

SEQUENCE LISTING

<110> Synthron Biopharmaceuticals B.V.

<120> Humanized Anti-SIRPalpha antibodies

<130> P1729PC00

<150> EP 18206594.6

<151> 2018-11-15

<160> 76

<170> PatentIn version 3.5

<210> 1

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 1

Val Gln Leu Val Glu Ser Gly Gly Arg Leu Gly Gln Pro Gly Thr Pro
1 5 10 15

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

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Gly
85 90 95

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 2
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized LCVR

<400> 2

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Trp His Tyr Ile Ser Arg
85 90 95

Ser Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 3
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized HCVR

<400> 3

Val Gln Leu Val Glu Ser Gly Gly Arg Leu Val Gln Pro Gly Thr Pro
1 5 10 15

Leu Thr Leu Ser Cys Thr Val Ser Gly Phe Ser Leu Ser Ser Tyr Val

20 25 30

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Gly
85 90 95

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 4
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized HCVR

<400> 4

Val Gln Leu Val Glu Ser Gly Gly Arg Leu Gly Gln Pro Gly Thr Ser
1 5 10 15

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

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

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

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 5
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized HCVR

<400> 5

Val Gln Leu Val Glu Ser Gly Gly Arg Leu Gly Gln Pro Gly Thr Ser
1 5 10 15

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

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Gly
85 90 95

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 6
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized HCVR

<400> 6

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

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

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

Thr Ile Gly Thr Gly Val Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Leu Gln Met Thr
65 70 75 80

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

Ala Trp Asn Asp Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 7
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized LCVR

<400> 7

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

Asp Arg Val Thr Leu Thr Cys Gln Ala Ser Gln Ser Val Tyr Gly Asn
20 25 30

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

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

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

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

Glu Ala Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 8

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 8

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

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

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

Thr Ile Gly Thr Gly Val Ile Thr Tyr Phe Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Met Glu Leu Ser
65 70 75 80

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Ser
85 90 95

Ala Trp Asn Asp Pro Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 9

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized LCVR

<400> 9

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

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

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

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

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

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

Glu Ala Asp Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 10

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 10

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

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

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

Thr Ile Gly Thr Gly Val Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Leu Gln Met Thr
65 70 75 80

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

Ala Trp Asn Asp Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 11

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 11

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

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

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

Thr Ile Gly Thr Gly Val Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Leu Gln Met Thr
65 70 75 80

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

Ala Trp Asn Asp Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 12

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 12

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

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

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

Thr Ile Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Met Glu Leu Ser
65 70 75 80

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

Ala Trp Asn Asp Pro Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 13

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized HCVR

<400> 13

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

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

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

Thr Ile Gly Thr Gly Val Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

Arg Phe Thr Gly Ser Lys Thr Ser Ser Thr Ala Tyr Leu Gln Met Thr
65 70 75 80

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

Ala Trp Asn Asp Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 14

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

<220>
<223> humanized HCVR

<400> 14

Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Gly Gln Pro Gly Thr Pro
1 5 10 15

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

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Gly
85 90 95

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 15
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized HCVR

<400> 15

Val Gln Leu Val Glu Ser Gly Gly Arg Leu Val Gln Pro Gly Thr Pro
1 5 10 15

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

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

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
50 55 60

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

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

Pro Leu Gly Val Asp Tyr Phe Asn Ile Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 16

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 12C4

<400> 16

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

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser

65 70 75 80

Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
85 90 95

Tyr Cys Ile Arg Asp Tyr Asp Tyr Asp Ala Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 17

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 12C4

<400> 17

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

1 5 10 15

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

Gly Tyr Asn Tyr Met Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 18
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain 29AM4-5 LALA mutant

<400> 18

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Ser Tyr Tyr
20 25 30

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

Ala Ser Val Tyr Ser Ser Phe Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Thr Phe Pro Gly Leu Phe Asp Gly Phe Phe Gly Ala Tyr
100 105 110

Leu Gly Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160

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

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

180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
210 215 220

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Ala Ala 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 His Glu Asp Pro Glu Val Lys 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 Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp
355 360 365

Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 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 Pro Gly Lys
450 455

<210> 19

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 29AM4-5 LALA mutant

<400> 19

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Val Asn Trp Val Gly
85 90 95

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

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu

115 120 125

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 20

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 12C4 LALA mutant

<400> 20

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

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
65 70 75 80

Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
85 90 95

Tyr Cys Ile Arg Asp Tyr Asp Tyr Asp Ala Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 21

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 12C4 LALA mutant

<400> 21

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

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

Gly Tyr Asn Tyr Met Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 22

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

<220>
<223> heavy chain KWAR23 LALA mutant

<400> 22

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

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

Tyr Ile His Trp Val Gln Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

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

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

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

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

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

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

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

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

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

405 410 415

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

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

<210> 23
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain KWAR23 LALA mutant

<400> 23

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

Glu Lys Val Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

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

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

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

Ala Glu Asp Ala Ala Ser Tyr Phe Cys His Gln Trp Ser Ser Tyr Pro
85 90 95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 24
<211> 330
<212> PRT
<213> Homo sapiens

<400> 24

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325

330

<210> 25

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> human IgG1 antibody heavy chain constant region LALA mutant

<400> 25

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

1 5 10 15

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

20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35 40 45

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

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr

65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

115 120 125

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

130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

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

165 170 175

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

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

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

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

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

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

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

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

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

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

<210> 26
<211> 107
<212> PRT
<213> Homo sapiens

<400> 26

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

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

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

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 27
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> HAVT20 leader sequence

<400> 27

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

Glu Phe Ser Met Ala
20

<210> 28
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain leader sequence

<400> 28

Met Gly Trp Thr Leu Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val His Ser

<210> 29
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain leader sequence

<400> 29

Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1 5 10 15

Gly Thr Arg Cys
20

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain CDR1

<400> 30

Ser Tyr Val Met Gly
1 5

<210> 31
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain CDR2

<400> 31

Ile Ile Ser Ser Ser Gly Ser Pro Tyr Tyr Ala Ser Trp Val Asn Gly
1 5 10 15

<210> 32
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> heavy chain CDR3

<400> 32

Val Gly Pro Leu Gly Val Asp Tyr Phe Asn Ile
1 5 10

<210> 33

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR1

<400> 33

Arg Ala Ser Gln Ser Ile Asn Ser Tyr Leu Ala
1 5 10

<210> 34

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR2

<400> 34

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 35

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR3

<400> 35

Gln Ser Trp His Tyr Ile Ser Arg Ser Tyr Thr
1 5 10

<210> 36

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR1

<400> 36

Ser His Gly Ile Ser

1 5

<210> 37

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR2

<400> 37

Thr Ile Gly Thr Gly Val Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

1 5 10 15

<210> 38

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR3

<400> 38

Gly Ser Ala Trp Asn Asp Pro Phe Asp Tyr

1 5 10

<210> 39

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR1

<400> 39

Gln Ala Ser Gln Ser Val Tyr Gly Asn Asn Asp Leu Ala

1 5 10

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR2

<400> 40

Leu Ala Ser Thr Leu Ala Thr
1 5

<210> 41

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR3

<400> 41

Leu Gly Gly Gly Asp Asp Glu Ala Asp Asn Thr
1 5 10

<210> 42

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR2

<400> 42

Thr Ile Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 43

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR3

<400> 43

Gly Ser Ala Trp Asn Asp Pro Phe Asp Ile
1 5 10

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR2

<400> 44

Thr Ile Gly Thr Gly Val Ile Thr Tyr Phe Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain CDR3

<400> 45

Gly Ser Ala Trp Asn Asp Pro Phe Asp Pro
1 5 10

<210> 46

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain CDR3

<400> 46

Leu Gly Gly Gly Asp Asp Glu Ala Asp Asn Val
1 5 10

<210> 47

<211> 443

<212> PRT

<213> Mus musculus

<400> 47

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

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

Tyr Ile His Trp Val Gln Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Arg Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser
180 185 190

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

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

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

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

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

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

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
290 295 300

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

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

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

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
355 360 365

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

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

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

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
420 425 430

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440

<210> 48

<211> 215

<212> PRT

<213> Mus musculus

<400> 48

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

Glu Lys Val Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

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

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

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

Ala Glu Asp Ala Ala Ser Tyr Phe Cys His Gln Trp Ser Ser Tyr Pro
85 90 95

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

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

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

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

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

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

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

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 49
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain humanized HEFLB

<400> 49

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

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

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

Gly Asn Ile Asp Pro Ser Asp Ser Asp Thr His Tyr Ser Pro Ser Phe
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 50

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain humanized HEFLB

<400> 50

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

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

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

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

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

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

<210> 51

<211> 618

<212> PRT

<213> Artificial Sequence

<220>

<223> human SIRPalpha1 extracellular domain 1-370, Avi-FXa-Fc tag

<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 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 Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
370 375 380

Trp His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro Cys
385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
435 440 445

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

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545 550 555 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
565 570 575

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 52

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> human SIRPalphaBIT, extracellular domain 1-370, Avi-FXa-Fc tag

<400> 52

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 Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
370 375 380

Glu Trp His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro
385 390 395 400

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
405 410 415

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
420 425 430

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
435 440 445

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
450 455 460

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
485 490 495

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
500 505 510

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
515 520 525

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
530 535 540

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
545 550 555 560

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
565 570 575

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
580 585 590

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
595 600 605

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 53

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> human SIRPbeta1v1, extracellular domain, Avi-FXa-Fc tag

<400> 53

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

Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu
20 25 30

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

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

Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn
65 70 75 80

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

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

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

Asp Asp Val 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 Val Arg Ala Thr
145 150 155 160

Pro 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

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

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

Val Ile Cys Glu Ile Ala His Ile 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 Thr Leu Glu
245 250 255

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

Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu
275 280 285

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

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

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

Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln
340 345 350

Lys Glu His Gly Ser Asp Ile Thr His Glu Ala Ala Leu Ala Pro Thr
355 360 365

Ala Pro Leu Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
370 375 380

Glu Trp His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro
385 390 395 400

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
405 410 415

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
420 425 430

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
435 440 445

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
450 455 460

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
485 490 495

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
500 505 510

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

515 520 525

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
530 535 540

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
545 550 555 560

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
565 570 575

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
580 585 590

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
595 600 605

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 54

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> human SIRPbeta1v2, extracellular domain, Avi-FXa-Fc tag

<400> 54

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

Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Glu Glu
20 25 30

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

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

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

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

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

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

Asp His Val 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 Ala Gly Asp 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 Leu 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 Pro Gly Pro Ala Leu Ala Ser Ala
355 360 365

Ala Pro Leu Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
370 375 380

Glu Trp His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro
385 390 395 400

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
405 410 415

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
420 425 430

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
435 440 445

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
450 455 460

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

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
485 490 495

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
500 505 510

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
515 520 525

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
530 535 540

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
545 550 555 560

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
565 570 575

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
580 585 590

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
595 600 605

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 55

<211> 649

<212> PRT

<213> Artificial Sequence

<220>

<223> human SIRPgamma, extracellular domain, Avi-FXa-Fc tag

<400> 55

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

Leu Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu Leu
20 25 30

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

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

Leu Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln

65 70 75 80

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

Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro Ala
 100 105 110

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

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

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

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

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

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

Ser Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln Val
 210 215 220

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

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

Thr Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys Gln
 260 265 270

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

Gly Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn Lys
290 295 300

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

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

Leu Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln Lys
340 345 350

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

Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu
370 375 380

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
385 390 395 400

Gly Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
405 410 415

His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro Cys Pro
420 425 430

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
435 440 445

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
450 455 460

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
465 470 475 480

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
485 490 495

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
500 505 510

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
515 520 525

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
530 535 540

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
545 550 555 560

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
565 570 575

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
580 585 590

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
595 600 605

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
610 615 620

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
625 630 635 640

Lys Ser Leu Ser Leu Ser Pro Gly Lys
645

<210> 56

<211> 618

<212> PRT

<213> Artificial Sequence

<220>

<223> cynomolgus monkey SIRPalph, extracellular domain, Avi-FXa-Fc tag

<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 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 Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
370 375 380

Trp His Glu Ile Glu Gly Arg Asp Lys Thr His Thr Cys Pro Pro Cys
385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
435 440 445

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

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545 550 555 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
565 570 575

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 57

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1H9 including leader sequence

<400> 57

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

Glu Phe Ser Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

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

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

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

His Ile Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser
85 90 95

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

Ala Val Tyr Tyr Cys Ala Thr Gly Tyr Gly Ser Ser Tyr Gly Tyr Phe
115 120 125

Asp 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 Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
370 375 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys

465

470

<210> 58

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 1H9 including leader sequence

<400> 58

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

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

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

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

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

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

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

Tyr Gly Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile 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> 59

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 40A-1 including leader sequence

<400> 59

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

Glu Phe Ser Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

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

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

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

His Ile Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser
85 90 95

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

Ala Val Tyr Tyr Cys Ala Thr Gly Tyr Gly Ser Ser Tyr Gly Tyr Phe
115 120 125

Asp 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 Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
370 375 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 60

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 40A-1 including leader sequence

<400> 60

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

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

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

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

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

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

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

Ala Ser Ser Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile 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> 61
<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 40A-2 including leader sequence

<400> 61

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

Glu Phe Ser Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser
35 40 45

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

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

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

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

Ala Val Tyr Tyr Cys Thr Arg Ser Phe Tyr Tyr Ser Leu Asp Ala Ala
115 120 125

Trp Phe Val Tyr Trp Gly Gln Gly Thr Leu 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
165 170 175

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
195 200 205

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
210 215 220

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
225 230 235 240

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
245 250 255

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

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

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

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

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

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

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

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

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

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

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

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

Leu Ser Pro Gly Lys
465

<210> 62

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 40A-2 including leader sequence

<400> 62

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

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

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

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

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

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

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

Ala Ser Ser Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile 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> 63

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain AB3-LALA including leader sequence

<400> 63

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

Glu Phe Ser Met Ala Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu
20 25 30

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

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

Gly Leu Glu Phe Val Ala Gln Ile Thr Ser Gly Ser Arg Thr Tyr Tyr
65 70 75 80

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

Ser Thr Val Lys Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly
100 105 110

Ile Tyr Phe Cys Ala Arg Asp Phe Gly Ser Gly Val Gly Ser Ile Asp
115 120 125

Ala Trp Gly Asn Gly Thr Glu Val Ile Val Ser Ser Ala Ser Thr Lys
130 135 140

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

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

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

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 Ala Leu Pro
340 345 350

Ala Pro 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 Arg Asp Glu Leu 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 Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 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 Pro Gly Lys
465 470

<210> 64
<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain AB3-LALA including leader sequence

<400> 64

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

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

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

Gly Trp Tyr Gln Gln Arg Ser Pro Gly Ser Ala Pro Val Thr Val Ile
50 55 60

Tyr Arg Asp Asn Gln Arg Pro Ser Asn Ile Pro Ser Arg Phe Ser Ser
65 70 75 80

Ser Thr Ser Gly Ser Thr Ser Thr Leu Thr Ile Thr Gly Val Gln Ala
85 90 95

Asp Asp Glu Ser Val Tyr Phe Cys Gly Ser Tyr Asp Gly Ser Ile Asp
100 105 110

Ile Phe Gly Ala Gly Thr Thr Leu Thr Val Leu Arg Thr Val Ala Ala
115 120 125

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
225 230

<210> 65

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain AB25-LALA including leader sequence

<400> 65

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

Glu Phe Ser Met Ala Asp Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Arg Pro Gly Glu Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe
35 40 45

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

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

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

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

Val Tyr Tyr Cys Ala Arg Glu Thr Trp Asn His Leu Phe Asp Tyr Trp
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
465

<210> 66

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain AB25-LALA including leader sequence

<400> 66

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

Glu Phe Ser Met Ala Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser
20 25 30

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

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

Val Thr Leu Ile Tyr Ser Asp Asp Lys Arg Pro Ser Asn Ile Pro Glu
65 70 75 80

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

Gly Val Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Gly Tyr Asp
100 105 110

Gln Ser Ser Tyr Thr Asn Pro Phe Gly Gly Gly Thr Lys Leu Thr Val
115 120 125

Leu Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 67

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain AB115-LALA including leader sequence

<400> 67

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

Glu Phe Ser Met Ala Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
20 25 30

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

Phe Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Glu Gly
50 55 60

Leu Glu Trp Val Ser Arg Ile Asn Ser Gly Gly Gly Gly Thr Asp Tyr
65 70 75 80

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

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

Val Tyr Tyr Cys Ala Lys Gln Tyr Asp Trp Asn Ser Phe Phe Asp Tyr
115 120 125

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

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
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 Gln Thr Tyr Ile Cys Asn Val
210 215 220

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
245 250 255

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

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

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

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

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

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

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

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

Leu Ser Pro Gly Lys
465

<210> 68

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain AB115-LALA including leader sequence

<400> 68

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

Glu Phe Ser Met Ala Glu Thr Val Leu Thr Gln Ser Pro Ala Thr Leu
20 25 30

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

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

Pro Arg Leu Leu Ile Tyr Asp Ala Thr Asn Arg Ala Thr Gly Ile Ser
65 70 75 80

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 69

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain AB119-LALA including leader sequence

<400> 69

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

Glu Phe Ser Met Ala Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val
20 25 30

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

Phe Ser Asn Phe Ala Met Thr Trp Val Arg Gln Ala Pro Gly Glu Gly
50 55 60

Leu Glu Trp Val Ser Thr Ile Gly Ser Gly Asp Thr Tyr Tyr Ala Asp

65 70 75 80

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

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

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

Tyr Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

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

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

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 Ala Leu Pro
340 345 350

Ala Pro 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 Arg Asp Glu Leu 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 Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 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 Pro Gly Lys
465 470

<210> 70

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain AB119-LALA including leader sequence

<400> 70

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

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

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

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

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

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 71

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain AB136-LALA including leader sequence

<400> 71

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

Glu Phe Ser Met Ala Asp Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Arg Pro Gly Glu Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Asp Met Asn Trp Val Arg Gln Ala Pro Gly Glu
50 55 60

Gly Leu Glu Trp Val Ser Leu Ile Ser Gly Ser Gly Glu Ile Ile Tyr
65 70 75 80

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

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

Ala Val Tyr Tyr Cys Ala Lys Glu Asn Asn Arg Tyr Arg Phe Phe Asp
115 120 125

Asp Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

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

145	150	155	160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro			
165	170	175	
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr			
180	185	190	
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val			
195	200	205	
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn			
210	215	220	
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro			
225	230	235	240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
245	250	255	
Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
260	265	270	
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
275	280	285	
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
290	295	300	
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
305	310	315	320
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 Ala Leu Pro			
340	345	350	
Ala Pro 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 Arg Asp Glu Leu 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 Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 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 Pro Gly Lys
465 470

<210> 72

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain AB136-LALA including leader sequence

<400> 72

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

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

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

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

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro

65 70 75 80

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 73

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 3F9-LALA including leader sequence

<400> 73

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

Glu Phe Ser Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys
50 55 60

Arg Leu Glu Trp Val Ala Thr Ile Ser Asp Tyr Gly Gly Ser Tyr Thr
65 70 75 80

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

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

Thr Ala Leu Tyr Tyr Cys Ala Arg Pro Pro Tyr Asp Asp Tyr Tyr Gly
115 120 125

Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala
130 135 140

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

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

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
195 200 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
210 215 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys

225	230	235	240
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro			
	245	250	255
Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys			
	260	265	270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
	275	280	285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr			
	290	295	300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu			
305	310	315	320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			
	325	330	335
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys			
	340	345	350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln			
	355	360	365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu			
	370	375	380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro			
385	390	395	400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn			
	405	410	415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu			
	420	425	430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
	435	440	445

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 74

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 3F9-LALA including leader sequence

<400> 74

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

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

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

Ser Val Ser Ser Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65 70 75 80

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
100 105 110

Cys Gln His Asn Arg Glu Leu Pro Cys Thr Phe Gly Gly Gly Thr Lys
115 120 125

Leu 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> 75

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 7H9-LALA including leader sequence

<400> 75

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

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

Val Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Phe
 35 40 45

Ser Ile Ser Arg Gly Tyr Asp Trp His Trp Ile Arg His Phe Pro Gly
 50 55 60

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

Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr His Asp Thr Ser
 85 90 95

Lys Asn His Phe Phe Leu Arg Leu Asn Ser Val Thr Ala Glu Asp Thr
100 105 110

Ala Thr Tyr Tyr Cys Ala Arg Gly Gly Gly Ala Trp Phe Thr Tyr Trp
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

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

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

305	310	315	320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
	325	330	335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
	340	345	350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
	355	360	365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
	370	375	380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
385	390	395	400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
	405	410	415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
	420	425	430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
	435	440	445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
	450	455	460
Ser Pro Gly Lys			
465			

<210> 76

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 7H9-LALA including leader sequence

<400> 76

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

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

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

Ser Ile Ser Asp Ser Leu His Trp Tyr His Gln Lys Ser His Glu Ser
50 55 60

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

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

Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
100 105 110

His Ser Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile 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