

SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION KOBE UNIVERSITY
DAIICHI SANKYO COMPANY, LTD.

<120> Anti-SIRPA Antibodies

<130> PH-7967-PCT

<150> JP 2018-131116

<151> 2018-07-10

<160> 86

<170> PatentIn version 3.5

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<211> 11

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<213> Artificial

<220>

<223> amino acid sequence of D13 CDR-L1

<400> 1

Gly Ala Ser Lys Ser Val Arg Thr Tyr Met His

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<210> 2

<211> 7

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Ser Ala Ser Asn Leu Glu Ala

1 5

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<220>
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Gln Gln Ser Asn Glu Pro Pro Tyr Thr
1 5

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Gly Phe Thr Phe Ser Asp Tyr Gly Met Ile
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Arg Tyr Tyr Gly Phe Asn Tyr Pro Phe Asp Tyr
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<220>
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<400> 7

Lys Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala
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<210> 8
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<220>
<223> amino acid sequence of F44 CDR-L2

<400> 8

Ser Gly Ser Thr Leu Gln Ser
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<220>
<223> amino acid sequence of F44 CDR-L3

<400> 9

Gln Gln His Asn Glu Tyr Pro Pro Thr
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<210> 10
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<223> amino acid sequence of F44 CDR-H1

<400> 10

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

<210> 11
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<220>
<223> amino acid sequence of F44 CDR-H2

<400> 11

Tyr Ile Thr Thr Gly Gly Gly Ser Thr Tyr
1 5 10

<210> 12
<211> 10
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<220>
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<400> 12

Ala Asn Tyr Gly Gly Ser Tyr Phe Asp Tyr
1 5 10

<210> 13
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<212> PRT
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<220>
<223> amino acid sequence of F63 CDR-L1

<400> 13

Glu Arg Ser Ser Gly Asp Ile Gly Asp Ser Tyr Val Ser
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<210> 14
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<212> PRT
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<220>
<223> amino acid sequence of F63 CDR-L2

<400> 14

Ala Asp Asp Gln Arg Pro Ser
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<210> 15
<211> 9
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of F63 CDR-L3

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Gln Ser Tyr Asp Ser Lys Ile Asp Ile
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<210> 16
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<220>
<223> amino acid sequence of F63 CDR-H1

<400> 16

Gly Phe Ser Leu Ala Ser Tyr Ser Leu Ser
1 5 10

<210> 17
<211> 9
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of F63 CDR-H2

<400> 17

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<210> 18
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 <223> amino acid sequence of F63 CDR-H3

<400> 18

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<220>
 <223> DNA fragment comprising nucleotide sequences coding human light chain signal sequence and human kappa light chain constant region

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cgtgttcattt ttccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg	180
cctgctgaat aacttctacc ccagagaggg caaggtgcag tggaaggtgg acaacgcct	240
gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag	300
cctgagcagc accctgacct tgagcaaagc cgactacgag aagcacaagg tgtacgcctg	360
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<210> 20
<211> 462
<212> DNA
<213> Artificial

<220>

<223> DNA fragment comprising nucleotide sequences coding human light chain signal sequence and human lambda light chain constant region

<400> 20

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cctaaggctg cccctagcgt gaccctgttc cctccttcca gcgaggagct tcaagctaac	180
aaggccaccc tgggtgtgtct tatctctgac ttctaccctg gcgctgtgac cgtggcctgg	240
aaggctgaca gctcccctgt gaaggccgga gtggagacca ccacacctag caagcagtct	300
aacaacaagt acgctgccag ctctacctg agccttacct ctgagcagtg gaagtctcac	360
agaagctact cctgtcaagt gaccacagag ggcagcaccg tggagaagac cgtggctcct	420
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<210> 21
<211> 1117
<212> DNA
<213> Artificial

<220>

<223> DNA fragment comprising nucleotide sequences coding human heavy chain signal sequence and human IgG4 Pro FALA heavy chain constant region

<400> 21

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aagggcccta gcgtgttccc tctggcccct tgtagcagaa gcaccagcga gtctacagcc	180
gccctgggct gcctcgtgaa ggactacttt cccgagcccg tgaccgtgtc ctggaactct	240
ggcgctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac	300
tctctgtcca gcgtcgtgac tgtgccagc agctctctgg gcaccaagac ctacacctgt	360
aacgtggacc acaagcccag caacaccaag gtggacaagc gggtggaatc taagtacggc	420
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<210> 22
 <211> 699
 <212> DNA
 <213> Artificial

<220>

<223> nucleotide sequence coding human chimeric antibody D13 light chain

<400> 22

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tcttgtgggg ccagcaaaag tgtccgtaca tatatgcaact ggtaccaaca aaaatcggga      180
cagcaacca aactcctgat ctatagtga tccaacctag aggtcggagt cccttcagg      240
ttcagtggga gtgggtctgg gacagacttt accctcacca tagatcctgt ggagcctgat      300
gacattgcaa actattactg tcagcagagt aatgaacctc cgtacacgtt tggagctggg      360
accaagctgg aactgaaacg gacggtggcc gccccctccg tgttcattct cccccctcc      420
gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc      480
agagaggcca aggtgcagtg gaaggtggac aacgcctgc agtcgggaa ctcccaggag      540
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg      600
agcaaagccg actacgagaa gcacaagtg tacgcctgcg aggtgacca ccagggcctg      660
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<210> 23

<211> 233

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of human chimeric antibody D13 light chain

<400> 23

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1           5           10           15
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Gly Ala Tyr Gly Asp Thr Val Leu Thr Gln Ser Pro Ala Leu Ala Val
20 25 30

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

Arg Thr Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Gln Gln Pro Lys
50 55 60

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

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

Val Glu Ala Asp Asp Ile Ala Asn Tyr Tyr Cys Gln Gln Ser Asn Glu
100 105 110

Pro Pro Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145 150 155 160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 24
<211> 1398
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding human chimeric antibody D13 heavy
chain

<400> 24
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tgtttagcct ctggattcac ttccagtac tatggaatga tctgggttcg ccaggctcca 180
gggaaggggc tggagtgggt tgcattctatt agtagtagta gcagttacat ctactatgca 240
gacacagtga agggccgatt caccatctcc agagaaaatg ccaagaacac cctgttcctg 300
cacatgacca gtctgaggtc tgaagacact gccttgtatt actgtgcaag aagatactat 360
gggtttaact acccttttga ttactggggc caaggagtca tggtcacagt cagctcagcc 420
tccaccaagg gccctagcgt gttccctctg gccccttgta gcagaagcac cagcgagtct 480

acagccgccc tgggctgcct cgtgaaggac tactttcccg agcccgtagc cgtgtcctgg	540
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cagccccgcg aaccccaggt gtacacactg cctccaagcc aggaagagat gaccaagaat	1140
caggtgtccc tgacctgtct cgtgaaaggc ttctaccct ccatatcgc cgtggaatgg	1200
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ggctcattct tcctgtacag cagactgacc gtggacaaga gccggtggca ggaaggcaac	1320
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<210> 25

<211> 466

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of human chimeric antibody D13 heavy chain

<400> 25

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Leu Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asp Tyr Gly Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
65 70 75 80

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

Thr Leu Phe Leu His Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Leu
100 105 110

Tyr Tyr Cys Ala Arg Arg Tyr Tyr Gly Phe Asn Tyr Pro Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

	165		170		175
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe					
	180		185		190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val					
	195		200		205
Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val					
	210		215		220
Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys					
	225		230		235
					240
Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly					
		245		250	255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile					
	260		265		270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu					
	275		280		285
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His					
	290		295		300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg					
	305		310		315
					320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys					
		325		330	335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
450 455 460

Gly Lys
465

<210> 26
<211> 702
<212> DNA
<213> Artificial

<220>

<223> nucleotide sequence coding human chimeric antibody F44 light chain

<400> 26

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atcaattgca aggcaagtaa gagcattagc aagtatttag cctggatatca acagaaacct      180
gggaaagcaa ataagcttct tatctactct gggtaactt tgcaatctgg aactccatcg      240
aggttcagtg gcagtggatc tggtagatc ttactctca ccatcagaaa cctggagcct      300
gaagattttg gactctatta ctgtcaacag cataatgaat acccaccac gtttgagct      360
gggaccaagt tggaactgaa acggacggcg gccgccccct ccgtgttcat cttccccccc      420
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ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc      660
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<210> 27

<211> 234

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of human chimeric antibody F44 light chain

<400> 27

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1           5           10           15
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Gly Ala Tyr Gly Asp Val Gln Met Thr Gln Ser Pro Ser Asn Leu Ala
20 25 30

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

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

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

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

Asn Leu Glu Pro Glu Asp Phe Gly Leu Tyr Tyr Cys Gln Gln His Asn
100 105 110

Glu Tyr Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 28
<211> 1395
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding human chimeric antibody F44 heavy
chain

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<210> 29

<211> 465

<212> PRT

<213> Artificial

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<223> amino acid sequence of human chimeric antibody F44 heavy chain

<400> 29

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu
50 55 60

Glu Trp Val Thr Tyr Ile Thr Thr Gly Gly Gly Ser Thr Tyr Phe Arg
65 70 75 80

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

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

Tyr Tyr Cys Thr Ala Ala Asn Tyr Gly Gly Ser Tyr Phe Asp Tyr Trp
115 120 125

Gly Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr

165

170

175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
225 230 235 240

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
305 310 315 320

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
340 345 350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385 390 395 400

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
420 425 430

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
450 455 460

Lys
465

<210> 30
<211> 708
<212> DNA
<213> Artificial

<220>

<223> nucleotide sequence coding human chimeric antibody F63 light chain

<400> 30

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atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
cagttcacgc tgactcaacc aaagtccgtg tcaggagctt taagaagcac taccaccatt      120
ccctgtgagc gcagcagtgg tgacattgga gatagctatg tgagctggta ccagegacac      180
ttgggaagac ccccatcaa tgtgatctat gctgatgac aaagaccatc tgaagtgtct      240
gatcggttct cgggtccat cgacagctcc tctaactcag cctcactgac catcactaat      300
ctgcagatgg atgatgaggc cgactacttc tgtcagtctt acgatagtaa gattgacatt      360
ttcggcggtg gaaccaagct cactgtccta ggccagccta aggctgcccc tagcgtgacc      420
ctgttcctc cttccagega ggagcttcaa gctaacaagg ccaccctggg gtgtcttacc      480
tctgacttct accctggcgc tgtgaccgtg gcctggaagg ctgacagctc ccctgtgaag      540
gccggagtgg agaccaccac acctagcaag cagtctaaca acaagtacgc tgccagctcc      600
tacctgagcc ttaccctga gcagtggaag tctcacagaa gctactcctg tcaagtgacc      660
cacgagggca gcaccgtgga gaagaccgtg gctcctaccg agtgttcc      708
```

<210> 31

<211> 236

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of human chimeric antibody F63 light chain

<400> 31

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1           5           10           15
```

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

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

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

Pro Ile Asn Val Ile Tyr Ala Asp Asp Gln Arg Pro Ser Glu Val Ser
65 70 75 80

Asp Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu
85 90 95

Thr Ile Thr Asn Leu Gln Met Asp Asp Glu Ala Asp Tyr Phe Cys Gln
100 105 110

Ser Tyr Asp Ser Lys Ile Asp Ile Phe Gly Gly Gly Thr Lys Leu Thr
115 120 125

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

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
145 150 155 160

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
165 170 175

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
180 185 190

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
195 200 205

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
210 215 220

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 32

<211> 1410

<212> DNA

<213> Artificial

<220>

<223> nucleotide sequence coding human chimeric antibody F63 heavy
chain

<400> 32

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctga aggagtcagg acctggtctg gtgcagccct cagagaccct gtcctcacc 120

tgcactgtct ctgggttctc actagccagc tatagtttaa gttgggttcg ccagccttca 180

ggaaaaggtc ctgagtggat gggaagaatg tactatgatg gagacacagc atataattca 240

gctctcaaat cccgactgag catcagcagg gacacctcca agaaccaagt tttcttaaaa 300

atgaacagtc tgcaaactga tgacacaggc acttactact gtaccagaga taggagtatg 360

tttggtacgg attatcccca ctggtacttt gacttctggg gccaggaac catggtcacc 420

gtgagctcag cctccaccaa gggccctagc gtgttcctc tgccccctg tagcagaagc 480

accagcgagt ctacagccgc cctgggctgc ctcggaagg actactttcc cgagcccgtg	540
accgtgtcct ggaactctgg cgctctgaca agcggcgtgc acacctttcc agccgtgctg	600
cagagcagcg gcctgtactc tctgtccagc gtcgtgactg tgcccagcag ctctctgggc	660
accaagacct acacctgtaa cgtggaccac aagcccagca acaccaaggt ggacaagcgg	720
gtggaatcta agtacggccc tccctgccct ccttgcccag cccctgaagc cgcgggcgga	780
ccctccgtgt tctgtttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc	840
gaagtgacct gcgtggtggt ggatgtgtcc caggaagatc ccgaggtgca gttcaattgg	900
tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagttcaac	960
agcacctacc ggggtggtgtc cgtgctgaca gtgctgcacc aggactggct gaacggcaaa	1020
gagtacaagt gcaaggtgtc caacaagggc ctgcccagct ccatcgagaa aaccatcagc	1080
aaggccaagg gccagccccg cgaaccccag gtgtacacac tgccccaag ccaggaagag	1140
atgaccaaga atcaggtgtc cctgacctgt ctcggaag gtttctaccc ctccgatatc	1200
gccgtggaat gggagagcaa cggccagccc gagaacaact acaagaccac cccccctgtg	1260
ctggactccg atggttcatt cttcctgtac agcagactga ccgtggacaa gagccggtgg	1320
caggaaggca acgtgttcag ctgctccgtg atgcacgagg ccctgcacaa ccactacacc	1380
cagaagtccc tgtctctgag cctgggcaaa	1410

<210> 33

<211> 470

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of human chimeric antibody F63 heavy chain

<400> 33

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

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

Glu Trp Met Gly Arg Met Tyr Tyr Asp Gly Asp Thr Ala Tyr Asn Ser
65 70 75 80

Ala Leu Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Asn Gln
85 90 95

Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Gly Thr Tyr
100 105 110

Tyr Cys Thr Arg Asp Arg Ser Met Phe Gly Thr Asp Tyr Pro His Trp
115 120 125

Tyr Phe Asp Phe Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Ala
130 135 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
145 150 155 160

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe

175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
340 345 350

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Leu Gly Lys
465 470

<210> 34
<211> 702
<212> DNA
<213> Artificial

<220>

<223> nucleotide sequence coding hL2 light chain of humanized D13

<400> 34

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atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
gccattcagc tgacacagag ccctagcagc ctgagcgcct ctgtgggcca gagagtgacc      120
attacctgcg gcgccagcaa gagcgtgcgg acctacatgc actggtatca gcagaagccc      180
ggcaaggccc ccaagctgct gatctacagc gcctccaatc tggaagccgg cgtgcccagc      240
agattttccg gctctggcag cggcaccgac ttcaccctga caatcagcag cctgcagccc      300
gaggacttcg ccacctacta ctgccagcag agcaacgagc cccctacac ctttggccag      360
ggcaccaagc tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc      420
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taactttctac      480
cccagagagg ccaaggtgca gtggaaggct gacaacgccc tgcaagtcgg gaactcccag      540
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc      600
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc      660
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt                          702
```

<210> 35

<211> 234

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of hL2 light chain of humanized D13

<400> 35

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1           5           10          15
```

Gly Ala Tyr Gly Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Gln Arg Val Thr Ile Thr Cys Gly Ala Ser Lys Ser
35 40 45

Val Arg Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

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

Glu Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

180

185

190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 36

<211> 702

<212> DNA

<213> Artificial

<220>

<223> nucleotide sequence coding hL3 light chain of humanized D13

<400> 36

atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatacccagc tgacacagag ccctagcagc ctgtctgcca gcgtgggcca gagagtgacc 120

attacctgcg gcgccagcaa gagcgtgcgg acctacatgc actggtatca gcagaagccc 180

ggcaagcagc ccaagctgct gatctacagc gcctccaacc tggaagccgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac ttcacctga caatcagcag cctgcagccc 300

gaggacttcg ccacctacta ctgccagcag agcaacgagc cccctacac ctttgccag 360

ggcaccaagc tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaagtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt 702

<210> 37

<211> 234

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of hL3 light chain of humanized D13

<400> 37

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Thr Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Gln Arg Val Thr Ile Thr Cys Gly Ala Ser Lys Ser
35 40 45

Val Arg Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Gln Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Asn Leu Glu Ala Gly Val Pro Ser
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 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn

100	105	110
Glu Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg		
115	120	125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln		
130	135	140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr		
145	150	155
		160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser		
	165	170
		175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr		
	180	185
		190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys		
	195	200
		205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro		
	210	215
		220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	

<210> 38

<211> 702

<212> DNA

<213> Artificial

<220>

<223> nucleotide sequence coding hL4 light chain of humanized D13

<400> 38

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atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
gataccgtgc tgaccagag ccctgatagc ctggccgtgt ccctgggaca gagagccacc      120
atcaattgcg gcgccagcaa gagcgtgcgg acctacatgc actggtatca gcagaagccc      180
ggccagcagc ccaagctgct gatctacagc gcctccaacc tggaagccgg cgtgcccagc      240
agattttctg gcagcggctc cggcaccgac ttcacctga caatcagctc cctgcaggcc      300
gaggacgtgg ccgtgtacta ctgccagcag agcaacgagc cccctacac ctttgccag      360
ggcaccaagg tggaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc      420
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttttac      480
cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag      540
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc      600
ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc      660
ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gt                          702
```

<210> 39

<211> 234

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of hL4 light chain of humanized D13

<400> 39

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1           5           10          15
```

```
Gly Ala Tyr Gly Asp Thr Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
```

20

25

30

Val Ser Leu Gly Gln Arg Ala Thr Ile Asn Cys Gly Ala Ser Lys Ser
 35 40 45

Val Arg Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Gln Pro
 50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Asn Leu Glu Ala Gly Val Pro Ser
 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 Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
 100 105 110

Glu Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 40
<211> 1398
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding hH1 heavy chain of humanized D13

<400> 40
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gtgcagctgg tggaatctgg cggcggagtg gtgcagcctg gcagaagcct gagactgagc 120
tgtgccgcca gcggtttcac cttcagcgac tacggcatga tctgggtgcg ccaggcccct 180
ggcaaaggcc tggaatgggt ggccagcatc agcagcagct ccagctacat ctactacgcc 240
gacagcgtga agggccggtt caccatcagc cgggacaaca gcaagaaccg gctgtacctg 300
cagatgaaca gcctgcgggc cgaggacacc gccgtgtact attgcgccag acggtactac 360
ggcttcaact accccttcga ctactggggc cagggcacaa tggtcaccgt cagctcagcc 420
tccaccaagg gccctagcgt gttccctctg gccccttgta gcagaagcac cagcgagtct 480
acagccgccc tgggctgcct cgtgaaggac tactttcccg agcccgtgac cgtgtcctgg 540
aactctggcg ctctgacaag cggcgtgcac acctttccag ccgtgctgca gagcagcggc 600

ctgtactctc tgtccagcgt cgtgactgtg cccagcagct ctctgggcac caagacctac	660
acctgtaacg tggaccacaa gcccagcaac accaaggtgg acaagcgggt ggaatctaag	720
tacggccctc cctgccctcc ttgcccagcc cctgaagccg cgggcggacc ctccgtgttc	780
ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc	840
gtggtggtgg atgtgtccca ggaagatccc gaggtgcagt tcaattggta cgtggacggc	900
gtggaagtgc acaacgccaa gaccaagcct agagaggaac agttcaacag cacctaccgg	960
gtggtgtccg tgctgacagt gctgcaccag gactggctga acggcaaaga gtacaagtgc	1020
aaggtgtcca acaaggcct gcccagctcc atcgagaaaa ccatcagcaa ggccaagggc	1080
cagccccgcg aaccccaggt gtacacactg cctccaagcc aggaagagat gaccaagaat	1140
caggtgtccc tgacctgtct cgtgaaaggc ttctaccctt ccgatatcgc cgtggaatgg	1200
gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgat	1260
ggctcattct tcctgtacag cagactgacc gtggacaaga gccggtggca ggaaggcaac	1320
gtgttcagct gctccgtgat gcacgaggcc ctgcacaacc actacacca gaagtcctg	1380
tctctgagcc tgggcaaa	1398

<210> 41

<211> 466

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of hH1 heavy chain of humanized D13

<400> 41

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1			5					10					15		

Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

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

Ser Asp Tyr Gly Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
65 70 75 80

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

Arg Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Tyr Tyr Gly Phe Asn Tyr Pro Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180	185	190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
195	200	205
Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val		
210	215	220
Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys		
225	230	235
		240
Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly		
	245	250
		255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile		
	260	265
		270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu		
	275	280
		285
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His		
290	295	300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg		
305	310	315
		320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys		
	325	330
		335
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu		
	340	345
		350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
450 455 460

Gly Lys
465

<210> 42
<211> 1398
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding hH2 heavy chain of humanized D13

<400> 42

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gtgcagctgg tggaatctgg cggcggagtg gtgcagcctg gcagaagcct gagactgagc	120
tgtgccgcca gcggtttcac cttcagcgac tacggcatga tctgggtgcg ccaggcccct	180
ggcaaaggcc tggaatgggt ggccagcatc agcagcagct ccagctacat ctactacgcc	240
gacagcgtga agggccggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg	300
cagatgaaca gcctgcgggc cgaggacacc gccgtgtact attgcgccag acggtactac	360
ggcttcaact accccttcga ctactggggc cagggcacaa tggtcaccgt cagctcagcc	420
tccaccaagg gccctagcgt gttccctctg gccccttgta gcagaagcac cagcgagtct	480
acagccgccc tgggctgcct cgtgaaggac tactttcccg agcccgtagc cgtgtcctgg	540
aactctggcg ctctgacaag cggcgtgcac acctttccag ccgtgctgca gagcagcggc	600
ctgtactctc tgtccagcgt cgtgactgtg cccagcagct ctctgggcac caagacctac	660
acctgtaacg tggaccacaa gccagcaac accaaggtgg acaagcgggt ggaatctaag	720
tacggccctc cctgccctcc ttgccagcc cctgaagccg cgggcggacc ctccgtgttc	780
ctgttccccc caaagcccaa ggacaccctg atgacagcc ggacccccga agtgacctgc	840
gtggtggtgg atgtgtccca ggaagatccc gaggtgcagt tcaattggta cgtggacggc	900
gtggaagtgc acaacgcaa gaccaagcct agagaggaac agttcaacag cacctaccgg	960
gtggtgtccg tgctgacagt gctgcaccag gactggctga acggcaaaga gtacaagtgc	1020
aaggtgtcca acaaggcct gccagctcc atcgagaaaa ccatcagcaa ggccaagggc	1080
cagccccgcg aaccccaggt gtacacactg cctccaagcc aggaagagat gaccaagaat	1140
caggtgtccc tgacctgtct cgtgaaaggc ttctaccctt ccgatatcgc cgtggaatgg	1200
gagagcaacg gccagccccg gaacaactac aagaccaccc cccctgtgct ggactccgat	1260

ggctcattct tcctgtacag cagactgacc gtggacaaga gccggtggca ggaaggcaac 1320

gtgttcagct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagtcctg 1380

tctctgagcc tgggcaaa 1398

<210> 43

<211> 466

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of hH2 heavy chain of humanized D13

<400> 43

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

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

Ser Asp Tyr Gly Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
65 70 75 80

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

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val

100	105	110
Tyr Tyr Cys Ala Arg Arg Tyr Tyr Gly Phe Asn Tyr Pro Phe Asp Tyr		
115	120	125
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
130	135	140
Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser		
145	150	155
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
165	170	175
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
180	185	190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
195	200	205
Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val		
210	215	220
Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys		
225	230	235
Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly		
245	250	255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile		
260	265	270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
305 310 315 320

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His

435

440

445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
 450 455 460

Gly Lys
 465

<210> 44

<211> 1140

<212> DNA

<213> Artificial

<220>

<223> nucleotide sequence coding human SIRPA variant 1 ECD

<400> 44

atggaacctg ccggacctgc ccctggcaga ctgggacctc tgctgtgtct gctgctggcc	60
gcctcttttg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac	120
aagagcgtgc tgggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg	180
atccccgtgg gccccatcca gtggtttaga ggcgctggcc ctggccgcga gctgatctac	240
aatcagaaaag agggccactt cccagagtg accaccgtgt ccgacctgac caagcggaac	300
aacatggact tcagcatccg gatcggaac atcacccctg ccgatgccgg cacctactac	360
tcgctgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc	420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct	480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc	540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct	600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca agtggtgtgt gacccgcgaa	660

gatgtgcaca gccaaagtgat ctgcgaggtg gccacgtga cactgcagg cgatcctctg 720
agaggaaccg ccaacctgtc cgagacaatc agagtgtccc ccacctgga agtgaccag 780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc 840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc 900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg 960
tcgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc 1020
gtgtccaaga gccacgatct gaaggtgtca gccatccca aagagcagg ctccaacaca 1080
gccgccgaga acaccggcag caacgagcgg aacatctacc accaccatca ccaccactga 1140

<210> 45

<211> 379

<212> PRT

<213> Artificial

<220>

<223> amino acid sequencde of human SIRPA variant 1 ECD

<400> 45

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu

225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr His His His His His His
370 375

<210> 46
<211> 468
<212> DNA

<213> Artificial

<220>

<223> nucleotide sequence coding human SIRPA variant 1 IgV

<400> 46

atggaacctg ccggacctgc ccctggcaga ctgggacctc tgctgtgtct gctgctggcc 60

gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac 120

aagagcgtgc tgggtggccgc tggcgaaacc gccacctga gatgtacagc caccagcctg 180

atccccgtgg gcccacatcca gtggttttaga ggcgctggcc ctggccgcga gctgatctac 240

aatcagaaaag agggccactt cccagagtg accaccgtgt ccgacctgac caagcggaac 300

aacatggact tcagcatccg gatcggaac atcaccctg ccgatgccgg cacctactac 360

tgctgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc 420

gagctgagcg tgcgggctaa acctagccac caccaccatc accactga 468

<210> 47

<211> 155

<212> PRT

<213> Artificial

<220>

<223> amino acid sequencde of human SIRPA variant 1 IgV

<400> 47

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

35	40	45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly		
50	55	60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr		
65	70	75
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu		
85	90	95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr		
100	105	110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser		
115	120	125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val		
130	135	140
Arg Ala Lys Pro Ser His His His His His His		
145	150	155

<210> 48
 <211> 1137
 <212> DNA
 <213> Artificial

<220>
 <223> nucleotide sequence coding human SIRPA variant 2 ECD

<400> 48
 atggaacctg ccggacctgc ccctggcaga ctgggacctc tgctgtgtct gctgctggcc

60

gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac	120
aagagcgtgt cagtggccgc tggcgagtct gccatcctgc actgtaccgt gaccagcctg	180
atccccgtgg gccccatcca gtggttttaga ggcgctggac ctgccagaga gctgatctac	240
aaccagaaag agggccactt cccagagtg accaccgtgt ccgagagcac caagcgcgag	300
aacatggact tcagcatcag catctccaac atcacccctg ccgacgccgg cacctactac	360
tgcgtgaagt tcagaaaggg cagccccgac accgagttca agagcggagc cggcacagag	420
ctgtctgtgc gggccaaacc ttctgcccct gtggtgtctg gaccagccgc cagagctaca	480
cctcagcaca ccgtgtcttt tacctgcgag agccacggct tcagccccag agacatcacc	540
ctgaagtggc tcaagaacgg caacgagctg agcgacttcc agaccaacgt ggaccctgtg	600
ggcgagtccg tgtcctacag catccacagc accgccaagg tggctgtgac ccgcgaagat	660
gtgcacagcc aagtgatctg cgaggtggcc cacgtgacac tgcagggcga tcctctgaga	720
ggaaccgcca acctgagcga gacaatcaga gtgccccca ccctggaagt gaccagcag	780
ccagtgcggg ccgagaacca agtgaacgtg acctgtcaag tgcggaagtt ctacccccag	840
cggtgcagc tgacctggct ggaaaacggc aatgtgtccc ggaccgagac agccagcacc	900
gtgacagaga acaaggatgg cacctacaat tggatgtctt ggctgctcgt gaacgtgtcc	960
gcccaccggg acgatgtgaa gctgacatgc caggtggaac acgacggcca gcctgccgtg	1020
tctaagagcc acgacctgaa ggtgtcagcc catcccaaag agcagggtc caacacagcc	1080
gccgagaaca ccggcagcaa cgagcggaac atctaccacc accatcacca ccaactga	1137

<210> 49
 <211> 378
 <212> PRT
 <213> Artificial

<220>

<223> amino acid sequencde of human SIRPA variant 2 ECD

<400> 49

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr

145	150	155	160
Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro			
	165	170	175
Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp			
	180	185	190
Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile			
	195	200	205
His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln			
	210	215	220
Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg			
225	230	235	240
Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu			
	245	250	255
Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys			
	260	265	270
Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu			
	275	280	285
Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn			
	290	295	300
Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser			
305	310	315	320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
355 360 365

Arg Asn Ile Tyr His His His His His His
370 375

<210> 50
<211> 465
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding human SIRPA variant 2 IgV

<400> 50
atggaacctg ccggacctgc ccctggcaga ctgggacctc tgctgtgtct gctgctggcc 60
gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgcac 120
aagagcgtgt cagtggccgc tggcgagtct gccatcctgc actgtaccgt gaccagcctg 180
atccccgtgg gccccatcca gtggtttaga ggcgctggac ctgccagaga gctgatctac 240
aaccagaaag agggccactt cccagagtg accaccgtgt ccgagagcac caagcgcgag 300
aacatggact tcagcatcag catctccaac atcaccctg ccgacgccgg cacctactac 360
tgctgaagt tcagaaaggg cagccccgcac accgagttca agagcggagc cggcacagag 420
ctgtctgtgc gggccaagcc tagccaccac caccatcacc attga 465

<210> 51
<211> 154
<212> PRT
<213> Artificial

<220>

<223> amino acid sequencde of human SIRPA variant 2 IgV

<400> 51

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser His His His His His His
145 150

<210> 52
<211> 1137
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence coding monkey SIRPA ECD

<400> 52
atggaacccg ccggaacctgc tcttggcaga ctgggacctc tgctgtgtct gctgctgacc 60
gccagctgtg cttggagcgg agtgctgggc gaagaggaac tgcaagtgat ccagcccgag 120
aagtccgtgt ctgtggccgc tggcgatagc gccaccctga attgcaccgt gtccagcctg 180
atccccgtgg gccctatcca gtggtttaga ggcgctggcc ctggcagaga gctgatctac 240
aacctgaaag agggccactt ccccagagt accgccgtgt ccgacccac caagcggaac 300
aacatggact tcagcatccg gatcagcaac atcacccctg ccgacgccgg cacctactac 360
tgcgtaagt tcagaaagg cagccccgac gtggaactga agtctggcgc cggaacagag 420
ctgagcgtgc gggccaaacc ttctgccct gtggtgtctg gacctgccgt gcgggctaca 480
gccgagcaca ccgtgtcttt tacctgcgag agccacggct tcagccccag agacatcacc 540
ctgaagtggg tcaagaacgg caacgagctg tccgacgtgc agaccaacgt ggaccctgcc 600
ggcaagagcg tgtcctacag catcagatcc accgccagag tgctgctgac aagacgggac 660
gtgcacagcc aagtgatctg cgaggtggcc cacgtgacac tgcagggcga tcctctgaga 720

ggcaccgcca atctgagcga ggctatccgg gtgcccccat tcctggaagt gaccacagcag 780
agcatgcggg ccgacaacca agtgaacgtg acctgccaag tgaccaagtt ctacccccag 840
cggctgcagc tgacctggct ggaaaacggc aatgtgtccc ggaccgagat ggcctctgcc 900
ctgcccgaga acaaggatgg cacctacaat tggaccagct ggctgctcgt gaacgtgtcc 960
gcccaccggg acgatgtgaa gctgacatgc caggtggaac acgacggcca gcccgccgtg 1020
aacaagagct tcagcgtgaa agtgtctgct cccccaaag agcagggcag caacactgcc 1080
gccgagaaca ccggcaccaa cgagcggaac atctaccatc accaccatca tcaactga 1137

<210> 53

<211> 378

<212> PRT

<213> Artificial

<220>

<223> amino acid sequencde of monkey SIRPA ECD

<400> 53

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Thr Ala Ser Cys Ala Trp Ser Gly Val Leu Gly Glu Glu
20 25 30

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

Asp Ser Ala Thr Leu Asn Cys Thr Val Ser Ser Leu Ile Pro Val Gly
50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr

65		70		75		80									
Asn	Leu	Lys	Glu	Gly	His	Phe	Pro	Arg	Val	Thr	Ala	Val	Ser	Asp	Pro
			85					90						95	
Thr	Lys	Arg	Asn	Asn	Met	Asp	Phe	Ser	Ile	Arg	Ile	Ser	Asn	Ile	Thr
			100					105					110		
Pro	Ala	Asp	Ala	Gly	Thr	Tyr	Tyr	Cys	Val	Lys	Phe	Arg	Lys	Gly	Ser
		115						120					125		
Pro	Asp	Val	Glu	Leu	Lys	Ser	Gly	Ala	Gly	Thr	Glu	Leu	Ser	Val	Arg
		130					135					140			
Ala	Lys	Pro	Ser	Ala	Pro	Val	Val	Ser	Gly	Pro	Ala	Val	Arg	Ala	Thr
145					150					155					160
Ala	Glu	His	Thr	Val	Ser	Phe	Thr	Cys	Glu	Ser	His	Gly	Phe	Ser	Pro
				165					170					175	
Arg	Asp	Ile	Thr	Leu	Lys	Trp	Phe	Lys	Asn	Gly	Asn	Glu	Leu	Ser	Asp
			180						185					190	
Val	Gln	Thr	Asn	Val	Asp	Pro	Ala	Gly	Lys	Ser	Val	Ser	Tyr	Ser	Ile
		195					200					205			
Arg	Ser	Thr	Ala	Arg	Val	Leu	Leu	Thr	Arg	Arg	Asp	Val	His	Ser	Gln
		210					215				220				
Val	Ile	Cys	Glu	Val	Ala	His	Val	Thr	Leu	Gln	Gly	Asp	Pro	Leu	Arg
225					230					235					240

Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Phe Leu Glu
245 250 255

Val Thr Gln Gln Ser Met Arg Ala Asp Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Thr Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Met Ala Ser Ala Leu Pro Glu Asn
290 295 300

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

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Asn Lys Ser Phe Ser Val Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Thr Asn Glu
355 360 365

Arg Asn Ile Tyr His His His His His His
370 375

<210> 54
<211> 1107
<212> DNA
<213> Artificial

<220>

<223> nucleotide sequence coding human CD47-Fc

<400> 54

atgtggcccc	tggtagcggc	gctgttgctg	ggctcggcgt	gctgcggatc	agctcagcta	60
ctatttaata	aaacaaaatc	tgtagaattc	acgttttgta	atgacactgt	cgtcattcca	120
tgctttgtta	ctaatatgga	ggcacaaaac	actactgaag	tatacgtaaa	gtggaaattt	180
aaaggaagag	atattttacac	ctttgatgga	gctctaaaca	agtccactgt	ccccactgac	240
tttagtagtg	caaaaattga	agtctcaca	ttactaaaag	gagatgcctc	tttgaagatg	300
gataagagtg	atgctgtctc	acacacagga	aactacactt	gtgaagtaac	agaattaacc	360
agagaaggtg	aaacgatcat	cgagctaaaa	tatcgtgttg	tttcatggtt	ttctccaaat	420
gaagacaaaa	ctcacacatg	cccaccctgc	ccagcacctg	aactcctggg	gggaccctca	480
gtcttcctct	tcccccaaaa	acccaaggac	accctcatga	tctcccgga	ccctgaggtc	540
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	600
gacggcgtgg	aggtgcataa	tgccaagaca	aagccccggg	aggagcagta	caacagcacg	660
taccgggtgg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	720
aagtgaagg	tctccaacaa	agccctccca	gcccccatcg	agaaaaccat	ctccaaagcc	780
aaaggccagc	cccgggaacc	acaggtgtac	accctgcccc	catcccggga	ggagatgacc	840
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	atcccagcga	catcgccgtg	900
gagtgggaga	gcaatggcca	gcccgagaac	aactacaaga	ccaccctcc	cgtgctggac	960
tccgacggct	ccttcttct	ctacagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1020
ggcaacgtct	tctcatgctc	cgtgatgcat	gaggtctctg	acaaccacta	caccagaag	1080
agcctctccc	tgtctcccgg	caaatga				1107

<210> 55
<211> 368
<212> PRT
<213> Artificial

<220>
<223> amino acid sequencde of human CD47-Fc

<400> 55

Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly
1 5 10 15

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

Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala
35 40 45

Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp
50 55 60

Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp
65 70 75 80

Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala
85 90 95

Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr
100 105 110

Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu
115 120 125

Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asp Lys Thr
130 135 140

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
145 150 155 160

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
195 200 205

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

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

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

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

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

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

290

295

300

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 325 330 335

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 340 345 350

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 355 360 365

<210> 56

<211> 504

<212> PRT

<213> Homo sapiens

<400> 56

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
 20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
 50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 57

<211> 503

<212> PRT

<213> Homo sapiens

<400> 57

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile

195		200		205
His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln				
210		215		220
Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg				
225		230		235
				240
Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu				
		245		250
				255
Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys				
		260		265
				270
Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu				
		275		280
				285
Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn				
		290		295
				300
Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser				
305		310		315
				320
Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly				
		325		330
				335
Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro				
		340		345
				350
Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu				
		355		360
				365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 58

<211> 503

<212> PRT

<213> Macaca fascicularis

<400> 58

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Thr Ala Ser Cys Ala Trp Ser Gly Val Leu Gly Glu Glu
20 25 30

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

Asp Ser Ala Thr Leu Asn Cys Thr Val Ser Ser Leu Ile Pro Val Gly
50 55 60

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

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

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Val Glu Leu Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr
145 150 155 160

Ala Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Val Gln Thr Asn Val Asp Pro Ala Gly Lys Ser Val Ser Tyr Ser Ile
195 200 205

Arg Ser Thr Ala Arg Val Leu Leu Thr Arg Arg Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Phe Leu Glu
245 250 255

Val Thr Gln Gln Ser Met Arg Ala Asp Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Thr Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Met Ala Ser Ala Leu Pro Glu Asn
290 295 300

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

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Asn Lys Ser Phe Ser Val Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Thr Asn Glu
355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Arg Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Gly Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 59
<211> 509
<212> PRT
<213> Mus musculus

<400> 59

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

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

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

Asp Ser Thr Val Leu Asn Cys Thr Leu Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Pro Ser Arg Leu Leu Ile Tyr
65 70 75 80

Ser Phe Ala Gly Glu Tyr Val Pro Arg Ile Arg Asn Val Ser Asp Thr
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

Pro Ala Asp Ala Gly Ile Tyr Tyr Cys Val Lys Phe Gln Lys Gly Ser
115 120 125

Ser Glu Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr
130 135 140

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

Gly Ile Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe
165 170 175

Ser Pro Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu
180 185 190

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

Asn Ile Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val Asn
210 215 220

Ser Lys Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro
225 230 235 240

Leu Arg Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr
245 250 255

Val Lys Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu
260 265 270

Thr Cys Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp
275 280 285

Leu Glu Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr

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

Thr Gly Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu
465 470 475 480

Asp Met Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro
485 490 495

Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 60

<211> 509

<212> PRT

<213> Mus musculus

<400> 60

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

Cys Leu Leu Leu Ser Ala Ser Cys Phe Cys Thr Gly Ala Thr Gly Thr
20 25 30

Glu Val Lys Val Thr Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly
35 40 45

Asp Ser Thr Ile Leu Asn Cys Thr Val Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Gln Ser Arg Leu Leu Ile Tyr
65 70 75 80

Ser Phe Thr Gly Glu His Phe Pro Arg Val Arg Asn Val Ser Asp Thr
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

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

Ser Glu Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr
130 135 140

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

Gly Ile Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe
165 170 175

Ser Pro Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu
180 185 190

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

Asn Ile Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val Asn
210 215 220

Ser Lys Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro
225 230 235 240

Leu Arg Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr
245 250 255

Val Lys Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu
260 265 270

Thr Cys Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp
275 280 285

Leu Glu Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr
290 295 300

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

Ser Ser Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His
325 330 335

Asp Gln Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Phe Ala
340 345 350

His Ser Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Asp Asn Asn Ala
355 360 365

Thr His Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu
370 375 380

Leu Val Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln
385 390 395 400

Lys Lys Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu
405 410 415

Lys Asn Ala Arg Glu Ile Thr Gln Ile Gln Asp Thr Asn Asp Ile Asn
420 425 430

Asp Ile Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu Lys Lys Pro Ala
435 440 445

Pro Arg Ala Pro Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Glu
450 455 460

Thr Gly Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu
465 470 475 480

Asp Met Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro
485 490 495

Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 61
<211> 513
<212> PRT
<213> Mus musculus

<400> 61

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

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

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

Asp Ser Thr Val Leu Asn Cys Thr Leu Thr Ser Leu Leu Pro Val Gly

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

Ser Lys Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro
225 230 235 240

Leu Arg Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr
245 250 255

Val Lys Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu
260 265 270

Thr Cys Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp
275 280 285

Leu Glu Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr
290 295 300

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

Ser Ser Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His
325 330 335

Asp Gln Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Leu Ala
340 345 350

His Ser Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Gly Asn Asn Ala
355 360 365

Thr His Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu
370 375 380

Leu Val Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln

385 390 395 400

Lys Lys Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu
405 410 415

Lys Asn Ala Arg Glu Ile Thr Gln Val Gln Ser Leu Ile Gln Asp Thr
420 425 430

Asn Asp Ile Asn Asp Ile Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu
435 440 445

Lys Lys Pro Ala Pro Arg Ala Pro Glu Pro Asn Asn His Thr Glu Tyr
450 455 460

Ala Ser Ile Glu Thr Gly Lys Val Pro Arg Pro Glu Asp Thr Leu Thr
465 470 475 480

Tyr Ala Asp Leu Asp Met Val His Leu Ser Arg Ala Gln Pro Ala Pro
485 490 495

Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Gln Arg
500 505 510

Lys

<210> 62

<211> 507

<212> PRT

<213> Mus musculus

<400> 62

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

Cys Leu Leu Leu Ser Ala Ser Cys Phe Cys Thr Gly Ala Thr Arg Thr
20 25 30

Glu Val Lys Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly
35 40 45

Asp Ser Thr Val Leu Asn Cys Thr Leu Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Gln Ser Arg Gln Leu Ile Tyr
65 70 75 80

Ser Phe Thr Thr Glu His Phe Pro Arg Val Thr Asn Val Ser Asp Ala
85 90 95

Thr Lys Arg Ser Asn Leu Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

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

Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr Val Leu
130 135 140

Ala Lys Pro Ser Pro Pro Glu Val Ser Gly Pro Ala Asp Arg Gly Ile
145 150 155 160

Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe Ser Pro
165 170 175

Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu His Pro
180 185 190

Leu Glu Thr Thr Val Asn Pro Ser Gly Lys Asn Val Ser Tyr Asn Ile
195 200 205

Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val His Ser Lys
210 215 220

Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro Leu Arg
225 230 235 240

Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr Val Lys
245 250 255

Val Thr Gln Gln Ser Pro Thr Ser Met Ser Gln Val Asn Leu Thr Cys
260 265 270

Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr Lys Asn
290 295 300

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

Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His Asp Gln
325 330 335

Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Leu Ala His Ser
340 345 350

Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Gly Asn Asn Ala Thr His
355 360 365

Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu Leu Val
370 375 380

Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln Lys Lys
385 390 395 400

Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Ile Gln Asp Thr Asn Asp Ile Asn Asp Ile
420 425 430

Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu Lys Lys Pro Ala Pro Arg
435 440 445

Ala Pro Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Glu Thr Gly
450 455 460

Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met
465 470 475 480

Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe
485 490 495

Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 63
<211> 503
<212> PRT
<213> Homo sapiens

<400> 63

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu Leu Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg

130	135	140																	
Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr																			
145	150	155	160																
Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro																			
	165	170	175																
Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp																			
	180	185	190																
Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile																			
	195	200	205																
His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln																			
	210	215	220																
Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg																			
225	230	235	240																
Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu																			
	245	250	255																
Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys																			
	260	265	270																
Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu																			
	275	280	285																
Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn																			
	290	295	300																

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr

465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 64
<211> 504
<212> PRT
<213> Homo sapiens

<400> 64

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 65
<211> 504
<212> PRT
<213> Homo sapiens

<400> 65

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu

225		230		235		240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu						
	245		250		255	
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr						
	260		265		270	
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu						
	275		280		285	
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu						
	290		295		300	
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val						
305		310		315		320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp						
	325		330		335	
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His						
	340		345		350	
Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn						
	355		360		365	
Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val						
	370		375		380	
Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys						
385		390		395		400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 66

<211> 504

<212> PRT

<213> Homo sapiens

<400> 66

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Pro Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 67

<211> 503

<212> PRT

<213> Homo sapiens

<400> 67

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Gly Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195 200 205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
245 250 255

Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
290 295 300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly

	325		330		335
Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro					
	340		345		350
Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu					
	355		360		365
Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala					
	370		375		380
Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala					
	385		390		395
					400
Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala					
	405		410		415
Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn					
	420		425		430
Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn					
	435		440		445
His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu					
	450		455		460
Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr					
	465		470		475
					480
Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala					
	485		490		495

Ser Val Gln Val Pro Arg Lys
500

<210> 68
<211> 503
<212> PRT
<213> Homo sapiens

<400> 68

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195 200 205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
245 250 255

Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
290 295 300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 69
<211> 504
<212> PRT
<213> Homo sapiens

<400> 69

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu

85

90

95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Ile Thr
 100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 115 120 125

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 130 135 140

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
 145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
 165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
 180 185 190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
 195 200 205

Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
 210 215 220

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
 225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
 245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu

420

425

430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
 435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
 450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
 465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
 485 490 495

Ala Ser Val Gln Val Pro Arg Lys
 500

<210> 70

<211> 503

<212> PRT

<213> Homo sapiens

<400> 70

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Arg Val Ala Gly Glu Glu
 20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195 200 205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
245 250 255

Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
260 265 270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
290 295 300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305 310 315 320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
325 330 335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
340 345 350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
485 490 495

Ser Val Gln Val Pro Arg Lys
500

<210> 71

<211> 296

<212> PRT

<213> Artificial

<220>

<223> amino acid sequencde of human SIRPA_V2_IgV form

<400> 71

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
165 170 175

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
180 185 190

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
195 200 205

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
210 215 220

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
225 230 235 240

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
245 250 255

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
260 265 270

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
275 280 285

Ala Ser Val Gln Val Pro Arg Lys
290 295

<210> 72

<211> 397

<212> PRT

<213> Artificial

<220>

<223> amino acid sequencde of human SIRPA V2_IgV_IgC1 form

<400> 72

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
50 55 60

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
85 90 95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
130 135 140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145 150 155 160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
180 185 190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
195 200 205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
210 215 220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225 230 235 240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
245 250 255

Val Thr Gln Gln Pro Val Arg Ala Ile Tyr Ile Val Val Gly Val Val
260 265 270

Cys Thr Leu Leu Val Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg
275 280 285

Ile Arg Gln Lys Lys Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His
290 295 300

Glu Pro Glu Lys Asn Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile
305 310 315 320

Thr Tyr Ala Asp Leu Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln
325 330 335

Ala Ala Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser
340 345 350

Pro Gln Pro Ala Ser Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met
355 360 365

Val His Leu Asn Arg Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro
370 375 380

Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Pro Arg Lys
385 390 395

<210> 73

<211> 507

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of mouse SIRPA mutant hmSIRPA_delta 0

<400> 73

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

Cys Leu Leu Leu Ser Ala Ser Cys Phe Cys Thr Gly Ala Thr Gly Thr
20 25 30

Glu Val Lys Val Thr Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly
35 40 45

Asp Ser Thr Ile Leu Asn Cys Thr Val Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Gln Ser Arg Leu Leu Ile Tyr
65 70 75 80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Arg Asn Val Ser Asp Thr
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

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

Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr Val Leu
130 135 140

Ala Lys Pro Ser Pro Pro Glu Val Ser Gly Pro Ala Asp Arg Gly Ile
145 150 155 160

Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe Ser Pro
165 170 175

Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu His Pro
180 185 190

Leu Glu Thr Thr Val Asn Pro Ser Gly Lys Asn Val Ser Tyr Asn Ile
195 200 205

Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val Asn Ser Lys
210 215 220

Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro Leu Arg
225 230 235 240

Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr Val Lys
245 250 255

Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu Thr Cys
260 265 270

Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp Leu Glu
275 280 285

Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr Lys Asn
290 295 300

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

Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His Asp Gln
325 330 335

Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Phe Ala His Ser
340 345 350

Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Asp Asn Asn Ala Thr His
355 360 365

Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu Leu Val
370 375 380

Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln Lys Lys
385 390 395 400

Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Ile Gln Asp Thr Asn Asp Ile Asn Asp Ile
420 425 430

Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu Lys Lys Pro Ala Pro Arg
435 440 445

Ala Pro Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Glu Thr Gly
450 455 460

Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met
465 470 475 480

Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe
485 490 495

Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 74

<211> 509

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of mouse SIRPA mutant hmSIRPA_delta 1

<400> 74

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

Cys Leu Leu Leu Ser Ala Ser Cys Phe Cys Thr Gly Ala Thr Gly Thr
20 25 30

Glu Val Lys Val Thr Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly
35 40 45

Asp Ser Thr Ile Leu Asn Cys Thr Val Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Gln Ser Arg Leu Leu Ile Tyr
65 70 75 80

Asn Gln Lys Glu Glu His Phe Pro Arg Val Arg Asn Val Ser Asp Thr
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

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

Ser Glu Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr
130 135 140

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

Gly Ile Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe
165 170 175

Ser Pro Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu
180 185 190

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

Asn Ile Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val Asn
210 215 220

Ser Lys Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro
225 230 235 240

Leu Arg Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr
245 250 255

Val Lys Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu
260 265 270

Thr Cys Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp
275 280 285

Leu Glu Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr
290 295 300

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

Ser Ser Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His
325 330 335

Asp Gln Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Phe Ala
340 345 350

His Ser Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Asp Asn Asn Ala
355 360 365

Thr His Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu
370 375 380

Leu Val Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln
385 390 395 400

Lys Lys Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu
405 410 415

Lys Asn Ala Arg Glu Ile Thr Gln Ile Gln Asp Thr Asn Asp Ile Asn
420 425 430

Asp Ile Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu Lys Lys Pro Ala
435 440 445

Pro Arg Ala Pro Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Glu
450 455 460

Thr Gly Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu
465 470 475 480

Asp Met Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro
485 490 495

Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 75
<211> 509
<212> PRT
<213> Artificial

<220>

<223> amino acid sequence of mouse SIRPA mutant hmSIRPA_delta 2

<400> 75

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

Cys Leu Leu Leu Ser Ala Ser Cys Phe Cys Thr Gly Ala Thr Gly Thr
20 25 30

Glu Val Lys Val Thr Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly
35 40 45

Asp Ser Thr Ile Leu Asn Cys Thr Val Thr Ser Leu Leu Pro Val Gly
50 55 60

Pro Ile Arg Trp Tyr Arg Gly Val Gly Gln Ser Arg Leu Leu Ile Tyr
65 70 75 80

Ser Phe Thr Glu Gly His Phe Pro Arg Val Arg Asn Val Ser Asp Thr
85 90 95

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Asn Val Thr
100 105 110

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

Ser Glu Pro Asp Thr Glu Ile Gln Ser Gly Gly Gly Thr Glu Val Tyr
130 135 140

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

Gly Ile Pro Asp Gln Lys Val Asn Phe Thr Cys Lys Ser His Gly Phe
165 170 175

Ser Pro Arg Asn Ile Thr Leu Lys Trp Phe Lys Asp Gly Gln Glu Leu
180 185 190

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

Asn Ile Ser Ser Thr Val Arg Val Val Leu Asn Ser Met Asp Val Asn
210 215 220

Ser Lys Val Ile Cys Glu Val Ala His Ile Thr Leu Asp Arg Ser Pro
225 230 235 240

Leu Arg Gly Ile Ala Asn Leu Ser Asn Phe Ile Arg Val Ser Pro Thr
245 250 255

Val Lys Val Thr Gln Gln Ser Pro Thr Ser Met Asn Gln Val Asn Leu
260 265 270

Thr Cys Arg Ala Glu Arg Phe Tyr Pro Glu Asp Leu Gln Leu Ile Trp
275 280 285

Leu Glu Asn Gly Asn Val Ser Arg Asn Asp Thr Pro Lys Asn Leu Thr
290 295 300

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

Ser Ser Ala His Arg Glu Asp Val Val Phe Thr Cys Gln Val Lys His
325 330 335

Asp Gln Gln Pro Ala Ile Thr Arg Asn His Thr Val Leu Gly Phe Ala
340 345 350

His Ser Ser Asp Gln Gly Ser Met Gln Thr Phe Pro Asp Asn Asn Ala
355 360 365

Thr His Asn Trp Asn Val Phe Ile Gly Val Gly Val Ala Cys Ala Leu
370 375 380

Leu Val Val Leu Leu Met Ala Ala Leu Tyr Leu Leu Arg Ile Lys Gln
385 390 395 400

Lys Lys Ala Lys Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu
405 410 415

Lys Asn Ala Arg Glu Ile Thr Gln Ile Gln Asp Thr Asn Asp Ile Asn
420 425 430

Asp Ile Thr Tyr Ala Asp Leu Asn Leu Pro Lys Glu Lys Lys Pro Ala
435 440 445

Pro Arg Ala Pro Glu Pro Asn Asn His Thr Glu Tyr Ala Ser Ile Glu
450 455 460

Thr Gly Lys Val Pro Arg Pro Glu Asp Thr Leu Thr Tyr Ala Asp Leu
465 470 475 480

Asp Met Val His Leu Ser Arg Ala Gln Pro Ala Pro Lys Pro Glu Pro
485 490 495

Ser Phe Ser Glu Tyr Ala Ser Val Gln Val Gln Arg Lys
500 505

<210> 76

<211> 5

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of 81st to 85th amino acids in amino acid
sequence of mouse SIRPA mutant hmSIRPA_delta 0

<400> 76

Asn Gln Lys Glu Gly
1 5

<210> 77

<211> 5

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of 81st to 85th amino acids in amino acid
sequence of mouse SIRPA mutant hmSIRPA_delta 1

<400> 77

Asn Gln Lys Glu Glu
1 5

<210> 78
<211> 5
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of 81st to 85th amino acids in amino acid
sequence of BALB/C mouse SIRPA

<400> 78

Ser Phe Thr Gly Glu
1 5

<210> 79
<211> 5
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of 126th to 130th amino acids in amino acid
sequence of BALB/C mouse SIRPA

<400> 79

Arg Gly Ser Ser Glu
1 5

<210> 80
<211> 5
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of 81st to 85th amino acids in amino acid
sequence of mouse SIRPA mutant hmSIRPA_delta 2

<400> 80

Ser Phe Thr Glu Gly

1

5

<210> 81

<211> 466

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of OSE-172 antibody heavy chain
(OSE-172_hG4Pro)

<400> 81

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1				5					10					15	

Val	Leu	Ser	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Glu	Ser	Leu	Arg	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
		35					40					45			

Thr	Ser	Tyr	Trp	Val	His	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu
	50					55				60					

Glu	Trp	Met	Gly	Asn	Ile	Asp	Pro	Ser	Asp	Ser	Asp	Thr	His	Tyr	Ser
65					70					75				80	

Pro	Ser	Phe	Gln	Gly	His	Val	Thr	Leu	Ser	Val	Asp	Lys	Ser	Ile	Ser
			85						90					95	

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

Tyr Tyr Cys Val Arg Gly Gly Thr Gly Thr Leu Ala Tyr Phe Ala Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
225 230 235 240

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
305 310 315 320

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 82
<211> 239
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of OSE-172 antibody light chain (OSE-172_hK)

<400> 82

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Leu Val His Ser Tyr Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Arg
50 55 60

Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Phe Gln Gly Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 83

<211> 459

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of KWAR23 antibody heavy chain
(KWAR23_hG4Pro)

<400> 83

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Ile His Trp Val Gln Gln Arg Thr Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Ala
65 70 75 80

Pro Lys Phe Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

Thr Ala Tyr Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu

145		150		155		160
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly						
	165		170		175	
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser						
	180		185		190	
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu						
	195		200		205	
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr						
	210		215		220	
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro						
225		230		235		240
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro						
	245		250		255	
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr						
	260		265		270	
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn						
	275		280		285	
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg						
	290		295		300	
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val						
305		310		315		320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
405 410 415

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
450 455

<210> 84
<211> 235
<212> PRT
<213> Artificial

<220>

<223> amino acid sequence of KWAR23 antibody light chain (KWAR23_hK)

<400> 84

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

Ala Ser Pro Gly Glu Lys Val Thr Leu Thr Cys Ser Ala Ser Ser Ser
35 40 45

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

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Ser Met Glu Ala Glu Asp Ala Ala Ser Tyr Phe Cys His Gln Trp
100 105 110

Ser Ser Tyr Pro Arg Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

145 150 155 160

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 85
<211> 467
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of ADU-1805 antibody heavy chain
(ADU-1805_hG2)

<400> 85

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser Thr Phe
35 40 45

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

Glu Trp Ile Gly Ala Ile Tyr Pro Val Asn Ser Asp Thr Thr Tyr Asn
65 70 75 80

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

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Ser Phe Tyr Tyr Ser Leu Asp Ala Ala Trp Phe
115 120 125

Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
145 150 155 160

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
210 215 220

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
225 230 235 240

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
305 310 315 320

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 86

<211> 234

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of ADU-1805 antibody light chain (ADU-1805_hK)

<400> 86

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

Ile Gly Ser Arg Leu Asn Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

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

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

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

Ser Ser Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230