

SEQUENCE LISTING

<110> UCB Biopharma SPRL

<120> Method

<130> PF0018W0

<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

<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

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

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
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

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

<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		
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
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

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

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
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
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

<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
 gctgaagtgc agctgggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120
 ctctcttgtg 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
 ggtgaaggta 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 ctcttgtgca 840
 gtaagcggca tcgacctgag caattacgcc atcaactggg tgagacaagc tccggggaag 900
 tgtttagaat ggatcggtat aatatgggcc agtgggacga ctttttatgc tacatgggcg 960
 aaaggaaggt ttacaattag ccgggacaat agcaaaaaca ccgtgtatct ccaaataaac 1020
 tccttgcgag cagaggacac ggcggtgtac tattgtgctc gcactgtccc aggttatagc 1080
 actgcaccct acttcgatct gtgggggaaa gggaccctgg tgactgtttc aagttaa 1137

<210> 22
<211> 1074
<212> DNA
<213> Artificial

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

<400> 22
gaagttcagc tggtcgagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc 60
tcttgtgcag caagcggttt cacgttcacc aactacggtg tccactggat tcgtcaggca 120
ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac 180
cgtgactctg tcaaaggctg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240
ctgcaaatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt 300
gaaggtatct tcgactactg gggtcagggt accctggtaa ctgtctcgag cgcttctaca 360
aagggcccaa gcgttttccc actggctccg tcctctaaat ccacctctgg tggtagggct 420
gcactgggtt gcctggtgaa agactacttc ccagaaccag ttaccgtgtc ttggaactct 480
gggtgcactga cctctggtgt tcacaccttt ccagcagttc tccagtcttc tggctctgtac 540
tccctgtcta gcgtgggttac cgttccgtct tcttctctgg gtactcagac ctacatctgc 600
aacgtcaacc acaaaccgtc caacaccaag gtcgacaaaa aagtcgagcc gaaatcctgt 660
agtggagggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720
cttgagtctg gaggaggcct agtccagcct ggaggagacc tgcgtctctc ttgtgcagta 780
agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840
ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900
ggaaggttta 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 gcgttggctg gtttcgcgac cgttgcgcaa	60
gctgatatcc agatgacca gagcccaagc agtctctccg ccagcgtagg cgatcgtgtg	120
actattacct gtcgtgcaac ccagagcatc tacaacgctc tggcttggtg tcagcagaaa	180
ccgggtaaag cgccaaaact cctgatctac aacgcgaaca ctctgcatac tgggtgttccg	240
tctcgtttct ctgcgtctgg ttctgggtacg gactctactc tgaccatctc ctctctccag	300
ccggaagatt tcgcgacctg ctactgccag cagtactacg attaccact gacgtttggt	360
ggtggtacca aagttgagat caaacgtacg gttgcagctc catccgtctt catctttcca	420
ccgtctgacg aacagctcaa atctgggtact gcttctgtcg ttgcctcct gaacaacttc	480
tatccgcgtg aagcgaaagt ccagtggaaa gtcgacaacg cactccagtc tggtaactct	540
caggaatctg tgaccgaaca ggactccaaa gactccacct actctctgtc tagcacctg	600
actctgtcca aagcagacta cgagaaacac aaagtgtacg cttgcgaagt taccatcag	660
ggtctgagct ctccggttac caaatccttt aatagagggg agtgtggtgg cgggtggcagt	720
ggtggtggag gttccggagg tggcggttca gacatacaaa tgaccagag tccttcacg	780
gtatccgcgt ccgttggcga tagggtgact attacatgtc aaagctctcc tagcgtctgg	840
agcaattttc tctctggtg tcaacagaaa ccggggaagg ctccaaaact tctgatttat	900
gaagcctcga aactcaccag tggagttccg tcaagattca gtggctctgg atcagggaca	960
gacttcacgt tgacaatcag ttcgctgcaa ccagaggact ttgcgacctg ctattgtggt	1020
ggaggttaca gtagcataag tgatacgaca tttgggtgcg gtactaaggt ggaaatcaaa	1080
cgtacctaa	1089

<210> 24

<211> 1026

<212> DNA

<213> Artificial

<220>

<223> Light chain A26-645(gL4)

<400> 24

gatatccaga tgacccagag cccaagcagt ctctccgcca gcgtaggcga tcgtgtgact	60
attacctgtc gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg	120
ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcatactgg tgttccgtct	180
cgtttctctg cgtctggttc tggtagggac tctactctga ccatctcctc tctccagccg	240
gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt	300
ggtaccaaag ttgagatcaa acgtacgggt gcagctccat ccgtcttcat ctttccaccg	360
tctgacgaac agctcaaadc tggtagtgct tctgtcgttt 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 tggcagtgggt	660
ggtggagggt ccggagggtg cggttcagac atacaaatga cccagagtcc ttcacggtgta	720
tccgcgtccg ttggcgatag ggtgactatt acatgtcaaa gctctcctag cgtctggagc	780
aattttctat cctggtatca acagaaaccg gggaaggctc caaaacttct gatttatgaa	840
gcctcgaaac tcaccagtgg agttccgtca agattcagtg gctctggatc agggacagac	900
ttcacgttga caatcagttc gctgcaacca gaggactttg cgacctacta ttgtggtgga	960
ggttacagta gcataagtga tacgacattt gggtgcggtg ctaaggtgga aatcaaacgt	1020
acctaa	1026

<210> 25

<211> 1131

<212> DNA

<213> Artificial

<220>

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

<400> 25

atggaatggg	cctgggtctt	cctgtttttc	ctttctgtca	caaccggggt	gcacagcgag	60
gtgcagctcg	tcgagtcctg	aggcgggctt	gtccagcctg	gaggagacct	gcgtctctct	120
tgtgcagcaa	gcggtttcac	gttcaccaac	tacggtatcc	actggattcg	tcaggcacca	180
ggtaaaggtc	tggaatgggt	agcctctatc	tctccgtctg	gtggctctgac	gtactaccgt	240
gactctgtca	aaggctgttt	caccatctct	cgtgatgacg	cgaaaaactc	tccgtacctg	300
cagatgaact	ctctgcgtgc	agaagatacc	gcagtgtact	actgcgctac	tggtggtgaa	360
ggatatcttc	actactgggg	tcagggtacc	ctggtaactg	tctcaagcgc	ttctacaaag	420
ggcccatcgg	tcttccccct	ggcacctcc	tccaagagca	cctctggggg	cacagcggcc	480
ctgggctgcc	tggtcaagga	ctacttcccc	gaaccgggtga	cggtgtcgtg	gaactcaggc	540
gccctgacca	gcggcgtgca	caccttcccg	gctgtcctac	agtcctctgg	actctactcc	600
ctcagcagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	660
gtgaatcaca	agcccagcaa	caccaagggt	gacaagaaag	ttgagcccaa	atcttgttcc	720
ggaggtggcg	gttccggagg	tggcgggtacc	ggtggcggtg	gatccgaagt	ccagctgctt	780
gaatccggag	gcggactcgt	gcagcccgga	ggcagtcctc	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	gctcgcactg	tcccaggtta	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
ctggaggggag	cctgcgtctc
	60

tcttgtgcag caagcggttt cacgttcacc aactacggta tccactggat tcgtcaggca	120
ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac	180
cgtgactctg tcaaaggtcg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac	240
ctgcagatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt	300
gaaggtatct tcgactactg gggtcagggt accctggtaa ctgtctcaag cgcttctaca	360
aagggcccat cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc cgggctgtcc tacagtcttc tggactctac	540
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
tccggaggtg gcggttccgg aggtggcggg 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 acgtacggtg gctgcaccat ctgtcttcat cttccccca	420
tctgatgagc agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac	480
cctagagagg ccaaagtcca gtggaagggtg gataacgccc 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 ccagagccc ttcctctgta	780
agcgccagtg tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc	840
aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa	900
gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac	960
tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga	1020
ggttacagta gcataagtga tacgacattt ggatgcggca ctaaagtgga aatcaagcgt	1080
acctga	1086

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

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

<400> 28	
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact	60
attacctgtc gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg	120
ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataaccgg tgttccgtct	180
cgtttctctg cgtctggttc tggtagcgac tctactctga ccatctcctc tctgcagccg	240

gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt	300
ggtaccaaag ttgagatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccccca	360
tctgatgagc agttgaagtc tggcactgcc tctgtttgtgt gcctgctgaa taacttctac	420
cctagagagg ccaaagtcca gtggaaggtg 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 acctgcaaaa gctccccttc agtctggtcc	780
aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa	840
gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac	900
tttaccctga caatctctc actccagccc gaggacttcg ccacctatta ctgcggtgga	960
ggttacagta gcataagtga tacgacattt ggatgcggca 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	

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
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
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> 33
<211> 16
<212> PRT
<213> Artificial

<220>
<223> Linker 1

<400> 5

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser

1 5 10 15

<210> 34
 <211> 15
 <212> PRT
 <213> Artificial

<220>
 <223> Linker 2

<400> 6

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

<210> 35
 <211> 789
 <212> DNA
 <213> Artificial

<220>
 <223> 645 gH5gL4

<400> 13

gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc	60
tcttgtgcag taagcggcat cgacctgtcc aactacgcga ttaactgggt acgtcaggca	120
ccgggtaaag gtctggaatg gatcggcatc atctgggcct ctggtacgac cttctacgct	180
acttgggccca aaggtcgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg	240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg taccgttccg	300
ggctattcta ctgcaccgta cttcgacctg tggggtcagg gtactctggt taccgtctcg	360
agtggaggtg gcggttctgg cggtggcggt tccggtggcg gtggatcggg aggtggcggt	420
tctgatatcc agatgacca gagtccaagc agtgtttccg ccagcgtagg cgatcgtgtg	480
actattacct gtcagtcctc tccgagcgtt tgggtccaact tcctgagctg gtaccagcag	540
aaaccgggta aagccccgaa actgctgata tacgaggcgt ctaaactgac ctctggtgta	600
ccgtcccgtt tctctggctc tggctctggt acggacttca ctctgacat ctcctctctg	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
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 aactacgca ttaactgggt acgtcaggca 120
ccgggtaaatt gcctggaatg gatcggcatc atctgggcct ctggtacgac cttctacgct 180
acttgggccca aaggtcgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240

```

cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg taccgttccg      300
ggctattcta ctgcaccgta cttcgacctg tggggtcagg gtactctggt taccgtctcg      360
agtggaggtg gcggttcttg cggtggcggt tccggtggcg gtggatcggg aggtggcggt      420
tctgatatcc agatgacca gagtccaagc agtgtttccg ccagcgtagg cgatcgtgtg      480
actattacct gtcagtcctc tccgagcgtt tgggtccaact tcctgagctg gtaccagcag      540
aaaccgggta aagccccgaa actgctgata tacgaggcgt ctaaactgac ctctggtgta      600
ccgtcccgtt tctctggctc tggctctggt acggacttca ctctgaccat ctctctcttg      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
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 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
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 Cys Gly Thr Lys Val Glu Ile Lys Arg Thr His His His
245 250 255

His His His His His His His
260