

eolf-seql (2)
SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Antigen Binding Molecules comprising a TNF family ligand trimer
and PD1 binding moiety

<130> P33618-EP

<160> 170

<170> PatentIn version 3.5

<210> 1

<211> 184

<212> PRT

<213> Homo sapiens

<400> 1

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

eolf-seql (2)

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu
180

<210> 2
<211> 170
<212> PRT
<213> Homo sapiens

<400> 2

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

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
20 25 30

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
35 40 45

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
50 55 60

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
65 70 75 80

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala

eolf-seql (2)

85

90

95

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
100 105 110

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
115 120 125

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
130 135 140

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
145 150 155 160

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
165 170

<210> 3
<211> 175
<212> PRT
<213> Homo sapiens

<400> 3

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

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

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

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

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

eolf-seql (2)

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
165 170 175

<210> 4
<211> 203
<212> PRT
<213> Homo sapiens

<400> 4

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
20 25 30

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
35 40 45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
50 55 60

eolf-seql (2)

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

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
115 120 125

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

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
145 150 155 160

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
180 185 190

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
195 200

<210> 5
<211> 178
<212> PRT
<213> Homo sapiens

<400> 5

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

eolf-seql (2)

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu

<210> 6

<211> 164

<212> PRT

<213> Homo sapiens

eolf-seql (2)

<400> 6

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

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
20 25 30

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
35 40 45

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
50 55 60

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
65 70 75 80

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
85 90 95

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
100 105 110

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
115 120 125

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
130 135 140

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
145 150 155 160

Pro Ala Gly Leu

<210> 7

eolf-seql (2)

<211> 169

<212> PRT

<213> Homo sapiens

<400> 7

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

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

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

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

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

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

Val Thr Pro Glu Ile Pro Ala Gly Leu
165

eolf-seql (2)

<210> 8
 <211> 197
 <212> PRT
 <213> Homo sapiens
 <400> 8

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
 1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
 20 25 30

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
 35 40 45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 50 55 60

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

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
 85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
 100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
 115 120 125

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

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
 145 150 155 160

eolf-seql (2)

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
180 185 190

Ile Pro Ala Gly Leu
195

<210> 9

<211> 378

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric hu 4-1BBL (71-254) connected by (G4S)₂ linker

<400> 9

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr

eolf-seql (2)

100

105

110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala

eolf-seql (2)

290

295

300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
370 375

<210> 10

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric hu 4-1BBL (71-248) connected by (G4S)₂ linker

<400> 10

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

eolf-seql (2)

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
180 185 190

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
195 200 205

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
245 250 255

eolf-seql (2)

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
260 265 270

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
305 310 315 320

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
325 330 335

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
355 360 365

<210> 11
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> dimeric hu 4-1BBL (80-254) connected by (G4S)₂ linker

<400> 11

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

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys

eolf-seql (2)

35

40

45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

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

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp
180 185 190

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
195 200 205

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
210 215 220

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val

eolf-seql (2)

225 230 235 240

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
245 250 255

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
260 265 270

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
275 280 285

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
290 295 300

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
305 310 315 320

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
325 330 335

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

Gly Leu Pro Ser Pro Arg Ser Glu
355 360

<210>	12
<211>	416
<212>	PRT
<213>	Artificial Sequence

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<220>
<223>    dimeric hu 4-1BBL (52-254) connected by (G4S)2 linker
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<400> 12

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

eolf-seql (2)

Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	Pro	Ala	Gly			
			20					25					30					
Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val	Ala	Gln	Asn			
		35					40					45						
Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp	Pro	Gly	Leu			
		50				55					60							
Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	Glu	Asp	Thr	Lys			
65					70					75					80			
Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	Phe	Phe	Gln	Leu			
				85					90					95				
Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser	Val	Ser	Leu			
			100					105					110					
Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala	Ala	Ala	Leu			
		115					120					125						
Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala	Arg	Asn	Ser			
		130				135					140							
Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala	Gly	Gln	Arg			
145					150					155					160			
Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His	Ala	Trp	Gln			
				165					170					175				
Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val	Thr	Pro	Glu			
			180					185					190					
Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu	Gly	Gly	Gly	Gly	Ser			
		195					200					205						

eolf-seql (2)

Gly Gly Gly Gly Ser Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro
210 215 220

Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro
225 230 235 240

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
245 250 255

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

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

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
290 295 300

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
305 310 315 320

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
325 330 335

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

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
355 360 365

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
370 375 380

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
385 390 395 400

eolf-seql (2)

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 405 410 415

<210> 13
 <211> 7
 <212> PRT
 <213> Mus Musculus

<400> 13

Gly Phe Ser Phe Ser Ser Tyr
 1 5

<210> 14
 <211> 3
 <212> PRT
 <213> Mus Musculus

<400> 14

Gly Gly Arg
 1

<210> 15
 <211> 9
 <212> PRT
 <213> Mus Musculus

<400> 15

Thr Gly Arg Val Tyr Phe Ala Leu Asp
 1 5

<210> 16
 <211> 11
 <212> PRT
 <213> Mus Musculus

<400> 16

Ser Glu Ser Val Asp Thr Ser Asp Asn Ser Phe
 1 5 10

eolf-seql (2)

<210> 17
 <211> 3
 <212> PRT
 <213> Mus Musculus

<400> 17

Arg Ser Ser
 1

<210> 18
 <211> 6
 <212> PRT
 <213> Mus Musculus

<400> 18

Asn Tyr Asp Val Pro Trp
 1 5

<210> 19
 <211> 120
 <212> PRT
 <213> Mus Musculus

<400> 19

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

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

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Asp Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

eolf-seql (2)

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 20
<211> 111
<212> PRT
<213> Mus Musculus
<400> 20

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro
35 40 45

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

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

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

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

eolf-seql (2)

<210> 21
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized variant -heavy chain variable domain VH of
 PD1-0103-0312, -0313, -0314 and -0315

<400> 21

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 22
 <211> 111
 <212> PRT
 <213> Artificial Sequence

eolf-seql (2)

<220>

<223> humanized variant -light chain variable domain VL of
PD1-0103-0312

<400> 22

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

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

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

Lys Leu Leu Ile Tyr Arg Ser Ser Thr 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 Asn Tyr
85 90 95

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

<210> 23

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized variant -light chain variable domain VL of
PD1-0103-0313

<400> 23

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

eolf-seql (2)

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ser Ser Thr Leu Glu Ser Gly Val Pro Asp
50 55 60

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

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Asn Tyr
85 90 95

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

<210> 24

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized variant -light chain variable domain VL of
PD1-0103-0314

<400> 24

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Thr Ser
20 25 30

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

eolf-seql (2)

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

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

<210> 25

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized variant -light chain variable domain VL of
PD1-0103-0315

<400> 25

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Thr Ser
20 25 30

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

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

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

eolf-seql (2)

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

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

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H1, PD1-0098

<400> 26

Gly Tyr Ser Ile Thr Ser Asp Tyr
1 5

<210> 27
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H2, PD1-0098

<400> 27

Tyr Ser Gly
1

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H3, PD1-0098

<400> 28

His Gly Ser Ala Pro Trp Tyr Phe Asp
1 5

eolf-seql (2)

<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L1, PD1-0098

<400> 29

Ser Gln Asn Ile Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 30
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L2, PD1-0098

<400> 30

Lys Val Ser
1

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L3, PD1-0098

<400> 31

Gly Ser His Phe Pro Leu
1 5

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

eolf-seql (2)

<220>

<223> heavy chain variable domain VH, PD1-0098

<400> 32

Asp	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	Thr	Val	Thr	Gly	Tyr	Ser	Ile	Thr	Ser	Asp
			20					25					30		

Tyr	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Phe	Pro	Gly	Asp	Lys	Leu	Glu	Trp
		35					40					45			

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

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

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

Ala	Arg	Trp	His	Gly	Ser	Ala	Pro	Trp	Tyr	Phe	Asp	Tyr	Trp	Gly	Arg
			100					105					110		

Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser
		115					120

<210> 33

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable domain VL, PD1-0098

<400> 33

eolf-seql (2)

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

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

Ser His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H1, PD1-0050

<400> 34

Gly Tyr Ser Ile Thr Ser Asp Tyr
1 5

<210> 35
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql (2)

<223> heavy chain HVR-H2, PD1-0050

<400> 35

Tyr Thr Gly

1

<210> 36

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H3, PD1-0050

<400> 36

Met Asp Tyr Tyr Gly Ser Thr Leu Asp

1

5

<210> 37

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, PD1-0050

<400> 37

Ser Glu Ser Val Asp Arg Tyr Gly Asn Ser Phe

1

5

10

<210> 38

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, PD1-0050

<400> 38

Arg Ala Ser

1

eolf-seql (2)

<210> 39
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L3, PD1-0050

<400> 39

Asn Asn Glu Asp Pro Tyr
 1 5

<210> 40
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, PD1-0050

<400> 40

Asp 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 Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20 25 30

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

Met Gly Tyr Ile Thr Tyr Thr Gly Arg Thr Ser Tyr Asn Pro Ser Leu
 50 55 60

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

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

eolf-seql (2)

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

Gly Thr Thr Leu Thr Val Ser Ser
 115 120

<210> 41
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL, PD1-0050

<400> 41

Lys Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Arg
 1 5 10 15

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

Gly Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

eolf-seql (2)

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

<220>
<223> heavy chain HVR-H1, PD1-0069

<400> 42

Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 43
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H2, PD1-0069

<400> 43

Tyr Ser Gly
1

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H3, PD1-0069

<400> 44

Gly Ile Thr Thr Gly Phe Ala
1 5

<210> 45
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql (2)

<223> light chain HVR-L1, PD1-0069

<400> 45

Ser Lys Gly Val Ser Thr Ser Ser Tyr Ser Phe
1 5 10

<210> 46

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, PD1-0069

<400> 46

Tyr Ala Ser
1

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, PD1-0069

<400> 47

Ser Arg Glu Phe Pro Trp
1 5

<210> 48

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable domain VH, PD1-0069

<400> 48

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

eolf-seql (2)

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

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

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

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

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

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

Leu Val Thr Val Ser Ala
115

<210> 49
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable domain VL, PD1-0069

<400> 49

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

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

eolf-seql (2)

Ser Tyr Ser Phe Met His Trp Tyr Gln Gln Lys Pro Arg Gln Pro Pro
35 40 45

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

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H1, PD1-0073

<400> 50

Gly Phe Thr Phe Ser Asn Tyr
1 5

<210> 51
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H2, PD1-0073

<400> 51

Gly Gly Arg
1

eolf-seql (2)

<210> 52
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H3, PD1-0073

<400> 52

Tyr Tyr Gly Ile Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L1, PD1-0073

<400> 53

Ser Gln Asp Val Thr Thr Ala
1 5

<210> 54
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L2, PD1-0073

<400> 54

Trp Ala Ser
1

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql (2)

<223> light chain HVR-L3, PD1-0073

<400> 55

His Tyr Ser Ile Pro Trp
1 5

<210> 56

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable domain VH, PD1-0073

<400> 56

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

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

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

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

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

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

Ala Ser Tyr Tyr Tyr Gly Ile Asp Tyr Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser
115

eolf-seql (2)

<210> 57
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL, PD1-0073

<400> 57

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

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

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

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

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

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Ile Pro Trp
 85 90 95

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

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

<220>
 <223> heavy chain HVR-H1, PD1-0078

eolf-seql (2)

<400> 58

Gly Tyr Thr Phe Thr Ser Thr
1 5

<210> 59

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H2, PD1-0078

<400> 59

Ser Asp Ser
1

<210> 60

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H3, PD1-0078

<400> 60

Pro Phe Asp
1

<210> 61

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, PD1-0078

<400> 61

Ser Gln Asp Val Ser Thr Ala
1 5

eolf-seql (2)

<210> 62
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L2, PD1-0078

<400> 62

Ser Ala Ser
 1

<210> 63
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L3, PD1-0078

<400> 63

His Tyr Ser His Pro Phe
 1 5

<210> 64
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, PD1-0078

<400> 64

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

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

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

eolf-seql (2)

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

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

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

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

Ser Ser

<210> 65
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable domain VL, PD1-0078

<400> 65

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

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

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

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

eolf-seql (2)

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

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

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

<210> 66
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H1, PD1-0102

<400> 66

Gly Tyr Ser Ile Thr Ser Gly Tyr
1 5

<210> 67
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H2, PD1-0102

<400> 67

Ser Ser Gly
1

<210> 68
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H3, PD1-0102

eolf-seql (2)

<400> 68

Arg Asn Trp Tyr Phe Asp
1 5

<210> 69

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, PD1-0102

<400> 69

Ser Gln Ser Leu Leu Asn Ser Gly Thr Gln Lys Asn Tyr
1 5 10

<210> 70

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, PD1-0102

<400> 70

Trp Ala Ser
1

<210> 71

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, PD1-0102

<400> 71

Asp Tyr Thr Phe Pro Leu
1 5

eolf-seql (2)

<210> 72
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, PD1-0102

<400> 72

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

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

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

Met Gly Phe Ile His Ser Ser Gly Asp Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

Val Thr Val Ser Ser
 115

<210> 73
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>

eolf-seql (2)

<223> light chain variable domain VL, PD1-0102

<400> 73

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

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

Gly Thr Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

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

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

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

Lys

<210> 74

<211> 722

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) - CL* Fc knob chain

<400> 74

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

eolf-seql (2)

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

eolf-seql (2)

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
 225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
 245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
 260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
 275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
 355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 385 390 395 400

eolf-seql (2)

Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
405 410 415

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
420 425 430

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
435 440 445

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
450 455 460

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
465 470 475 480

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
485 490 495

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
500 505 510

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
515 520 525

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
530 535 540

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
545 550 555 560

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
565 570 575

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
580 585 590

eolf-seql (2)

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
595 600 605

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
610 615 620

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
625 630 635 640

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
645 650 655

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
660 665 670

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
675 680 685

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
690 695 700

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
705 710 715 720

Gly Lys

<210> 75
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-254) - CH1*

<400> 75

eolf-seql (2)

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

eolf-seql (2)

Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
195 200 205

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

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
225 230 235 240

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
245 250 255

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
260 265 270

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
275 280 285

Asp Glu Lys Val Glu Pro Lys Ser Cys
290 295

<210> 76

<211> 722

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) - CL Fc knob chain

<400> 76

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

eolf-seql (2)

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

eolf-seql (2)

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
385 390 395 400

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
405 410 415

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
420 425 430

eolf-seql (2)

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 435 440 445

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 450 455 460

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 465 470 475 480

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
 485 490 495

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 500 505 510

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 515 520 525

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 530 535 540

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 545 550 555 560

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 565 570 575

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 580 585 590

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 595 600 605

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 610 615 620

eolf-seql (2)

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
625 630 635 640

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
645 650 655

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
660 665 670

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
675 680 685

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
690 695 700

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
705 710 715 720

Gly Lys

<210> 77

<211> 297

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-254) - CH1

<400> 77

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

eolf-seql (2)

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
195 200 205

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
210 215 220

eolf-seql (2)

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
225 230 235 240

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
245 250 255

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
260 265 270

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
275 280 285

Asp Lys Lys Val Glu Pro Lys Ser Cys
290 295

<210> 78

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-248) - CL* Fc knob chain

<400> 78

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

eolf-seql (2)

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
180 185 190

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
195 200 205

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
245 250 255

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
260 265 270

eolf-seql (2)

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
305 310 315 320

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
325 330 335

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val
370 375 380

Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser
385 390 395 400

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
405 410 415

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
420 425 430

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
435 440 445

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
450 455 460

eolf-seql (2)

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
465 470 475 480

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
485 490 495

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
500 505 510

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
515 520 525

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
530 535 540

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
545 550 555 560

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
565 570 575

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
580 585 590

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
595 600 605

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
610 615 620

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
625 630 635 640

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
645 650 655

eolf-seql (2)

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
660 665 670

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
675 680 685

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
690 695 700

Ser Leu Ser Pro Gly Lys
705 710

<210> 79
<211> 291
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-248) - CH1*

<400> 79

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

eolf-seql (2)

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Thr Lys
180 185 190

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
195 200 205

Gly Thr Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro
210 215 220

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
225 230 235 240

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
245 250 255

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
260 265 270

eolf-seql (2)

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro
275 280 285

Lys Ser Cys
290

<210> 80
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Dimeric hu 4-1BBL (71-248) - CL Fc knob chain

<400> 80

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

eolf-seql (2)

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
180 185 190

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
195 200 205

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
245 250 255

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
260 265 270

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
305 310 315 320

eolf-seql (2)

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
 325 330 335

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
 340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val
 370 375 380

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 385 390 395 400

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 405 410 415

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 420 425 430

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
 435 440 445

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 450 455 460

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 465 470 475 480

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 485 490 495

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 500 505 510

eolf-seql (2)

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
515 520 525

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
530 535 540

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
545 550 555 560

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
565 570 575

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
580 585 590

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
595 600 605

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
610 615 620

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
625 630 635 640

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
645 650 655

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
660 665 670

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
675 680 685

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
690 695 700

eolf-seql (2)

Ser Leu Ser Pro Gly Lys
705 710

<210> 81
<211> 291
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-248) - CH1

<400> 81

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

eolf-seql (2)

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
 165 170 175

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Thr Lys
 180 185 190

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 195 200 205

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 210 215 220

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 225 230 235 240

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 245 250 255

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 260 265 270

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 275 280 285

Lys Ser Cys
 290

<210> 82
 <211> 450
 <212> PRT
 <213> Artificial Sequence

eolf-seql (2)

<220>

<223> anti-PD1 (0314) Fc hole chain

<400> 82

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

Gly Lys
450

<210> 83
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-PD1 (0314) light chain

<400> 83

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Thr Ser
20 25 30

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

eolf-seql (2)

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

Asp Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 84

<211> 837

<212> PRT

<213> Artificial Sequence

eolf-seql (2)

<220>

<223> anti-PD1(0314) Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 84

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu
450 455 460

Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
465 470 475 480

Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
485 490 495

Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
500 505 510

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
515 520 525

Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
530 535 540

Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
545 550 555 560

eolf-seql (2)

Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
565 570 575

Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
580 585 590

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
595 600 605

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
610 615 620

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro
625 630 635 640

Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly
645 650 655

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
660 665 670

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
675 680 685

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
690 695 700

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
705 710 715 720

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
725 730 735

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
740 745 750

eolf-seql (2)

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
755 760 765

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
770 775 780

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
785 790 795 800

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
805 810 815

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
820 825 830

Ser Pro Arg Ser Glu
835

<210> 85

<211> 643

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD1(0314) Fc knob chain fused to monomeric hu 4-1BBL
(71-254)

<400> 85

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu
450 455 460

Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
465 470 475 480

Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
485 490 495

Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
500 505 510

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
515 520 525

Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
530 535 540

Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
545 550 555 560

Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
565 570 575

Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
580 585 590

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
595 600 605

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
610 615 620

eolf-seql (2)

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro
625 630 635 640

Arg Ser Glu

<210> 86
<211> 825
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-PD1(0314) Fc hole chain fused to dimeric hu 4-1BBL (71-248)

<400> 86

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

eolf-seql (2)

115

120

125

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

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

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

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

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

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

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

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

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

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

eolf-seql (2)

305		310		315		320
Glu	Tyr	Lys	Cys	Lys	Val	Glu
			325			335
Lys	Thr	Ile	Ser	Lys	Ala	Lys
			340			345
Thr	Leu	Pro	Pro	Ser	Arg	Asp
			355			360
Ser	Cys	Ala	Val	Lys	Gly	Phe
			370			375
Glu	Ser	Asn	Gly	Gln	Pro	Glu
385					390	
Leu	Asp	Ser	Asp	Gly	Ser	Phe
				405		410
Lys	Ser	Arg	Trp	Gln	Gln	Gly
			420			425
Glu	Ala	Leu	His	Asn	His	Tyr
			435			440
Gly	Gly	Gly	Gly	Gly	Ser	Gly
	450					455
Leu	Ser	Pro	Asp	Asp	Pro	Ala
465						470
Phe	Ala	Gln	Leu	Val	Ala	Gln
			485			490
Ser	Trp	Tyr	Ser	Asp	Pro	Gly
						495

eolf-seql (2)

500

505

510

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
 515 520 525

Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
 530 535 540

Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
 545 550 555 560

Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
 565 570 575

Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
 580 585 590

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
 595 600 605

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
 610 615 620

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly Gly
 625 630 635 640

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
 645 650 655

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 660 665 670

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 675 680 685

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys

eolf-seql (2)

690

695

700

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
705 710 715 720

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
725 730 735

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
740 745 750

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
755 760 765

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
770 775 780

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
785 790 795 800

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
805 810 815

Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825

<210> 87

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-PD1(0314) Fc knob chain fused to monomeric hu 4-1BBL
(71-248)

<400> 87

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

eolf-seql (2)

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Ser	Tyr	20	25	30	
Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ala	Thr	Ile	Ser	Gly	Gly	Gly	Arg	Asp	Ile	Tyr	Tyr	Pro	Asp	Ser	Val	50	55	60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	65	70	75	80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Val	Leu	Leu	Thr	Gly	Arg	Val	Tyr	Phe	Ala	Leu	Asp	Ser	Trp	Gly	Gln	100	105	110	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	130	135	140	
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	145	150	155	160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	165	170	175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	180	185	190	
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	195	200	205	

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu
450 455 460

Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
465 470 475 480

Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
485 490 495

Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
500 505 510

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
515 520 525

Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
530 535 540

Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
545 550 555 560

Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
565 570 575

Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
580 585 590

eolf-seql (2)

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
595 600 605

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
610 615 620

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630 635

<210> 88
<211> 602
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc hole dimeric ligand (71-248) chain

<400> 88

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
225 230 235 240

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
245 250 255

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
260 265 270

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
275 280 285

eolf-seql (2)

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
290 295 300

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
305 310 315 320

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
325 330 335

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

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
355 360 365

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
370 375 380

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
385 390 395 400

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
420 425 430

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
435 440 445

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
450 455 460

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
465 470 475 480

eolf-seql (2)

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
 485 490 495

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
 500 505 510

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
 515 520 525

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
 530 535 540

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
 545 550 555 560

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
 565 570 575

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
 580 585 590

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
 595 600

<210> 89

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc hole monomeric ligand (71-248) chain

<400> 89

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

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

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

eolf-seql (2)

Pro Gly Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
225 230 235 240

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
245 250 255

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
260 265 270

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
275 280 285

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
290 295 300

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
305 310 315 320

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
325 330 335

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
340 345 350

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
355 360 365

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
370 375 380

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
385 390 395 400

Pro Ala Gly Leu

eolf-seql (2)

<210> 90
 <211> 815
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-PD1(0314) Fc knob chain fused to dimeric hu 4-1BBL (71-248)

<400> 90

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

Gly Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
450 455 460

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
465 470 475 480

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
485 490 495

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
500 505 510

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
515 520 525

eolf-seql (2)

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
530 535 540

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
545 550 555 560

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
565 570 575

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
580 585 590

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
595 600 605

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
610 615 620

Ala Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly
625 630 635 640

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
645 650 655

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
660 665 670

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
675 680 685

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
690 695 700

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
705 710 715 720

eolf-seql (2)

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
725 730 735

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
740 745 750

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
755 760 765

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
770 775 780

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
785 790 795 800

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
805 810 815

<210> 91

<211> 414

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc knob chain fused to monomeric hu 4-1BBL (71-248)

<400> 91

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
225 230 235 240

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
245 250 255

eolf-seql (2)

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
260 265 270

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
275 280 285

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
290 295 300

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
305 310 315 320

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
325 330 335

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

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
355 360 365

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
370 375 380

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
385 390 395 400

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
405 410

<210> 92

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql (2)

<223> anti-PD1(0314) Fc hole monomeric ligand (71-248) chain

<400> 92

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu
450 455 460

Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
465 470 475 480

Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
485 490 495

Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
500 505 510

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly
515 520 525

Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly
530 535 540

Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg
545 550 555 560

eolf-seql (2)

Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro
565 570 575

Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu
580 585 590

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
595 600 605

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
610 615 620

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630 635

<210> 93
<211> 602
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc knob chain fused to dimeric hu 4-1BBL (71-248)

<400> 93

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
225 230 235 240

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
245 250 255

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
260 265 270

eolf-seql (2)

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
275 280 285

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
290 295 300

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
305 310 315 320

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
325 330 335

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

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
355 360 365

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
370 375 380

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
385 390 395 400

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
420 425 430

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
435 440 445

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
450 455 460

eolf-seql (2)

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
465 470 475 480

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
485 490 495

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
500 505 510

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
515 520 525

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
530 535 540

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
545 550 555 560

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
565 570 575

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
580 585 590

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
595 600

<210> 94
<211> 288
<212> PRT
<213> Homo sapiens

<400> 94

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

eolf-seql (2)

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

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

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
180 185 190

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

eolf-seql (2)

Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
 210 215 220

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
 225 230 235 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
 245 250 255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
 260 265 270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
 275 280 285

<210> 95
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 95

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

Leu His Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
 20 25 30

Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
 35 40 45

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
 50 55 60

Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
 65 70 75 80

eolf-seql (2)

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

Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
100 105 110

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

Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
130 135 140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
145 150 155 160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
165 170 175

Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
180 185 190

Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
195 200 205

<210> 96

<211> 233

<212> PRT

<213> Homo sapiens

<400> 96

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe

eolf-seql (2)

35

40

45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu

eolf-seql (2)

225

230

<210> 97
 <211> 244
 <212> PRT
 <213> Homo sapiens
 <400> 97

Met Gly Ala Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg
 1 5 10 15

Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
 20 25 30

Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
 35 40 45

Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
 50 55 60

Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
 65 70 75 80

Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
 85 90 95

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
 100 105 110

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

Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
 130 135 140

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

eolf-seql (2)

Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
165 170 175

Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala
180 185 190

Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
195 200 205

Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
210 215 220

His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala
225 230 235 240

Val Met Val Gly

<210> 98

<211> 183

<212> PRT

<213> Homo sapiens

<400> 98

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

Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val Ala Ser Val Ile Gln
20 25 30

Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser
35 40 45

Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val
50 55 60

eolf-seql (2)

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

Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn
85 90 95

Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu
100 105 110

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

Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr
130 135 140

Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu
145 150 155 160

Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn
165 170 175

Pro Gly Glu Phe Cys Val Leu
180

<210> 99
<211> 261
<212> PRT
<213> Homo sapiens

<400> 99

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

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

eolf-seql (2)

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
85 90 95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
100 105 110

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
130 135 140

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155 160

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220

eolf-seql (2)

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

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255

Gly Leu Leu Lys Leu
260

<210> 100
<211> 281
<212> PRT
<213> Homo sapiens

<400> 100

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
1 5 10 15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu

eolf-seql (2)

115

120

125

Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
130 135 140

Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
145 150 155 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
165 170 175

Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
180 185 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
225 230 235 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu
275 280

<210> 101

<211> 193

<212> PRT

<213> Homo sapiens

eolf-seql (2)

<400> 101

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu
35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His
50 55 60

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

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

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu
115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg
130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro
145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu
165 170 175

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

eolf-seql (2)

Pro

<210> 102
 <211> 234
 <212> PRT
 <213> Homo sapiens

<400> 102

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
 1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly
 20 25 30

Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu
 35 40 45

Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
 50 55 60

Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly
 65 70 75 80

Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys
 85 90 95

Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
 100 105 110

Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
 115 120 125

Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln
 130 135 140

eolf-seql (2)

Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu
145 150 155 160

Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val
165 170 175

Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln
180 185 190

Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val
195 200 205

Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val
210 215 220

Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
225 230

<210> 103
<211> 254
<212> PRT
<213> Homo sapiens

<400> 103

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

eolf-seql (2)

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

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

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
115 120 125

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

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
245 250

eolf-seql (2)

<210> 104

<211> 281

<212> PRT

<213> Homo sapiens

<400> 104

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

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile

eolf-seql (2)

165

170

175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 105
<211> 317
<212> PRT
<213> Homo sapiens

<400> 105

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
1 5 10 15

Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
20 25 30

Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
35 40 45

eolf-seql (2)

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

eolf-seql (2)

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

<210> 106
<211> 249
<212> PRT
<213> Homo sapiens

<400> 106

Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro
1 5 10 15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu
20 25 30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala
35 40 45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu
50 55 60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp
65 70 75 80

eolf-seql (2)

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro
85 90 95

Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala His Tyr Glu
100 105 110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly
115 120 125

Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu
130 135 140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu
145 150 155 160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr
165 170 175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu
180 185 190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg
195 200 205

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

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His
245

<210> 107
<211> 250
<212> PRT

eolf-seql (2)

<213> Homo sapiens

<400> 107

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
1 5 10 15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
20 25 30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
35 40 45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
50 55 60

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

Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
85 90 95

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

Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
115 120 125

Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
130 135 140

Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
145 150 155 160

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
165 170 175

eolf-seql (2)

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
180 185 190

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
195 200 205

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
210 215 220

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
225 230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 108
<211> 285
<212> PRT
<213> Homo sapiens

<400> 108

Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

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

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly

eolf-seql (2)

85

90

95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 130 135 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 145 150 155 160

Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 165 170 175

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 180 185 190

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 195 200 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
 245 250 255

Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
 260 265 270

Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu

eolf-seql (2)

275

280

285

<210> 109
 <211> 240
 <212> PRT
 <213> Homo sapiens
 <400> 109

Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
 1 5 10 15

Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
 20 25 30

Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
 35 40 45

Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
 50 55 60

Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
 65 70 75 80

Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
 85 90 95

His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
 100 105 110

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

His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
 130 135 140

Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
 145 150 155 160

eolf-seql (2)

Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
165 170 175

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

Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
195 200 205

Leu Glu Ala Gly Glu Lys Val Val Val Arg Val Leu Asp Glu Arg Leu
210 215 220

Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
225 230 235 240

<210> 110
<211> 251
<212> PRT
<213> Homo sapiens

<400> 110

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

Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
20 25 30

Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
35 40 45

Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
50 55 60

Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
65 70 75 80

eolf-seql (2)

His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
85 90 95

Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
100 105 110

Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
115 120 125

Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
130 135 140

Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
145 150 155 160

Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
165 170 175

Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
180 185 190

Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
195 200 205

Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
210 215 220

Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225 230 235 240

Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
245 250

<210> 111
<211> 199
<212> PRT

eolf-seql (2)

<213> Homo sapiens

<400> 111

Met Thr Leu His Pro Ser Pro Ile Thr Cys Glu Phe Leu Phe Ser Thr
1 5 10 15

Ala Leu Ile Ser Pro Lys Met Cys Leu Ser His Leu Glu Asn Met Pro
20 25 30

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

Trp Leu Phe Cys Ser Ile Val Met Leu Leu Phe Leu Cys Ser Phe Ser
50 55 60

Trp Leu Ile Phe Ile Phe Leu Gln Leu Glu Thr Ala Lys Glu Pro Cys
65 70 75 80

Met Ala Lys Phe Gly Pro Leu Pro Ser Lys Trp Gln Met Ala Ser Ser
85 90 95

Glu Pro Pro Cys Val Asn Lys Val Ser Asp Trp Lys Leu Glu Ile Leu
100 105 110

Gln Asn Gly Leu Tyr Leu Ile Tyr Gly Gln Val Ala Pro Asn Ala Asn
115 120 125

Tyr Asn Asp Val Ala Pro Phe Glu Val Arg Leu Tyr Lys Asn Lys Asp
130 135 140

Met Ile Gln Thr Leu Thr Asn Lys Ser Lys Ile Gln Asn Val Gly Gly
145 150 155 160

Thr Tyr Glu Leu His Val Gly Asp Thr Ile Asp Leu Ile Phe Asn Ser
165 170 175

eolf-seql (2)

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

Ala Asn Pro Gln Phe Ile Ser
 195

<210> 112
 <211> 391
 <212> PRT
 <213> Homo sapiens
 <400> 112

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

Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
 20 25 30

Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
 35 40 45

Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
 50 55 60

Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
 65 70 75 80

Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
 85 90 95

Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
 100 105 110

Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
 115 120 125

Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys

eolf-seql (2)

130

135

140

Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145 150 155 160

Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
165 170 175

Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
180 185 190

Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
195 200 205

Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
210 215 220

Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225 230 235 240

Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
245 250 255

Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
260 265 270

Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
275 280 285

Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
290 295 300

Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305 310 315 320

Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile

eolf-seql (2)

325

330

335

Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
340 345 350

Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
355 360 365

Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
370 375 380

Leu Gly Glu Ala Pro Ala Ser
385 390

<210> 113
<211> 205
<212> PRT
<213> Homo sapiens

<400> 113

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
20 25 30

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
35 40 45

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

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

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
85 90 95

eolf-seql (2)

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
 100 105 110

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
 115 120 125

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

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
 145 150 155 160

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
 165 170 175

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
 180 185 190

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 195 200 205

<210> 114
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 114

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

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

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
 35 40 45

eolf-seql (2)

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn
50 55 60

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
115 120 125

Glu Phe Cys Val Leu
130

<210> 115
<211> 132
<212> PRT
<213> Homo sapiens

<400> 115

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

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

Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
35 40 45

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
50 55 60

eolf-seql (2)

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
65 70 75 80

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

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

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
115 120 125

Phe Cys Val Leu
130

<210> 116
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker G4S

<400> 116

Gly Gly Gly Gly Ser
1 5

<210> 117
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker (G4S)2

<400> 117

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

eolf-seql (2)

<210> 118
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker (SG4)2

<400> 118

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10

<210> 119
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker (G4S)3

<400> 119

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 120
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker G4(SG4)2

<400> 120

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10

<210> 121
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>

eolf-seql (2)

<223> Peptide linker (G4S)4

<400> 121

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 122

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GSPGSSSSGS

<400> 122

Gly Ser Pro Gly Ser Ser Ser Ser Gly Ser
1 5 10

<210> 123

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GSGSGSGS

<400> 123

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 124

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GSGSGNGS

eolf-seql (2)

<400> 124

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 125

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GGSGSGSG

<400> 125

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 126

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GGSGSG

<400> 126

Gly Gly Ser Gly Ser Gly
1 5

<210> 127

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker GGSG

<400> 127

Gly Gly Ser Gly
1

eolf-seql (2)

<210> 128
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> GGSGNGSG

<400> 128

Gly Gly Ser Gly Asn Gly Ser Gly
1 5

<210> 129
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide inker GGNGSGSG

<400> 129

Gly Gly Asn Gly Ser Gly Ser Gly
1 5

<210> 130
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker GGNGSG

<400> 130

Gly Gly Asn Gly Ser Gly
1 5

<210> 131
<211> 2166
<212> DNA
<213> Artificial Sequence

<220>

eolf-seql (2)

<223> nucleotide sequence of dimeric hu 4-1BBL (71-254) - CL* Fc knob chain

<400> 131

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atgtttgctc	agctgggtggc	ccagaacgtg	ctgctgatcg	atggccccct	gtcctggtac	120
agcgatcctg	gactggctgg	cgtgtcactg	acaggcggcc	tgagctacaa	agaggacacc	180
aaagaactgg	tggtggccaa	ggccggcgtg	tactacgtgt	tctttcagct	ggaactgcgg	240
agagtgggtg	ccggcgaagg	atctggctct	gtgtctctgg	ccctgcatct	gcagcctctg	300
agaagcgctg	ctggcgctgc	agctctggca	ctgacagtgg	atctgcctcc	tgccagctcc	360
gaggccccga	atagcgcatt	tgggtttcaa	ggcaggctgc	tgcacctgtc	tgccggccag	420
aggctggggag	tgcatctgca	cacagaggcc	agggctagac	acgcctggca	gctgacacag	480
ggcgctacag	tgctgggcct	gttcagagtg	acccccgaga	ttccagccgg	cctgccttct	540
ccaagaagcg	aaggcggagg	cggatctggc	ggcggaggat	ctagagaggg	acccgaactg	600
tcccctgacg	atccagccgg	gctgctggat	ctgagacagg	gaatgttcgc	ccagctggtg	660
gctcagaatg	tgctgctgat	tgacggacct	ctgagctggt	actccgaccc	agggctggca	720
ggggtgtccc	tgactggggg	actgtcctac	aaagaagata	caaaagaact	ggtggtggct	780
aaagctgggg	tgtactatgt	gttttttcag	ctggaactga	ggcgggtggt	ggctggggag	840
ggctcaggat	ctgtgtccct	ggctctgcat	ctgcagccac	tgcgctctgc	tgctggcgca	900
gctgcactgg	ctctgactgt	ggacctgcca	ccagcctcta	gcgaggccag	aaacagcgcc	960
ttcgggttcc	aaggacgcct	gctgcatctg	agcgccggac	agcgcttggg	agtgcattctg	1020
catactgaag	ccagagcccc	gcatgcttgg	cagctgactc	agggggcaac	tgtgctggga	1080
ctgttttcgc	tgacacctga	gatccctgcc	ggactgcca	gccctagatc	agaagggggc	1140
ggagggttcc	gagggggagg	atctcgtacg	gtggctgcac	catctgtctt	tatcttccca	1200
cccagcgacc	ggaagctgaa	gtctggcaca	gccagcgctg	tgtgcctgct	gaataacttc	1260
tacccccgcg	aggccaaggt	gcagtggga	gtggacaatg	ccctgcagag	cggcaacagc	1320

eolf-seql (2)

caggaaaagcg tgaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg	1380
accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag	1440
ggcctgtcta gccccgtgac caagagcttc aaccggggcg agtgcgacaa gacccacacc	1500
tgtcctccat gccctgcccc tgaagctgct ggcgggcccta gcgtgttcct gttcccccca	1560
aagcccaagg acaccctgat gatcagccgg acccctgaag tgacctgcgt ggtggtggat	1620
gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac	1680
aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1740
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac	1800
aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa	1860
ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg	1920
tgggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg	1980
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc	2040
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc	2100
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg	2160
ggtaaa	2166

<210> 132

<211> 891

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of monomeric hu 4-1BBL (71-254) - CH1*

<400> 132

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240

eolf-seql (2)

agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccgga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag	420
agactgggag tgcatctgca cacagaggcc agagccaggc acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc	540
cctagatctg aaggcggcgg aggttccgga ggccggaggat ctgctagcac aaagggtccc	600
agcgtgttcc ctctggcccc tagcagcaag agcacatctg gcggaacagc cgccctgggc	660
tgcttgggtg aagattactt ccccgagccc gtgaccgtgt cctggaattc tggcgccctg	720
acaagcggcg tgacacactt tccagccgtg ctgcagagca gcggcctgta ctctctgagc	780
agcgtcgtga cagtgtccag cagctctctg ggaccccaga cctacatctg caacgtgaac	840
cacaagccca gcaacaccaa ggtggacgag aaggtggaac ccaagtcctg c	891

<210> 133

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc hole chain

<400> 133

gaagtgcagc tgctcgaaag cggcggggga ctggtccagc ccggcgggtc cctgaggctg	60
tcttgcgccg cttcagggtt cagcttttcc tcttacacca tgagttgggt cagacaggca	120
cctggcaagg gactggagtg ggtcgccaca atcagcgggt gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actactgtgt gtcctgacc	300
ggccgcgtct attttgccct tgactcctgg ggacaaggca ctctggtgac cgtatctagt	360
gctagcacca agggccccct cgtgttcccc ctggcccca gcagcaagag caccagcggc	420
ggcacagccg ctctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc	480

eolf-seql (2)

tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagttct	540
ggcctgtata gcctgagcag cgtgggtcacc gtgccttcta gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
aagagctgcg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctccggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtaaa	1350

<210> 134

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of anti-PD1 (0314) light chain

<400> 134

gagatcgtgc tgaccagag ccccgccaca ctctccctgt ctctggcga aagggtacc	60
ctttcatgca gagcaagcga gtccgtggac acttctgata acagtttcat tcttggtat	120
cagcagaagc cagggcagag ccccgccctg ctcatctatc ggtcctctac actggagtca	180
gggattcctg ccagggttag cggctccggt tctgggaccg acttcacttt gaccatcagt	240

eolf-seql (2)

agcctggaac cagaggattt tgctgtgtac tattgtcaac agaattacga cgtcccctgg	300
acattcggcc agggaaacaa agtggagata aagcgtacgg tggctgcacc atctgtcttc	360
atcttccccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	420
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg	480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acagggggaga gtgt	654

<210> 135

<211> 2166

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of dimeric hu 4-1BBL (71-254) - CL Fc knob chain

<400> 135

agagaggggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtgg ccggcgaagg atctggctct gtgtctcttg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctagagaggg acccgaactg	600
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctgggtg	660
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	720

eolf-seql (2)

ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	780
aaagctggggg tgtactatgt gtttttttcag ctggaactga ggcggggtggt ggctgggggag	840
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca	900
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	960
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgcttggg agtgcatctg	1020
catactgaag ccagagcccc gcatgcttgg cagctgactc aggggggcaac tgtgctggga	1080
ctgttttcgcg tgacacctga gatccctgcc ggactgcca gccctagatc agaagggggc	1140
ggagggttccg gggggggagg atctcgtacg gtggccgctc cctccgtgtt tatctttccc	1200
ccatccgatg aacagctgaa aagcggcacc gcctccgtcg tgtgtctgct gaacaatttt	1260
taccctaggg aagctaaagt gcagtggaaa gtggataacg cactgcagtc cggcaactcc	1320
caggaatctg tgacagaaca ggactccaag gacagcacct actccctgtc ctccaccctg	1380
acactgtcta aggctgatta tgagaaacac aaagtctacg cctgcgaagt caccatcag	1440
ggcctgagct cgccccgtcac aaagagcttc aacaggggag agtgtgacaa gaccacacc	1500
tgtccccctt gtcctgcccc tgaagctgct ggcgccctt ctgtgttcct gttccccca	1560
aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggat	1620
gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac	1680
aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1740
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac	1800
aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa	1860
ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg	1920
tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg	1980
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc	2040
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc	2100
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg	2160

eolf-seql (2)

ggtaaaa

2166

<210> 136
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of monomeric hu 4-1BBL (71-254) - CH1

<400> 136
agagaggggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300
agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc 360
gaggccccga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag 420
agactgggag tgcattctgca cacagaggcc agagccaggc acgcctggca gctgacacag 480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc 540
cctagatctg aaggcggcgg aggttccgga ggccggaggat ctgctagcac caaaggccct 600
tccgtgtttc ctctggctcc tagctccaag tccacctctg gaggcaccgc tgctctcgga 660
tgctctgtga aggattatct tcctgagcct gtgacagtgt cctggaatag cggagcactg 720
acctctggag tgcatacttt ccccgctgtg ctgcagtcct ctggactgta cagcctgagc 780
agcgtggtga cagtggccag cagcagcctg ggaccccaga cctacatctg caacgtgaac 840
cacaagccca gcaacaccaa ggtggacaag aaggtggaac ccaagtcttg t 891

<210> 137
<211> 2511
<212> DNA
<213> Artificial Sequence

eolf-seql (2)

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 137

gaagtgcagc tgctcgaaag cggcggggga ctggtccagc ccggcgggtt cctgaggctg	60
tcttgcgccg cttcagggtt cagcttttcc tcttacacca tgagttgggt cagacaggca	120
cctggcaagg gactggagtg ggtcgccaca atcagcgggt gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actacttgtt gctcctgacc	300
ggccgcgtct attttgccct tgactcctgg ggacaaggca ctctggtgac cgtatctagt	360
gctagcacca agggcccctc cgtgttcccc ctggcccca gcagcaagag caccagcggc	420
ggcacagccg ctctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc	480
tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagttct	540
ggcctgtata gcctgagcag cgtggtcacc gtgccttcta gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
aagagctgcg acaaaaactca cacatgcca ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgccccatc ccgggatgag	1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcagggtg	1260

eolf-seql (2)

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccaga	1380
gagggccctg agctgagccc cgatgatcct gctggactgc tggacctgcg gcagggcatg	1440
tttgctcagc tgggtggcca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc	1500
gatcctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaga ggacaccaaa	1560
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	1620
gtggtggccg gcgaaggatc tggctctgtg tctctggccc tgcattctgca gcctctgaga	1680
agcgctgctg gcgctgcagc tctggcactg acagtggatc tgcctcctgc cagctccgag	1740
gcccgggaata gcgcatttgg gtttcaaggc aggctgctgc acctgtctgc cggccagagg	1800
ctgggagtgatc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc	1860
gctacagtgc tgggcctgtt cagagtgacc cccgagattc cagccggcct gccttctcca	1920
agaagcgaag gcggaggcgg atctggcggc ggaggatcta gagagggacc cgaactgtcc	1980
cctgacgatc cagccgggct gctggatctg agacagggaa tggtcgccca gctggtggct	2040
cagaatgtgc tgctgattga cggacctctg agctggtact ccgacccagg gctggcaggg	2100
gtgtccctga ctgggggact gtcctacaaa gaagatacaa aagaactggt ggtggctaaa	2160
gctgggggtgt actatgtgtt ttttcagctg gaactgaggc ggggtggtggc tggggagggc	2220
tcaggatctg tgtccctggc tctgcatctg cagccactgc gctctgctgc tggcgcagct	2280
gcactggctc tgactgtgga cctgccacca gcctctagcg aggccagaaa cagcgccttc	2340
gggttccaag gacgcctgct gcatctgagc gccggacagc gcctgggagt gcatctgcat	2400
actgaagcca gagcccggca tgcttggcag ctgactcagg gggcaactgt gctgggactg	2460
tttcgcgtga cacctgagat ccctgccgga ctgccaagcc ctagatcaga a	2511

<210> 138

<211> 1929

<212> DNA

<213> Artificial Sequence

eolf-seql (2)

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc knob chain fused to monomeric hu 4-1BBL (71-254)

<400> 138

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tcttgcgccg cttcagggtt cagcttttcc tcttacacca tgagttgggt cagacaggca	120
cctggcaagg gactggagtg ggtcgccaca atcagcgggtg gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actactgtgt gtcctgacc	300
ggccgcgtct attttgcctt tgactcctgg ggacaaggca ctctgggtgac cgtatctagt	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttggtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc gcggggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccctg cagagatgag	1080
ctgaccaaga accagggtgtc cctgtgggtgt ctgggtcaagg gcttctaccc cagcgatatc	1140
gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg	1200
ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccgggtg	1260
cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc	1320

eolf-seql (2)

cagaagtccc ttagcctgag ccccggcgga ggcggcggaa gcgaggagg aggatccaga	1380
gagggccctg agctgagccc cgatgatcct gctggactgc tggacctgcg gcagggcatg	1440
tttgctcagc tgggtggcca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc	1500
gacacctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaga ggacaccaaa	1560
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	1620
gtggtggccg gcgaaggatc tggctctgtg tctctggccc tgcactctgca gcctctgaga	1680
agcgtgctg gcgctgcagc tctggcactg acagtggatc tgcctcctgc cagctccgag	1740
gcccggaata gcgcatttgg gtttcaaggc aggctgctgc acctgtctgc cggccagagg	1800
ctgggagtgc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc	1860
gctacagtgc tgggcctgtt cagagtgacc cccgagattc cagccggcct gccttctcca	1920
agaagcgaa	1929

<210> 139

<211> 2130

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of dimeric hu 4-1BBL (71-248) - CL* Fc knob chain

<400> 139

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggcca ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	360
gagggcccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420

eolf-seql (2)

aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg actgggaggc	540
ggcggatctg gcggcggagg atctagagaa ggacccgagc tgtcccctga cgatccagcc	600
gggctgctgg atctgagaca gggaatgttc gccagctgg tggctcagaa tgtgctgctg	660
attgacggac ctctgagctg gtactccgac ccagggctgg cagggtgtc cctgactggg	720
ggactgtcct acaaagaaga taaaaaaga ctggtggtgg ctaaagctgg ggtgtactat	780
gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc	840
ctggctctgc atctgcagcc actgcgtctt gcagcagggg ctgcagcact ggccctgact	900
gtggacctgc cccagcttc ttccgaggcc agaaacagcg ctttcgggtt ccaaggacgc	960
ctgctgcatc tgagcgccgg acagcgcttg ggagtgcac tgcatactga agccagagcc	1020
cggcatgctt ggagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	1080
gagatccccg ctggactggg cggaggcggg tccggagggg gaggatctcg tacggtggct	1140
gcaccatctg tctttatctt cccaccagc gaccggaagc tgaagtctgg cacagccagc	1200
gtcgtgtgcc tgctgaataa cttctacccc cgcgaggcca aggtgcagtg gaagggtggac	1260
aatgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggacag caaggactcc	1320
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaagggtg	1380
tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaaccgg	1440
ggcgagtgcg acaagacca cacctgtcct ccatgccctg cccctgaagc tgctggcggc	1500
cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccctt	1560
gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtga gttcaattgg	1620
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac	1680
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1740
gagtacaagt gcaaggcttc caacaaagcc ctcggcgccc ccatcgagaa aacctctcc	1800
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag	1860

eolf-seql (2)

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc	1920
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1980
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg	2040
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	2100
cagaagagcc tctccctgtc tccgggtaaa	2130

<210> 140

<211> 873

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of monomeric hu 4-1BBL (71-248) - CH1*

<400> 140

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
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ttccccgagc ccgtgaccgt gtcctggaat tctggcgccc tgacaagcgg cgtgcacacc	720
tttccagccg tgctgcagag cagcggcctg tactctctga gcagcgtcgt gacagtgtccc	780
agcagctctc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc	840

eolf-seql (2)

aaggtggacg agaaggtgga acccaagtcc tgc 873

<210> 141

<211> 2130

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of dimeric hu 4-1BBL (71-248) - CL Fc knob chain

<400> 141

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
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eolf-seql (2)

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gtcgtgtgtc tgctgaacaa tttttaccct aggggaagcta aagtgcagtg gaaagtggat 1260
aacgcactgc agtccggcaa ctcccaggaa tctgtgacag aacaggactc caaggacagc 1320
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cagaagagcc tctccctgtc tccgggtaaa 2130

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<210> 142

<211> 873

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of monomeric hu 4-1BBL (71-248) - CH1

<400> 142

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eolf-seql (2)

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aaggtggaca agaaggtgga acccaagtct tgt	873

<210> 143

<211> 2475

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc hole chain fused to dimeric hu 4-1BBL (71-248)

<400> 143

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cctggcaagg gactggagtg ggtcgccaca atcagcgggt gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240

eolf-seql (2)

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gctagcacca agggccccctc cgtgttcccc ctggccccca gcagcaagag caccagcggc	420
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tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagttct	540
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tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
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eolf-seql (2)

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atcccagccg ggctc	2475

<210> 144
 <211> 1911
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence anti-PD1(0314) Fc knob chain fused to monomeric hu 4-1BBL (71-248)

<400> 144	
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cctggcaagg gactggagtg ggtcgccaca atcagcgggtg gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actactgtgt gtcctgacc	300

eolf-seql (2)

ggccgcgtct attttgccct tgactcctgg ggacaaggca ctctgggtgac cgtatctagt	360
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eolf-seql (2)

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gctacagtgc tgggcctgtt cagagtgacc cccgagattc ctgccgggct c	1911

<210> 145

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of Fc hole dimeric ligand (71-248) chain

<400> 145

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tgcgtgggtg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	180
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacaa cagcacgtac	240
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eolf-seql (2)

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gggctc	1806

<210> 146

<211> 1212

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of Fc hole monomeric ligand (71-248) chain

<400> 146

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tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	180
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	240

eolf-seql (2)

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cctgccgggc tc	1212

<210> 147

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc knob chain fused to dimeric hu 4-1BBL (71-248)

<400> 147

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eolf-seql (2)

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ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
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gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg	1200
ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg	1260
cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc	1320
cagaagtccc tgagcctgag ccccggcaga gagggccctg agctgagccc tgatgatcct	1380
gccggactgc tggacctgcg gcagggaatg tttgcccagc tgggtggcca gaacgtgtg	1440
ctgatcgatg gccccctgtc ctggtacagc gatcctggac tggctggcgt gtcactgaca	1500

eolf-seql (2)

ggcggcctga gctacaaaga ggacaccaaa gaactggtgg tggccaaggc cggcgtgtac	1560
tacgtgttct ttcagctgga actgcggaga gtggtggccg gcgaaggatc tggctctgtg	1620
tctctggccc tgcatctgca gcctctgaga tctgctgctg gcgccgctgc tctggcactg	1680
acagtggatc tgcctcctgc cagcagcgag gcccggaata gcgcatttgg gtttcaaggc	1740
aggctgctgc acctgtctgc cggccagagg ctgggagtgc atctgcacac agaggccagg	1800
gctagacacg cctggcagct gacacagggc gctacagtgc tgggcctgtt cagagtgacc	1860
cccgagattc cagcaggcct gggaggcggc ggatctggcg gcggaggatc tagagaagga	1920
cccgagctgt ccccccacga tcccgtggg ctgctggatc tgagacaggg catgttcgct	1980
cagctggtgg ctcagaatgt gctgctgatt gacggacctc tgagctggta ctccgaccca	2040
gggctggcag ggggtgtccct gactggggga ctgtcctaca aagaagatac aaaagaactg	2100
gtggtggcta aagctgggggt gtactatgtg ttttttcagc tggaactgag gcgggtggtg	2160
gctggggagg gctcaggatc tgtgtccctg gctctgcatc tgcagccact gcgctctgca	2220
gcaggggctg cagcactggc cctgactgtg gacctgcccc cagcttcttc cgaggccaga	2280
aacagcgctt tcgggttcca aggacgcctg ctgcatctga gcgccggaca gcgcctggga	2340
gtgcatctgc atactgaagc cagagcccgg catgcttggc agctgactca gggggcaact	2400
gtgctgggac tgtttcgctg gacacctgag atcccagccg ggctc	2445

<210> 148

<211> 1242

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of Fc knob chain fused to monomeric hu 4-1BBL
(71-248)

<400> 148

gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcaggggg accgtcagtc	60
ttcctcttcc ccccaaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	120
tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	180

eolf-seql (2)

```

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      240
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      300
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa      360
gggcagcccc gagaaccaca ggtgtacacc ctgccccctt gcagagatga gctgaccaag      420
aaccaggtgt ccctgtgggtg tctgggtcaag ggcttctacc ccagcgatat cgccgtggag      480
tgggagagca acggccagcc tgagaacaac tacaagacca cccccctgt gctggacagc      540
gacggcagct tcttcctgta ctccaaactg accgtggaca agagccgggtg gcagcagggc      600
aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc      660
ctgagcctga gccccggcgg aggcggcgga agcggaggag gaggatccag agagggccct      720
gagctgagcc ctgatgatcc tgccggactg ctggacctgc ggcagggaat gtttgcccag      780
ctgggtggccc agaacgtgct gctgatcgat ggccccctgt cctggtacag cgatcctgga      840
ctggctggcg tgtcactgac aggcggcctg agctacaaag aggacaccaa agaactgggtg      900
gtggccaagg ccggcgtgta ctacgtgttc tttcagctgg aactgcggag agtgggtggcc      960
ggcgaaggat ctggctctgt gtctctggcc ctgcatctgc agcctctgag atctgctgct     1020
ggcgccgctg ctctggcact gacagtggat ctgcctcctg ccagcagcga ggcccggaat     1080
agcgcatttg ggtttcaagg caggctgctg cacctgtctg ccggccagag gctgggagtg     1140
catctgcaca cagaggccag ggctagacac gcctggcagc tgacacaggg cgctacagtg     1200
ctgggcctgt tcagagtgac ccccgagatt cctgccgggc tc                          1242

```

<210> 149

<211> 1911

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of anti-PD1(0314) Fc hole monomeric ligand
(71-248) chain

<400> 149

eolf-seql (2)

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tcttgcgccg cttcagggtt cagcttttcc tcttacacca tgagttgggt cagacaggca	120
cctggcaagg gactggagtg ggtcgccaca atcagcgggtg gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actactgtgt gtcctgacc	300
ggccgcgtct attttgccct tgactcctgg ggacaaggca ctctgggtgac cgtatctagt	360
gctagcacca agggcccctc cgtgttcccc ctggcccca gcagcaagag caccagcggc	420
ggcacagccg ctctgggctg cctggtaag gactacttcc ccgagcccgt gaccgtgtcc	480
tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagttct	540
ggcctgtata gcctgagcag cgtggtcacc gtgccttcta gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
aagagctgcg aaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcagggtg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtgga ggccggcgaa gcggaggagg aggatccaga	1380
gagggccctg agctgagccc tgatgatcct gccggactgc tggacctgcg gcagggaatg	1440

eolf-seql (2)

tttccccagc tggctggcca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc	1500
gatcctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaaga ggacacccaaa	1560
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	1620
gtggtggccg gcgaaggatc tggctctgtg tctctggccc tgcattctgca gcctctgaga	1680
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gcccggaaata gcgcatttgg gtttcaaggc aggctgctgc acctgtctgc cggccagagg	1800
ctgggagtgatc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc	1860
gctacagtgc tgggcctgtt cagagtgacc cccgagattc ctgccgggct c	1911

<210> 150

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of Fc knob chain fused to dimeric hu 4-1BBL
(71-248)

<400> 150

gacaaaactc acacatgccc accgtgccc gcacctgaag ctgcaggggg accgtcagtc	60
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	120
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	180
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	240
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	300
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	360
gggcagcccc gagaaccaca ggtgtacacc ctgccccctt gcagagatga gctgaccaag	420
aaccaggtgt ccctgtggtg tctggtcaag ggcttctacc ccagcgatat cggcgtggag	480
tgggagagca acggccagcc tgagaacaac tacaagacca cccccctgt gctggacagc	540
gacggcagct tcttctgtga ctccaaactg accgtggaca agagccggtg gcagcagggc	600
aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc	660

eolf-seql (2)

ctgagcctga gccccggcgg aggcggcgga agcggaggag gaggatccag agagggccct	720
gagctgagcc ctgatgatcc tgccggactg ctggacctgc ggcagggaat gtttggccag	780
ctggtggccc agaactgct gctgatcgat ggccccctgt cctggtacag cgatcctgga	840
ctggctggcg tgtcactgac aggcggcctg agctacaaag aggacaccaa agaactgggtg	900
gtggccaagg ccggcgtgta ctacgtgttc tttcagctgg aactgcggag agtggtggcc	960
ggcgaaggat ctggctctgt gtctctggcc ctgcatctgc agcctctgag atctgctgct	1020
ggcgccgctg ctctggcact gacagtggat ctgcctcctg ccagcagcga ggcccggaaat	1080
agcgcatttg ggtttcaagg caggctgctg cacctgtctg ccggccagag gctgggagtg	1140
catctgcaca cagaggccag ggctagacac gcctggcagc tgacacaggg cgctacagtg	1200
ctgggcctgt tcagagtgac ccccgagatt ccagcaggcc tgggaggcgg cggatctggc	1260
ggcggaggat ctagagaagg acccgagctg tccccgacg atcccgtgg gctgctggat	1320
ctgagacagg gcatgttcgc tcagctgggtg gctcagaatg tgctgctgat tgacggacct	1380
ctgagctgggt actccgaccc agggctggca ggggtgtccc tgactggggg actgtcctac	1440
aaagaagata caaaagaact ggtgggtggct aaagctgggg tgactatgt gttttttcag	1500
ctggaactga ggcgggtgggt ggctggggag ggctcaggat ctgtgtccct ggctctgcat	1560
ctgcagccac tgcgctctgc agcaggggct gcagcactgg ccctgactgt ggacctgccc	1620
ccagcttctt ccgaggccag aaacagcgcc ttcgggttcc aaggacgcct gctgcatctg	1680
agcgccggac agcgctggg agtgcatctg catactgaag ccagagcccg gcatgcttgg	1740
cagctgactc agggggcaac tgtgctggga ctgtttcgcg tgacacctga gatcccagcc	1800
gggctc	1806

<210> 151

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

eolf-seql (2)

<223> nucleotide sequence of DP47 Fc hole chain

<400> 151

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	600
aatcacaagc ccagcaacac caaggtggac aagaaaagttg agcccaaatac ttgtgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	960
gtctccaaca aagccctcgg cgtcccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgtg caccctgccc ccatcccggt atgagctgac caagaaccag	1080
gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200
tccttcttcc tcgtgagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc	1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1320
ctgtctccgg gtaaa	1335

eolf-seql (2)

<210> 152
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of DP47 light chain

<400> 152
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacagggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc 300
 cagggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
 ggcttgagct cgcccgtcac aaagagcttc aacagggggag agtgt 645

<210> 153
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47 Fc hole chain

<400> 153

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

<210> 154

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> DP47 light chain

<400> 154

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

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

eolf-seql (2)

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 155

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of DP47 Fc hole chain fused to dimeric hu
4-1BBL (71-254)

<400> 155

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tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

eolf-seql (2)

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccctccgtgt tccccctggc cccagcagc aagagcacca gcggcggcac agccgctctg	420
ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc	480
ctgacctccg gcgtgcacac cttccccgcc gtgctgcaga gttctggcct gtatagcctg	540
agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg	600
aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtgggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	960
gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgtg caccctgccc ccatcccgga atgagctgac caagaaccag	1080
gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200
tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1260
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gcccagaacg tgctgctgat cgatggcccc ctgtcctggg acagcgatcc tggactggct	1500
ggcgtgtcac tgacaggcgg cctgagctac aaagaggaca ccaaagaact ggtgggtggcc	1560
aaggccggcg tgtactacgt gttctttcag ctggaactgc ggagagtggg ggccggcgaa	1620
ggatctggct ctgtgtctct ggccctgcat ctgcagcctc tgagaagcgc tgctggcgct	1680

eolf-seql (2)

gcagctcttg cactgacagt ggatctgcct cctgccagct ccgaggcccg gaatagcgca	1740
tttgggtttc aaggcaggct gctgcacctg tctgccggcc agaggctggg agtgcacatctg	1800
cacacagagg ccagggctag acacgcctgg cagctgacac agggcgctac agtgctgggc	1860
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ggactgtcct acaaagaaga taaaaagaa ctggtggtgg ctaaagctgg ggtgtactat	2160
gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc	2220
ctggctctgc atctgcagcc actgcgctct gctgctggcg cagctgcact ggctctgact	2280
gtggacctgc caccagcctc tagcgaggcc agaaacagcg ccttcgggtt ccaaggacgc	2340
ctgctgcatc tgagcgccgg acagcgctg ggagtgcac tgcatactga agccagagcc	2400
cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	2460
gagatccctg ccggactgcc aagccctaga tcagaa	2496

<210> 156

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of DP47 Fc knob chain fused to monomeric hu
4-1BBL (71-254)

<400> 156

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300

eolf-seql (2)

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttccccggct gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatac ttgtgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtgggtggacg tgagccacga agaccctgag gtcaagttca actgggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag	960
gtctccaaca aagccctcgg cgccccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgta caccctgccc ccctgcagag atgagctgac caagaaccag	1080
gtgtccctgt ggtgtctggt caagggcttc taccacagcg atatcgccgt ggagtgggag	1140
agcaacggcc agcctgagaa caactacaag accaccccc ctgtgctgga cagcgacggc	1200
agcttcttcc tgtactcaa actgaccgtg gacaagagcc ggtggcagca gggcaacgtg	1260
ttcagctgca gcgtgatgca cgaggccctg cacaaccact acaccagaa gtccctgagc	1320
ctgagccccg gcggaggcgg cggaagcgga ggaggaggat ccagagaggg ccctgagctg	1380
agccccgatg atcctgctgg actgctggac ctgcggcagg gcatgtttgc tcagctgggtg	1440
gcccagaacg tgctgctgat cgatggcccc ctgtcctggt acagcgatcc tggactggct	1500
ggcgtgtcac tgacaggcgg cctgagctac aaagaggaca ccaaagaact ggtggtggcc	1560
aaggccggcg tgtactacgt gttctttcag ctggaactgc ggagagtggg ggccggcgaa	1620
ggatctggct ctgtgtctct ggccctgcat ctgcagcctc tgagaagcgc tgctggcgct	1680
gcagctctgg cactgacagt ggatctgcct cctgccagct ccgaggcccc gaatagcgca	1740

eolf-seql (2)

tttgggtttc aaggcaggct gctgcacctg tctgccggcc agaggctggg agtgcacatctg 1800
cacacagagg ccagggctag acacgcctgg cagctgacac agggcgctac agtgctgggc 1860
ctgttcagag tgacccccga gattccagcc ggcctgcctt ctccaagaag cgaa 1914

<210> 157
<211> 832
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47 Fc hole chain fused to dimeric hu 4-1BBL (71-254)
<400> 157

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
450 455 460

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
465 470 475 480

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
485 490 495

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
500 505 510

eolf-seql (2)

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
515 520 525

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
530 535 540

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
545 550 555 560

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
565 570 575

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
580 585 590

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
595 600 605

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
610 615 620

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
645 650 655

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
660 665 670

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
675 680 685

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
690 695 700

eolf-seql (2)

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
705 710 715 720

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
725 730 735

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
740 745 750

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
755 760 765

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
770 775 780

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
785 790 795 800

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
805 810 815

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
820 825 830

<210> 158
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47 Fc knob chain fused to monomeric hu 4-1BBL (71-254)

<400> 158

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
450 455 460

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
465 470 475 480

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
485 490 495

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
500 505 510

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
515 520 525

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
530 535 540

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
545 550 555 560

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
565 570 575

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
580 585 590

eolf-seql (2)

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
595 600 605

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
610 615 620

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
625 630 635

<210> 159
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of DP47 heavy chain (hu IgG1 PGLALA)

<400> 159
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgttag caccaagggc 360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgcgtggaa ctcaggcgcc 480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc 540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatac ttgtgacaaa 660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

eolf-seql (2)

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gagggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg      900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag      960
gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag     1020
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag     1080
gtcagcctga cctgcctggg caaaggcttc tatcccagcg acatcgccgt ggagtgggag     1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc     1200
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc     1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc     1320
ctgtctccgg gtaaa                                           1335

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<210> 160
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47 heavy chain (hu IgG1 PGLALA)

<400> 160

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

<210> 161
 <211> 1350

eolf-seql (2)

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of PD1(0314) heavy chain (huIgG1 PGLALA)

<400> 161

gaagtgcagc tgctcgaaag cggcggggga ctggtccagc ccggcgggtc cctgaggctg	60
tcttgcgccg cttcagggtt cagcttttcc tcttacacca tgagttgggt cagacaggca	120
cctggcaagg gactggagtg ggctgccaca atcagcgggtg gcgggcgcga catttattac	180
ccagattccg tgaaaggacg gttcaccatc tctagggaca actcaaagaa tactctgtat	240
ttgcagatga acagcctgag agctgaggat acagcagttt actactgtgt gctcctgacc	300
ggccgcgtct attttggcct tgactcctgg ggacaaggca ctctgggtgac cgtatctagt	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttggtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag	1080
ctgaccaaga accagggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcagggtg	1260

eolf-seql (2)

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 162

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1(0314) heavy chain (huIgG1 PGLALA)

<400> 162

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql (2)

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 163
<211> 163
<212> PRT
<213> Homo sapiens

<400> 163

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser

eolf-seql (2)

20

25

30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

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

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln

<210> 164

<211> 681

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of Fc hole chain

<400> 164

eolf-seql (2)

gacaaaaactc acacatgccc accgtgccc	gcacctgaac tcctgggggg accgtcagtc	60
ttcctcttcc ccccaaaacc caaggacacc	ctcatgatct cccggacccc tgaggtcaca	120
tgcgtggtgg tggacgtgag ccacgaagac	cctgagggtca agttcaactg gtacgtggac	180
ggcgtggagg tgcataatgc caagacaaag	ccgcggggagg agcagtacaa cagcacgtac	240
cgtgtggtca gcgtcctcac cgtcctgcac	caggactggc tgaatggcaa ggagtacaag	300
tgcaagggtct ccaacaaagc cctcccagcc	cccatcgaga aaaccatctc caaagccaaa	360
gggcagcccc gagaaccaca ggtgtgcacc	ctgcccccat cccgggatga gctgaccaag	420
aaccagggtca gcctctctgt cgcagtcaaa	ggcttctatc ccagcgacat cgccgtggag	480
tgggagagca atgggcagcc ggagaacaac	tacaagacca cgcctcccgt gctggactcc	540
gacggctcct tcttcctcgt gagcaagctc	accgtggaca agagcagggtg gcagcagggg	600
aacgtcttct catgctccgt gatgcatgag	gctctgcaca accactacac gcagaagagc	660
ctctccctgt ctccgggtaa a		681

<210> 165

<211> 1266

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of human 4-1BB antigen Fc knob chain

<400> 165

ctgcaggacc cctgcagcaa ctgccctgcc	ggcaccttct gcgacaacaa ccggaaccag	60
atctgcagcc cctgcccccc caacagcttc	agctctgccg gcggacagcg gacctgcgac	120
atctgcagac agtgcaaggg cgtgttcaga	acccggaaaag agtgcagcag caccagcaac	180
gccgagtgcg actgcacccc cggcttccat	tgtctggggag ccggctgcag catgtgcgag	240
caggactgca agcagggcca ggaactgacc	aagaagggtc gcaaggactg ctgcttcggc	300
accttcaacg accagaagcg gggcatctgc	cggccctgga ccaactgtag cctggacggc	360
aagagcgtgc tgggtcaacgg caccaaagaa	cgggacgtcg tgtgcggccc cagccctgct	420

eolf-seql (2)

gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac	480
tctcctcagg tcgacgaaca gttatatattt cagggcggct caccctaaatc tgcagacaaa	540
actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	600
ttccccccaa aacccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg	660
gtgggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	720
gagggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	780
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcag	840
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag	900
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag	960
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1020
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1080
tccttcttcc tctacagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc	1140
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gacccctctc	1200
ctgtctccgg gtaaattccgg aggcctgaac gacatcttcg agggccagaa gattgaatgg	1260
cacgag	1266

<210> 166
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc hole chain

<400> 166

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
1				5				10					15		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			20					25					30		

eolf-seql (2)

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

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

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

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

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

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

eolf-seql (2)

Pro Gly Lys
225

<210> 167
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> human 4-1BB antigen Fc knob chain

<400> 167

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro

eolf-seql (2)

130

135

140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
165 170 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
180 185 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
195 200 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
210 215 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
225 230 235 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
245 250 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
260 265 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
275 280 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
290 295 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305 310 315 320

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

eolf-seql (2)

325

330

335

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
340 345 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
355 360 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
370 375 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
385 390 395 400

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
405 410 415

Lys Ile Glu Trp His Glu
420

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> avi tag

<400> 168

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
1 5 10 15

<210> 169
<211> 594
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of human 4-1BB His

eolf-seql (2)

```

<400> 169
ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag      60
atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac      120
atctgcagac agtgcaaggg cgtgttcaga acccggaaag agtgcagcag caccagcaac      180
gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag      240
caggactgca agcagggcca ggaactgacc aagaagggct gcaaggactg ctgcttcggc      300
accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc      360
aagagcgtgc tgggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct      420
gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac      480
tctcctcagg tcgacgaaca gttatatttt cagggcggct caggcctgaa cgacatcttc      540
gaggcccaga agatcgagtg gcacgaggct cgagctcacc accatcacca tcac          594

```

```

<210> 170
<211> 198
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> human 4-1BB His

```

<400> 170

```

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1           5           10          15

```

```

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
          20          25          30

```

```

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
          35          40          45

```

```

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
          50          55          60

```

eolf-seql (2)

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

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

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu
165 170 175

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala
180 185 190

His His His His His His
195