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<140> US 16/371,964

<141> 2019-04-01

<150> US 62/651,605

<151> 2018-04-02

<160> 85

<170> PatentIn version 3.5

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Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
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Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
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Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
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Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
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Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
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Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
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Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
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Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
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Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80

Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95

Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
 100 105 110

Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125

Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
 130 135 140

Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160

Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175

Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190

Thr Asn Val Thr Asp Ile Ile Arg Tyr Ser Phe Gln Val Pro Gly Pro
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Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
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Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
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Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
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Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
 100 105 110

Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
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 35 40 45

Ala Asn Ser Arg Lys Ala Trp Gln Lys Met Glu Gly Lys Met Pro Lys
 50 55 60

Ile Leu Ala Lys Thr Glu Arg Pro Ser Glu Asn Ser His Pro Val Gln
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Val Gly Arg Ile Thr Leu Glu Asp Tyr Pro Asp His Gly Leu Leu Gln
 85 90 95

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

Val Ile Tyr Gln His Pro Lys Glu Ser His Val Leu Phe Asn Pro Ile
 115 120 125

Cys Leu Val Val Thr Lys Gly Ser Ser Gly Thr Pro Gly Ser Ser Glu
 130 135 140

Asn Ser Thr Gln Asn Val Tyr Arg Thr Pro Ser Thr Thr Ala Lys Ala
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Leu Gly Pro Arg Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro Pro
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Glu Ser Thr Val Val Val Ser Thr Pro Gly Ser Glu Ile Asn Leu Thr
 180 185 190

Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile Ile
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Val Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu Phe
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Ala Val Thr Leu Arg Ser Phe Gly Pro
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<400> 8

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 35 40 45

His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly
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Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val
 65 70 75 80

Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn
 85 90 95

Phe Leu Ile Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn
 100 105 110

Phe Thr Gly Ala His Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly
 115 120 125

Ile Ser Phe Met Gly Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala
 130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 11
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1-Aba Heavy Chain Constant Region

<400> 11

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 Ser Pro Pro Ser
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG4-Aba Heavy Chain Constant Region

<400> 12

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 13
 <211> 107
 <212> PRT
 <213> homo sapiens

<400> 13

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> 14
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mAb 0318 VH

<400> 14

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 15
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mAb 0318 VL

<400> 15

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

115

120

125

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

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

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

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

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

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

<210> 16
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VH

<400> 16

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 17
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VL

<400> 17

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 18
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH

<400> 18

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 19
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG1.1f VL

<400> 19

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

<210> 20

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VH

<400> 20

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

$\langle 210 \rangle$	21
$\langle 211 \rangle$	111
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> 0318-IgG1-Aba VL

<400> 21

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 22

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VH

<400> 22

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 23
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VL

<400> 23

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

<210> 24
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VH CDR1

<400> 24

Thr Tyr Ala Met His
1 5

<210> 25
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VH CDR2

<400> 25

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

Val Lys Gly

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VH CDR3

<400> 26

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
1 5 10

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VL CDR1

<400> 27

Arg Ala Ser Gln Ser Val Asp Thr Phe Asp Tyr Ser Phe Leu His
1 5 10 15

<210> 28

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

<220>
 <223> 0318-IgG1.3f VL CDR2

<400> 28

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 29
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VL CDR3

<400> 29

Gln Gln Ser Asn Gln Asp Pro Tyr Thr
 1 5

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

<220>
 <223> 0318-IgG1.1f VH CDR1

<400> 30

Thr Tyr Ala Met His
 1 5

<210> 31
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH CDR2

<400> 31

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

Val Lys Gly

<210> 32
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH CDR3

<400> 32

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 33
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VL CDR1

<400> 33

Arg Ala Ser Gln Ser Val Asp Thr Phe Asp Tyr Ser Phe Leu His
 1 5 10 15

<210> 34
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VL CDR2

<400> 34

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 35

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

<220>
 <223> 0318-IgG1.1f VL CDR3

<400> 35

Gln Gln Ser Asn Gln Asp Pro Tyr Thr
 1 5

<210> 36
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba VH CDR1

<400> 36

Thr Tyr Ala Met His
 1 5

<210> 37
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba VH CDR2

<400> 37

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

Val Lys Gly

<210> 38
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VH CDR3

<400> 38

Asp	Met	Gly	Ile	Arg	Arg	Gln	Phe	Ala	Tyr
1				5					10

<210> 39

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR1

<400> 39

Arg	Ala	Ser	Gln	Ser	Val	Asp	Thr	Phe	Asp	Tyr	Ser	Phe	Leu	His
1				5					10					15

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR2

<400> 40

Arg	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR3

<400> 41

Gln	Gln	Ser	Asn	Gln	Asp	Pro	Tyr	Thr
1				5				

<210> 42

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

<220>
 <223> 0318-IgG4-Aba VH CDR1

<400> 42

Thr Tyr Ala Met His
 1 5

<210> 43
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VH CDR2

<400> 43

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

Val Lys Gly

<210> 44
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VH CDR3

<400> 44

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 45
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR1

<400> 45

Arg	Ala	Ser	Gln	Ser	Val	Asp	Thr	Phe	Asp	Tyr	Ser	Phe	Leu	His
1				5					10					15

<210> 46

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR2

<400> 46

Arg	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR3

<400> 47

Gln	Gln	Ser	Asn	Gln	Asp	Pro	Tyr	Thr
1				5				

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> LSPGK (C-terminal end of heavy chain)

<400> 48

Leu	Ser	Pro	Gly	Lys
1				5

<210> 49

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

<220>
 <223> LSPG (C-terminal end of heavy chain)

<400> 49

Leu Ser Pro Gly
 1

<210> 50
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f HC

<400> 50

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
 450

<210> 51
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f HC

<400> 51

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly
 450

<210> 52
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba HC

<400> 52

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
 450

<210> 53
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba HC

<400> 53

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435

440

445

Pro Gly Lys
450

<210> 54
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f LC

<400> 54

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 55
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f LC

<400> 55

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 56
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba LC

<400> 56

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 57
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba LC

<400> 57

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 58
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f HC

<400> 58
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 ctcgtggagt ccggcggagg actggtccaa cctggcggct ccctgaagct gtcctgcgct 120
 gcctccggct tcaccttctc cacctacgcc atgcactggg tcaggcaggc ctccggaaag 180
 ggcttggaaat gggtcggccg gattaggacc aagtccagca actacgctac ctactacgcc 240
 gccagcgtca agggccgggt cacaatctcc cgggacgact ccaagaacac cgcctatctc 300
 cagatgaaca gcctgaagac agaggacacc gccgtgtact attgcacccg ggatatgggc 360
 attcggaggc agttcgcta ttggggccag ggcaccctgg tgacagtcag ctccgccagc 420
 acaaaaggac ctagcgtgtt ccccttggcc cctagcagca agtccacaag cggcggcacc 480
 gctgccctgg gctgtctggt gaaagactac tttcccagac ccgtgacagt gagctggaac 540
 tctggcgcgc tgacatccgg agtgcacacc ttccctgccg tgctccagtc cagcggcctg 600
 tacagcctga gcagcgtcgt gaccgtccct agcagcagcc tgggaacca gacctacatc 660
 tgcaacgtga accacaagcc ctccaacacc aaggtggaca agagggtgga gccaagtcc 720
 tgtgacaaga cccatacctg ccccccctgt cctgctcctg aagctgaggg cgcccccttc 780

gtcttcctgt tccctcctaa gccaagac accctgatga tctccaggac ccccgagggtg	840
acctgtgtgg tgggtgatgt gtccacgag gaccccgagg tgaagttcaa ttggtacgtc	900
gacggcgtgg aggtgcacaa cgccaagacc aaaccccggg aggagcagta taacagcacc	960
taccgggtgg tgtccgtgct caccgtgctg caccaggact ggctgaacgg caaggagtac	1020
aagtgttaagg tcagcaataa ggccctgcct gcccctatcg agaagaccat tagcaaggct	1080
aagggccagc ccagggaacc ccagggtgtat accctcccc ctagccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctgggtg aaaggattct accctagcga catcgctgtg	1200
gagtgggaga gcaatggaca gcccgagaac aactacaaaa ccacccctcc cgtcctggac	1260
tccgatggca gcttctttct gtactccaag ctcaccgtcg acaagagccg gtggcagcag	1320
ggcaatgtgt ttagctgtc cgtgatgcac gaggctctgc acaaccacta tacccaaaag	1380
tccctgtccc tcagccccgg caagtga	1407

<210> 59
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f HC

<400> 59	
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ctgggtgaaa gcggcggagg actggtgcag ccaggcggca gcctgaagct gtcttgcgcc	120
gccagcggct tcaccttcag cacctacgcc atgcactggg tccgccaggc cagcggcaag	180
ggcctggaat gggtcggacg gatccggacc aagagcagca actacgccac ctactacgcc	240
gcctccgtga agggccggtt caccatcagc cgggacgaca gcaagaacac cgcctacctg	300
cagatgaaca gcctgaaaac cgaggacacc gccgtgtact actgcacccg ggacatgggc	360
atccggcggc agtttgccta ctggggccag ggcaccctgg tcacagtgtc cagcgcgtcg	420
accaagggcc catcgtctt cccctggca ccctcctcca agagcacctc tgggggcaca	480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgaagg ggccccgtca	780
gtcttctctt tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc	840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	900
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	960
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1020
aagtgcagg tctccaacaa agccctccca agcagcatcg agaaaaccat ctcaaagcc	1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1200
gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac	1260
tccgacggct ctttcttctt ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtccccggg ttga	1404

<210> 60
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba HC

<400> 60	
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ctggtggaga gcgaggagg actcgtgcag cctggaggat ccctgaagct gtcctgcgct	120
gcctccggct ttaccttctc cacctacgcc atgcattggg tgaggcaggc ctccggcaag	180
ggcctggaat ggggtgggcag gatcaggaca aagagctcca actacgccac ctactacgcc	240
gccagcgtga aaggacggtt caccatctcc cgggacgatt ccaaaaacac cgcttacctc	300
cagatgaata gcctgaagac cgaggacacc gccgtctact actgcaccag ggatatgggc	360

atccggcggc agtttgccta ctggggccag ggcaccctgg tgacagtgtc cagcgctagc	420
accaaaggcc cctccgtgtt cccctggct ccctccagca agtccacatc cggcggaacc	480
gccgctctgg gatgtctggt gaaggactac ttccccgagc ccgtgacagt gagctggaac	540
tctggcgctc tgacctccgg cgtgcacacc tttcctgctg tgctgcagtc ctccggcctc	600
tacagcctgt cctccgtcgt gacagtgtcc tcctccagcc tgggcaccca gacctacatc	660
tgcaacgtga accacaagcc ttccaacacc aagggtggata agcgggtcga acccaagagc	720
tgcgacaaga cccacaccag ccccccttcc cctgctcccg agctcctggg aggcagctcc	780
gtgtttctgt ttcccccaa gcctaaggac accctgatga tcagcaggac ccccgaaagt	840
acatgcgtgg tggctgacgt gtcccacgag gaccccgagg tcaagttcaa ctggtacgtg	900
gatggagtgg aggtccataa tgccaagacc aagccccggg aggagcagta caattccacc	960
taccgggtgg tgtccgtgct gacagtcctg catcaggact ggctcaacgg caaggagtac	1020
aaatgcaagg tgtccaacaa ggctctgtcc gccccatcg agaagacaat cagcaaggct	1080
aagggccagc ctagggagcc ccaggtgtac accctgtccc cttccaggga cgagctcacc	1140
aagaaccagg tgtccctgac atgcctcgtg aagggtttt accctagcga catcgctgtg	1200
gagtgggagt ccaacggaca gcccgagaac aactacaaga caacaccccc tgtgctggac	1260
tccgacggct ctttcttctt gtacagcaag ctcaccgtgg acaaattccc gtggcagcag	1320
ggaaacgtgt tcagctgtc cgtgatgcat gaggccctgc acaaccatta caccagaaa	1380
tccctgtccc tgtcccccg caagtga	1407

<210> 61
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba HC

<400> 61	
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ctggctgaga gcggcggagg actggtccag cctggaggat ccctgaagct ctcctgtgcc	120
gctagcggat ttaccttcag cacctacgct atgcattggg tgaggcaggc ttccggcaag	180

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ggactggagt ggggtgggacg gattcggacc aagagctcca attacgccac ctattacgcc      240
gcttccgtga agggccggtt caccatctcc agggacgact ccaagaacac cgcttacctg      300
cagatgaact ccctcaagac cgaggacacc gccgtgtatt actgcacccg ggacatgggc      360
atccggaggc agttcgctta ttggggacag ggcaccctgg tgaccgtgag ctccgcctcc      420
accaagggcc cttccgtgtt ccctctggcc ccctgtagca ggtccaccag cgagtccaca      480
gctgctctgg gctgtctggt gaaggattat ttccccgagc ccgtgacagt gtcctggaat      540
agcggcgccc tgacctccgg cgtgcatacc ttccctgccg tcctgcaaag cagcggcctg      600
tacagcctgt cctccgtggt gacagtccct tcctccagcc tgggaaccaa gacctacacc      660
tgcaatgtgg accacaagcc tagcaacacc aagggtggaca agagggtcga gccaagtcc      720
tgcgataaga cacacacctc ccctccttcc cctgctcctg agctgctcgg cggaagcagc      780
gtgttcctgt tccctcctaa gcctaaggac accctgatga tcagccggac ccctgaggtg      840
acctgtgtcg tgggtggacgt gtcccacgaa gaccccgagg tgaaattcaa ctggtacgtg      900
gacggcgctc aggtgcacaa cgctaagaca aaacccaggg aggagcagta caattccacc      960
taccgggtcg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac     1020
aagtgttaagg tcagcaataa ggccctgcct gccccattg agaagaccat ttccaaggcc     1080
aagggccagc ccagggaacc tcaggtgtac accctgcctc cctcccggga cgagctgacc     1140
aagaaccagg tcagcctgac ctgcctcgtg aagggttctt accctagcga catcgccgtg     1200
gagtgggagt ccaacggcca gcctgagaac aattacaaga ccaccccccc tgcctggac      1260
tccgacggat ctttcttctt gtactccaag ctgacagtgg ataagtcccg gtggcagcag      1320
ggaaatgtgt tctcctgctc cgtcatgcac gaagccctgc ataaccacta cacacagaag      1380
agcctgtccc tgagccctgg caagtga                                           1407

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<210> 62
<211> 708
<212> DNA
<213> Artificial Sequence

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<220>
<223> 0318-IgG1.3f LC

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<400> 62
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 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccacaggg agggcaaggt gcagtgggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gaccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 63
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f LC

<400> 63
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 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480

taccccaggg aggccaaggt gcagtggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gacccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 64
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba LC

<400> 64
 atgagggctt ggatcttctt tctgctctgc ctggccgggc ggccttggc cgatatcgtg 60
 ctgaccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggacccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttccct 420
 cccagcgacg agcagctgaa gagcggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccccaggg aggccaaggt gcagtggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gacccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 65
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba LC

<400> 65
 atgagggctt ggatcttctt tctgctctgc ctggccgggc gcgccttggc cgatatcgtg 60
 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccacaggg agggccaaggt gcagtgggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gaccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 66
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR1

<400> 66

Thr Tyr Ala Met His
 1 5

<210> 67
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR2

<400> 67

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

Val Lys Asp

<210> 68
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR3

<400> 68

Asp Met Gly Gln Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 69
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VL CDR1

<400> 69

Arg Ala Ser Glu Ser Val Asp Thr Phe Asp Tyr Ser Phe Leu His
 1 5 10 15

<210> 70
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VL CDR2

<400> 70

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 71

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

<220>
 <223> 0318 Ab - VL CDR3

<400> 71

Gln Gln Ser Asn Glu Asp Pro Tyr Thr
 1 5

<210> 72
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 AB - VH CDR3 (mutant)

<400> 72

Asp Gln Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 73
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 AB - VH CDR3 (mutant)

<400> 73

Asp Leu Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 74
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR1 (mutant)

<400> 74

Thr Tyr Ala Gln His
1 5

<210> 75
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318 Ab - VH CDR1 (mutant)

<400> 75

Thr Tyr Ala Leu His
1 5

<210> 76
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318 Ab - HC (IgG4)

<400> 76

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu His Asn Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val
 435 440 445

Ser Leu Gly
 450

<210> 77
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> WT IgG1 Constant Region (Allotypic Variant)

<400> 77

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

<210> 78

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1.1f HC Constant Region

<400> 78

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 Ala Glu Gly Ala 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 Ser Ser 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> 79

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1.3f HC Constant Region

<400> 79

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 80
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 80

Pro Val Gly Val Val
 1 5

<210> 81
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 318 Ab - Mutant

<400> 81

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

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

Ala Met His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val

35

40

45

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 82
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 319 Ab - Mutant

<400> 82

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 83
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 320 Ab - Mutant

<400> 83

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 84
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 321 Ab - Mutant

<400> 84

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 85
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG1.3f HC Kdel

<400> 85

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

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

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

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

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala 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 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180

185

190

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly
450