221> VARIANT
<222> 48, 58
<223> Xaa = Val or Ile

<220>
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<223> Xaa = Ser or Tyr

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<400> 271
Xaa Ile Xaa Xaa Thr Gln Ser Pro Ala Thr Leu Ser Xaa Ser Xaa Gly
 1   5   10   15
Glu Xaa Xaa Thr Xaa Xaa Cys Arg Xaa Ser Glu Asn Val Tyr Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Xaa Gly Xaa Xaa Pro Xaa Leu Leu Xaa
        35   40   45
Xaa Phe Ala Lys Thr Leu Ala Glu Gly Xaa Pro Xaa Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Xaa Phe Xaa Leu Xaa Ile Ser Ser Leu Xaa Pro
65   70   75   80
Glu Asp Xaa Xaa Xaa Tyr Xaa Cys Gln His His Ser Asp Asn Pro Trp
                85   90   95
Thr Phe Gly Xaa Gly Thr Xaa Xaa Glu Ile Lys
            100   105

<210> 272
<211> 5
<212> PRT
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<220>
<223> Linker peptide

<400> 272
Gly Gly Gly Gly Ser
1   5

<210> 273
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 273
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker peptide

<400> 274
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 275
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 275
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser
            20

<210> 276
<211> 4
<212> PRT
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<220>
<223> Linker peptide

<400> 276
Gly Ser Gly Ser
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<210> 277
<211> 6
<212> PRT
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<220>
<223> Linker peptide

<400> 277
Gly Ser Gly Ser Gly Ser
 1   5

<210> 278
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<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 278
Gly Ser Gly Ser Gly Ser Gly Ser
 1   5

<210> 279
<211> 10
<212> PRT
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<220>
<223> Linker peptide

<400> 279
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 280
<211> 6
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<220>
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<400> 280
Gly Gly Ser Gly Gly Ser
1 5

<210> 281
<211> 9
<212> PRT
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<220>
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<400> 281
Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5

<210> 282
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 282
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10

<210> 283
<211> 15
<212> PRT
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<220>
<223> Linker peptide

<400> 283
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10 15

<210> 284
<211> 4
<212> PRT
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<220>
<223> Linker peptide

<400> 284
Gly Gly Gly Ser
1

<210> 285
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 285
Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 286
<211> 12
<212> PRT
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<220>
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<400> 286
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 287
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<212> PRT
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<220>
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<400> 287
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 288
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
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<400> 288
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15
Gly Gly Gly Ser
20

<210> 289
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 289
Gly Gly Gly Gly Gly Ser
1 5

<210> 290
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 290
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
 1   5   10

<210> 291
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 291
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Gly Ser

<210> 292
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 292
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Gly Ser Gly Gly Gly Gly Gly Ser
            20

<210> 293
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 293
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25   30