

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

eolf-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
Page 4

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

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 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

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 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

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

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

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

Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys Leu Thr Ser Gly

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 tttcacgttc accaactacg gtatccactg gattcgtcag 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 gcaactgtcc 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 gggtcagggt accctggtaa ctgtctcgag cgcttctaca 360
aagggcccaa gcgttttccc actggctccg tcctctaaat ccacctctgg tggtagcgct 420
gcactgggtt gcctgggtgaa 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
ggaagggttta 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 tcgcgacctc ctactgccag cagtactacg attacccact gacgtttggt 360
ggtggtacca aagttgagat caaacgtacg gttgcagctc catccgtctt catctttcca 420

	eolf-seq1	
ccgtctgacg aacagctcaa atctggtact 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
ggtctgagct ctccggttac caaatccttt aatagagggg agtgtggtgg cgggtggcagt		720
ggtggtggag gttccggagg tggcgggttca gacatacaaa tgaccagag tccttcatcg		780
gtatccgcgt ccgttggcga tagggtgact 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
ggaggttaca gtagcataag tgatacgaca tttgggtgcg gtactaaggt ggaaatcaaa		1080
cgtaacataa		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 gtgcaaccca gagcatctac aacgctctgg cttggtatca gcagaaaccg		120
ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcatactgg tgttccgtct		180
cgtttctctg cgtctggttc tggtagcgac tctactctga ccatctcctc tctccagccg		240
gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt		300
ggtaccaaag ttgagatcaa acgtacggtt gcagctccat ccgtcttcat ctttccaccg		360
tctgacgaac agctcaaadc tggtagtctg 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 gtggtggcgg tggcagtggt		660
ggtggagggt ccggagggtg cggttcagac atacaaatga ccagaggtcc ttcacggtga		720
tccgcgtccg ttggcgatag ggtgactatt acatgtcaaa gctctcctag cgtctggagc		780
aattttctat cctggtatca acagaaaccg gggagggctc caaaacttct gatttatgaa		840
gcctcgaaac tcaccagtgg agttccgtca agattcagt gctctggatc agggacagac		900
ttcacgttga caatcagttc gctgcaacca gaggactttg cgacctacta ttgtggtgga		960
ggttacagta gcataagtga tacgacattt ggggtgcggt ctaagggtgga aatcaaacgt		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
 ctcagcagcg 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	gggtcagggt	accctggtaa	ctgtctcaag	cgcttctaca	360
aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	420
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	480
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	tggactctac	540
tccctcagca	gcgtgggtgac	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 tgcataccgg tgttccgtct 240
cgtttctctg	cgtctggttc tggtagcgac tctactctga ccatctcctc tctgcagccg 300
gaagatttcg	cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 360
ggtaccaaag	ttgagatcaa acgtacgggt gctgcaccat ctgtcttcat cttcccccca 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	

co1f-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
ccgggtaaatt gcctggaatg gatcggcatc atctgggcct ctggtacgac cttctacgct 180
acttgggcca aaggtcgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg taccgttccg 300
ggctattcta ctgcaccgta cttcgacctg tggggtcagg gtactctggt 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 tggctctggt acggacttca ctctgaccat ctctctctctg 660
cagccggaag actttgcaac gtactactgc ggtgggtggtt 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

