

eolf-seq1  
SEQUENCE LISTING

<110> UCB Biopharma SPRL

<120> Method

<130> PF0019WO

<150>

<151>

<160> 38

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial

<220>

<223> CDRH1

<400> 1

Asn Tyr Gly Ile His  
1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial

<220>

<223> CDRH2

<400> 2

Ser Ile Ser Pro Ser Gly Gly Leu Thr Tyr Tyr Arg Asp Ser Val Lys  
1 5 10 15

Gly

<210> 3

<211> 8

<212> PRT

<213> Artificial

<220>

<223> CDRH3

<400> 3

Gly Gly Glu Gly Ile Phe Asp Tyr  
1 5

<210> 4

<211> 11

<212> PRT

<213> Artificial

<220>

<223> CDRL1

# e0lf-seq1

<400> 4

Arg Ala Thr Gln Ser Ile Tyr Asn Ala Leu Ala  
1 5 10

<210> 5

<211> 7

<212> PRT

<213> Artificial

<220>

<223> CDRL2

<400> 5

Asn Ala Asn Thr Leu His Thr  
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial

<220>

<223> CDRL3

<400> 6

Gln Gln Tyr Tyr Asp Tyr Pro Leu Thr  
1 5

<210> 7

<211> 108

<212> PRT

<213> Artificial

<220>

<223> Light chain variable region of antibody A26

<400> 7

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

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

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

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

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

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

eo1f-seq1

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

<210> 8  
<211> 117  
<212> PRT  
<213> Artificial

<220>  
<223> Heavy chain variable region of antibody A26

<400> 8

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

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

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

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

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

Val Thr Val Ser Ser  
115

<210> 9  
<211> 214  
<212> PRT  
<213> Artificial

<220>  
<223> Light chain of anti-OX40 antibody Fab component

<400> 9

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

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

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

eo1f-seq1

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 10  
<211> 220  
<212> PRT  
<213> Artificial

<220>  
<223> Heavy chain of anti-OX40 antibody Fab component

<400> 10

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

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

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

Ala Ser Ile Ser Pro Ser Gly Gly Leu Thr Tyr Tyr Arg Asp Ser Val

eo1f-seq1

50

55

60

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

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

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

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

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

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

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

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

<210> 11  
<211> 121  
<212> PRT  
<213> Artificial

<220>  
<223> Heavy chain of anti-albumin Fv component

<400> 11

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr  
20 25 30

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys  
50 55 60

eo1f-seq1

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 12

<211> 112

<212> PRT

<213> Artificial

<220>

<223> Light chain of anti-albumin Fv component

<400> 12

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
20 25 30

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile  
85 90 95

Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr  
100 105 110

<210> 13

<211> 16

<212> PRT

<213> Artificial

<220>

<223> Linker 1

<400> 13

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser  
1 5 10 15

eo1f-seq1

<210> 14  
 <211> 15  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Linker 2

<400> 14

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

<210> 15  
 <211> 357  
 <212> PRT  
 <213> Artificial

<220>  
 <223> A26 Fab Heavy-(G4S,G4T,G4S)-645dsFv(gH5)

<400> 15

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

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

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

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

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

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

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

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160

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

eo1f-seq1

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

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

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

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

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

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

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly Ile Ile Trp  
275 280 285

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr  
290 295 300

Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser  
305 310 315 320

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro  
325 330 335

Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu  
340 345 350

Val Thr Val Ser Ser  
355

<210> 16  
<211> 341  
<212> PRT  
<213> Artificial

<220>  
<223> A26 Fab Light-(3xG4S)-645dsFv(gL4)

<400> 16

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

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
Page 8

self-seq1

35

40

45

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
210 215 220

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val  
225 230 235 240

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

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

Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys Leu Thr Ser Gly Val  
275 280 285

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

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

colf-seq1  
315

305 310 320

Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val  
325 330 335

Glu Ile Lys Arg Thr  
340

<210> 17  
<211> 119  
<212> PRT  
<213> Artificial

<220>  
<223> 645gH1 heavy chain variable domain

<400> 17

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr  
20 25 30

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Thr Thr Val Tyr Leu Gln Met  
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser  
115

<210> 18  
<211> 110  
<212> PRT  
<213> Artificial

<220>  
<223> 645gL1 light chain variable domain

<400> 18

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
Page 10

eo1f-seq1

20

25

30

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile  
85 90 95

Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 19  
<211> 355  
<212> PRT  
<213> Artificial

<220>  
<223> A26 Fab Heavy-( 3xG4S)-645dsFv(gH1)

<400> 19

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

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

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

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

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

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

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

eo1f-seq1

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu  
225 230 235 240

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

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

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly Ile Ile Trp  
275 280 285

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr  
290 295 300

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

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro Gly Tyr  
325 330 335

Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr  
340 345 350

Val Ser Ser  
355

<210> 20  
<211> 340  
<212> PRT  
<213> Artificial

<220>  
<223> A26 Fab Light-(3xG4S)-645dsFv(gL1)

<400> 20

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
Page 12

eo1f-seq1

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Asp | Arg | Val | Thr | Ile | Thr | Asn |
|     |     | 20  |     |     | 25  | 30  |
| Leu | Ala | Trp | Tyr | Gln | Gln | Lys |
|     |     | 35  |     |     | 40  | 45  |
| Tyr | Asn | Ala | Asn | Thr | Leu | His |
|     | 50  |     |     |     | 55  | 60  |
| Ser | Gly | Ser | Gly | Thr | Asp | Ser |
| 65  |     |     |     | 70  |     | 75  |
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr |
|     |     |     | 85  |     |     | 90  |
| Thr | Phe | Gly | Gly | Gly | Thr | Lys |
|     |     | 100 |     |     | 105 | 110 |
| Pro | Ser | Val | Phe | Ile | Phe | Pro |
|     |     | 115 |     |     | 120 | 125 |
| Thr | Ala | Ser | Val | Val | Cys | Leu |
|     | 130 |     |     |     | 135 | 140 |
| Lys | Val | Gln | Trp | Lys | Val | Asp |
| 145 |     |     |     | 150 |     | 155 |
| Glu | Ser | Val | Thr | Glu | Gln | Asp |
|     |     |     | 165 |     | 170 | 175 |
| Ser | Thr | Leu | Thr | Leu | Ser | Lys |
|     |     | 180 |     |     | 185 | 190 |
| Ala | Cys | Glu | Val | Thr | His | Gln |
|     |     | 195 |     |     | 200 | 205 |
| Phe | Asn | Arg | Gly | Glu | Cys | Ser |
|     | 210 |     |     |     | 215 | 220 |
| Ser | Gly | Gly | Gly | Gly | Ser | Asp |
| 225 |     |     |     | 230 |     | 235 |
| Val | Ser | Ala | Ser | Val | Gly | Asp |
|     |     |     | 245 |     | 250 | 255 |
| Pro | Ser | Val | Trp | Ser | Asn | Phe |
|     |     | 260 |     |     | 265 | 270 |
| Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     |     |     |     |     |     |

eo1f-seq1

275

280

285

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

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly  
305 310 315 320

Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys  
325 330 335

Val Glu Ile Lys  
340

<210> 21  
<211> 1137  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain A26-645(gH5) including E.coli OmpA leader

<400> 21  
atgaagaaga ctgctatagc gatcgagtg gcgctagctg gtttcgccac cgtggcgcaa 60  
gctgaagttc agctggtcga gtctggaggc gggcttgctc agcctggagg gagcctgcgt 120  
ctctcttggt cagcaagcgg ttccacgttc accaactacg gtatccactg gattcgctcag 180  
gcaccaggta aaggtctgga atgggtagcc tctatctctc cgtctggtgg tctgacgtac 240  
taccgtgact ctgtcaaagg tcgtttcacc atctctcgtg atgacgcgaa aaactctccg 300  
tacctgcaaa tgaactctct gcgtgcagaa gataccgcag tgtactactg cgctactggt 360  
gggtgaaggta tcttcgacta ctgggggtcag ggtaccctgg taactgtctc gagcgcttct 420  
acaaagggcc caagcgtttt cccactggct ccgtcctcta aatccacctc tgggtggtacg 480  
gctgcactgg gttgcctggt gaaagactac ttcccagaac cagttaccgt gtcttggaac 540  
tctggtgcac tgacctctgg tgttcacacc tttccagcag ttctccagtc ttctggtctg 600  
tactccctgt ctagcgtggt taccgttccg tcttcttctc tgggtactca gacctacatc 660  
tgcaacgtca accacaaacc gtccaacacc aaggtcgaca aaaaagtcga gccgaaatcc 720  
tgtagtggag gtgggggctc aggtggaggc gggaccggtg gaggtggcag cgaggttcaa 780  
ctgcttgagt ctggaggagg cctagtccag cctggaggga gcctgcgtct ctcttggtgca 840  
gtaagcggca tcgacctgag caattacgcc atcaactggg tgagacaagc tccggggaag 900  
tgtttagaat ggatcgggtat aatatgggcc agtgggacga ctttttatgc tacatgggcg 960  
aaaggaaggt ttacaattag ccgggacaat agcaaaaaca ccgtgtatct ccaaataaac 1020  
tccttgcgag cagaggacac ggcgggtgtac tattgtgtct gactgtccc aggttatagc 1080  
actgcaccct acttcgatct gtgggggacaa gggaccctgg tgactgtttc aagttaa 1137

<210> 22

eo1f-seq1

<211> 1074  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain A26-645(gH5)

<400> 22  
gaagttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60  
tcttgtgcag caagcggttt cacgttcacc aactacggta tccactggat tcgtcaggca 120  
ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac 180  
cgtgactctg tcaaaggctg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240  
ctgcaaataa actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt 300  
gaaggtatct tcgactactg gggtcagggg accctggtaa ctgtctcgag cgcttctaca 360  
aagggcccaa gcgttttccc actggctccg tcctctaaat ccacctctgg tggtagcggt 420  
gcactgggtt gcctggtgaa agactacttc ccagaaccag ttaccgtgtc ttggaactct 480  
ggtgcactga cctctggtgt tcacaccttt ccagcagttc tccagtcttc tggctctgtac 540  
tccctgtcta gcgtgggttac cgttccgtct tcttctctgg gtactcagac ctacatctgc 600  
aacgtcaacc acaaacctgc caacaccaag gtcgacaaaa aagtcgagcc gaaatcctgt 660  
agtggaggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720  
cttgagtctg gaggaggcct agtccagcct ggaggggagcc tgcgtctctc ttgtgcagta 780  
agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840  
ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900  
ggaagggtta caattagccg ggacaatagc aaaaacaccg tgtatctcca aatgaactcc 960  
ttgcgagcag aggacacggc ggtgtactat tgtgctcgca ctgtcccagg ttatagcact 1020  
gcaccctact tcgatctgtg gggacaaggg accctgggtga ctgtttcaag ttaa 1074

<210> 23  
<211> 1089  
<212> DNA  
<213> Artificial

<220>  
<223> Light chain A26-645(gL4) including E.coli OmpA leader

<400> 23  
atgaaaaaga cagctatcgc aattgcagtg gcgttggtg gtttcgcgac cgttgcgcaa 60  
gctgatatcc agatgaccca gagcccaagc agtctctccg ccagcgtagg cgatcgtgtg 120  
actattacct gtcgtgcaac ccagagcatc tacaacgctc tggcttggtg tcagcagaaa 180  
ccgggtaaag cgccaaaact cctgatctac aacgcgaaca ctctgcatac tgggtgttccg 240  
tctcgtttct ctgcgtctgg ttctggtacg gactctactc tgaccatctc ctctctccag 300  
ccggaagatt tcgcgacctt ctactgccag cagtactacg attacccact gacgtttggt 360  
ggtggtacca aagttgagat caaacgtacg gttgcagctc catccgtctt catctttcca 420

|                                                                      | eol-f-seq1 |      |
|----------------------------------------------------------------------|------------|------|
| ccgtctgacg aacagctcaa atctgggtact gcttctgtcg tttgcctcct gaacaacttc   |            | 480  |
| tatccgcgtg aagcgaaagt ccagtggaaa gtcgacaacg cactccagtc tggtaactct    |            | 540  |
| caggaatctg tgaccgaaca ggactccaaa gactccacct actctctgtc tagcaccctg    |            | 600  |
| actctgtcca aagcagacta cgagaaacac aaagtgtacg cttgcgaagt taccatcag     |            | 660  |
| ggctctgagct ctccgggttac caaatccttt aatagagggg agtgtggtgg cgggtggcagt |            | 720  |
| gggtgggtggag gttccggagg tggcgggttca gacatacaaa tgaccagag tccttcatcg  |            | 780  |
| gtatccgcgt ccgttggcga taggggtgact attacatgtc aaagctctcc tagcgtctgg   |            | 840  |
| agcaattttc tatcctggta tcaacagaaa ccggggaagg ctccaaaact tctgatttat    |            | 900  |
| gaagcctcga aactcaccag tggagttccg tcaagattca gtggctctgg atcagggaca    |            | 960  |
| gacttcacgt tgacaatcag ttcgctgcaa ccagaggact ttgcgaccta ctattgtggt    |            | 1020 |
| ggagggttaca gtagcataag tgatacgaca tttgggtgcg gtactaaggt ggaaatcaaa   |            | 1080 |
| cgtaaccta                                                            |            | 1089 |

<210> 24  
 <211> 1026  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Light chain A26-645(gL4)

|                                                                      |  |      |
|----------------------------------------------------------------------|--|------|
| <400> 24                                                             |  |      |
| gatatccaga tgaccagag cccaagcagt ctctccgcca gcgtaggcga tctgtgtgact    |  | 60   |
| attacctgtc gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg     |  | 120  |
| ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcatactgg tgttccgtct    |  | 180  |
| cgtttctctg cgtctggttc tgggtacggac tctactctga ccatctcctc tctccagccg   |  | 240  |
| gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttgggtgg    |  | 300  |
| ggtagcaaaag ttgagatcaa acgtacggtt gcagctccat ccgtcttcat ctttccaccg   |  | 360  |
| tctgacgaac agctcaaadc tgggtactgct tctgtcggtt gcctcctgaa caacttctat   |  | 420  |
| ccgcgtgaag cgaaagtcca gtggaaagtc gacaacgcac tccagtctgg taactctcag    |  | 480  |
| gaatctgtga ccgaacagga ctccaaagac tccacctact ctctgtctag caccctgact    |  | 540  |
| ctgtccaaag cagactacga gaaacacaaa gtgtacgctt gcgaagttac ccatcagggt    |  | 600  |
| ctgagctctc cggttaccaa atcctttaat agaggggagt gtgggtggcg tggcagtggt    |  | 660  |
| gggtggagggt ccggagggtgg cggttcagac atacaaatga cccagagtc ttcacggtga   |  | 720  |
| tccgcgtccg ttggcgatag ggtgactatt acatgtcaaa gctctcctag cgtctggagc    |  | 780  |
| aattttctat cctggtatca acagaaaccg gggagggctc caaaacttct gatttatgaa    |  | 840  |
| gcctcgaaac tcaccagtgg agttccgtca agattcagtg gctctggatc agggacagac    |  | 900  |
| ttcacgttga caatcagttc gctgcaacca gaggactttg cgacctacta ttgtggtgga    |  | 960  |
| ggttacagta gcataagtga tacgacattt ggggtgcggtga ctaagggtgga aatcaaaccg |  | 1020 |

<210> 25  
 <211> 1131  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain A26-645(gH5) including B72.3 leader sequence

<400> 25  
 atggaatggg cctgggtcct cctgtttttc ctttctgtca caaccggggg gcacagcgag 60  
 gtgcagctcg tcgagtctgg aggcgggctt gtccagcctg gaggagacct gcgtctctct 120  
 tgtgcagcaa gcggtttcac gttcaccaac tacggatatcc actggattcg tcaggcacca 180  
 ggtaaagggtc tggaatgggt agcctctatc tctccgtctg gtgggtctgac gtactaccgt 240  
 gactctgtca aaggctcgttt caccatctct cgtgatgacg cgaaaaactc tccgtacctg 300  
 cagatgaact ctctgcgtgc agaagatacc gcagtgtact actgcgctac tgggtggtgaa 360  
 ggtatcttcg actactgggg tcagggtacc ctggtaactg tctcaagcgc ttctacaaag 420  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 480  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc 540  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctctgg actctactcc 600  
 ctgagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac 660  
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttggtcc 720  
 ggaggtggcg gttccggagg tggcgggtacc ggtggcgggt gatccgaagt ccagctgctt 780  
 gaatccggag gcggactcgt gcagcccgga ggcagtcttc gcttgtcctg cgctgtatct 840  
 ggaatcgacc tgagcaatta cgccatcaac tgggtgagac aggcacctgg gaaatgcctc 900  
 gaatggatcg gcattatatg ggctagtggg acgacctttt atgctacatg ggcgaagggt 960  
 agattcacia tctcacggga taatagtaag aacacagtgt acctgcagat gaactccctg 1020  
 cgagcagagg ataccgccgt ttactattgt gctcgactg tcccagggtta tagcactgca 1080  
 ccctactttg atctgtgggg gcagggcact ctggtcaccg tctcgagttg a 1131

<210> 26  
 <211> 1074  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain A26-645(gH5)

<400> 26  
 gaggtgcagc tcgtcgagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc 60  
 tcttgtgcag caagcggttt cacgttcacc aactacggtc tccactggat tcgtcaggca 120  
 ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctgggtggtct gacgtactac 180  
 cgtgactctg tcaaagggtc tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240

|             |            |             |            |             |            | eof-seq1 |      |
|-------------|------------|-------------|------------|-------------|------------|----------|------|
| ctgcagatga  | actctctgcg | tgcagaagat  | accgcagtgt | actactgcgc  | tactggtggt |          | 300  |
| gaaggatatct | tcgactactg | gggtcaggggt | accctggtaa | ctgtctcaag  | cgcttctaca |          | 360  |
| aagggcccat  | cggtcttccc | cctggcaccc  | tcctccaaga | gcacctctgg  | gggcacagcg |          | 420  |
| gccctgggct  | gcctggtcaa | ggactacttc  | cccgaaccgg | tgacgggtgtc | gtggaactca |          | 480  |
| ggcgccctga  | ccagcggcgt | gcacaccttc  | ccggctgtcc | tacagtcctc  | tggactctac |          | 540  |
| tccctcagca  | gcgtggtgac | cgtgccctcc  | agcagcttgg | gcaccagac   | ctacatctgc |          | 600  |
| aacgtgaatc  | acaagcccag | caacaccaag  | gtggacaaga | aagttgagcc  | caaatcttgt |          | 660  |
| tccggagggtg | gcggttccgg | aggtggcgggt | accggtggcg | gtggatccga  | agtccagctg |          | 720  |
| cttgaatccg  | gaggcggact | cgtgcagccc  | ggaggcagtc | ttcgcttgtc  | ctgcgctgta |          | 780  |
| tctggaatcg  | acctgagcaa | ttacgccatc  | aactgggtga | gacaggcacc  | tgggaaatgc |          | 840  |
| ctcgaatgga  | tcggcattat | atgggctagt  | gggacgacct | tttatgctac  | atgggcgaag |          | 900  |
| ggtagattca  | caatctcacg | ggataatagt  | aagaacacag | tgtacctgca  | gatgaactcc |          | 960  |
| ctgcgagcag  | aggataccgc | cgtttactat  | tgtgctcgca | ctgtcccagg  | ttatagcact |          | 1020 |
| gcaccctact  | ttgatctgtg | ggggcagggc  | actctggtca | ccgtctcgag  | ttga       |          | 1074 |

<210> 27  
 <211> 1086  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Light chain A26-645(gL4) including B72.3 leader sequence

|            |                                                             |
|------------|-------------------------------------------------------------|
| <400> 27   |                                                             |
| atgtcagttc | ccacacaggt gctgggcctg cttctgttgt ggctcaccga tgctaggtgt 60   |
| gatatccaga | tgaccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 120   |
| attacctgtc | gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg 180   |
| ggtaaagcgc | caaaactcct gatctacaac gcgaacactc tgcataaccgg tgttccgtct 240 |
| cgtttctctg | cgtctggttc tggtagcgac tctactctga ccatctcctc tctgcagccg 300  |
| gaagatttcg | cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 360  |
| ggtaccaaag | ttgagatcaa acgtacgggt gctgcacat ctgtcttcat cttccccca 420    |
| tctgatgagc | agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac 480  |
| cctagagagg | caaagtcca gtggaagggt gataacgcc ttcaatccgg aaactcccag 540    |
| gagagtgtca | ctgagcagga ctcaaaggac tccacctata gccttagcag cacactgaca 600  |
| ctgagcaagg | ctgactacga gaaacacaag gtctacgcct gcgaagtgac acatcaaggc 660  |
| ctgagctcac | ccgtgacaaa gagctttaac aggggagagt gtggtggagg tggctctggc 720  |
| ggtggtggct | ccggaggcgg aggaagcgac atccagatga cccagagccc ttcctctgta 780  |
| agcgccagtg | tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc 840  |
| aattttctat | cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa 900  |

eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtggggtc tggaactgac | 960  |
| tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga  | 1020 |
| ggttacagta gcataagtga tacgacattt ggatgcgga ctaaagtgga aatcaagcgt   | 1080 |
| acctga                                                             | 1086 |

<210> 28  
 <211> 1026  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Light chain A26-645(gL4)

|                                                                    |      |
|--------------------------------------------------------------------|------|
| <400> 28                                                           |      |
| gatatccaga tgaccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact   | 60   |
| attacctgtc gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg   | 120  |
| ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataccgg tgttccgtct  | 180  |
| cgtttctctg cgtctggttc tggtagcgac tctactctga ccactctcctc tctgcagccg | 240  |
| gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt  | 300  |
| ggtaccaaag ttgagatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccccca  | 360  |
| tctgatgagc agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac  | 420  |
| cctagagagg ccaaagtcca gtggaagggtg gataacgccc ttcaatccgg aaactcccag | 480  |
| gagagtgtca ctgagcagga ctcaaaggac tccacctata gccttagcag cacactgaca  | 540  |
| ctgagcaagg ctgactacga gaaacacaag gtctacgcct gcgaagtgac acatcaaggc  | 600  |
| ctgagctcac ccgtgacaaa gagctttaac aggggagagt gtggtggagg tggctctggc  | 660  |
| ggtggtggct ccggaggcgg aggaagcgac atccagatga cccagagccc ttcctctgta  | 720  |
| agcgccagtg tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc  | 780  |
| aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa  | 840  |
| gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtggggtc tggaactgac | 900  |
| tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga  | 960  |
| ggttacagta gcataagtga tacgacattt ggatgcgga ctaaagtgga aatcaagcgt   | 1020 |
| acctga                                                             | 1026 |

<210> 29  
 <211> 121  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Heavy chain variable domain of anti-albumin antibody (no ds)

<400> 1

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

eo1f-seq1

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

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys  
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 30  
<211> 121  
<212> PRT  
<213> Artificial

<220>  
<223> Heavy chain variable domain of anti-albumin antibody (ds)  
<400> 2

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr  
20 25 30

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys  
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser

## eolf-seql

115

120

<210> 31  
 <211> 112  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Light chain variable domain of anti-albumin antibody (no ds)  
 <400> 3

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
 20 25 30

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile  
 85 90 95

Ser Asp Thr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105 110

<210> 32  
 <211> 112  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Light chain variable domain of anti-albumin antibody (ds)  
 <400> 4

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
 20 25 30

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln  
 Page 21



eof-seq1

ccgtcccggt tctctggctc tggctctggt acggacttca ctctgaccat ctctctctctg 660  
cagccggaag actttgcaac gtactactgc ggtggtggtt actcttccat ctctgacacc 720  
acgttcggtg gaggcaccaa agttgaaatc aaacgtacgc atcaccatca ccatcaccat 780  
caccatcac 789

<210> 36  
<211> 263  
<212> PRT  
<213> Artificial

<220>  
<223> 645 gH5gL4

<400> 14

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr  
20 25 30

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys  
50 55 60

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln  
130 135 140

Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val  
145 150 155 160

Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser  
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu  
180 185 190

Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
Page 23

eo1f-seq1

195

200

205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
210 215 220

Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr  
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr His His His  
245 250 255

His His His His His His His  
260

<210> 37  
<211> 789  
<212> DNA  
<213> Artificial

<220>  
<223> 645 gH5gL4ds

<400> 15  
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60  
tcttgtgcag taagcggcat cgacctgtcc aactacgcga ttaactgggt acgtcaggca 120  
ccgggtaaata gcctggaatg gatcggcatc atctgggcct ctggtacgac cttctacgct 180  
acttgggcca aaggtcgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240  
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg taccgttccg 300  
ggctattcta ctgcaccgta cttcgacctg tggggtcagg gtactctgggt taccgtctcg 360  
agtggagggtg gcggttcttg cggtggcggg tccgggtggcg gtggatcggg aggtggcggg 420  
tctgatatcc agatgaccca gagtccaagc agtggtttccg ccagcgtagg cgatcgtgtg 480  
actattacct gtcagtcctc tccgagcgtt tgggtccaact tcctgagctg gtaccagcag 540  
aaaccgggta aagccccgaa actgctgatac tacgaggcgt ctaaactgac ctctgggtgta 600  
ccgtcccgtt tctctggctc tggctctgggt acggacttca ctctgaccat ctctctctctg 660  
cagccggaag actttgcaac gtactactgc ggtgggtgggt actcttccat ctctgacacc 720  
acgttcgggt gtggcaccaa agttgaaatc aaacgtacgc atcaccatca ccatcaccat 780  
caccatcac 789

<210> 38  
<211> 263  
<212> PRT  
<213> Artificial

<220>  
<223> 645 gH5gL4ds

<400> 16

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

| eolf-seq1  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 1          |            |            |            | 5          |            |            |            | 10         |            |            |            | 15         |            |            |            |
| Ser        | Leu        | Arg        | Leu<br>20  | Ser        | Cys        | Ala        | Val        | Ser<br>25  | Gly        | Ile        | Asp        | Leu        | Ser<br>30  | Asn        | Tyr        |
| Ala        | Ile        | Asn<br>35  | Trp        | Val        | Arg        | Gln        | Ala<br>40  | Pro        | Gly        | Lys        | Cys        | Leu<br>45  | Glu        | Trp        | Ile        |
| Gly        | Ile<br>50  | Ile        | Trp        | Ala        | Ser        | Gly<br>55  | Thr        | Thr        | Phe        | Tyr        | Ala<br>60  | Thr        | Trp        | Ala        | Lys        |
| Gly<br>65  | Arg        | Phe        | Thr        | Ile        | Ser<br>70  | Arg        | Asp        | Asn        | Ser        | Lys<br>75  | Asn        | Thr        | Val        | Tyr        | Leu<br>80  |
| Gln        | Met        | Asn        | Ser        | Leu<br>85  | Arg        | Ala        | Glu        | Asp        | Thr<br>90  | Ala        | Val        | Tyr        | Tyr        | Cys<br>95  | Ala        |
| Arg        | Thr        | Val        | Pro<br>100 | Gly        | Tyr        | Ser        | Thr        | Ala<br>105 | Pro        | Tyr        | Phe        | Asp        | Leu<br>110 | Trp        | Gly        |
| Gln        | Gly        | Thr<br>115 | Leu        | Val        | Thr        | Val        | Ser<br>120 | Ser        | Gly        | Gly        | Gly        | Gly<br>125 | Ser        | Gly        | Gly        |
| Gly        | Gly<br>130 | Ser        | Gly        | Gly        | Gly        | Gly<br>135 | Ser        | Gly        | Gly        | Gly        | Gly<br>140 | Ser        | Asp        | Ile        | Gln        |
| Met<br>145 | Thr        | Gln        | Ser        | Pro        | Ser<br>150 | Ser        | Val        | Ser        | Ala        | Ser<br>155 | Val        | Gly        | Asp        | Arg        | Val<br>160 |
| Thr        | Ile        | Thr        | Cys        | Gln<br>165 | Ser        | Ser        | Pro        | Ser        | Val<br>170 | Trp        | Ser        | Asn        | Phe        | Leu<br>175 | Ser        |
| Trp        | Tyr        | Gln        | Gln<br>180 | Lys        | Pro        | Gly        | Lys        | Ala<br>185 | Pro        | Lys        | Leu        | Leu        | Ile<br>190 | Tyr        | Glu        |
| Ala        | Ser        | Lys<br>195 | Leu        | Thr        | Ser        | Gly        | Val<br>200 | Pro        | Ser        | Arg        | Phe        | Ser<br>205 | Gly        | Ser        | Gly        |
| Ser        | Gly<br>210 | Thr        | Asp        | Phe        | Thr        | Leu<br>215 | Thr        | Ile        | Ser        | Ser        | Leu<br>220 | Gln        | Pro        | Glu        | Asp        |
| Phe<br>225 | Ala        | Thr        | Tyr        | Tyr        | Cys<br>230 | Gly        | Gly        | Gly        | Tyr        | Ser<br>235 | Ser        | Ile        | Ser        | Asp        | Thr<br>240 |
| Thr        | Phe        | Gly        | Cys        | Gly<br>245 | Thr        | Lys        | Val        | Glu        | Ile<br>250 | Lys        | Arg        | Thr        | His        | His<br>255 | His        |
| His        | His        | His        | His<br>260 | His        | His        | His        |            |            |            |            |            |            |            |            |            |