

SEQUENCE LISTING

<110> Genmab A/S

<120> ANTIBODIES

<130> P/0155-WO-PCT

<160> 71

<170> PatentIn version 3.5

<210> 1

<211> 282

<212> PRT

<213> Homo Sapiens

<400> 1

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
 145 150 155 160

Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
 225 230 235 240

Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
 245 250 255

Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
 260 265 270

Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
 275 280

<210> 2

<211> 282

<212> PRT

<213> *Macaca fascicularis*

<400> 2

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
 1 5 10 15

Phe Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Ile Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
 145 150 155 160

Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
 225 230 235 240

Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
 245 250 255

Lys Ala Ser Leu Cys Val Ser Ser Phe Leu Ala Ile Ser Trp Ala Leu
 260 265 270

Leu Pro Leu Ala Pro Tyr Leu Met Leu Lys
 275 280

<210> 3
 <211> 282
 <212> PRT
 <213> Canis familiaris

<400> 3

Met Ala Ser Pro Gly Gln Asn Ile Phe Trp Ser Ile Ile Ser Val Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Leu Thr Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Met Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Asp Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Ile Pro Glu Val Asn Val Asp Tyr Asn
 145 150 155 160

Ala Ser Ser Glu Asn Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Val Trp Ala Ser Gln Ala Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Phe Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
 225 230 235 240

Thr Asp Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
 245 250 255

Lys Ala Ser Leu Gly Val Ser Ser Phe Phe Ala Ile Ser Trp Val Leu
 260 265 270

Leu Pro Leu Ser Ser Tyr Leu Met Leu Lys
 275 280

<210> 4

<211> 282
 <212> PRT
 <213> *Oryctolagus cuniculus*

<400> 4

Met Ala Ser Leu Gly Gln Ile Ile Phe Trp Ser Ile Ile Ser Ile Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Leu Thr Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Arg Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Val Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Asp Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Leu Asp Tyr Asn
 145 150 155 160

Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Val Asn Asn Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
 225 230 235 240

Thr Asp Ser Glu Ile Lys Arg Arg Ser Ser Leu Gln Leu Leu Asn Ser
 245 250 255

Arg Ala Ala Pro Ser Val Ser Pro Arg Ser Ala Val Gly Trp Leu Leu
 260 265 270

Leu Pro Leu Ser Ser Tyr Val Met Leu Lys
 275 280

<210> 5
 <211> 282
 <212> PRT
 <213> Rattus norvegicus

<400> 5

Met Ala Ser Leu Gly Gln Ile Ile Phe Trp Ser Ile Ile Asn Val Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Val Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Lys His Phe Ile Thr Val Thr Thr Phe Thr Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Thr Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Asn Gly Ile Val Ile Gln Trp Leu Lys Glu Gly Ile Lys Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Gln Gln His Glu Met
 85 90 95

Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Val Val Gly Asn
 100 105 110

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Thr Cys Tyr Ile His Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Ile Asn Val Asp Tyr Asn
 145 150 155 160

Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Ala Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
 225 230 235 240

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

Gly Pro Ser Pro Cys Val Ser Ser Val Ser Ala Ala Gly Trp Ala Leu

260

265

270

Leu Ser Leu Ser Cys Cys Leu Met Leu Arg
 275 280

<210> 6
 <211> 283
 <212> PRT
 <213> Mus musculus

<400> 6

Met Ala Ser Leu Gly Gln Ile Ile Phe Trp Ser Ile Ile Asn Ile Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Lys His Phe Ile Thr Val Thr Thr Phe Thr Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Thr Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Asn Gly Ile Val Ile Gln Trp Leu Lys Glu Gly Ile Lys Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Gln Gln His Glu Met
 85 90 95

Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Val Val Gly Asn
 100 105 110

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Thr Cys Tyr Ile Arg Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Ile Asn Val Asp Tyr Asn
145 150 155 160

Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
165 170 175

Pro Thr Val Ala Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225 230 235 240

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

Gly Pro Ser Pro Cys Val Phe Ser Ser Ala Phe Val Ala Gly Trp Ala
260 265 270

Leu Leu Ser Leu Ser Cys Cys Leu Met Leu Arg
275 280

<210> 7
<211> 282
<212> PRT
<213> Sus scrofa

<400> 7

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

Ile Ile Leu Ala Gly Ala Ile Ala Phe Ile Ile Gly Phe Gly Ile Ser
20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Leu Thr Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Thr Gly Leu Val
 65 70 75 80

His Glu Phe Lys Lys Gly Lys Asp Asp Leu Ser Asp Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Lys Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Phe Ser Ile Pro Glu Val Asn Val Asp Ser Asn
 145 150 155 160

Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
 165 170 175

Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
 180 185 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Pro Glu Asn Val Thr Met
 195 200 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Thr Thr Tyr Ser
 210 215 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Arg Val

Thr Asp Ser Glu Ile Lys Arg Gln Ser His Leu Gln Leu Leu Asn Ser
245 250 255

Thr Asp Ser Glu Ile Lys Arg Gln Ser His Leu Gln Leu Leu Asn Ser
245 250 255

245

250

255

Lys Ala Ser Leu Cys Leu Ser Ser Phe Val Ala Ile Ser Trp Val Leu
260 265 270

260

265

270

Leu Pro Leu Cys Pro Tyr Leu Met Leu Lys
275 280

275

280

$\langle 210 \rangle$ 8

<211> 9

<212> PRT

<213> Artificial sequence

 $\langle 220 \rangle$

<223> Nucleic acid motif for translation

<400> 8

Gly Cys Cys Gly Cys Cys Ala Cys Cys
1 5

1

5

$\langle 210 \rangle$ 9

<211> 534

<212> PRT

<213> Homo Sapiens

<400> 9

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

1

5

10

15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
20 25 30

20

25

30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

35

40

45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

50

55

60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
 65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
 85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
 100 105 110

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

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

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
 145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
 165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
 180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
 195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
 225 230 235 240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
 245 250 255

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

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
 275 280 285

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

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
 305 310 315 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
 325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
 340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
 355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
 370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
 385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
 405 410 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
 420 425 430

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

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
 450 455 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu
 465 470 475 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
 485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
 500 505 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
 515 520 525

Asp Gly Gln Glu Ile Ala
 530

<210> 10
 <211> 325
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Domain swap

<400> 10

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
 1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
 20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
 35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
 50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
 65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
 85 90 95

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

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
 115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
 130 135 140

Tyr Lys Thr Gly Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro
 145 150 155 160

Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser
 165 170 175

Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly
 180 185 190

Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln
 195 200 205

Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala Asn
 210 215 220

Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala
 225 230 235 240

His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro Glu
 245 250 255

Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
 260 265 270

Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
 275 280 285

Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
 290 295 300

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

Gly Gln Glu Ile Ala
 325

<210> 11
 <211> 273
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Domain swap

<400> 11

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

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
 20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
 35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
 50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
 65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
 85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
 100 105 110

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

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Phe Ser Met Pro
 130 135 140

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

Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser Gln Val
 165 170 175

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

Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val Leu Tyr Asn Val
 195 200 205

Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn Asp Ile Ala Lys
 210 215 220

Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile Lys Arg Arg Ser
 225 230 235 240

His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys Val Ser Ser Phe
 245 250 255

Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met Leu
 260 265 270

Lys

<210> 12

<211> 484

<212> PRT
 <213> Artificial sequence

<220>
 <223> Tagged protein

<400> 12

Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile Thr Val Thr
 1 5 10 15

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

Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu
 35 40 45

Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp
 50 55 60

Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe
 65 70 75 80

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

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser Lys
 100 105 110

Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser Met
 115 120 125

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

Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser Gln
 145 150 155 160

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

Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val Leu Tyr Asn
 180 185 190

Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn Asp Ile Ala
 195 200 205

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

Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Ile Glu Gly Arg Met
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys His His His His His His His
 465 470 475 480

Glu Pro Glu Ala

<210> 13
 <211> 186
 <212> PRT
 <213> Homo Sapiens

<400> 13

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> 14

<211> 127

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 14

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 Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe
 20 25 30

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

Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe
 50 55 60

Gln Asp Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr
 65 70 75 80

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

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

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
 115 120 125

<210> 15

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 15

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

Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg
 20 25 30

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

Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser
 50 55 60

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys
 100 105

<210> 16

<211> 125

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 16

Glu Val Lys 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 Asn Thr Tyr
 20 25 30

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

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

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

Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met 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> 17

<211> 125

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 17

Glu Val Lys 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 Asn Thr Tyr
 20 25 30

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

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

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

Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
 85 90 95

Tyr Cys Val Arg Gly 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> 18
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 18

Gly Phe Thr Phe Asn Thr Tyr Ala
 1 5

<210> 19
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 19

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

<210> 20
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 20

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
 1 5 10 15

<210> 21
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 21

Val Arg Gly Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 22

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 22

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

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

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

Gln Ala Asp Asp Glu Ser Ile Tyr Phe 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> 23

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 23

Thr Gly Ala Val Thr Thr Ser Asn Tyr

1 5

<210> 24

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 24

Ala Leu Trp Tyr Ser Asn Leu Trp Val

1 5

<210> 25

<211> 117

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 25

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu

$\langle 210 \rangle$	26
$\langle 211 \rangle$	8
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

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<220>
<223> binding domain sequence
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<400> 26

Gly Gly Ser Phe Ser Gly Tyr Tyr
1 5

$\langle 210 \rangle$	27
$\langle 211 \rangle$	7
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

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<220>
<223> binding domain sequence
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<400> 27

Ile Asn His Ser Gly Ser Thr
1 5

$\langle 210 \rangle$	28
$\langle 211 \rangle$	11
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

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<220>
<223> binding domain sequence
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<400> 28

Ala Arg Gly Leu Phe Asn Trp Asn Phe Asp Ser
1 5 10

<210> 29

<211> 117

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 29

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

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

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

Gly Glu Ile Ser His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Gly Leu Phe Asn Trp Asn Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 30

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

<220>
 <223> binding domain sequence

<400> 30

Ile Ser His Ser Gly Ser Thr
 1 5

<210> 31
 <211> 117
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 31

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

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

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

Gly Glu Ile Gln His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

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

Arg Gly Leu Phe Asn Trp Asn Phe Asp Ser Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
115

<210> 32
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 32

Ile Gln His Ser Gly Ser Thr
1 5

<210> 33
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<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 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 Gly 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 Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Arg

85

90

95

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

<210> 34
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
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<400> 34

Gln Gly Ile Arg Asn Asp
 1 5

<210> 35
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 35

Leu Gln His Asn Ser Tyr Pro Arg Thr
 1 5

<210> 36
 <211> 116
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 36

Glu 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 Phe

20

25

30

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

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

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

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

Ala Arg Glu Ile Thr Thr Val Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 37
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 37

Gly Tyr Thr Phe Thr Asn Phe Trp
 1 5

<210> 38
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 38

Ile Asp Pro Ser Asp Ser Tyr Thr
1 5

<210> 39
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 39

Ala Arg Glu Ile Thr Thr Val Asp Tyr
1 5

<210> 40
<211> 106
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 40

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 Ser Ala Thr Ser Ser Ile Ser Tyr Met
20 25 30

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Arg Ser Tyr Pro Phe Thr

85

90

95

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

<210> 41
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 41

Ser Ser Ile Ser Tyr
 1 5

<210> 42
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 42

His Gln Arg Arg Ser Tyr Pro Phe Thr
 1 5

<210> 43
 <211> 121
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 43

Glu 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

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 Asn Glu Lys Phe
 50 55 60

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

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

Ala Arg Leu Asp Gly Ser Ser Tyr Arg Gly Ala Met Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 44

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 44

Gly Tyr Thr Phe Thr Ser Tyr Trp
 1 5

<210> 45

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 45

Ile Tyr Pro Gly Gly Gly Tyr Thr
1 5

<210> 46
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 46

Ala Arg Leu Asp Gly Ser Ser Tyr Arg Gly Ala Met Asp Ser
1 5 10

<210> 47
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 47

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 Gly Phe Asn Lys Tyr
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Gly Asn Leu Leu Tyr

85

90

95

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 48
 <211> 6
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> binding domain sequence
 <400> 48

Gln Gly Phe Asn Lys Tyr
 1 5

<210> 49
 <211> 9
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> binding domain sequence
 <400> 49

Leu Gln Tyr Gly Asn Leu Leu Tyr Ala
 1 5

<210> 50
 <211> 115
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> binding domain sequence
 <400> 50

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

Ser Val Ile Tyr Gly Ser Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Val 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 Asp Thr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 100 105 110

Val Ser Ser
 115

<210> 51
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 51

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 52
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 52

Ile Tyr Gly Ser Gly Arg Thr
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 53

Ala Arg Asp Thr Tyr Ala Met Asp Val
1 5

<210> 54
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 54

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85

90

95

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

<210> 55
 <211> 7
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> binding domain sequence
 <400> 55

Gln Ser Val Ser Ser Ser Tyr
 1 5

<210> 56
 <211> 10
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> binding domain sequence
 <400> 56

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

<210> 57
 <211> 330
 <212> PRT
 <213> Homo Sapiens
 <400> 57

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

Arg 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

$\langle 210 \rangle$	58
$\langle 211 \rangle$	330
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> Constant region

<400> 58

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

Arg 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 Leu
 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> 59
 <211> 330
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Constant region

<400> 59

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

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

Pro Ala Pro Glu Phe Glu 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> 60

<211> 330

<212> PRT

<213> Artificial sequence

<220>

<223> Constant region

<400> 60

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

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

Pro Ala Pro Glu Phe Glu 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 Leu
 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> 61
 <211> 330
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Constant region

<400> 61

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

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

Pro Ala Pro Glu Phe Glu 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 Arg 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> 62
 <211> 330
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Constant region

<400> 62

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

Arg 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 Arg 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

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 <211> 107
 <212> PRT
 <213> Homo Sapiens

<400> 63

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> 64

<211> 106

<212> PRT

<213> Homo Sapiens

<400> 64

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> 65

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> binding domain sequence

<400> 65

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

Leu Arg 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 Glu Gly Ser Tyr Pro Asn Gln Phe Asp Pro Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 66
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 66

Gly Gly Ser Ile Lys Ser Gly Ser Tyr Tyr
 1 5 10

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

<220>
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<400> 67

Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 68
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
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<400> 68

Ala Arg Glu Gly Ser Tyr Pro Asn Gln Phe Asp Pro
 1 5 10

<210> 69
 <211> 107
 <212> PRT
 <213> Artificial sequence

<220>
 <223> binding domain sequence

<400> 69

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

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

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

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

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

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

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

<210> 70
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 <212> PRT
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<220>
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<400> 70

Gln Ser Val Ser Ser Asn
 1 5

<210> 71
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> binding domain sequence

<400> 71

Gln Gln Tyr His Ser Phe Pro Phe Thr
1 5