

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Antibodies binding to CD3

<130> P35214

<150> EP18214994.8

<151> 2018-12-21

<160> 122

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3orig HCDR1

<400> 1

Thr Tyr Ala Met Asn

1 5

<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3opt HCDR1

<400> 2

Ser Tyr Ala Met Asn

1 5

<210> 3

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3orig / CD3opt HCDR2

<400> 3

Arg	Ile	Arg	Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser
1				5					10					15	

Val Lys Gly

<210> 4

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3orig HCDR3

<400> 4

His	Gly	Asn	Phe	Gly	Asn	Ser	Tyr	Val	Ser	Trp	Phe	Ala	Tyr
1				5					10				

<210> 5

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3opt HCDR3

<400> 5

His	Thr	Thr	Phe	Pro	Ser	Ser	Tyr	Val	Ser	Tyr	Tyr	Gly	Tyr
1				5					10				

<210> 6

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3orig VH

<400> 6

Glu Val Gln Leu Leu 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 Thr Tyr
20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

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

<210> 7
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3opt VH

<400> 7

Glu Val Gln Leu Leu 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 Gln Phe Ser Ser Tyr
20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
100 105 110

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

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3orig / CD3opt LCDR1

<400> 8

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3orig / CD3opt LCDR2

<400> 9

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3orig / CD3opt LCDR3

<400> 10

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 11
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3orig / CD3opt VL

<400> 11

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 Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly 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 Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 12
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3orig IgG HC

<400> 12

Glu Val Gln Leu Leu 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 Thr Tyr
20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

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

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

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

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

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

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
325 330 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

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

Leu Ser Leu Ser Pro
450

<210> 13
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3opt IgG HC

<400> 13

Glu Val Gln Leu Leu 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 Gln Phe Ser Ser Tyr
20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
100 105 110

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

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

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

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

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

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
325 330 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

405

410

415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430

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

Leu Ser Leu Ser Pro
 450

<210> 14
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3orig / CD3opt IgG LC

<400> 14

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 Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
 35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly 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 Tyr Ser Asn
 85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu 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> 15
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 HCDR1

<400> 15

Asp Tyr Phe Leu His
1 5

<210> 16
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> TYRP1 HCDR2

<400> 16

Trp Ile Asn Pro Asp Asn Gly Asn Thr Val Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 17

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TYRP1 HCDR3

<400> 17

Arg Asp Tyr Thr Tyr Glu Lys Ala Ala Leu Asp Tyr
1 5 10

<210> 18

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> TYRP1 VH

<400> 18

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 Phe Asn Ile Lys Asp Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asp Asn Gly Asn Thr Val 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

Thr Arg Arg Asp Tyr Thr Tyr Glu Lys Ala Ala Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 19
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 LCDR1

<400> 19

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

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 LCDR2

<400> 20

Asp Ala Lys Thr Leu Ala Asp
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 LCDR3

<400> 21

Gln His Phe Trp Ser Leu Pro Phe Thr
1 5

<210> 22
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 VL

<400> 22

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 Gly Asn Ile Tyr Asn Tyr
20 25 30

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

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

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

<210> 23
<211> 674
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 VH-CH1(EE) - CD3orig/CD3opt VL-CH1 - Fc (knob, PGLALA)

<400> 23

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 Phe Asn Ile Lys Asp Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asp Asn Gly Asn Thr Val 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

Thr Arg Arg Asp Tyr Thr Tyr Glu Lys Ala Ala Leu Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
 225 230 235 240

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
 245 250 255

Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
 260 265 270

Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly Leu Ile Gly Gly Thr
 275 280 285

Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
 290 295 300

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp Glu
 305 310 315 320

Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly
 325 330 335

Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala Ser Thr Lys Gly Pro
340 345 350

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
355 360 365

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
385 390 395 400

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
405 410 415

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
420 425 430

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
435 440 445

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
450 455 460

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
465 470 475 480

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
485 490 495

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
500 505 510

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
515 520 525

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

530

535

540

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 545 550 555 560

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 565 570 575

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
 580 585 590

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 595 600 605

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 610 615 620

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 625 630 635 640

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 645 650 655

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 660 665 670

Ser Pro

<210> 24

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> TYRP1 VH-CH1(EF) -Fc (hole, PGLALA)

<400> 24

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 Phe Asn Ile Lys Asp Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asp Asn Gly Asn Thr Val 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

Thr Arg Arg Asp Tyr Thr Tyr Glu Lys Ala Ala Leu Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

195

200

205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro

<210> 25
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TYRP1 VL-CL(RK)

<400> 25

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 Gly Asn Ile Tyr Asn Tyr
20 25 30

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

Tyr Asp Ala Lys Thr Leu Ala Asp 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 Val Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Leu 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 Arg Lys 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> 26
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3orig VH-CL

<400> 26

Glu Val Gln Leu Leu 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 Thr Tyr
20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

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

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

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

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

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

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

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr

210

215

220

Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 27

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3opt VH-CL

<400> 27

Glu Val Gln Leu Leu 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 Gln Phe Ser Ser Tyr
 20 25 30

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60

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

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

Tyr Cys Val Arg His Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
 100 105 110

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 28
 <211> 360
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human CD3 epsilon stalk - Fc(knob) - Avi

<400> 28

Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys
 1 5 10 15

Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
 20 25 30

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

Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys
50 55 60

Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg
65 70 75 80

Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg
85 90 95

Val Ser Glu Asn Cys Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
115 120 125

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
130 135 140

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

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
165 170 175

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
180 185 190

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
195 200 205

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
210 215 220

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
245 250 255

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
260 265 270

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
275 280 285

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

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
325 330 335

Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu
340 345 350

Ala Gln Lys Ile Glu Trp His Glu
355 360

<210> 29
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD3 delta stalk - Fc (hole) - Avi

<400> 29

Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1 5 10 15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
20 25 30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
35 40 45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
50 55 60

Val Gln Val His Tyr Arg Met Cys Arg Ser Glu Gln Leu Tyr Phe Gln
65 70 75 80

Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
85 90 95

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
100 105 110

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
115 120 125

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
130 135 140

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
145 150 155 160

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
165 170 175

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
180 185 190

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
195 200 205

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

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 225 230 235 240

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 245 250 255

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 275 280 285

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 290 295 300

Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
 305 310 315 320

Ile Glu Trp His Glu
 325

<210> 30
 <211> 351
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cynomolgus CD3 epsilon stalk - Fc (knob) - Avi

<400> 30

Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr Gln Thr Pro Tyr Gln
 1 5 10 15

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

Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys Asn Lys Glu Asp Ser
 35 40 45

Gly Asp Arg Leu Phe Leu Pro Glu Phe Ser Glu Met Glu Gln Ser Gly
50 55 60

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

His Leu Tyr Leu Lys Ala Arg Val Ser Glu Asn Cys Val Asp Glu Gln
85 90 95

Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr
100 105 110

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
130 135 140

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145 150 155 160

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
165 170 175

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
180 185 190

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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
210 215 220

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
225 230 235 240

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
245 250 255

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
275 280 285

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
305 310 315 320

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly
325 330 335

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
340 345 350

<210> 31
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgus CD3 delta stalk - Fc (hole) - Avi

<400> 31

Phe Lys Ile Pro Val Glu Glu Leu Glu Asp Arg Val Phe Val Lys Cys
1 5 10 15

Asn Thr Ser Val Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Thr
20 25 30

Asn Asn Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
35 40 45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Ala
50 55 60

Val Gln Val His Tyr Arg Met Ser Gln Asn Cys Val Asp Glu Gln Leu
65 70 75 80

Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys
85 90 95

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

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
115 120 125

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
130 135 140

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

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
165 170 175

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
180 185 190

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

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

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

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
245 250 255

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
260 265 270

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
275 280 285

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
290 295 300

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly
305 310 315 320

Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
325 330

<210> 32
<211> 699
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TYRP1 ECD - Fc (knob) - Avi

<400> 32

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

Cys Cys Pro Asp Leu Ser Pro Val Ser Gly Pro Gly Thr Asp Arg Cys
20 25 30

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

Arg Pro His Ser Pro Gln Tyr Pro His Asp Gly Arg Asp Asp Arg Glu
50 55 60

Val Trp Pro Leu Arg Phe Phe Asn Arg Thr Cys His Cys Asn Gly Asn
65 70 75 80

Phe Ser Gly His Asn Cys Gly Thr Cys Arg Pro Gly Trp Arg Gly Ala
85 90 95

Ala Cys Asp Gln Arg Val Leu Ile Val Arg Arg Asn Leu Leu Asp Leu
100 105 110

Ser Lys Glu Glu Lys Asn His Phe Val Arg Ala Leu Asp Met Ala Lys
115 120 125

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

Ile Leu Gly Pro Asp Gly Asn Thr Pro Gln Phe Glu Asn Ile Ser Ile
145 150 155 160

Tyr Asn Tyr Phe Val Trp Thr His Tyr Tyr Ser Val Lys Lys Thr Phe
165 170 175

Leu Gly Val Gly Gln Glu Ser Phe Gly Glu Val Asp Phe Ser His Glu
180 185 190

Gly Pro Ala Phe Leu Thr Trp His Arg Tyr His Leu Leu Arg Leu Glu
195 200 205

Lys Asp Met Gln Glu Met Leu Gln Glu Pro Ser Phe Ser Leu Pro Tyr
210 215 220

Trp Asn Phe Ala Thr Gly Lys Asn Val Cys Asp Ile Cys Thr Asp Asp
225 230 235 240

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

Ser Val Phe Ser Gln Trp Arg Val Val Cys Asp Ser Leu Glu Asp Tyr
260 265 270

Asp Thr Leu Gly Thr Leu Cys Asn Ser Thr Glu Asp Gly Pro Ile Arg
275 280 285

Arg Asn Pro Ala Gly Asn Val Ala Arg Pro Met Val Gln Arg Leu Pro
290 295 300

Glu Pro Gln Asp Val Ala Gln Cys Leu Glu Val Gly Leu Phe Asp Thr
305 310 315 320

Pro Pro Phe Tyr Ser Asn Ser Thr Asn Ser Phe Arg Asn Thr Val Glu
325 330 335

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

His Asn Leu Ala His Leu Phe Leu Asn Gly Thr Gly Gly Gln Thr His
355 360 365

Leu Ser Pro Asn Asp Pro Ile Phe Val Leu Leu His Thr Phe Thr Asp
370 375 380

Ala Val Phe Asp Glu Trp Leu Arg Arg Tyr Asn Ala Asp Ile Ser Thr
385 390 395 400

Phe Pro Leu Glu Asn Ala Pro Ile Gly His Asn Arg Gln Tyr Asn Met
405 410 415

Val Pro Phe Trp Pro Pro Val Thr Asn Thr Glu Met Phe Val Thr Ala
420 425 430

Pro Asp Asn Leu Gly Tyr Thr Tyr Glu Ile Gln Trp Pro Ser Arg Glu
435 440 445

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

450

455

460

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 465 470 475 480

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 485 490 495

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 500 505 510

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 515 520 525

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 530 535 540

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 545 550 555 560

Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 565 570 575

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
 580 585 590

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
 595 600 605

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 610 615 620

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 625 630 635 640

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 645 650 655

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
660 665 670

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp
675 680 685

Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695

<210> 33
<211> 698
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgus TYRP1 ECD - Fc (knob) - Avi

<400> 33

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

Cys Cys Pro Asp Leu Ser Pro Met Ser Gly Pro Gly Thr Asp Arg Cys
20 25 30

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

Arg Pro His Ser Pro Arg Tyr Pro His Asp Gly Arg Asp Asp Arg Glu
50 55 60

Val Trp Pro Leu Arg Phe Phe Asn Arg Thr Cys His Cys Asn Gly Asn
65 70 75 80

Phe Ser Gly His Asn Cys Gly Thr Cys Arg Pro Gly Trp Arg Gly Ala
85 90 95

Ala Cys Asp Gln Arg Val Leu Val Val Arg Arg Asn Leu Leu Asp Leu

100	105	110
Ser Lys Glu Glu Lys Asn His Phe Val Arg Ala Leu Asp Met Ala Lys		
115	120	125
Arg Thr Thr His Pro Leu Phe Val Ile Ala Thr Arg Arg Ser Glu Glu		
130	135	140
Ile Leu Gly Pro Asp Gly Asn Thr Pro Gln Phe Glu Asn Ile Ser Ile		
145	150	155
Tyr Asn Tyr Phe Val Trp Thr His Tyr Tyr Ser Val Lys Lys Thr Phe		
165	170	175
Leu Gly Ala Gly Gln Glu Ser Phe Gly Glu Val Asp Phe Ser His Glu		
180	185	190
Gly Pro Ala Phe Leu Thr Trp His Arg Tyr His Leu Leu Arg Leu Glu		
195	200	205
Lys Asp Met Gln Glu Met Leu Gln Glu Pro Ser Phe Ser Leu Pro Tyr		
210	215	220
Trp Asn Phe Ala Thr Gly Lys Asn Val Cys Asp Ile Cys Thr Asp Asp		
225	230	235
Leu Met Gly Ser Arg Ser Asn Phe Asp Ser Thr Leu Ile Ser Pro Asn		
245	250	255
Ser Val Phe Ser Gln Trp Arg Val Val Cys Asp Ser Leu Glu Asp Tyr		
260	265	270
Asp Thr Leu Gly Thr Leu Cys Asn Ser Thr Glu Ser Gly Pro Ile Arg		
275	280	285
Arg Asn Pro Ala Gly Asn Val Ala Arg Pro Met Val Gln Arg Leu Pro		
290	295	300

Glu Pro Gln Asp Val Ala Gln Cys Leu Glu Val Gly Leu Phe Asp Thr
305 310 315 320

Pro Pro Phe Tyr Ser Asn Ser Thr Asn Ser Phe Arg Asn Thr Val Glu
325 330 335

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

His Asn Leu Ala His Leu Phe Leu Asn Gly Thr Gly Gly Gln Thr His
355 360 365

Leu Ser Pro Asn Asp Pro Ile Phe Val Leu Leu His Thr Phe Thr Asp
370 375 380

Ala Val Phe Asp Glu Trp Leu Arg Arg Tyr Asn Ala Asp Ile Ser Thr
385 390 395 400

Phe Pro Leu Glu Asn Ala Pro Ile Gly His Asn Arg Gln Tyr Asn Met
405 410 415

Val Pro Phe Trp Pro Pro Val Thr Asn Thr Glu Met Phe Val Thr Ala
420 425 430

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

Phe Ser Val Pro Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
450 455 460

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
465 470 475 480

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
485 490 495

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
500 505 510

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
515 520 525

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
530 535 540

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
545 550 555 560

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
565 570 575

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
580 585 590

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
595 600 605

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
610 615 620

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
625 630 635 640

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
645 650 655

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
660 665 670

Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile
675 680 685

Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695

<210> 34
<211> 699
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse TYRP1 ECD - Fc (knob) - Avi

<400> 34

Gln Phe Pro Arg Glu Cys Ala Asn Ile Glu Ala Leu Arg Arg Gly Val
1 5 10 15

Cys Cys Pro Asp Leu Leu Pro Ser Ser Gly Pro Gly Thr Asp Pro Cys
20 25 30

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

Arg Pro His Ser Arg His Tyr Pro His Asp Gly Lys Asp Asp Arg Glu
50 55 60

Ala Trp Pro Leu Arg Phe Phe Asn Arg Thr Cys Gln Cys Asn Asp Asn
65 70 75 80

Phe Ser Gly His Asn Cys Gly Thr Cys Arg Pro Gly Trp Arg Gly Ala
85 90 95

Ala Cys Asn Gln Lys Ile Leu Thr Val Arg Arg Asn Leu Leu Asp Leu
100 105 110

Ser Pro Glu Glu Lys Ser His Phe Val Arg Ala Leu Asp Met Ala Lys
115 120 125

Arg Thr Thr His Pro Gln Phe Val Ile Ala Thr Arg Arg Leu Glu Asp
130 135 140

Ile Leu Gly Pro Asp Gly Asn Thr Pro Gln Phe Glu Asn Ile Ser Val
145 150 155 160

Tyr Asn Tyr Phe Val Trp Thr His Tyr Tyr Ser Val Lys Lys Thr Phe
165 170 175

Leu Gly Thr Gly Gln Glu Ser Phe Gly Asp Val Asp Phe Ser His Glu
180 185 190

Gly Pro Ala Phe Leu Thr Trp His Arg Tyr His Leu Leu Gln Leu Glu
195 200 205

Arg Asp Met Gln Glu Met Leu Gln Glu Pro Ser Phe Ser Leu Pro Tyr
210 215 220

Trp Asn Phe Ala Thr Gly Lys Asn Val Cys Asp Val Cys Thr Asp Asp
225 230 235 240

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

Ser Val Phe Ser Gln Trp Arg Val Val Cys Glu Ser Leu Glu Glu Tyr
260 265 270

Asp Thr Leu Gly Thr Leu Cys Asn Ser Thr Glu Gly Gly Pro Ile Arg
275 280 285

Arg Asn Pro Ala Gly Asn Val Gly Arg Pro Ala Val Gln Arg Leu Pro
290 295 300

Glu Pro Gln Asp Val Thr Gln Cys Leu Glu Val Arg Val Phe Asp Thr
305 310 315 320

Pro Pro Phe Tyr Ser Asn Ser Thr Asp Ser Phe Arg Asn Thr Val Glu
325 330 335

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

His Asn Leu Ala His Leu Phe Leu Asn Gly Thr Gly Gly Gln Thr His
355 360 365

Leu Ser Pro Asn Asp Pro Ile Phe Val Leu Leu His Thr Phe Thr Asp
370 375 380

Ala Val Phe Asp Glu Trp Leu Arg Arg Tyr Asn Ala Asp Ile Ser Thr
385 390 395 400

Phe Pro Leu Glu Asn Ala Pro Ile Gly His Asn Arg Gln Tyr Asn Met
405 410 415

Val Pro Phe Trp Pro Pro Val Thr Asn Thr Glu Met Phe Val Thr Ala
420 425 430

Pro Asp Asn Leu Gly Tyr Ala Tyr Glu Val Gln Trp Pro Gly Gln Glu
435 440 445

Phe Thr Val Ser Glu Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
450 455 460

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
465 470 475 480

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
485 490 495

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
500 505 510

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
515 520 525

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

530

535

540

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 545 550 555 560

Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 565 570 575

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
 580 585 590

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
 595 600 605

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 610 615 620

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 625 630 635 640

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 645 650 655

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 660 665 670

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp
 675 680 685

Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 690 695

<210> 35

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc (hole)

<400> 35

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

180

185

190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro
 225

<210> 36
 <211> 393
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII ECD - Avi - His

<400> 36

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
 1 5 10 15

Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val
 20 25 30

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
 35 40 45

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
 50 55 60

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

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

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
100 105 110

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
115 120 125

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
130 135 140

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
145 150 155 160

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
165 170 175

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
180 185 190

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
195 200 205

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

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
225 230 235 240

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
245 250 255

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
260 265 270

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
275 280 285

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys

290

295

300

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
 305 310 315 320

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
 325 330 335

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile
 340 345 350

Pro Ser Val Asp Gly Gly Ser Pro Thr Pro Pro Thr Pro Gly Gly Gly
 355 360 365

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

Ala Arg Ala His His His His His His
 385 390

<210> 37
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.021 HCDR1

<400> 37

Ser Tyr Trp Ile Ala
 1 5

<210> 38
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.021 HCDR2

<400> 38

Val Ile His Pro Tyr Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 39

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.021 HCDR3

<400> 39

Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr
1 5 10

<210> 40

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.021 VH

<400> 40

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asp Ser Tyr
20 25 30

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

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

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

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

Ala Arg Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 41
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.021 LCDR1

<400> 41

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.021 LCDR2

<400> 42

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.021 LCDR3

<400> 43

Gln Gln Val His Ser Gly Pro Pro Val Thr
1 5 10

<210> 44
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.021 VL

<400> 44

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Val His Ser Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu

100

105

110

Ile Lys

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.052 HCDR1

<400> 45

Asn Tyr Trp Ile Gly
1 5

<210> 46
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.052 HCDR2

<400> 46

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

Gly

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.052 HCDR3

<400> 47

Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr
1 5 10

<210> 48
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.052 VH

<400> 48

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

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

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

Gly Thr Ile Tyr Pro Gly Asp Ser Asp Arg Arg Tyr Ser Pro Ser Phe
50 55 60

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

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

Ala Arg Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 49
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.052 LCDR1

<400> 49

Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	Ser	Asn	Asn	Lys	Asn	Tyr	Leu
1				5					10					15	

Ala

<210> 50

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.052 LCDR2

<400> 50

Trp	Ala	Ser	Thr	Arg	Glu	Ser
1					5	

<210> 51

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.052 LCDR3

<400> 51

Gln	Gln	Val	His	Ser	Gly	Pro	Pro	Val	Thr
1				5					10

<210> 52

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P056.052 VL

<400> 52

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Val His Ser Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P047.019 HCDR1

<400> 53

Ser Ile Trp Ile His
1 5

<210> 54
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 HCDR2

<400> 54

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

Gly

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 HCDR3

<400> 55

Thr Gly Pro Gly Leu Ala Phe Asp Tyr
1 5

<210> 56
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 VH

<400> 56

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Pro Ser Ile
20 25 30

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

Gly Thr Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 LCDR1

<400> 57

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 58
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 LCDR2

<400> 58

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 LCDR3

<400> 59

Gln Gln Ser Tyr Ser Thr Pro Ile Thr
1 5

<210> 60
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P047.019 VL

<400> 60

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

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

Lys

<210> 61
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 HCDR1

<400> 61

Asn Tyr Trp Ile Ala
1 5

<210> 62
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 HCDR2

<400> 62

Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 63

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

<220>
<223> EGFRvIII P057.012 HCDR3

<400> 63

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

<210> 64
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 VH

<400> 64

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

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

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

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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

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

Ala Arg Ala Thr Asn Ile Ala Ser Gly Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> EGFRvIII P057.012 LCDR1

<400> 65

Lys Ser Ser Gln Ser Val Leu Trp Asn Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 66
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 LCDR2

<400> 66

Trp Ala Ser Lys Arg Glu Ser
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 LCDR3

<400> 67

Gln Gln Ser Tyr Ser Ala Pro Ile Thr

1

5

<210> 68
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.012 VL

<400> 68

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

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

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

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

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

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

Ser Tyr Ser Ala Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 69
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> EGFRvIII P057.011 HCDR1

<400> 69

Arg Arg Trp Ile Ala
1 5

<210> 70

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P057.011 HCDR2

<400> 70

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

Gly

<210> 71

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P057.011 HCDR3

<400> 71

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

<210> 72

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P057.011 VH

<400> 72

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

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

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

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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

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

Ala Arg Ala Thr Asn Ile Ala Ser Gly Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 73

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P057.011 LCDR1

<400> 73

Lys Ser Ser Gln Ser Val Leu Trp Asn Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 74
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.011 LCDR2

<400> 74

Trp Ala Ser Lys Arg Glu Ser
1 5

<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.011 LCDR3

<400> 75

Gln Gln Ser Tyr Ser Ala Pro Ile Thr
1 5

<210> 76
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P057.011 VL

<400> 76

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

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

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

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

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

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

Ser Tyr Ser Ala Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 77
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.027 HCDR1

<400> 77

Asn Asn Trp Ile Ala
1 5

<210> 78
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.027 HCDR2

<400> 78

Val Ile Tyr Pro Gly Asp Ser Asp Lys Arg Tyr Ser Pro Ser Phe Gln
 1 5 10 15

Gly

<210> 79
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.027 HCDR3

<400> 79

Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr
 1 5 10

<210> 80
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.027 VH

<400> 80

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

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

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

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

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

65		70		75		80
Leu	Gln	Trp	Ser	Ser	Leu	Lys
			85			Ala
				90	Ser	Asp
					Thr	Ala
					Met	Tyr
						Tyr
						Cys

Ala	Arg	Val	Ser	Arg	Ser	Ser	Tyr	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		

Thr	Leu	Val	Thr	Val	Ser	Ser
						115

<210> 81
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.027 LCDR1

<400> 81

Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	Ser	Asn	Asn	Lys	Asn	Tyr	Leu
1				5					10					15	

Ala

<210> 82
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFRvIII P056.027 LCDR2

<400> 82

Trp	Ala	Ser	Thr	Arg	Glu	Ser
1					5	

<210> 83
 <211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.027 LCDR3

<400> 83

Gln Gln Val His Ser Gly Pro Pro Val Thr
1 5 10

<210> 84
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P056.027 VL

<400> 84

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Val His Ser Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 85
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P063.056 HCDR1

<400> 85

Ser Tyr Trp Ile Ala
1 5

<210> 86
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P063.056 HCDR2

<400> 86

Val Ile His Pro Tyr Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 87
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P063.056 HCDR3

<400> 87

Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr
1 5 10

<210> 88
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P063.056 VH

<400> 88

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asp Ser Tyr
20 25 30

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

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

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

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

Ala Arg Val Ser Arg Ser Ser Tyr Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 89
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> EGFRvIII P063.056 LCDR1

<400> 89

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 90

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P063.056 LCDR2

<400> 90

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 91

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P063.056 LCDR3

<400> 91

Gln Gln Gln Arg Asp Gly Pro Pro Val Thr
1 5 10

<210> 92

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P063.056 VL

<400> 92

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Gln Arg Asp Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 93

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P064.078 HCDR1

<400> 93

Ser Tyr Trp Ile Ala
1 5

<210> 94

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

<220>
<223> EGFRvIII P064.078 HCDR2

<400> 94

Val	Ile	His	Pro	Tyr	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe	Gln
1				5					10					15	

Gly

<210> 95
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P064.078 HCDR3

<400> 95

Val	Ser	Arg	Leu	Ser	Tyr	Ala	Leu	Asp	Tyr
1				5					10

<210> 96
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P064.078 VH

<400> 96

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

Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Asp	Ser	Tyr
			20					25					30		

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 97
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P064.078 LCDR1

<400> 97

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P064.078 LCDR2

<400> 98

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 99

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P064.078 LCDR3

<400> 99

Gln Gln Val His Ser Gly Pro Pro Val Thr
1 5 10

<210> 100

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P064.078 VL

<400> 100

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Val His Ser Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 HCDR1

<400> 101

Ser Tyr Trp Ile Ala
1 5

<210> 102
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 HCDR2

<400> 102

Val Ile His Pro Tyr Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 103
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P065.036 HCDR3

<400> 103

Val Ser Arg Ser Ser Tyr Ala Leu Asp Tyr
1 5 10

<210> 104

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFRvIII P065.036 VH

<400> 104

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asp Ser Tyr
20 25 30

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 105
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 LCDR1

<400> 105

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 106
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 LCDR2

<400> 106

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 107
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 LCDR3

<400> 107

Gln Gln Val Tyr Ser Gly Pro Pro Val Thr
1 5 10

<210> 108
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII P065.036 VL

<400> 108

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Val Tyr Ser Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 109
<211> 672
<212> PRT
<213> Artificial Sequence

<220>

<223> EGFRvIII VH-CH1(EE) - CD3orig/CD3opt VL-CH1 - Fc (knob, PGLALA)

<400> 109

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asp Ser Tyr
20 25 30

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr Gln Glu
 225 230 235 240

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
 245 250 255

Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln
 260 265 270

Glu Lys Pro Gly Gln Ala Phe Arg Gly Leu Ile Gly Gly Thr Asn Lys
 275 280 285

Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
 290 295 300

Lys Ala Ala Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp Glu Ala Glu
 305 310 315 320

Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly Gly Gly
 325 330 335

Thr Lys Leu Thr Val Leu Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 340 345 350

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 355 360 365

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 385 390 395 400

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 405 410 415

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 420 425 430

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 435 440 445

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 450 455 460

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 465 470 475 480

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 485 490 495

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 500 505 510

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 515 520 525

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 530 535 540

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 545 550 555 560

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 565 570 575

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
580 585 590

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
595 600 605

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
610 615 620

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
625 630 635 640

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
645 650 655

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
660 665 670

<210> 110
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII VH-CH1(EF) -Fc (hole, PGLALA)

<400> 110

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asp Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 111
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFRvIII VL-CL(RK)

<400> 111

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

Gln Arg Asp Gly Pro Pro Val Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
115 120 125

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

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

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

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

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

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 112
<211> 186
<212> PRT
<213> Homo sapiens

<400> 112

Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys
1 5 10 15

Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
20 25 30

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

Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys
50 55 60

Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg
65 70 75 80

Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg
85 90 95

Val Cys Glu Asn Cys Met Glu Met Asp Val Met Ser Val Ala Thr Ile

100

105

110

Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu Leu Leu Leu Val Tyr
 115 120 125

Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly
 130 135 140

Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro
 145 150 155 160

Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp
 165 170 175

Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
 180 185

<210> 113
 <211> 177
 <212> PRT
 <213> Macaca fascicularis

<400> 113

Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr Gln Thr Pro Tyr Gln
 1 5 10 15

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

Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys Asn Lys Glu Asp Ser
 35 40 45

Gly Asp Arg Leu Phe Leu Pro Glu Phe Ser Glu Met Glu Gln Ser Gly
 50 55 60

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

His Leu Tyr Leu Lys Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp
85 90 95

Val Met Ala Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Leu
100 105 110

Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys
115 120 125

Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly
130 135 140

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

Ile Arg Lys Gly Gln Gln Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg
165 170 175

Ile

<210> 114
<211> 513
<212> PRT
<213> Homo sapiens

<400> 114

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

Cys Cys Pro Asp Leu Ser Pro Val Ser Gly Pro Gly Thr Asp Arg Cys
20 25 30

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

Arg Pro His Ser Pro Gln Tyr Pro His Asp Gly Arg Asp Asp Arg Glu

50

55

60

Val Trp Pro Leu Arg Phe Phe Asn Arg Thr Cys His Cys Asn Gly Asn
65 70 75 80

Phe Ser Gly His Asn Cys Gly Thr Cys Arg Pro Gly Trp Arg Gly Ala
85 90 95

Ala Cys Asp Gln Arg Val Leu Ile Val Arg Arg Asn Leu Leu Asp Leu
100 105 110

Ser Lys Glu Glu Lys Asn His Phe Val Arg Ala Leu Asp Met Ala Lys
115 120 125

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

Ile Leu Gly Pro Asp Gly Asn Thr Pro Gln Phe Glu Asn Ile Ser Ile
145 150 155 160

Tyr Asn Tyr Phe Val Trp Thr His Tyr Tyr Ser Val Lys Lys Thr Phe
165 170 175

Leu Gly Val Gly Gln Glu Ser Phe Gly Glu Val Asp Phe Ser His Glu
180 185 190

Gly Pro Ala Phe Leu Thr Trp His Arg Tyr His Leu Leu Arg Leu Glu
195 200 205

Lys Asp Met Gln Glu Met Leu Gln Glu Pro Ser Phe Ser Leu Pro Tyr
210 215 220

Trp Asn Phe Ala Thr Gly Lys Asn Val Cys Asp Ile Cys Thr Asp Asp
225 230 235 240

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

Ser Val Phe Ser Gln Trp Arg Val Val Cys Asp Ser Leu Glu Asp Tyr
260 265 270

Asp Thr Leu Gly Thr Leu Cys Asn Ser Thr Glu Asp Gly Pro Ile Arg
275 280 285

Arg Asn Pro Ala Gly Asn Val Ala Arg Pro Met Val Gln Arg Leu Pro
290 295 300

Glu Pro Gln Asp Val Ala Gln Cys Leu Glu Val Gly Leu Phe Asp Thr
305 310 315 320

Pro Pro Phe Tyr Ser Asn Ser Thr Asn Ser Phe Arg Asn Thr Val Glu
325 330 335

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

His Asn Leu Ala His Leu Phe Leu Asn Gly Thr Gly Gly Gln Thr His
355 360 365

Leu Ser Pro Asn Asp Pro Ile Phe Val Leu Leu His Thr Phe Thr Asp
370 375 380

Ala Val Phe Asp Glu Trp Leu Arg Arg Tyr Asn Ala Asp Ile Ser Thr
385 390 395 400

Phe Pro Leu Glu Asn Ala Pro Ile Gly His Asn Arg Gln Tyr Asn Met
405 410 415

Val Pro Phe Trp Pro Pro Val Thr Asn Thr Glu Met Phe Val Thr Ala
420 425 430

Pro Asp Asn Leu Gly Tyr Thr Tyr Glu Ile Gln Trp Pro Ser Arg Glu
435 440 445

Phe Ser Val Pro Glu Ile Ile Ala Ile Ala Val Val Gly Ala Leu Leu
450 455 460

Leu Val Ala Leu Ile Phe Gly Thr Ala Ser Tyr Leu Ile Arg Ala Arg
465 470 475 480

Arg Ser Met Asp Glu Ala Asn Gln Pro Leu Leu Thr Asp Gln Tyr Gln
485 490 495

Cys Tyr Ala Glu Glu Tyr Glu Lys Leu Gln Asn Pro Asn Gln Ser Val
500 505 510

Val

<210> 115
<211> 919
<212> PRT
<213> Homo sapiens

<400> 115

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val
20 25 30

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
35 40 45

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
50 55 60

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

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu

85

90

95

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
 100 105 110

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
 115 120 125

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
 130 135 140

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
 145 150 155 160

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
 165 170 175

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
 180 185 190

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
 195 200 205

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

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
 225 230 235 240

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
 245 250 255

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
 260 265 270

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
 275 280 285

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
290 295 300

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
305 310 315 320

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
325 330 335

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile
340 345 350

Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Val
355 360 365

Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His Ile Val Arg
370 375 380

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

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

Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe
420 425 430

Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys
435 440 445

Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala
450 455 460

Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn
465 470 475 480

Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln
485 490 495

Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg
500 505 510

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

Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His
530 535 540

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val
545 550 555 560

Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys
565 570 575

Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu
580 585 590

Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser
595 600 605

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr
610 615 620

Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu
625 630 635 640

Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met
645 650 655

Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu
660 665 670

Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu
675 680 685

Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro Thr Asp Ser
690 695 700

Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp Asp Val Val
705 710 715 720

Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe Phe Ser Ser Pro
725 730 735

Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu Ser Ala Thr Ser Asn
740 745 750

Asn Ser Thr Val Ala Cys Ile Asp Arg Asn Gly Leu Gln Ser Cys Pro
755 760 765

Ile Lys Glu Asp Ser Phe Leu Gln Arg Tyr Ser Ser Asp Pro Thr Gly
770 775 780

Ala Leu Thr Glu Asp Ser Ile Asp Asp Thr Phe Leu Pro Val Pro Glu
785 790 795 800

Tyr Ile Asn Gln Ser Val Pro Lys Arg Pro Ala Gly Ser Val Gln Asn
805 810 815

Pro Val Tyr His Asn Gln Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro
820 825 830

His Tyr Gln Asp Pro His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu
835 840 845

Asn Thr Val Gln Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala
850 855 860

His Trp Ala Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp

Tyr Gln Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe
885 890 895

Lys Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
900 905 910

Ser Ser Glu Phe Ile Gly Ala
915

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<210> 116
<211> 1186
<212> PRT
<213> Homo sapiens
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$\langle 400 \rangle$ 116

Leu Glu Glu Lys Lys Val Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln
1 5 10 15

Leu Gly Thr Phe Glu Asp His Phe Leu Ser Leu Gln Arg Met Phe Asn
20 25 30

Asn Cys Glu Val Val Leu Gly Asn Leu Glu Ile Thr Tyr Val Gln Arg
35 40 45

Asn Tyr Asp Leu Ser Phe Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr
50 55 60

Val Leu Ile Ala Leu Asn Thr Val Glu Arg Ile Pro Leu Glu Asn Leu
65 70 75 80

Gln Ile Ile Arg Gly Asn Met Tyr Tyr Glu Asn Ser Tyr Ala Leu Ala
85 90 95

Val Leu Ser Asn Tyr Asp Ala Asn Lys Thr Gly Leu Lys Glu Leu Pro
100 105 110

Met Arg Asn Leu Gln Glu Ile Leu His Gly Ala Val Arg Phe Ser Asn
115 120 125

Asn Pro Ala Leu Cys Asn Val Glu Ser Ile Gln Trp Arg Asp Ile Val
130 135 140

Ser Ser Asp Phe Leu Ser Asn Met Ser Met Asp Phe Gln Asn His Leu
145 150 155 160

Gly Ser Cys Gln Lys Cys Asp Pro Ser Cys Pro Asn Gly Ser Cys Trp
165 170 175

Gly Ala Gly Glu Glu Asn Cys Gln Lys Leu Thr Lys Ile Ile Cys Ala
180 185 190

Gln Gln Cys Ser Gly Arg Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys
195 200 205

His Asn Gln Cys Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys
210 215 220

Leu Val Cys Arg Lys Phe Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys
225 230 235 240

Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn
245 250 255

Pro Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro
260 265 270

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

Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys
290 295 300

Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu
305 310 315 320

Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys
325 330 335

Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe
340 345 350

Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu
355 360 365

Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln
370 375 380

Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu
385 390 395 400

Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val
405 410 415

Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile
420 425 430

Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala
435 440 445

Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr
450 455 460

Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
465 470 475 480

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
485 490 495

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val

500

505

510

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
 515 520 525

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
 530 535 540

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
 545 550 555 560

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
 565 570 575

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
 580 585 590

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
 595 600 605

Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr
 610 615 620

Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile
 625 630 635 640

Gly Leu Phe Met Arg Arg Arg His Ile Val Arg Lys Arg Thr Leu Arg
 645 650 655

Arg Leu Leu Gln Glu Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
 660 665 670

Glu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe
 675 680 685

Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
 690 695 700

Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile Pro Val Ala Ile
705 710 715 720

Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
725 730 735

Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His Val Cys Arg
740 745 750

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile Thr Gln Leu
755 760 765

Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg Glu His Lys Asp Asn
770 775 780

Ile Gly Ser Gln Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly
785 790 795 800

Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His Arg Asp Leu Ala Ala
805 810 815

Arg Asn Val Leu Val Lys Thr Pro Gln His Val Lys Ile Thr Asp Phe
820 825 830

Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys Glu Tyr His Ala Glu
835 840 845

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu His
850 855 860

Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
865 870 875 880

Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala
885 890 895

Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
900 905 910

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
915 920 925

Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe
930 935 940

Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp
945 950 955 960

Glu Arg Met His Leu Pro Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala
965 970 975

Leu Met Asp Glu Glu Asp Met Asp Asp Val Val Asp Ala Asp Glu Tyr
980 985 990

Leu Ile Pro Gln Gln Gly Phe Phe Ser Ser Pro Ser Thr Ser Arg Thr
995 1000 1005

Pro Leu Leu Ser Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val
1010 1015 1020

Ala Cys Ile Asp Arg Asn Gly Leu Gln Ser Cys Pro Ile Lys Glu
1025 1030 1035

Asp Ser Phe Leu Gln Arg Tyr Ser Ser Asp Pro Thr Gly Ala Leu
1040 1045 1050

Thr Glu Asp Ser Ile Asp Asp Thr Phe Leu Pro Val Pro Glu Tyr
1055 1060 1065

Ile Asn Gln Ser Val Pro Lys Arg Pro Ala Gly Ser Val Gln Asn
1070 1075 1080

Pro Val Tyr His Asn Gln Pro Leu Asn Pro Ala Pro Ser Arg Asp
1085 1090 1095

Pro His Tyr Gln Asp Pro His Ser Thr Ala Val Gly Asn Pro Glu
1100 1105 1110

Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn Ser Thr Phe Asp
1115 1120 1125

Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln Ile Ser Leu
1130 1135 1140

Asp Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu Ala Lys
1145 1150 1155

Pro Asn Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu Tyr
1160 1165 1170

Leu Arg Val Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala
1175 1180 1185

<210> 117
<211> 225
<212> PRT
<213> Homo sapiens

<400> 117

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro
225

<210> 118
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 118

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 119

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 119

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 120

<211> 107

<212> PRT

<213> Homo sapiens

<400> 120

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

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<210> 121
<211> 105
<212> PRT
<213> Homo sapiens
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<400> 121

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

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

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

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

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

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

Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

$\langle 210 \rangle$	122
$\langle 211 \rangle$	328
$\langle 212 \rangle$	PRT

<213> Homo sapiens

<400> 122

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

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

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

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

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

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

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

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

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

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

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

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

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