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<130> 41800P WO

<140> PCT/EP2008/009548
<141> 2008-11-12

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35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
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Glu Asp Met Ala Asp Tyr Tyr Cys Leu Gln Ser Lys Glu Ser Pro Trp
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35 40 45

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

Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu
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35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
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Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg
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20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

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

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

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
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Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
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Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Arg Thr Ile Ser Ser Leu Glu Ser
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Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
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35 40 45

Gly Tyr Ile Thr Asn Ser Gly Gly Thr Ala Tyr Asn Pro Ser Leu Lys
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Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu
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gtgcaccagg actggctgaa cggcaaggag tacaagtgca aggtctccaa caaaggcctc 960

ccagccccca tcgagaaaac catctccaaa accaaagggc agccccgaga accacaggtg 1020

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1080

gtcaaaggct tctaccccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1140

aacaactaca agaccacacc tcccatgctg gactccgacg gctccttctt cctctacagc 1200

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1260

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatga 1320

<210> 37
<211> 214
<212> PRT
<213> Artificial

<220>
<223> 11B7 LC kappa

<400> 37

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

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

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 38
<211> 443
<212> PRT
<213> Artificial

<220>
<223> 11B7-HCgamma1

<400> 38

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asp Lys Met Glu Trp Met
35 40 45

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

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

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

Ile Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 39
<211> 439
<212> PRT
<213> Artificial

<220>
<223> 11B7 HC gamma2

<400> 39

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asp Lys Met Glu Trp Met
35 40 45

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

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

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

Ile Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

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

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

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

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

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

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

Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
210 215 220

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

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

Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
275 280 285

Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp
290 295 300

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

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg
325 330 335

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 40
<211> 214
<212> PRT
<213> Artificial

<220>
<223> 11D5 LC kappa

<400> 40

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

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

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

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

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

Glu Asp Met Ala Ile Tyr Tyr Cys Leu Gln Tyr Ile Gln Phe Pro Leu
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 41
<211> 443
<212> PRT
<213> Artificial

<220>
<223> 11D5 HC gamma1

<400> 41

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

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

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

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

Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

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

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

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

145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 42
<211> 439
<212> PRT
<213> Artificial

<220>
<223> 11D5 HC gamma2

<400> 42

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

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

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

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

Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

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

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

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

145 150 155 160

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

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

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

Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
210 215 220

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

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

Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
275 280 285

Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp
290 295 300

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

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg
325 330 335

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 43
<211> 128
<212> PRT
<213> Artificial

<220>
<223> Hum11B7-VLk

<400> 43

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

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

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

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

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

Lys Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

<210> 44
<211> 132
<212> PRT
<213> Artificial

<220>
<223> Hum11B7-VH

<400> 44

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

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

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

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

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

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

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
100 105 110

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

Thr Val Ser Ser
130

<210> 45
<211> 132
<212> PRT
<213> Artificial

<220>
<223> Hum11D5-VH

<400> 45

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

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

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

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

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

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

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 46
<211> 129
<212> PRT
<213> Artificial

<220>
<223> Hum11D5-VLk

<400> 46

Met Asp Met Arg Val Leu Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

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

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

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

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln

100 105 110

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

Lys

<210> 47
<211> 427
<212> DNA
<213> Artificial

<220>
<223> Hum11B7-VLk

<400> 47
aattaaaagc tagcaagctt gccaccatgg atatgcgtgt acctgcacag ctgttaggac 60

tgcttctgct ctggcttagg ggagcaagat gcgacatcca gatgactcag agcccaagct 120

ccttgtctgc cagtgtgggt gatagggtca ccataacctg tcgagcttca caggatatcg 180

gcaactacct acgctggtat cagcagaaac cgggcaaagc cccaaagctg ctgatctatg 240

gcgccaccaa tctggctgct ggtgttccct ctcggttcag tgggtctgga tcaggcacag 300

acttcacact caccatttcc agcctccaac ccgaggactt tgcgacgtac tactgcttgc 360

agtccaagga atccccttgg acatttgggc aagggactaa ggtggagatt aagcgtacga 420

attaaaa 427

<210> 48
<211> 429
<212> DNA
<213> Artificial

<220>
<223> Hum11B7-VH

<400> 48
aattaaggta ccaagcttgc caccatgaag cacctctggt tctttctcct gctagtggct 60

gctcctcgct gggtgttgag ccaggttcag ttgcaggaat ctggaccagg actggtcaaa 120

ccctctgaga cactgtcact gacatgcact gtgtcaggtg gctccatttc ctccaactat 180

tggggctgga ttcggcaacc tccgggaaaa gggcttgagt ggataggcta catcacctat 240

ctgggagta cctcctacaa tcccagtctt aagagcaggg tgactatcag cgtagacacc 300

ccaagaacc agtttagcct caagctgagt tctgtgactg cagcggatac agccgtctac 360

attgtgcca gaaccacgtt ctactattgg ggtcagggca cattagtcac cgttagctca 420

gcgaattaa 429

<210> 49
<211> 427
<212> DNA
<213> Artificial

<220>
<223> Hum11D5-VLk

<400> 49
aattaaaagc tagcaagctt gccaccatgg atatgcgcgt cttagcccaa ctactcggtc 60

tgcttctgtt gtgctttcca ggagccaggt gtgacatcca gatgacacag tcccctagta 120

gcctgtctgc gtctgtaggc gatcgagtga ccattaccig cagagcttcc caggatattg 180

gcaactatct gagctggttt cagcagaaac caggcaaagc acccaagagt ctcatctatg 240

gggccatcaa gctcgctgtt ggtgtgcctt cacggttttc cggatctggg tcaggcacag 300

acttcactct gaccatttcc agccttcaac cggaagactt cgcaacgtac tactgtctgc 360

agtacatcca gttccccttg actttcggtg gagggacaaa ggtggagata aagcgtacga 420

attaaaa 427

<210> 50
<211> 429
<212> DNA
<213> Artificial

<220>
<223> Hum11D5-VH

<400> 50
aattaaggta ccaagcttgc caccatgaag catctgtggt tctttctgct gcttgtggct 60

gctcctaggt gggtgttaag ccaggttcag ctccaggaat ctggtcccgg attggtgaaa 120

ccgagtgaga ctctatccct gacatgcacc gttagtggag gcagtatctc tagcaactat 180

tggggctgga ttcggcaacc acctggtaag ggccttgagt ggattgggca catcaccaac 240

tctgggaata ccacctacaa tccctccctg aaatcacgcg tcacgataag cgtggacact 300

tccaagaacc agttctccct caagctctca agcgtcacag cagcggatac agccgtatac 360

tactgtgcaa gaggggcctt tgactattgg ggacagggca cattggtgac tgtcagctca 420

gcgaattaa 429

<210> 51
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer kappa_GSP1

<400> 51
gatggatgca ttggtgcagc 20

<210> 52
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer new_kappa_GSP1

<400> 52
atagatacag ttggtgcagc 20

<210> 53
<211> 19
<212> DNA
<213> Artificial

<220>
<223> primer heavy_GSP1

<400> 53
cagggtcacc atggagtta 19

<210> 54
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer XhoI-hGSP2

<400> 54
ccgctcgagc ggccgtttca gctccagctt gg 32

<210> 55
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer XhoI-hGSP2

<400> 55
ccgctcgagc gggccagtgg atagacagat gg 32

<210> 56
<211> 21
<212> DNA
<213> Artificial

<220>
<223> primer RT-gamma

<400> 56
gcgtgtagtg gttgtgcaga g 21

<210> 57
<211> 16
<212> DNA
<213> Artificial

<220>
<223> primer RT-gamma2

<400> 57
gggcttgccg gccgtg 16

<210> 58
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer RT-kappa

<400> 58
tggaactgag gagcaggtgg 20

<210> 59
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer 5' Blp

<400> 59
agataagctt tgctcagcgt ccaccaaggg cccatcggt 39

<210> 60
<211> 34
<212> DNA
<213> Artificial

<220>
<223> primer 3' Bam(GAG)

<400> 60
agatggatcc tcatttaccc ggagacaggg agag 34

<210> 61
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer 5' Bsi:

<400> 61

agataagctt cgtacggtgg ctgcaccatc tgtcttcat 39

<210> 62
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer 3' Bam(CTT)

<400> 62
agatggatcc ctaacactct cccctgttga agctct 36

<210> 63
<211> 42
<212> DNA
<213> Artificial

<220>
<223> primer VL-11B7-5'

<400> 63
agataagctt gtgcattccg acatccagat gacccaggct cc 42

<210> 64
<211> 33
<212> DNA
<213> Artificial

<220>
<223> primer VL-11B7-3'

<400> 64
agatcgtacg tttcagctcc agcttggtgc ctc 33

<210> 65
<211> 45
<212> DNA
<213> Artificial

<220>
<223> primer VL-11D5-5'

<400> 65
agataagctt gtgcattccg acatccagat gacccagtct ccatc 45

<210> 66
<211> 27
<212> DNA
<213> Artificial

<220>
<223> primer VL-11D5-3'

<400> 66
agatcgtacg tttcagcttg gtcccag 27

<210> 67
<211> 42
<212> DNA
<213> Artificial

<220>
<223> primer VH-11B7/11D5-5'

<400> 67
agataagctt gtgcattccg aggtgcagct tcaggagtca gg 42

<210> 68
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer VH-11B7/11D5-3'

<400> 68
agatgctgag ctgacagtga ccatgactcc ttggcc 36

<210> 69
<211> 37
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE1

<400> 69
gcgaattcgc caccatgggc agggtcccgc tggcctg 37

<210> 70
<211> 34
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE2

<400> 70
cagccgaggt ataggctgtc acagacacag tcag 34

<210> 71
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE3

<400> 71
tcaccctgtt agggtaccgg ctggcatatc 30

<210> 72
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE4

<400> 72
ataagaatgc ggccgctcag gctccgtcct cctgccctg 39

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<213> Artificial

<220>
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<210> 82

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<220>
<223> leader sequence

<400> 82

Met Gly Asp Asn Asp Ile His Phe Ala Phe Leu Ser Thr Gly Val His
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Ser

<210> 83
<211> 2682
<212> DNA
<213> Macaca fascicularis

<400> 83
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ccagggaata tcacaggtgc ccggggactc acgggcaccc ttcggtgtca gctccaggtt 180

cagggagagc cccccgaggt acactggctt cgggacggac agatcctgga gctcgcggac 240

agtacccaga cccaggtgcc cctgggtgaa gatgagcagg atgactggat agtggtcagc 300

cagctcagaa tcgcctccct acagctttcc gacgcgggac agtaccagtg tttggtgttt 360

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caagcccagg gacccccaga gcccgtggac ctactctggc tccaggatgc tgtccccctg 540

gccacagctc caggtcatgg tccccagcgc aacctgcatg ttccagggct gaacaagaca 600

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<212> PRT
<213> Macaca fascicularis

<400> 84

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Leu Ala Leu Cys Gly Trp Val Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Ala Ser Leu Gln Leu Ser Asp Ala
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Asn Phe Val Ser
115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

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

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Asn Leu
180 185 190

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

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
225 230 235 240

Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr
245 250 255

His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln
260 265 270

Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Leu Gln Ala Ser
275 280 285

Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Thr Pro
290 295 300

Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp
305 310 315 320

Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro
325 330 335

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

Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg
355 360 365

Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly
370 375 380

Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser
385 390 395 400

Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
405 410 415

Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Gln Ala Gln
420 425 430

Pro Val His Gln Leu Val Lys Glu Thr Ser Ala Pro Ala Phe Ser Trp
435 440 445

Pro Trp Trp Tyr Ile Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val
450 455 460

Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg
465 470 475 480

Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val
485 490 495

Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr
500 505 510

Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp
515 520 525

Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu
530 535 540

Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn Gln Asp Asp Ser
545 550 555 560

Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg
565 570 575

Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe
580 585 590

Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
595 600 605

Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
610 615 620

His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Asp Gln
625 630 635 640

Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile
645 650 655

Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
660 665 670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
675 680 685

Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
690 695 700

Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Leu Asp Pro
835 840 845

Lys Asp Ser Cys Ser Cys Leu Thr Ser Ala Glu Val His Pro Ala Gly
850 855 860

Arg Tyr Val Leu Cys Pro Ser Thr Ala Pro Ser Pro Ala Gln Pro Ala
865 870 875 880

Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala
885 890