

P-2019-16740 TRADUCCIÓN LISTADO DE SECUENCIAS.txt
SEQUENCE LISTING

<110> Compugen Ltd.
<120> ANTI-TIGIT ANTIBODIES AND METHODS OF USE
<130> 114386-5008-WO
<140> Filed herewith
<141> 2017-08-17
<150> US 62/477,974
<151> 2017-03-28
<150> US 62/513,775
<151> 2017-06-01
<150> US 62/417,217
<151> 2016-11-03
<150> US 62/376,335
<151> 2016-08-17
<150> US 62/513,771
<151> 2017-06-01
<150> US 62/376,334
<151> 2016-08-17
<150> US 62/376,334
<151> 2016-08-17
<150> US 62/376,334
<151> 2016-08-17
<150> US 62/513,916
<151> 2017-06-01
<150> US 62/538,561
<151> 2017-07-28
<160> 611
<170> PatentIn version 3.5
<210> 1
<211> 204
<212> PRT
<213> Artificial Sequence
<220>
<223> Human PVRIG sequence starting from position 21
<400> 1
Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys
1 5 10 15
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala
20 25 30
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly
35 40 45
Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asn Gly Ala Gly
50 55 60
Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
65 70 75 80
Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
85 90 95
Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
100 105 110
Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
115 120 125
Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
130 135 140
Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
145 150 155 160
Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
165 170 175
Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
180 185 190

Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala
195 200

<210> 2
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PVRIG sequence starting from position 1

<400> 2

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

Leu Glu Gly Ala Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu
20 25 30

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

Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe
50 55 60

Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro
65 70 75 80

Asn Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly
85 90 95

Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser
100 105 110

Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala
115 120 125

Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp
130 135 140

Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala
145 150 155 160

Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu
165 170 175

Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu
180 185 190

Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg
195 200 205

Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala
210 215 220

<210> 3
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PVLR2 alpha isoform

<400> 3

Met Ala Arg Ala Ala Ala Leu Leu Pro Ser Arg Ser Pro Pro Thr Pro
1 5 10 15

Leu Leu Trp Pro Leu Leu Leu Leu Leu Leu Glu Thr Gly Ala Gln
20 25 30

Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly
35 40 45

Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr
50 55 60

Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln
65 70 75 80

Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro
85 90 95

P-2019-16740 TRADUCCIÓN LISTADO DE SECUENCIAS.txt

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

Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His
115 120 125

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

Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala
145 150 155 160

Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp
165 170 175

Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala
180 185 190

Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln
195 200 205

Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr
210 215 220

Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val
225 230 235 240

Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu Ser
245 250 255

Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn Trp
260 265 270

Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser Asn
275 280 285

Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe Pro
290 295 300

Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val Asp
305 310 315 320

Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val Gly
325 330 335

Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Arg Ala
340 345 350

Ser Pro Arg Asp Val Gly Pro Leu Val Trp Gly Ala Val Gly Gly Thr
355 360 365

Leu Leu Val Leu Leu Leu Leu Ala Gly Gly Ser Leu Ala Phe Ile Leu
370 375 380

Leu Arg Val Arg Arg Arg Arg Lys Ser Pro Gly Gly Ala Gly Gly Gly
385 390 395 400

Ala Ser Gly Asp Gly Gly Phe Tyr Asp Pro Lys Ala Gln Val Leu Gly
405 410 415

Asn Gly Asp Pro Val Phe Trp Thr Pro Val Val Pro Gly Pro Met Glu
420 425 430

Pro Asp Gly Lys Asp Glu Glu Glu Glu Glu Glu Lys Ala Glu
435 440 445

Lys Gly Leu Met Leu Pro Pro Pro Pro Ala Leu Glu Asp Asp Met Glu
450 455 460

Ser Gln Leu Asp Gly Ser Leu Ile Ser Arg Arg Ala Val Tyr Val
465 470 475

<210> 4
<211> 518
<212> PRT
<213> Artificial Sequence

<220>

<223> Human PVLR2 delta isoform

<400> 4

Met Ala Arg Ala Ala Ala Leu Leu Pro Ser Arg Ser Pro Pro Thr Pro
1 5 10 15

Leu Leu Trp Pro Leu Leu Leu Leu Leu Leu Glu Thr Gly Ala Gln
20 25 30

Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly
35 40 45

Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr
50 55 60

Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln
65 70 75 80

Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro
85 90 95

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

Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His
115 120 125

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

Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala
145 150 155 160

Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp
165 170 175

Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala
180 185 190

Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln
195 200 205

Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr
210 215 220

Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val
225 230 235 240

Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu Ser
245 250 255

Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn Trp
260 265 270

Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser Asn
275 280 285

Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe Pro
290 295 300

Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val Asp
305 310 315 320

Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val Gly
325 330 335

Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn Thr
340 345 350

Ala Gly Ala Gly Ala Thr Gly Gly Ile Ile Gly Gly Ile Ile Ala Ala
355 360 365

Ile Ile Ala Thr Ala Val Ala Ala Thr Gly Ile Leu Ile Cys Arg Gln
370 375 380

Gln Arg Lys Glu Gln Thr Leu Gln Gly Ala Glu Glu Asp Glu Asp Leu
385 390 395 400

Glu Gly Pro Pro Ser Tyr Lys Pro Pro Thr Pro Lys Ala Lys Leu Glu
405 410 415

Ala Gln Glu Met Pro Ser Gln Leu Phe Thr Leu Gly Ala Ser Glu His
420 425 430

Ser Pro Leu Lys Thr Pro Tyr Phe Asp Ala Gly Ala Ser Cys Thr Glu
435 440 445

Gln Glu Met Pro Arg Tyr His Glu Leu Pro Thr Leu Glu Glu Arg Ser
450 455 460

Gly Pro Leu His Pro Gly Ala Thr Ser Leu Gly Ser Pro Ile Pro Val
465 470 475 480

Pro Pro Gly Pro Pro Ala Val Glu Asp Val Ser Leu Asp Leu Glu Asp
485 490 495

Glu Glu Gly Glu Glu Glu Glu Tyr Leu Asp Lys Ile Asn Pro Ile
500 505 510

Tyr Asp Ala Leu Ser Tyr
515

<210> 5
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy (vh) domain

<400> 5

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 6

Gly Tyr Thr Phe Thr Asp Tyr Asn
1 5

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 7

Ile Tyr Pro Tyr Ile Gly Gly Ser
1 5

<210> 8
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 8

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr
 1 5 10

<210> 9
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC

<400> 9

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp 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> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 10

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 Val Ser Glu Asn Ile Tyr Ser Asn
20 25 30

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

Tyr Glu Ala Thr Asn Leu Ala Glu 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 His Phe Trp Gly Thr Pro Tyr
85 90 95

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

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

<220>
<223> vLCDR1

<400> 11

Glu Asn Ile Tyr Ser Asn
1 5

<210> 12
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 12

Glu Ala Thr
1

<210> 13
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 13

Gln His Phe Trp Gly Thr Pro Tyr Thr
1 5

<210> 14

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 14

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 Val Ser Glu Asn Ile Tyr Ser Asn
20 25 30

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

Tyr Glu Ala Thr Asn Leu Ala Glu 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 His Phe Trp Gly Thr Pro Tyr
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 15

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable heavy (vh) domain

<400> 15

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80 85 90

```

65              70              75              80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
           85           90           95

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
           100          105          110

Thr Leu Val Thr Val Ser Ser
      115

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 16
Gly Tyr Ala Phe Thr Asn Tyr Leu
1              5

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 17
Ile Asn Pro Gly Ser Gly Gly Ile
1              5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 18
Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr
1              5              10

<210> 19
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC

<400> 19
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1              5              10              15

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65           70           75           80

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

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
           100          105          110

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 20
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 20

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

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

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

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

65 70 75 80

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

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

<210> 21
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 21

Gln Ser Val Arg Ile Ala
 1 5

<210> 22
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 22

Leu Ala Ser
 1

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

<220>
 <223> vLCDR3

<400> 23

Leu Gln His Trp Asn Tyr Pro Tyr Thr
 1 5

<210> 24
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 24

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 25
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VH

<400> 25

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

<210> 26
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VH

<400> 26

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10 15

<210> 27
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VH

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Asn, Gln, Ser or Ala

<400> 27

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

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

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

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

Lys Ser Lys Ala Thr Leu Ser Ala Asp Asn Pro Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Xaa Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Pro Val Thr Val Ser Ser
115 120

<210> 28
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.518 antibody VH

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Tyr, Gln, Ser or Ala

<400> 28

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg

<210> 29
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.518 antibody VH

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Asn, Gln, Ser or Ala

<220>
<221> MOD_RES
<222> (105)..(105)
<223> Asn, Gln, Ser or Ala

<400> 29

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Xaa Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 30
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VH

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Asn, Gln, Ser or Ala

<400> 30

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

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

Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Xaa Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 31
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VH

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Asn, Gln, Ser or Ala

<400> 31

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

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

Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

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

Gln Gly Arg Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

Ala Arg Glu Asp Lys Thr Ala Arg Xaa Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.518 antibody VH

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Asn, Gln, Ser or Ala

<220>
<221> MOD_RES
<222> (105)..(105)
<223> Asn, Gln, Ser or Ala

<400> 32

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

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

Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

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

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

Ala Arg Glu Asp Lys Thr Ala Arg Xaa Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 33
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.518 antibody VL

<400> 33

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

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

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

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

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

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

<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VL

<400> 34

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 1 5 10

<210> 35
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VL

<220>
 <221> MOD_RES
 <222> (28)..(28)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (53)..(53)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (92)..(92)
 <223> Trp, Tyr, Phe or His

<400> 35

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

Glu Thr Val Thr Ile Ile Cys Arg Val Ser Glu Xaa Ile Tyr Ser Xaa
 20 25 30

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

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

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

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Xaa Gly Thr Pro Tyr
 85 90 95

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

<210> 36
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VL

<220>
 <221> MOD_RES
 <222> (28)..(28)
 <223> Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Tyr, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (53)..(53)
 <223> Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (92)..(92)
 <223> Tyr, Phe or His

<400> 36

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 Xaa Ile Ser Ser Xaa
 20 25 30

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

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

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

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

<210> 37
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VL

<220>
 <221> MOD_RES
 <222> (28)..(28)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (53)..(53)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (92)..(92)
 <223> Trp, Tyr, Phe or His

<400> 37

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 Val Ser Glu Xaa Ile Tyr Ser Xaa
 20 25 30

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

Tyr Glu Ala Thr Xaa Leu Ala Glu 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 His Phe Xaa Gly Thr Pro Tyr
 85 90 95

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

<210> 38
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.518 antibody VL

<220>
 <221> MOD_RES
 <222> (28)..(28)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Asn, Gln, Ser, Ala or Asp

<220>
 <221> MOD_RES
 <222> (53)..(53)
 <223> Asn, Gln, Ser, Ala or Asp

```

<220>
<221> MOD_RES
<222> (92)..(92)
<223> Trp, Tyr, Phe or His

<400> 38

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 Val Ser Glu Xaa Ile Tyr Ser Xaa
          20          25          30

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

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

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

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

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

```

```

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Humanized sequences of CHA.7.518 antibody VL

```

```

<220>
<221> MOD_RES
<222> (28)..(28)
<223> Asn, Gln, Ser, Ala or Asp

```

```

<220>
<221> MOD_RES
<222> (32)..(32)
<223> Asn, Gln, Ser, Ala or Asp

```

```

<220>
<221> MOD_RES
<222> (53)..(53)
<223> Asn, Gln, Ser, Ala or Asp

```

```

<220>
<221> MOD_RES
<222> (92)..(92)
<223> Trp, Tyr, Phe or His

```

```

<400> 39

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 Val Ser Glu Xaa Ile Tyr Ser Xaa
          20          25          30

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

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

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

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

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

```

```

<210> 40
<211> 98
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VH

```

```

<400> 40

```

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg

<210> 41
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VH

<400> 41

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10 15

<210> 42
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VH

<220>
<221> MOD_RES
<222> (31)..(31)
<223> Asn, Gln, Ser or Ala

<220>
<221> MOD_RES
<222> (52)..(52)
<223> Asn, Gln, Ser or Ala

<220>
<221> MOD_RES
<222> (105)..(105)
<223> Trp, Tyr, Phe or His

<400> 42

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

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

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

Gly Val Ile Xaa Pro Gly Ser Gly Gly Ile Tyr Tyr Asn Asp Lys Phe
50 55 60

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

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

Ala Arg Ser Glu Thr His Asp Thr Xaa Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 43
<211> 98

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Humanized sequences of CHA.7.538_1 antibody VH

 <220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Gln, Ser or Ala

 <220>
 <221> MOD_RES
 <222> (52)..(52)
 <223> Asn, Gln, Ser or Ala

 <400> 43

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

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

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

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

 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

 Ala Arg

<210> 44
 <211> 119
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Humanized sequences of CHA.7.538_1 antibody VH

 <220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

 <220>
 <221> MOD_RES
 <222> (52)..(52)
 <223> Asn, Gln, Ser or Ala

 <220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Trp, Tyr, Phe or His

 <400> 44

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

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

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

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

 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

 Ala Arg Ser Glu Thr His Asp Thr Xaa Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

 Thr Leu Val Thr Val Ser Ser
 115

<210> 45
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_1 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (52)..(52)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Trp, Tyr, Phe or His

<400> 45

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Ser Glu Thr His Asp Thr Xaa Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 46
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_1 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (52)..(52)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (105)..(105)
 <223> Trp, Tyr, Phe or His

<400> 46

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

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

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

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

Gln Gly Arg Val Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr

```
<210> 47
<211> 119
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VH

```
<220>
<221> MOD_RES
<222> (31)..(31)
<223> Asn, Gln, Ser or Ala
```

```
<220>
<221> MOD_RES
<222> (52)..(52)
<223> Asn, Gln, Ser or Ala
```

```
<220>
<221> MOD_RES
<222> (105)..(105)
<223> Trp, Tyr, Phe or His
```

<400> 47

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Ala Phe Thr Xaa Tyr

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

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

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

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

Ala Arg Ser Glu Thr His Asp Thr Xaa Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210>	48
<211>	96
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<400> 48

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

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

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

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

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

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

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<400> 49

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 50
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<400> 50

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 Gly Ile Arg Asn Asp
20 25 30

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

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

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

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

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<220>
<221> MOD_RES
<222> (92)..(92)
<223> Trp, Tyr, Phe or His

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Asn, Gln, Ser, Ala or Asp

<400> 51

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Ile Ser Thr Ser Val Gly
1 5 10 15

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

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

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

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

Glu Asp Leu Ala Asp Tyr Phe Cys Leu Gln His Xaa Xaa Tyr Pro Tyr
85 90 95

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

<210> 52
<211> 96

```

<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<220>
<221> MOD_RES
<222> (92)..(92)
<223> Tyr, Phe or His

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Gln, Ser, Ala or Asp

<400> 52
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1          5          10          15

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

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

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

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

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

```

```

<210> 53
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<220>
<221> MOD_RES
<222> (92)..(92)
<223> Trp, Tyr, Phe or His

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Asn, Gln, Ser, Ala or Asp

<400> 53
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 Lys Ala Ser Gln Ser Val Arg Ile Ala
          20          25          30

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

Tyr Leu Ala Ser Thr Arg His Thr 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 Leu Gln His Xaa Xaa Tyr Pro Tyr
          85          90          95

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

```

```

<210> 54
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequences of CHA.7.538_1 antibody VL

<220>
<221> MOD_RES

```

<222> (92)..(92)
 <223> Trp, Tyr, Phe or His

 <220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Asn, Gln, Ser, Ala or Asp

 <400> 54
 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 Lys Ala Ser Gln Ser Val Arg Ile Ala
 20 25 30

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

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

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

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

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

<210> 55
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<400> 55
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

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

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

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

 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg

<210> 56
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<400> 56
 Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10 15

<210> 57
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Trp, Tyr, Phe or His

<220>
 <221> MOD_RES
 <222> (59)..(59)
 <223> Asn, Gln, Ser or Ala

<400> 57

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

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

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

Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Xaa Tyr Asn Glu Lys Phe
 50 55 60

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

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

Ala Ser Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ala
 115 120

<210> 58
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Tyr, Phe or His

<220>
 <221> MOD_RES
 <222> (59)..(59)
 <223> Gln, Ser or Ala

<400> 58

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg

<210> 59
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Trp, Tyr, Phe or His

<220>
 <221> MOD_RES
 <222> (59)..(59)
 <223> Asn, Gln, Ser or Ala

<400> 59

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

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

Xaa Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Xaa Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 60
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Trp, Tyr, Phe or His

<220>
 <221> MOD_RES
 <222> (59)..(59)
 <223> Asn, Gln, Ser or Ala

<400> 60

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

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

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

Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Xaa Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Ser Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 61
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized sequences of CHA.7.538_2 antibody VH

<220>
 <221> MOD_RES
 <222> (31)..(31)
 <223> Asn, Gln, Ser or Ala

<220>
 <221> MOD_RES
 <222> (33)..(33)
 <223> Trp, Tyr, Phe or His

<220>
 <221> MOD_RES
 <222> (59)..(59)
 <223> Asn, Gln, Ser or Ala

<400> 61

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

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

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

Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Xaa Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Ser Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 62
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.518 VH h518HH1

<400> 62

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 63
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.518 VH h518HH2

<400> 63

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 64
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.518 VH h518HH3

<400> 64

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

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

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

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

Gln Gly Arg Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 65
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.518 VH h518HH4

<400> 65

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Asn Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Tyr Ile Gly Gly Ser Gly Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Ala Thr Leu Thr Ala Asp Asn Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Asp Lys Thr Ala Arg Asn Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120
 <210> 66
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> humanized CHA.7.518 VL h518HL1
 <400> 66
 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 Val Ser Glu Asn Ile Tyr Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Glu Ala Thr Asn Leu Ala Glu 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 His Phe Trp Gly Thr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105
 <210> 67
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> humanized CHA.7.518 VL h518HL2
 <400> 67
 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 Val Ser Glu Asn Ile Tyr Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Glu Ala Thr Asn Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 68
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.518 VL h518HL3

<400> 68

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 Val Ser Glu Asn Ile Tyr Ser Asn
 20 25 30

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

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

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

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

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

<210> 69
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1 VH h5381HH1

<400> 69

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 70
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1 VH h5381HH2

<400> 70

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 71
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.538_1 VH h5381HH3

<400> 71

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

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

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

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

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

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

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 72
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.538_1 VH h5381HH4

<400> 72

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

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

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

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

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

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

Ala Arg Ser Glu Thr His Asp Thr Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 73
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1/538_2 VL h538HL1

<400> 73

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

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

Tyr Leu Ala Ser Thr Arg His Thr 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 Leu Gln His Trp Asn Tyr Pro Tyr
 85 90 95

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

<210> 74
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1/538_2 VL h538HL2

<400> 74

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

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

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

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

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

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

<210> 75
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_2 VH h5382HH1

<400> 75

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 76
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.538_2 VH h5382HH2

<400> 76

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Ser Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 77
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CHA.7.538_2 VH h5382HH3

<400> 77

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

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

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

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

Gln Gly Arg Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Ser Pro Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Phe Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 78
<211> 107

<212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1/538_2 VL h538HL1

<400> 78

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

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

Tyr Leu Ala Ser Thr Arg His Thr 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 Leu Gln His Trp Asn Tyr Pro Tyr
 85 90 95

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

<210> 79
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized CHA.7.538_1/538_2 VL h538HL2

<400> 79

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

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

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

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

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

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

<210> 80
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sequence alignment of PVRIG orthologs

<400> 80

Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala Thr Glu Leu Ser
 1 5 10 15

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

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

Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp Ala Pro Ala Arg
 50 55 60

Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu Ile Leu Glu Gly
 65 70 75 80

Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe Cys Cys Lys Phe
85 90 95

Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly Ser Leu Pro Pro
100 105 110

Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro Ala Pro Ile Leu
115 120 125

Arg Ala Asp
130

<210> 81
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence alignment of PVRIG orthologs

<400> 81

Thr Pro Glu Val Trp Val Gln Val Gln Met Glu Ala Thr Glu Leu Ser
1 5 10 15

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

Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly Gly Thr Lys Leu
35 40 45

Ala Val Leu His Pro Glu Leu Gly Thr Arg Gln Trp Ala Pro Ala Arg
50 55 60

Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu Ala Leu Glu Asp
65 70 75 80

Ser Gly Ala Ser Ser Pro Phe Ala Asn Thr Thr Phe Cys Cys Lys Phe
85 90 95

Ala Ser Phe Pro Glu Gly Ser Trp Glu Ser Cys Gly Ser Leu Pro Pro
100 105 110

Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro Val Pro Ile Leu
115 120 125

Arg Ala Asp
130

<210> 82
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence alignment of PVRIG orthologs

<400> 82

Thr Pro Glu Val Trp Val Gln Val Gln Met Lys Ala Thr Glu Leu Ser
1 5 10 15

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

Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly Gly Thr Arg Leu
35 40 45

Ala Val Leu His Pro Glu Leu Gly Thr Arg Gln Trp Ala Pro Ala His
50 55 60

Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu Val Leu Glu Glu
65 70 75 80

Pro Gly Ala Ser Ser Pro Ser Ala Asn Thr Thr Phe Cys Cys Lys Phe
85 90 95

Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly Ser Leu Pro Pro
100 105 110

Ser Ser Asp Pro Gly Leu Ser Ala Pro Ile Leu Arg Ala Asp
115 120 125

<210> 83
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sequence alignment of PVRIG orthologs

<400> 83

Thr Pro Glu Val Trp Val Gln Val Gln Met Glu Ala Thr Glu Leu Ser
 1 5 10 15

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

Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly Gly Thr Lys Leu
 35 40 45

Ala Val Leu His Pro Glu Leu Gly Thr Arg Gln Trp Ala Pro Ala Arg
 50 55 60

Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu Ala Leu Glu Asp
 65 70 75 80

Ser Gly Ala Ser Ser Pro Phe Ala Asn Thr Thr Phe Cys Cys Lys Phe
 85 90 95

Ala Ser Phe Pro Glu Gly Ser Trp Glu Ser Cys Gly Ser Leu Pro Pro
 100 105 110

Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro Val Pro Ile Leu
 115 120 125

Arg Ala Asp
 130

<210> 84
 <211> 166
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain: Amino acid sequence

<400> 84

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

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
 20 25 30

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

Thr Asn Tyr Ala Val His Trp Ile Lys Gln Thr Thr Gly Gln Ala Leu
 50 55 60

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

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

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Pro Val Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Ser Gly Thr Thr Arg Phe Ala Tyr Trp Gly Gln Gly
 115 120 125

Thr Leu Val Thr Val Ser Ser Ala Gln Thr Thr Ala Pro Ser Val Tyr
 130 135 140

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

Gly Cys Leu Val Lys Gly
 165

<210> 85

<211> 498
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Heavy chain: DNA sequence

<400> 85
 atggaatgga actgggtctt tctcttcctc ctgtcagtaa ctgcaggagt ccactcccag 60
 gtccagctgc agcagtctgg agctgagctg gcaaagcctg gctcttcagt gatgatttcc 120
 tgcaaggctt ctggttacac ctttaccac tatgctgtgc actggataaa gcagacgact 180
 ggacaggccc ttgagtggac tggatatatt gctcctggaa gtggagttac taaatacaat 240
 gagaagtca agggcaaggc cacattgact gtagacaaat cctcaaccac agcctacatg 300
 caactcagca gcctgacacc tgtggacact gcggtctatt actgtgcaag cggaactacg 360
 aggtttgctt attggggcca aggcactctg gtcactgtct cttcagccca aacaacagcc 420
 ccatctgtct atccactggc tcctggatgt ggtgatacaa ccagctccac ggtgactctg 480
 ggatgcctgg tcaagggc 498

<210> 86
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain: Amino acid sequence

<400> 86

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

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

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

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

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

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

Thr Ile Asp Pro Val Gln Ala Asp Asp Ile Ala Thr Tyr Tyr Cys Gln
 100 105 110

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

Ile Lys
 130

<210> 87
 <211> 390
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Light chain: DNA sequence

<400> 87
 atggagacag acacactcct gctatgggtg ctgctgctct gggttccagg ctccactggt 60
 gacattgtgc tgaccagtc tcctgctttg gctgtgtctc tagggcagag ggccacaatc 120
 tcctgtagag ccagccaaag tgtcagttta tccagctata atctcatgca gtggtaccaa 180
 cagaaaccag gacaggaacc caaaatcctc atctatgatg catccaacct accatctggg 240
 atccctgccca gggttcagtgg cagtgggtct gggacagact tcaccctcac cattgatcct 300
 gtgcaggctg atgatattgc aacctattac tgtcagcaga gtaaggatga cccgctcacg 360
 ttcggttctg ggaccaagct ggagatcaaa 390

<210> 88
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Human IgG1 constant region

<400> 88

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 Glu Glu
225 230 235 240

Met 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> 89

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG1 D265A constant region

<400> 89

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 Ala 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 Glu Glu
225 230 235 240

Met 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> 90
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 N297A constant region

<400> 90

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 Ala 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 Glu Glu
 225 230 235 240
 Met 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> 91
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IgG2 constant region

<400> 91

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 115 120 125
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 130 135 140
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 145 150 155 160
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 165 170 175
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 180 185 190
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 195 200 205
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 210 215 220
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 225 230 235 240
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 260 265 270
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 275 280 285
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 290 295 300
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 305 310 315 320
 Ser Leu Ser Pro Gly Lys
 325
 <210> 92
 <211> 377
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Human IgG3 constant region
 <400> 92
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
 100 105 110
 Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 93
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG4 constant region (Wild Type)

<400> 93

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

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

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

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

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

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

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

115

120

125

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 325

<210> 94
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IgG4 constant region (S241P hinge mutant)

<400> 94

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
325

<210> 95
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human kappa light chain

<400> 95

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> 96
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Human lambda light chain

<400> 96

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

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

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro

35

40

45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 97
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TIGIT ECD

<400> 97

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1 5 10 15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
20 25 30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
35 40 45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
50 55 60

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

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
85 90 95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
100 105 110

His Gly Ala Arg Phe Gln Ile Pro
115 120

<210> 98
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyno macaque TIGIT ECD

<400> 98

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Lys Lys
1 5 10 15

Gly Gly Ser Val Ile Leu Gln Cys His Leu Ser Ser Thr Met Ala Gln
20 25 30

Val Thr Gln Val Asn Trp Glu Gln His Asp His Ser Leu Leu Ala Ile
35 40 45

Arg Asn Ala Glu Leu Gly Trp His Ile Tyr Pro Ala Phe Lys Asp Arg
50 55 60

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

Asn Asp Thr Gly Glu Tyr Phe Cys Thr Tyr His Thr Tyr Pro Asp Gly
85 90 95

Thr Tyr Arg Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala
100 105 110

Glu His Ser Ala Arg Phe Gln Ile Pro
115 120

```

<210> 99
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PVR ECD

<400> 99
Asp Val Val Val Gln Ala Pro Thr Gln Val Pro Gly Phe Leu Gly Asp
1      5      10      15

Ser Val Thr Leu Pro Cys Tyr Leu Gln Val Pro Asn Met Glu Val Thr
20      25      30

His Val Ser Gln Leu Thr Trp Ala Arg His Gly Glu Ser Gly Ser Met
35      40      45

Ala Val Phe His Gln Thr Gln Gly Pro Ser Tyr Ser Glu Ser Lys Arg
50      55      60

Leu Glu Phe Val Ala Ala Arg Leu Gly Ala Glu Leu Arg Asn Ala Ser
65      70      75      80

Leu Arg Met Phe Gly Leu Arg Val Glu Asp Glu Gly Asn Tyr Thr Cys
85      90      95

Leu Phe Val Thr Phe Pro Gln Gly Ser Arg Ser Val Asp Ile Trp Leu
100     105     110

Arg Val Leu Ala Lys Pro Gln Asn Thr Ala Glu Val Gln Lys Val Gln
115     120     125

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

Arg Pro Pro Ala Gln Ile Thr Trp His Ser Asp Leu Gly Gly Met Pro
145     150     155     160

Asn Thr Ser Gln Val Pro Gly Phe Leu Ser Gly Thr Val Thr Val Thr
165     170     175

Ser Leu Trp Ile Leu Val Pro Ser Ser Gln Val Asp Gly Lys Asn Val
180     185     190

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

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

Asp Asn Asn Trp Tyr Leu Gly Gln Asn Glu Ala Thr Leu Thr Cys Asp
225     230     235     240

Ala Arg Ser Asn Pro Glu Pro Thr Gly Tyr Asn Trp Ser Thr Thr Met
245     250     255

Gly Pro Leu Pro Pro Phe Ala Val Ala Gln Gly Ala Gln Leu Leu Ile
260     265     270

Arg Pro Val Asp Lys Pro Ile Asn Thr Thr Leu Ile Cys Asn Val Thr
275     280     285

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

Gly Pro Pro Ser Glu His Ser Gly Met Ser Arg Asn
305     310     315

<210> 100
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA.9.018 Variable heavy (vh) domain

<400> 100
Gln 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 Thr Phe Ser Ser Tyr
20 25 30

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

Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Glu Met Leu Val Gln Asp Tyr Tyr Tyr Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 101
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 101

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 102

Ile Arg Tyr Asp Gly Ser Asn Lys
1 5

<210> 103
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 103

Ala Lys Glu Met Leu Val Gln Asp Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 104
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 104

Gln 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 Thr Phe Ser Ser Tyr
20 25 30

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

Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Glu Met Leu Val Gln Asp Tyr Tyr Tyr Met Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270
 Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 105
 <211> 113
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 105
 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Pro Gly
 1 5 10 15

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

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

Pro Gln Leu Leu Ile Tyr Trp Gly Ser Asn Arg Ala 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 Met Gln Gly
85 90 95

Leu Gln Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg

<210> 106
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 106

Gln Asn Leu Leu His Arg Asn Gly Ile Asn Tyr
1 5 10

<210> 107
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 107

Trp Gly Ser
1

<210> 108
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 108

Met Gln Gly Leu Gln Ile Pro Pro Thr
1 5

<210> 109
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 109

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

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

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

Pro Gln Leu Leu Ile Tyr Trp Gly Ser Asn Arg Ala 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 Met Gln Gly
85 90 95

Leu Gln Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp 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> 110
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA.9.027 Variable heavy (vh) domain

<400> 110

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 111
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 111

Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 112
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 112

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 113
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 113

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 114
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 114

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 115
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 115

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ser Leu
85 90 95

Ser Ser Leu Gln Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly
100 105 110

<210> 116
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR1

<400> 116

Ser Ser Asn Met Gly Arg Arg Pro
1 5

<210> 117
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR2

<400> 117

Ser Gln Asn
1

<210> 118
<211> 11
<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 118

Ala Val Trp Asp Asp Ser Leu Ser Ser Leu Gln
1 5 10

<210> 119

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 119

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ser Leu
85 90 95

Ser Ser Leu Gln Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly Gln
100 105 110

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 120

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CPA.9.049 Variable heavy (vh) domain

<400> 120

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 121
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR1

<400> 121

Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 122
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR2

<400> 122

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 123
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR3

<400> 123

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 124
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 124

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270
 Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 125
 <211> 111
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 125
 Gln Ser Ala Leu Thr Gln Pro Arg Ser Ala Ser Gly Asn Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30
 Pro Val Asn Trp Tyr Gln Gln Ile Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Ser Gln Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ser Leu
 85 90 95

Phe Ser Leu Leu Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly
 100 105 110

<210> 126
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 126

Ser Ser Asn Met Gly Arg Arg Pro
 1 5

<210> 127
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 127

Ser Gln Asn
 1

<210> 128
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 128

Ala Val Trp Asp Asp Ser Leu Phe Ser Leu Leu
 1 5 10

<210> 129
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 129

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ser Leu
 85 90 95

Phe Ser Leu Leu Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly Gln
 100 105 110

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 130
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA.9.057 Variable heavy (vh) domain

<400> 130

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

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

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

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Gln Gly Ala Ala Ala Gly Asn Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 131

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

<210> 132
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 132

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 133
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 133

Ala Arg Gln Gly Ala Ala Ala Gly Asn Pro Phe Asp Ile
1 5 10

<210> 134
<211> 448

```

<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 134

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

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

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

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50     55     60

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

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

Cys Ala Arg Gln Gly Ala Ala Ala Gly Asn Pro Phe Asp Ile Trp Gly
100    105    110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
195    200    205

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

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

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

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

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

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

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

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

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

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

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

```

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

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

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

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

<210> 135
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 135

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Phe Val Tyr Trp His Gln Gln Leu Thr Gly Thr Ala Pro Lys Leu Leu
35 40 45

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Gly Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 136

Ser Ser Asn Ile Gly Ser Asn Phe
1 5

<210> 137
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 137

Arg Asn Thr
1

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 138

Ala Thr Trp Asp Asp Ser Leu Ser Ala Trp Val
1 5 10

<210> 139
<211> 216
<212> PRT
<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 139

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Phe Val Tyr Trp His Gln Gln Leu Thr Gly Thr Ala Pro Lys Leu Leu
35 40 45

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Gly Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

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

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 140

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CPA.9.059 Variable heavy (vh) domain

<400> 140

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Gly Ala Arg Tyr Ser Tyr Gly Gln Tyr Pro Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 141

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

<220>
 <223> vhCDR1

<400> 141

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 142
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 142

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 143
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 143

Ala Arg Gly Ala Arg Tyr Ser Tyr Gly Gln Tyr Pro Tyr
 1 5 10

<210> 144
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 144

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
 1 5 10 15

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

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

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

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

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

Arg Gly Ala Arg Tyr Ser Tyr Gly Gln Tyr Pro Tyr Trp Gly Gln Gly
 100 105 110

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

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

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

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

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 145
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 145
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1      5      10      15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Asp Ile Ser Ser Leu
      20      25      30

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

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

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

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

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

```

```

<210> 146
<211> 6
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223>  vLCDR1

<400>  146

His Asp Ile Ser Ser Leu
1      5

<210>  147
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vLCDR2

<400>  147

Ala Ala Ser
1

<210>  148
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vLCDR3

<400>  148

Leu Gln Leu Asp Ser Phe Pro Thr Trp Thr
1      5      10

<210>  149
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Full length light chain

<400>  149

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Asp Ile Ser Ser Leu
      20      25      30

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

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

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile 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> 150
 <211> 121
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> CPA.9.083 Variable heavy (vh) domain

 <400> 150
 Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Gly Thr Pro Val Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 151
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

 <400> 151

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 152
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

 <400> 152

Ile Ser Tyr Asp Gly Thr Pro Val
1 5

<210> 153
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

 <400> 153

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
1 5 10

<210> 154
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

 <400> 154

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

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

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
Página 65

35

40

45

Ala Val Ile Ser Tyr Asp Gly Thr Pro Val Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 155
 <211> 111
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Variable light (vl) domain

 <400> 155

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

 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30

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

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

 Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
 65 70 75 80

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

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

<210> 156
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 156

Ser Ser Asn Met Gly Arg Arg Pro
 1 5

<210> 157
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 157

Ser Gln Asn
 1

<210> 158
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 158

Ala Val Trp Asp Gly Asp Arg Arg Ser Leu Gln
 1 5 10

<210> 159
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 159

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30

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

Ile Tyr Ser Gln Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

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

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

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 160
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA.9.086 Variable heavy (vh) domain

<400> 160

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

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

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

Ala Val Ile Ser Tyr Ala Gly Glu Val Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 161
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 161

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 162
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 162

Ile Ser Tyr Ala Gly Glu Val Lys
 1 5

<210> 163

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 163

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 164

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 164

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

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

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

Ala Val Ile Ser Tyr Ala Gly Glu Val Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

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

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

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

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

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 280 285 290 295

275

280

285

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

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

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

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

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

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

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

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

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

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

<210> 165
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 165

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ile Gly
 85 90 95

Arg Val Leu Gln Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly
 100 105 110

<210> 166
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR1

<400> 166

Ser Ser Asn Met Gly Arg Arg Pro
 1 5

<210> 167
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR2

<400> 167

Ser Gln Asn

1

<210> 168

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 168

Ala Val Trp Asp Asp Ile Gly Arg Val Leu Gln

1

5

10

<210> 169

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 169

Gln Ser Ala Leu Thr Gln Pro Arg Ser Ala Ser Gly Asn Pro Gly Gln

1

5

10

15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg

20

25

30

Pro Val Asn Trp Tyr Gln Gln Ile Pro Gly Thr Ala Pro Lys Leu Leu

35

40

45

Ile Tyr Ser Gln Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln

65

70

75

80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Val Trp Asp Asp Ile Gly

85

90

95

Arg Val Leu Gln Leu Gly Gly Gly Thr Gln Leu Ala Val Leu Gly Gln

100

105

110

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

115

120

125

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

130

135

140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys

145

150

155

160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr

165

170

175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His

180

185

190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys

195

200

205

Thr Val Ala Pro Thr Glu Cys Ser

210

215

<210> 170

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CPA.9.089 Variable heavy (vh) domain

<400> 170

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

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

Ala Val Ile Ser Tyr Asp Arg Thr Pro Val Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 171
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR1

<400> 171

Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 172
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR2

<400> 172

Ile Ser Tyr Asp Arg Thr Pro Val
 1 5

<210> 173
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vHCDR3

<400> 173

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 174
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 174

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

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

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

Ala Val Ile Ser Tyr Asp Arg Thr Pro Val Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270
 Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 175
 <211> 111
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 175
 Gln Ser Ala Leu Thr Gln Pro Arg Ser Ala Ser Gly Asn Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
 20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Pro Arg Leu Asn Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
100 105 110

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 176

Ser Ser Asn Met Gly Arg Arg Pro
1 5

<210> 177
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 177

Ser Gln Asn
1

<210> 178
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 178

Ala Thr Trp Asp Asp Ser Leu Pro Arg Leu Asn
1 5 10

<210> 179
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 179

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Pro Arg Leu Asn Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly Gln
100 105 110

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 180
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA.9.093 Variable heavy (vh) domain

<400> 180

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

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

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

Ala Val Ile Ser Tyr Glu Gly Asp Arg Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 181

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 182
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 182

Ile Ser Tyr Glu Gly Asp Arg Lys
1 5

<210> 183
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 183

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 184

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 184

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

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

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

Ala Val Ile Ser Tyr Glu Gly Asp Arg Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 185
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 185

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Thr Trp Asp Asp Ser Thr
85 90 95

Pro His Gly Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
100 105 110

<210> 186
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 186

Ser Ser Asn Met Gly Arg Arg Pro
1 5

<210> 187
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 187

Ser Gln Asn
1

<210> 188
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 188

Ala Thr Trp Asp Asp Ser Thr Pro His Gly Val

1 5

<210> 189
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 189

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Arg
20 25 30

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

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

Gly Ser Gln Ser Gly Thr Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Phe Cys Ala Thr Trp Asp Asp Ser Thr
85 90 95

Pro His Gly Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly Gln
100 105 110

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 190
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA.9.101 Variable heavy (vh) domain

<400> 190

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
 115

<210> 191
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 191

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 192
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 192

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 193
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 193

Ala Arg Gly Ala Pro Leu Phe Gly Gln Tyr Pro Tyr
 1 5 10

<210> 194
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 194

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
 1 5 10 15

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

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

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

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

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

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

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

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

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 195
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 195
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 His Ala Ile Ala Ser Leu
      20      25      30

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

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

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

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

```

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

<210> 196
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 196

His Ala Ile Ala Ser Leu
1 5

<210> 197
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 197

Ala Ala Ser
1

<210> 198
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 198

Leu Gln Leu Asp Ser Phe Pro Thr Trp Thr
1 5 10

<210> 199
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 199

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 His Ala Ile Ala Ser Leu
20 25 30

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

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

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile 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> 200
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA.9.103 Variable heavy (vh) domain
 <400> 200

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
 1 5 10 15

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

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

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

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

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

Arg Gly Ala Arg Pro Asn Gly Gln Tyr Pro Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 201
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1
 <400> 201

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 202
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2
 <400> 202

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 203
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3
 <400> 203

Ala Arg Gly Ala Arg Pro Asn Gly Gln Tyr Pro Tyr
 1 5 10

<210> 204
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))
 <400> 204

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
 20 25 30
 Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Ala Arg Pro Asn Gly Gln Tyr Pro Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
 210 215 220
 Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255
 Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320
 Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 340 345 350
 Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400
 Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415

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

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

<210> 205
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 205

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Gly Ile Lys Ser Leu
 20 25 30

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

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

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

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

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

<210> 206
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 206

His Gly Ile Lys Ser Leu
 1 5

<210> 207
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 207

Ala Ala Ser
 1

<210> 208
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 208

Leu Gln Leu Asp Ser Phe Pro Thr Trp Thr
 1 5 10

<210> 209
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 209

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Gly Ile Lys Ser Leu
 20 25 30
 Phe Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Ala Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Leu Asp Ser Phe Pro Thr
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile 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> 210
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Clone 31C6 Variable heavy (vh) domain

<400> 210

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
 20 25 30
 Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asp Pro Tyr Asn Asp Gly Ala Lys Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val Trp Gly Ala Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

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

<220>
 <223> vhCDR1

<400> 211

Gly Tyr Thr Phe Ser Ser Tyr Val
1 5

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

<220>
<223> vhCDR2

<400> 212

Ile Asp Pro Tyr Asn Asp Gly Ala
1 5

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

<220>
<223> vhCDR3

<400> 213

Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val
1 5 10

<210> 214
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 214

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

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

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

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

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

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

Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

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

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

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

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

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

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

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

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

P-2019-16740 TRADUCCIÓN LISTADO DE SECUENCIAS.txt
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

<210> 215
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain
 <400> 215

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

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

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

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

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

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

Thr Phe Gly Ala Gly Thr Thr Leu Glu Leu Lys
 100 105

<210> 216
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1
 <400> 216

Glu His Ile Tyr Ser Tyr
 1 5

<210> 217
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 217

Asn Ala Lys
 1

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

<220>
 <223> vLCDR3

<400> 218

Gln His His Phe Gly Ser Pro Leu Thr
 1 5

<210> 219
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 219

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 220
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Clone 22G2 Variable heavy (vh) domain

<400> 220

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

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

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
 50 55 60

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

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

Cys Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr
 100 105 110

Tyr Phe Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
 115 120 125

Ser Ser
 130

<210> 221

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR1

<400> 221

Gly Gly Ser Val Ser Ser Gly Ile Tyr Tyr
 1 5 10

<210> 222

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 222

Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 223

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 223

Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr Tyr
 1 5 10 15

Phe Phe Gly Val Asp Val
 20

<210> 224

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 224

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

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

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

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr
100 105 110

Tyr Phe Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

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

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

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

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

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

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

Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
225 230 235 240

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
245 250 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
260 265 270

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
275 280 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
290 295 300

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305 310 315 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
325 330 335

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
355 360 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

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

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 225
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 225

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 226
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 226

Gln Ser Val Ser Ser Tyr
1 5

<210> 227
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 227

Asp Ala Ser
1

<210> 228
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 228

Gln Gln Arg Ser Asn Trp Pro Pro Leu Phe Thr
1 5 10

<210> 229
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 229

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

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
Página 91

35

40

45

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 230
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.536.1 Variable heavy (vh) domain

<400> 230

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 231
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 231

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
1 5 10

<210> 232
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 232

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
 1 5 10

<210> 233
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 233

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

<210> 234
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 234

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

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

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

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

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

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

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

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val

260

265

270

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

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

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

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

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

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

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

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

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

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

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

<210> 235
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 235

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 Asp Val Lys Asn Ala
20 25 30

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

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

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

<210> 236
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR1

<400> 236

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

<210> 237
<211> 7
<212> PRT
<213> Artificial Sequence

```

<220>
<223>  vLCDR2

<400>  237

Ser Pro Ser Tyr Arg Tyr Thr
1      5

<210>  238
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vLCDR3

<400>  238

Gln Gln His Tyr Ser Thr Pro Phe Thr
1      5

<210>  239
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Full length light chain

<400>  239

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 Asp Val Lys Asn Ala
      20      25      30

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

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
      85      90      95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
      210

<210>  240
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CHA.9.536.3 Variable heavy (vh) domain

<400>  240

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

```

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 241
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 241

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
1 5 10

<210> 242
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 242

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
1 5 10

<210> 243
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 243

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

<210> 244
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 244

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 245
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 245
 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 Asp Val Lys Asn Ala
20 25 30

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

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

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

<210> 246
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 246

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

<210> 247
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 247

Ser Pro Ser Tyr Arg Tyr Thr
1 5

<210> 248
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 248

Gln Gln His Tyr Ser Thr Pro Phe Thr
1 5

<210> 249
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 249

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 Asp Val Lys Asn Ala
20 25 30

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

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 250
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.536.4 Variable heavy (vh) domain

<400> 250

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 251
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 251

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
1 5 10

<210> 252
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 252

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
1 5 10

<210> 253
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 253

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

<210> 254

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 254

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

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

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

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 255
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 255

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 Asp Val Lys Asn Ala
20 25 30

Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 256
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 256

Arg Ala Ser Gln Asp Val Lys Asn Ala Val Val
1 5 10

<210> 257
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 257

Ser Pro Ser Tyr Arg Tyr Thr
1 5

<210> 258
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 258

Gln Gln His Tyr Ser Thr Pro Phe Thr
1 5

<210> 259

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 259

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 Asp Val Lys Asn Ala
20 25 30

Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 260

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.536.5 Variable heavy (vh) domain

<400> 260

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 261
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 261

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
1 5 10

<210> 262
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 262

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
1 5 10

<210> 263
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 263

Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr
1 5 10

<210> 264
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 264

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 265
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 265
 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 Asp Val Lys Asn Ala
 20 25 30
 Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 266
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 266

Arg Ala Ser Gln Asp Val Lys Asn Ala Val Val
1 5 10

<210> 267
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 267

Ser Pro Ser Tyr Arg Tyr Thr
1 5

<210> 268
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 268

Gln Gln His Tyr Ser Thr Pro Phe Thr
1 5

<210> 269
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 269

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 Asp Val Lys Asn Ala
20 25 30

Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 270
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.536.6 Variable heavy (vh) domain

<400> 270

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 271
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 271

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
 1 5 10

<210> 272
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 272

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
 1 5 10

<210> 273
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 273

Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr
 1 5 10

<210> 274
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 274

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 275
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 275

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 Asp Val Lys Asn Ala
 20 25 30

Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Phe
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 276
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 276

Arg Ala Ser Gln Asp Val Lys Asn Ala Val Val
 1 5 10

<210> 277
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 277

Ser Pro Ser Tyr Arg Tyr Thr
 1 5

<210> 278
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 278

Gln Gln His Tyr Ser Thr Pro Phe Thr
 1 5

<210> 279
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 279

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 Asp Val Lys Asn Ala
 20 25 30
 Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Phe
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 280
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.536.7 Variable heavy (vh) domain

<400> 280

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30
 Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 281
 <211> 10
 <212> PRT
 <213> Artificial Sequence

```

<220>
<223>  vhCDR1

<400>  281

Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
1      5      10

<210>  282
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vhCDR2

<400>  282

Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
1      5      10

<210>  283
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vhCDR3

<400>  283

Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr
1      5      10

<210>  284
<211>  446
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Full length HC (IgG4(S241P))

<400>  284

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1      5      10      15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
      20      25      30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35      40      45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
      50      55      60

Gln Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65      70      75      80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
      85      90      95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
      100      105      110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
      115      120      125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
      130      135      140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145      150      155      160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
      165      170      175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
      180      185      190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
      195      200      205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
      210      215      220

```

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 285
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 285
 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 Asp Val Lys Asn Ala
 20 25 30
 Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 286
 <211> 11
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> vlCDR1
 <400> 286

Arg Ala Ser Gln Asp Val Lys Asn Ala Val Val
1 5 10

<210> 287
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 287

Ser Pro Ser Tyr Arg Tyr Thr
1 5

<210> 288
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 288

Gln Gln His Tyr Ser Thr Pro Phe Thr
1 5

<210> 289
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 289

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 Asp Val Lys Asn Ala
20 25 30

Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Pro Ser Tyr Arg Tyr Thr 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 Gln His Tyr Ser Thr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 290
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
 <223> CHA.9.536.8 Variable heavy (vh) domain
 <400> 290
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30
 Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 291
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 291
 Gly Tyr Thr Phe Thr Glu Tyr Thr Leu His
 1 5 10

<210> 292
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 292
 Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser
 1 5 10

<210> 293
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 293
 Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr
 1 5 10

<210> 294
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 294
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30
 Thr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Ser Gly Tyr Tyr Asp Tyr Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 295
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
 <223> Variable light (vl) domain
 <400> 295
 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 Asp Val Lys Asn Ala
 20 25 30
 Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Phe
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 296
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR1

<400> 296

Arg Ala Ser Gln Asp Val Lys Asn Ala Val Val
 1 5 10

<210> 297
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR2

<400> 297

Ser Pro Ser Tyr Arg Tyr Thr
 1 5

<210> 298
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR3

<400> 298

Gln Gln His Tyr Ser Thr Pro Phe Thr
 1 5

<210> 299
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 299

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 Asp Val Lys Asn Ala
 20 25 30
 Val Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Pro Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Pro

```
<210> 300
<211> 119
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223>  CHA.9.560.1 Variable heavy (vh) domain
```

<400> 300

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

```
<210> 301
<211> 10
<212> PRT
<213> Artificial Sequence
```

<220>
<223> vhCDR1

<400> 301

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

```
<210> 302
<211> 10
<212> PRT
<213> Artificial Sequence
```

<220>
<223> vhCDR2

<400> 302

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
 1 5 10

<210> 303

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 303

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
 1 5 10

<210> 304

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 304

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val

290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 305
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 305

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr
35 40 45

Leu Ile Tyr Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 306
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 306

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
1 5 10

<210> 307
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 307

Gly Thr Asn Gly Arg Gly Ser
1 5

<210> 308
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 308

Ala Leu Trp Phe Ser Asn His Trp Val
 1 5

<210> 309
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 309

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn His Ala Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr
 35 40 45

Leu Ile Tyr Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
 50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
 65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
 100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205

Ala Pro Thr Glu Cys Ser
 210

<210> 310
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.560.3 Variable heavy (vh) domain

<400> 310

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 311
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 311

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 312
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 312

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 313
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 313

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
1 5 10

<210> 314
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 314

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 315
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 315

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 316
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 316

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
1 5 10

<210> 317
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 317

Gly Thr Asn Gly Arg Gly Ser
1 5

<210> 318
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 318

Ala Leu Trp Phe Ser Asn His Trp Val
1 5

<210> 319
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 319

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 320
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.560.4 Variable heavy (vh) domain

<400> 320

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 321
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 321

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 322
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 322

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 323
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 323

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr

```

1          5          10
<210> 324
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 324

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
          20          25          30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50          55          60

Gln Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65          70          75          80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
          100          105          110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
          115          120          125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
          130          135          140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145          150          155          160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
          165          170          175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
          180          185          190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
          195          200          205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210          215          220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225          230          235          240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
          245          250          255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
          260          265          270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
          275          280          285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290          295          300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305          310          315          320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
          325          330          335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
          340          345          350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
          355          360          365

```

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 325
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 325

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
 50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 326
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 326

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
 1 5 10

<210> 327
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 327

Gly Thr Asn Gly Arg Gly Ser
 1 5

<210> 328
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 328

Ala Leu Trp Phe Ser Asn His Trp Val
 1 5

<210> 329

<211> 214
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Full length light chain

 <400> 329
 Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15
 Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45
 Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80
 Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95
 His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
 100 105 110
 Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160
 Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190
 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Cys Ser
 210

<210> 330
 <211> 119
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> CHA.9.560.5 Variable heavy (vh) domain

 <400> 330
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 331
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 331

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 332
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 332

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 333
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 333

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
1 5 10

<210> 334
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 334

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 335
 <211> 109
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 335
 Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15
 Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45
 Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80
 Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95
 His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 336
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 336

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
 1 5 10

<210> 337
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 337

Gly Thr Asn Gly Arg Gly Ser
 1 5

<210> 338
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 338

Ala Leu Trp Phe Ser Asn His Trp Val
 1 5

<210> 339
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 339

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
 50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
 100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 340
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.560.6 Variable heavy (vh) domain

<400> 340

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 341
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 341

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 342
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 342

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 343
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 343

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
1 5 10

<210> 344
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 344

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 345
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 345

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
 50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 346
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR1

<400> 346

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
 1 5 10

<210> 347
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR2

<400> 347

Gly Thr Asn Gly Arg Gly Ser
 1 5

<210> 348
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR3

<400> 348

Ala Leu Trp Phe Ser Asn His Trp Val
 1 5

<210> 349
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 349

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45
 Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80
 Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95
 His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
 100 105 110
 Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160
 Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190
 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Cys Ser
 210

<210> 350
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.560.7 Variable heavy (vh) domain

<400> 350

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Phe Thr Phe Thr Leu Asp Ala Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 351
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 351

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
 1 5 10

<210> 352
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 352

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
 1 5 10

<210> 353
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 353

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
 1 5 10

<210> 354
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 354

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 355
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 355

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
 1 5 10 15
 Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45
 Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
 65 70 75 80
 Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
 85 90 95
 His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 356
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 356

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
 1 5 10

<210> 357
 <211> 7
 <212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR2

<400> 357

Gly Thr Asn Gly Arg Gly Ser
1 5

<210> 358

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 358

Ala Leu Trp Phe Ser Asn His Trp Val
1 5

<210> 359

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 359

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 360

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.560.8 Variable heavy (vh) domain

<400> 360

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Phe Thr Leu Asp Ala Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 361
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 361

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 362
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 362

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 363
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 363

Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr
1 5 10

<210> 364
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 364

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Phe Thr Leu Asp Ala Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

Ser Arg Gly Asn Gly Tyr Tyr Val Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 365
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 365

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 366
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 366

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn His Ala Asn
1 5 10

<210> 367
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 367

Gly Thr Asn Gly Arg Gly Ser
1 5

<210> 368
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 368

Ala Leu Trp Phe Ser Asn His Trp Val
1 5

<210> 369
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 369

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn His Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Arg Gly Thr Asn Gly Arg Gly Ser Gly Val Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Phe Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gln Pro Lys

100

105

110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205

Ala Pro Thr Glu Cys Ser
 210

<210> 370
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.546.1 Variable heavy (vh) domain

<400> 370

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 371
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 371

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1 5 10

<210> 372
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 372

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 373
 <211> 10

<212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 373

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 374
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 374

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser

325

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 375
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 375

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 Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 376
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 376

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
1 5 10

<210> 377
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 377

Lys Ala Ser Asn Leu His Thr
1 5

<210> 378
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 378

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 379

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 379

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Tyr
85 90 95Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205Phe Asn Arg Gly Glu Cys
210

<210> 380

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.547.1 Variable heavy (vh) domain

<400> 380

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 381
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vHCDR1

<400> 381

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 382
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vHCDR2

<400> 382

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1 5 10

<210> 383
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vHCDR3

<400> 383

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 384
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 384

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 385
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 385

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 Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 386
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 386

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
1 5 10

<210> 387
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 387

Lys Ala Ser Asn Leu His Thr
1 5

<210> 388
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 388

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 389
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 389

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 Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 390
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.547.2 Variable heavy (vh) domain

<400> 390

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 391
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 391

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1 5 10

<210> 392
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 392

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 393
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 393

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 394
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 394

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 395
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 395

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 Asn Ile Asn Val Trp
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 396
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR1

<400> 396

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
 1 5 10

<210> 397
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR2

<400> 397

Lys Ala Ser Asn Leu His Thr
 1 5

<210> 398
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR3

<400> 398

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 399
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 399

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 Asn Ile Asn Val Trp
 20 25 30
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 400
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.547.3 Variable heavy (vh) domain

<400> 400

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 Thr Phe Ser Ser Tyr
 20 25 30
 Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 401
 <211> 10
 <212> PRT
 <213> Artificial Sequence

```

<220>
<223>  vhCDR1

<400>  401

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1      5      10

<210>  402
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vhCDR2

<400>  402

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1      5      10

<210>  403
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  vhCDR3

<400>  403

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1      5      10

<210>  404
<211>  446
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Full length HC (IgG4(S241P))

<400>  404

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 Thr Phe Ser Ser Tyr
      20      25      30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35      40      45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50      55      60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
      100      105      110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
      115      120      125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
      130      135      140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145      150      155      160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
      165      170      175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
      180      185      190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
      195      200      205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210      215      220

```

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 <210> 405
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variable light (vl) domain
 <400> 405
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 406
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 406

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
 1 5 10

<210> 407

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR2

<400> 407

Lys Ala Ser Asn Leu His Thr
 1 5

<210> 408

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 408

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 409

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 409

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 410

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.547.4 Variable heavy (vh) domain

<400> 410

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 411

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR1

<400> 411

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 412

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 412

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1 5 10

<210> 413

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 413

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 414

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 414

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 415
<211> 107
<212> PRT

<213> Artificial Sequence

<220>

<223> Variable light (vl) domain

<400> 415

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 416

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR1

<400> 416

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
1 5 10

<210> 417

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR2

<400> 417

Lys Ala Ser Asn Leu His Thr
1 5

<210> 418

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 418

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 419

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 419

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 420
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.547.6 Variable heavy (vh) domain
<400> 420

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 421
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1
<400> 421

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 422
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 422

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 423

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 423

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 424

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 424

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 425
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain
 <400> 425

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 Asn Ile Asn Val Trp
 20 25 30
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 426
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1
 <400> 426

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
 1 5 10

<210> 427
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2
 <400> 427

Lys Ala Ser Lys Ser His Thr

1 5

<210> 428
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 428

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 429
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 429

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 Asn Ile Asn Val Trp
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 430
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.547.7 Variable heavy (vh) domain

<400> 430

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 431
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 431

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 432
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 432

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1 5 10

<210> 433
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 433

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 434
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 434

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe

115

120

125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 435
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 435

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 Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 436
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 436

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
 1 5 10

<210> 437
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 437

Lys Ala Ser Lys Ser His Thr
 1 5

<210> 438
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 438

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 439
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 439

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 Asn Ile Asn Val Trp
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 440
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.547.8 Variable heavy (vh) domain

<400> 440

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 Thr Phe Ser Ser Tyr
20 25 30
Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 441
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 441

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 442
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 442

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1 5 10

<210> 443
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 443

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 444
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 444

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val

355

360

365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 445
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 445

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 446
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 446

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
1 5 10

<210> 447
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 447

Lys Ala Ser Lys Ser His Thr
1 5

<210> 448
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 448

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 449
 <211> 214
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Full length light chain

 <400> 449
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 450
 <211> 119
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> CHA.9.547.9 Variable heavy (vh) domain

 <400> 450
 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 Thr Phe Ser Ser Tyr
 20 25 30
 Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 451
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 451

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 452
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 452

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
1 5 10

<210> 453
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 453

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 454
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 454

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 455
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 455

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 456
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 456

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Thr
 1 5 10

<210> 457
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 457

Lys Ala Ser Lys Ser His Thr
 1 5

<210> 458
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 458

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 459
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 459

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 460
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.541.1 Variable heavy (vh) domain

<400> 460

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 461
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 461

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 462
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 462

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 463
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 463

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 464
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 464

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

P-2019-16740 TRADUCCIÓN LISTADO DE SECUENCIAS.txt

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 465
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 465

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 466
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 466

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
 1 5 10

<210> 467
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 467

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 468
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 468

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 1 5

<210> 469
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 469

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 470
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.541.3

<400> 470

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 471
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 471

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 472
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 472

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
 1 5 10

<210> 473
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 473

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
 1 5 10

<210> 474
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC (IgG4(S241P))

<400> 474

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 475
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 475

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 476
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 476

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 477
<211> 7

<212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 477

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 478
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 478

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 1 5

<210> 479
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 479

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 480
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.541.4 Variable heavy (vh) domain

<400> 480

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 481
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 481

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 482
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 482

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 483
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 483

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 484
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 484

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 485
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 485

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1 5
Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80
Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 486
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 486

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 487
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 487

Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 488
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 488

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
1 5

<210> 489
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 489

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 490
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.541.5 Variable heavy (vh) domain

<400> 490

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 491
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 491

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
 1 5 10

<210> 492
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 492

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
 1 5 10

<210> 493

```

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 493
Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1          5          10

<210> 494
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 494
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
          20          25          30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50          55          60

Gln Gly Arg Phe Thr Met Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65          70          75          80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
          100          105          110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
          115          120          125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
          130          135          140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145          150          155          160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
          165          170          175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
          180          185          190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
          195          200          205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
          210          215          220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225          230          235          240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
          245          250          255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
          260          265          270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
          275          280          285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
          290          295          300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305          310          315          320

```

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 495
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 495

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Val Thr Met Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30
 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Met Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 496
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 496

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
 1 5 10

<210> 497
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 497

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 498
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> vLCDR3

<400> 498

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
1 5

<210> 499

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 499

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Met Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Met Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 500

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.541.6 Variable heavy (vh) domain

<400> 500

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 501
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 501

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 502
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 502

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 503
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 503

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 504
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC (IgG4(S241P))

<400> 504

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

```

145          150          155          160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
          165          170          175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
          180          185          190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
          195          200          205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
          210          215          220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
          225          230          235          240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
          245          250          255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
          260          265          270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
          275          280          285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
          290          295          300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
          305          310          315          320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
          325          330          335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
          340          345          350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
          355          360          365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
          370          375          380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
          385          390          395          400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
          405          410          415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
          420          425          430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
          435          440          445

```

```

<210> 505
<211> 106
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variable light (vl) domain

```

```

<400> 505

```

```

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1          5          10          15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
          20          25          30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
          35          40          45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
          50          55          60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65          70          75          80

```

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 506
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 506

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
 1 5 10

<210> 507
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 507

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 508
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 508

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 1 5

<210> 509
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 509

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 510
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.541.7 Variable heavy (vh) domain

<400> 510

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 511
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 511

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 512
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 512

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 513
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 513

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 514
<211> 446
<212> PRT
<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 514

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp

385 390 395 400
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 515
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 515

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 516
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 516

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 517
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 517

Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 518
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 518

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
1 5

<210> 519
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 519

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 520

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> CHA.9.541.8 Variable heavy (vh) domain

<400> 520

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 521

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR1

<400> 521

Gly Tyr Thr Ile Thr Asn Tyr Gly Met Asn
1 5 10

<210> 522

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 522

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr
1 5 10

<210> 523

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 523

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
1 5 10

<210> 524

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC (IgG4(S241P))

<400> 524

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Phe Thr Ile Thr Leu Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 525
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 525

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Met Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Met Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 526
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 526

Gly Asn Gly Asn Pro Leu Gly Met Asp Tyr
 1 5 10

<210> 527

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR2

<400> 527

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 528

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 528

Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 1 5

<210> 529

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 529

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Val Thr Met Ser Cys Gly Asn Gly Asn Pro Leu Gly Met Asp
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Met Glu Pro Glu
 65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 530

<211> 119

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> CHA.9.547.10 Variable heavy (vh) domain

 <400> 530
 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 Thr Phe Ser Ser Tyr
 20 25 30
 Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 531
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 531

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1 5 10

<210> 532
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 532

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 533
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 533

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 534
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC

<400> 534

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

P-2019-16740 TRADUCCIÓN LISTADO DE SECUENCIAS.txt

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 535
<211> 107

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Variable light (vl) domain

 <400> 535
 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 Asn Ile Asn Val Trp
 20 25 30

 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

 Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 536
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR1

<400> 536

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
 1 5 10

<210> 537
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR2

<400> 537

Lys Ala Ser Lys Ser His Thr
 1 5

<210> 538
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vlCDR3

<400> 538

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 539
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 539

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 Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 540
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.547.11 Variable heavy (vh) domain

<400> 540

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 541
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 541

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
1 5 10

<210> 542
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 542

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 543

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 543

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 544

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC

<400> 544

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 545
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 545

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 546
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR1

<400> 546

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 547
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR2

<400> 547

Lys Ala Ser Lys Ser His Thr
1 5

<210> 548
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 548

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 549
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 549

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 550
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CHA.9.547.12 Variable heavy (vh) domain

<400> 550

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 551
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 551

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1 5 10

<210> 552
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 552

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 553
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 553

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> 554
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length HC

<400> 554

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270
 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 555
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 555

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 Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 556
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 556

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 557
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR2

<400> 557

Lys Ala Ser Lys Ser His Thr
1 5

<210> 558
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR3

<400> 558

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
1 5

<210> 559
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length light chain

<400> 559

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 Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 560
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.547.13 Variable heavy (vh) domain

<400> 560

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 Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 561
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR1

<400> 561

Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1 5 10

<210> 562
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR2

<400> 562

Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr
 1 5 10

<210> 563
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vhCDR3

<400> 563

Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 564
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC

<400> 564

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 Thr Phe Ser Ser Tyr
20 25 30

Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Trp Leu Leu Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 565
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable light (vl) domain

<400> 565

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 566
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR1

<400> 566

Arg Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
 1 5 10

<210> 567
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 567

Lys Ala Ser Lys Ser His Thr
 1 5

<210> 568
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 568

Gln Gln Gly Gln Ser Tyr Pro Tyr Thr
 1 5

<210> 569
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 569

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Lys Ser His Thr 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 Gln Gly Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 570
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CHA.9.543 Variable heavy (vh) domain

<400> 570

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ser His Gly Lys Asn Leu Glu Trp Leu
 35 40 45

Gly Leu Ile Phe Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Asn Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Val Arg Phe Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser
 100 105 110

Val Ser Val Ser Ser
115

<210> 571
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 571

Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
1 5 10

<210> 572
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR2

<400> 572

Leu Ile Phe Pro Tyr Asn Gly Gly Thr Ser
1 5 10

<210> 573
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR3

<400> 573

Gly Val Arg Phe Ala Leu Asp Tyr
1 5

<210> 574
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length HC

<400> 574

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Arg Gln Ser His Gly Lys Asn Leu Glu Trp Leu
35 40 45

Gly Leu Ile Phe Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Val Arg Phe Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Ser Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu
115 120 125

Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys
130 135 140

Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser
145 150 155 160

Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp

180

185

190

Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr
195 200 205

Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys
210 215 220

Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val
245 250 255

Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
260 265 270

Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu
275 280 285

Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala
305 310 315 320

Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg
325 330 335

Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met
340 345 350

Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro
355 360 365

Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn
370 375 380

Tyr Lys Asn Thr
385

<210> 575
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 575

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Phe Gly
1 5 10 15

Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Asn Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Ile 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 Asn Ile
65 70 75 80

Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Gln Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 576
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> vLCDR1

<400> 576

Arg Ser Ser Gln Ser Leu Ala Asn Ser Tyr Gly Asn Thr Tyr Leu Ser
 1 5 10 15

<210> 577
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 577

Glu Ile Ser Asn Arg Phe Ser
 1 5

<210> 578
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 578

Leu Gln Gly Thr His Gln Pro Trp Thr
 1 5

<210> 579
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 579

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Phe Gly
 1 5 10 15

Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Asn Ser
 20 25 30

Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Glu Ile 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 Asn Ile
 65 70 75 80

Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr Cys Leu Gln Gly
 85 90 95

Thr His Gln Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 115 120 125

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 580
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Clone 31C6 Variable heavy (vh) domain

<400> 580

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
 20 25 30

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asp Pro Tyr Asn Asp Gly Ala Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val Trp Gly Ala Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser
 115

<210> 581

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR1

<400> 581

Gly Tyr Thr Phe Ser Ser Tyr Val
 1 5

<210> 582

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 582

Ile Asp Pro Tyr Asn Asp Gly Ala
 1 5

<210> 583

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 583

Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val
 1 5 10

<210> 584

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC

<400> 584

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
 20 25 30

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asp Pro Tyr Asn Asp Gly Ala Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Pro Tyr Gly Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu
340 345 350

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 585

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable light (vl) domain

<400> 585

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu His Ile Tyr Ser Tyr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
 35 40 45

Tyr Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His His Phe Gly Ser Pro Leu
 85 90 95

Thr Phe Gly Ala Gly Thr Thr Leu Glu Leu Lys
 100 105

<210> 586

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR1

<400> 586

Glu His Ile Tyr Ser Tyr
 1 5

<210> 587

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR2

<400> 587

Asn Ala Lys
 1

<210> 588

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> vLCDR3

<400> 588

Gln His His Phe Gly Ser Pro Leu Thr
 1 5

<210> 589

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length light chain

<400> 589

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu His Ile Tyr Ser Tyr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
 35 40 45

Tyr Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His His Phe Gly Ser Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Thr Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 590
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 22G2 Variable heavy (vh) domain

<400> 590

Gln Val His Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Ile Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr
100 105 110

Tyr Phe Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

Ser Ser
130

<210> 591
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> vhCDR1

<400> 591

Gly Gly Ser Val Ser Ser Gly Ile Tyr Tyr
1 5 10

<210> 592
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> vhCDR2

<400> 592

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 593

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> vhCDR3

<400> 593

Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr Tyr
1 5 10 15

Phe Phe Gly Val Asp Val
20

<210> 594

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length HC

<400> 594

Gln Val His Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Ile Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Tyr Tyr Val Ser Gly Asn Tyr Tyr Asn Val Asp Tyr
100 105 110

Tyr Phe Phe Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly
130 135 140

Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys
145 150 155 160

Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu
165 170 175

Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr
180 185 190

Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu
195 200 205

Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp
210 215 220

Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr
225 230 235 240

Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
245 250 255

Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp
260 265 270

Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp
275 280 285

Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn
290 295 300

Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala
340 345 350

Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp
355 360 365

Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile
370 375 380

Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn
385 390 395 400

Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys
405 410 415

Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys
420 425 430

Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu
435 440 445

Ser His Ser Pro Gly Lys
450

<210> 595
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light (vl) domain

<400> 595

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 596
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> vlCDR1

<400> 596

Gln Ser Val Ser Ser Tyr
1 5

<210> 597

<211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR2

<400> 597

Asp Ala Ser
 1

<210> 598
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> vLCDR3

<400> 598

Gln Gln Arg Ser Asn Trp Pro Pro Leu Phe Thr
 1 5 10

<210> 599
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length light chain

<400> 599

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Asp
 100 105 110

Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr
 115 120 125

Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys
 130 135 140

Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly
 145 150 155 160

Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn
 180 185 190

Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val
 195 200 205

Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 600
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA9.086 CDR sequences

<400> 600

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 601
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 601

Ile Ser Tyr Ala Gly Glu Val Lys
1 5

<210> 602
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 602

Ala Arg Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
1 5 10

<210> 603
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 603

Ser Ser Asn Met Gly Arg Arg Pro
1 5

<210> 604
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 604

Ser Gln Asn
1

<210> 605
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 605

Ala Val Trp Asp Asp Ile Gly Arg Val Leu Gln
1 5 10

<210> 606
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 606

Ser Tyr Ala Met His
1 5

<210> 607
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CPA9.086 CDR sequences

<400> 607

Val Ile Ser Tyr Ala Gly Glu Val Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 608
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA9.086 CDR sequences

<400> 608

Asp Pro Leu Pro Leu His Tyr Tyr Gly Met Asp Val
 1 5 10

<210> 609
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA9.086 CDR sequences

<400> 609

Ser Gly Ser Ser Ser Asn Met Gly Arg Arg Pro Val Asn
 1 5 10

<210> 610
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA9.086 CDR sequences

<400> 610

Ser Gln Asn Gln Arg Pro Ser
 1 5

<210> 611
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CPA9.086 CDR sequences

<400> 611

Ala Val Trp Asp Asp Ile Gly Arg Val Leu Gln
 1 5 10