

eolf-seq1

SEQUENCE LISTING

<110> UCB BIOPHARMA SPRL

<120> METHOD FOR PROTEIN PURIFICATION

<130> PF0017 WO

<150> GB1506868.7

<151> 2015-04-22

<160> 38

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H1

<400> 1

Asn Tyr Gly Ile His
1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> CDR-H2

<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

eolf-seql

<211> 8
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<220>
<223> CDR-H3

<400> 3

Gly Gly Glu Gly Ile Phe Asp Tyr
1 5

<210> 4
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<213> Artificial Sequence

<220>
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<400> 4

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

<210> 5
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<223> CDR-L2

<400> 5

Asn Ala Asn Thr Leu His Thr
1 5

<210> 6
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eolf-seql

<400> 6

Gln Gln Tyr Tyr Asp Tyr Pro Leu Thr
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<210> 7

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> LV region of Ab 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

eolf-seql

<213> Artificial Sequence

<220>

<223> HV of Ab 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 Sequence

<220>

<223> LC of Fab component

<400> 9

eolf-seql

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

eolf-seql

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
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC of 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

eolf-seql

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 Sequence

<220>

<223> HC 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

eolf-seql

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 Sequence

<220>
<223> LC 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

									eolf-seql					
65					70				75				80	
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gly	Gly	Tyr	Ser	Ser
				85					90				95	Ile

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 Sequence

<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 Sequence

<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 Sequence

<220>
 <223> A26 H(g4s, g4t, g4s)-645ds Fv(Gh5)

<400> 15

eolf-seql

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

eolf-seql

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

eolf-seql

<213> Artificial Sequence

<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
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eolf-seql

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
305 310 315 320

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

eolf-seql

<211> 119
 <212> PRT
 <213> Artificial Sequence

<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 Sequence

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

eolf-seql

<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
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 Sequence

<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

eolf-seql

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

eolf-seql

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 Sequence

<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

eolf-seql

1	5	10	15
Asp	Arg	Val	Thr
	20	Ile	Thr
		Cys	Arg
		Ala	Thr
		25	Gln
		Ser	Ile
			30
		Tyr	Asn
			Ala
Leu	Ala	Trp	Tyr
	35	Gln	Gln
		Lys	Pro
		40	Gly
		Lys	Ala
		Pro	Lys
			45
		Leu	Leu
			Ile
Tyr	Asn	Ala	Asn
	50	Thr	Leu
		His	Thr
		55	Gly
		Val	Pro
		Ser	Arg
			60
		Phe	Ser
			Ala
Ser	Gly	Ser	Gly
	65	Thr	Asp
		Ser	Thr
		Leu	Thr
		70	Ile
		Ser	Ser
		Leu	Gln
			80
		Pro	
Glu	Asp	Phe	Ala
		85	Thr
		Tyr	Tyr
		Cys	Gln
			90
		Gln	Tyr
		Tyr	Asp
		Tyr	Pro
			95
		Leu	
Thr	Phe	Gly	Gly
		100	Gly
		Thr	Lys
		Val	Val
		Glu	Ile
		105	Lys
		Arg	Thr
			110
		Val	Ala
			Ala
Pro	Ser	Val	Phe
		115	Ile
		Phe	Pro
		Pro	Pro
		Ser	Asp
		Glu	Gln
		Leu	Lys
			125
		Ser	Gly
Thr	Ala	Ser	Val
		130	Val
		Cys	Leu
		135	Leu
		Asn	Asn
		Phe	Tyr
			140
		Pro	Arg
		Glu	Ala
Lys	Val	Gln	Trp
	145	Lys	Val
		Asp	Asn
		Ala	Leu
		150	Gln
		Ser	Gly
			155
		Asn	Ser
			160
Glu	Ser	Val	Thr
		165	Glu
		Gln	Asp
		Ser	Lys
		Asp	Ser
		170	Thr
		Tyr	Ser
			175
		Leu	Ser
Ser	Thr	Leu	Thr
		180	Leu
		Ser	Lys
		Ala	Asp
		185	Tyr
		Glu	Lys
		His	Lys
			190
		Val	Tyr
Ala	Cys	Glu	Val
		Thr	His
		Gln	Gly
		Leu	Ser
		Ser	Pro
		Val	Thr
		Lys	Ser

eolf-seql

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
340

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

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

<400> 21

eolf-seql

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gctgaagttc agctggtcga gtctggaggc gggcttggtc agcctggagg gagcctgcgt	120
ctctcttggtg cagcaagcgg tttcacgttc accaactacg gtatccactg gattcgtcag	180
gcaccaggta aaggtctgga atgggtagcc tctatctctc cgtctgggtg 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 ctcttggtgca	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 gtggggacaa gggaccctgg tgactgtttc aagttaa	1137

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

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

<400> 22

eolf-seq1

gaagttcagc tggtcgagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc	60
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ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac	180
cgtgactctg tcaaaggctg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac	240
ctgcaaatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt	300
gaaggatatct tcgactactg gggtcagggt accctggtaa ctgtctcgag cgcttctaca	360
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gcactgggtt gcctggtgaa agactacttc ccagaaccag ttaccgtgtc ttggaactct	480
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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 Sequence

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

<400> 23
 atgaaaaaga cagctatcgc aattgcagtg gcgttggctg gtttcgacac cgttgcgcaa 60

eolf-seql

gctgatatcc agatgacca gagcccaagc agtctctccg ccagcgtagg cgatcgtgtg	120
actattacct gtcgtgcaac ccagagcatc tacaacgctc tggcttggtg tcagcagaaa	180
ccgggtaaag cgccaaaact cctgatctac aacgcgaaca ctctgcatac tgggtgttccg	240
tctcgtttct ctgctgtctgg ttctggtacg gactctactc tgaccatctc ctctctccag	300
ccggaagatt tcgcgacctg ctactgccag cagtactacg attacccact gacgtttggt	360
ggtggtacca aagttgagat caaacgtacg gttgcagctc catccgtctt catctttcca	420
ccgtctgacg aacagctcaa atctggtact gcttctgtcg ttgacctcct gaacaacttc	480
tatccgcgtg aagcgaaagt ccagtggaaa gtcgacaacg cactccagtc tggtaactct	540
caggaatctg tgaccgaaca ggactccaaa gactccacct actctctgtc tagcaccctg	600
actctgtcca aagcagacta cgagaaacac aaagtgtacg cttgcgaagt tacccatcag	660
ggtctgagct ctccggttac caaatccttt aatagagggg agtgtggtgg cggtggcagt	720
ggtggtggag gttccggagg tggcggttca gacatacaaa tgaccagag tccttcatcg	780
gtatccgcgt ccgttggcga tagggtgact attacatgtc aaagctctcc tagcgtctgg	840
agcaattttc tatcctggta tcaacagaaa ccggggaagg ctccaaaact tctgatttat	900
gaagcctcga aactcaccag tggagtccg tcaagattca gtggctctgg atcagggaca	960
gacttcacgt tgacaatcag ttcgctgcaa ccagaggact ttgcgacctg ctattgtggt	1020
ggagggttaca gtagcataag tgatacgaca tttgggtgcg gtactaaggt ggaaatcaaa	1080
cgtacctaa	1089

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

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

gatatccaga tgaccagag cccaagcagt ctctccgcca gcgtaggcga tcgtgtgact	60
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eolf-seql

attacctgtc gtgcaacca gagcatctac aacgctctgg cttggatatca gcagaaaccg	120
ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcatactgg tgttccgtct	180
cgtttctctg cgtctgggtc tggtagcgac 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 gtgggtggcgg tggcagtggt	660
ggtggagggt ccggagggtg cggttcagac atacaaatga cccagagtcc ttcacggta	720
tccgcgtccg ttggcgatag ggtgactatt acatgtcaaa gctctcctag cgtctggagc	780
aattttctat cctggatatca acagaaaccg gggaaggctc caaaacttct gatttatgaa	840
gcctcgaaac tcaccagtgg agttccgtca agattcagtg gctctggatc agggacagac	900
ttcacgttga caatcagttc gctgcaacca gaggactttg cgacctacta ttgtggtgga	960
ggttacagta gcataagtga tacgacattt ggggtgcggt ctaagggtgga aatcaaaccg	1020
acctaa	1026

<210> 25

<211> 1131

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 25

atggaatggt cctgggtcct cctgtttttc ctttctgtca caaccggggt gcacagcgag	60
---	----

gtgcagctcg tcgagtctgg aggcgggctt gtccagcctg gagggagcct gcgtctctct	120
---	-----

eolf-seql

tgtgcagcaa gcggtttcac gttcaccaac tacggatatcc actggattcg tcaggcacca	180
ggtaaagggtc tggaatgggt agcctctatc tctccgtctg gtggctctgac gtactaccgt	240
gactctgtca aaggctcgttt caccatctct cgtgatgacg cgaaaaactc tccgtacctg	300
cagatgaact ctctgcgtgc agaagatacc gcagtgtact actgcgctac tgggtggtgaa	360
ggatatcttcg 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 cccagaccta catctgcaac	660
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgttcc	720
ggagggtggcg gttccggagg tggcgggtacc ggtggcgggtg gatccgaagt ccagctgctt	780
gaatccggag gcggactcgt gcagcccga ggcagtcttc gcttgtcctg cgctgtatct	840
ggaatcgacc tgagcaatta cgccatcaac tgggtgagac aggcacctgg gaaatgcctc	900
gaatggatcg gcattatatg ggctagtggg acgacctttt atgctacatg ggcgaagggt	960
agattcaciaa 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 Sequence

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

<400> 26	
gagggtgcagc tcgtcgagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc	60
tcttgtgcag caagcgggtt cacgttcacc aactacggta tccactggat tcgtcaggca	120

eolf-seql

ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac	180
cgtgactctg tcaaaggctg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac	240
ctgcagatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt	300
gaaggatatct tcgactactg gggtcagggt accctggtaa ctgtctcaag cgcttctaca	360
aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa 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 accgggtggcg 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 actctgggtca ccgtctcgag ttga	1074

<210> 27

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 27

atgtcagttc ccacacaggt gctgggcctg cttctgttgt ggctcaccga tgctaggtgt	60
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact	120
attacctgtc gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg	180

eolf-seql

ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataaccgg tgttccgtct	240
cgtttctctg cgtctgggtc tggtagggac tctactctga ccatctcctc tctgcagccg	300
gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt	360
ggtaccaaag ttgagatcaa acgtacgggtg gctgcaccat ctgtcttcat cttcccccca	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 cccagagccc ttcctctgta	780
agcgccagtg tcggagacag agtgactatt acctgcaaaa gctccccctt 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 Sequence

<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 tgcataaccgg tgttccgtct	180

eolf-seql

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cgtttctctg cgtctggttc tggtagggac tctactctga ccatctcctc tctgcagccg      240
gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt      300
ggtaccaaag ttgagatcaa acgtacgggtg 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 gctccccctc agtctggtcc      780
aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa      840
gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac      900
tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga      960
ggttacagta gcataagtga tacgacattt ggatgcggca ctaaagtgga aatcaagcgt     1020
acctga                                             1026

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<210> 29

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 29

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

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```

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

```

eolf-seql

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 Sequence

<220>

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

<400> 30

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

eolf-seql

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 Sequence

<220>

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

<400> 31

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

eolf-seql

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 Sequence

<220>

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

<400> 32

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

eolf-seql

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

<220>
 <223> LINKER 1

<400> 33

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 Sequence

<220>
 <223> LINKER 2

<400> 34

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

<210> 35
 <211> 789
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 645 gH5gL4 specific to albumin

<400> 35

Gly Ala Gly Gly Thr Thr Cys Ala Gly Cys Thr Gly Cys Thr Gly Gly
 1 5 10 15

Ala Gly Thr Cys Thr Gly Gly Ala Gly Gly Cys Gly Gly Gly Cys Thr
 20 25 30

Thr Gly Thr Cys Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Gly Gly
 35 40 45

eolf-seql

Ala Gly Cys Cys Thr Gly Cys Gly Thr Cys Thr Cys Thr Cys Thr Thr
50 55 60

Gly Thr Gly Cys Ala Gly Thr Ala Ala Gly Cys Gly Gly Cys Ala Thr
65 70 75 80

Cys Gly Ala Cys Cys Thr Gly Thr Cys Cys Ala Ala Cys Thr Ala Cys
85 90 95

Gly Cys Gly Ala Thr Thr Ala Ala Cys Thr Gly Gly Gly Thr Ala Cys
100 105 110

Gly Thr Cys Ala Gly Gly Cys Ala Cys Cys Gly Gly Gly Thr Ala Ala
115 120 125

Ala Gly Gly Thr Cys Thr Gly Gly Ala Ala Thr Gly Gly Ala Thr Cys
130 135 140

Gly Gly Cys Ala Thr Cys Ala Thr Cys Thr Gly Gly Gly Cys Cys Thr
145 150 155 160

Cys Thr Gly Gly Thr Ala Cys Gly Ala Cys Cys Thr Thr Cys Thr Ala
165 170 175

Cys Gly Cys Thr Ala Cys Thr Thr Gly Gly Gly Cys Cys Ala Ala Ala
180 185 190

Gly Gly Thr Cys Gly Thr Thr Thr Cys Ala Cys Cys Ala Thr Cys Thr
195 200 205

Cys Cys Cys Gly Thr Gly Ala Cys Ala Ala Cys Thr Cys Thr Ala Ala
210 215 220

Ala Ala Ala Cys Ala Cys Cys Gly Thr Gly Thr Ala Cys Cys Thr Gly
225 230 235 240

eolf-seql

Cys Ala Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr Cys Thr Gly Cys
245 250 255

Gly Thr Gly Cys Gly Gly Ala Ala Gly Ala Cys Ala Cys Thr Gly Cys
260 265 270

Gly Gly Thr Thr Thr Ala Cys Thr Ala Thr Thr Gly Cys Gly Cys Gly
275 280 285

Cys Gly Thr Ala Cys Cys Gly Thr Thr Cys Cys Gly Gly Gly Cys Thr
290 295 300

Ala Thr Thr Cys Thr Ala Cys Thr Gly Cys Ala Cys Cys Gly Thr Ala
305 310 315 320

Cys Thr Thr Cys Gly Ala Cys Cys Thr Gly Thr Gly Gly Gly Gly Thr
325 330 335

Cys Ala Gly Gly Gly Thr Ala Cys Thr Cys Thr Gly Gly Thr Thr Ala
340 345 350

Cys Cys Gly Thr Cys Thr Cys Gly Ala Gly Thr Gly Gly Ala Gly Gly
355 360 365

Thr Gly Gly Cys Gly Gly Thr Thr Cys Thr Gly Gly Cys Gly Gly Thr
370 375 380

Gly Gly Cys Gly Gly Thr Thr Cys Cys Gly Gly Thr Gly Gly Cys Gly
385 390 395 400

Gly Thr Gly Gly Ala Thr Cys Gly Gly Gly Ala Gly Gly Thr Gly Gly
405 410 415

Cys Gly Gly Thr Thr Cys Thr Gly Ala Thr Ala Thr Cys Cys Ala Gly
420 425 430

eolf-seql

Ala Thr Gly Ala Cys Cys Cys Ala Gly Ala Gly Thr Cys Cys Ala Ala
435 440 445

Gly Cys Ala Gly Thr Gly Thr Thr Thr Cys Cys Gly Cys Cys Ala Gly
450 455 460

Cys Gly Thr Ala Gly Gly Cys Gly Ala Thr Cys Gly Thr Gly Thr Gly
465 470 475 480

Ala Cys Thr Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Ala Gly Thr
485 490 495

Cys Cys Thr Cys Thr Cys Cys Gly Ala Gly Cys Gly Thr Thr Thr Gly
500 505 510

Gly Thr Cys Cys Ala Ala Cys Thr Thr Cys Cys Thr Gly Ala Gly Cys
515 520 525

Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys Ala Gly Ala Ala Ala Cys
530 535 540

Cys Gly Gly Gly Thr Ala Ala Ala Gly Cys Cys Cys Cys Gly Ala Ala
545 550 555 560

Ala Cys Thr Gly Cys Thr Gly Ala Thr Cys Thr Ala Cys Gly Ala Gly
565 570 575

Gly Cys Gly Thr Cys Thr Ala Ala Ala Cys Thr Gly Ala Cys Cys Thr
580 585 590

Cys Thr Gly Gly Thr Gly Thr Ala Cys Cys Gly Thr Cys Cys Cys Gly
595 600 605

Thr Thr Thr Cys Thr Cys Thr Gly Gly Cys Thr Cys Thr Gly Gly Cys
610 615 620

eolf-seql

Thr Cys Thr Gly Gly Thr Ala Cys Gly Gly Ala Cys Thr Thr Cys Ala
625 630 635 640

Cys Thr Cys Thr Gly Ala Cys Cys Ala Thr Cys Thr Cys Cys Thr Cys
645 650 655

Thr Cys Thr Gly Cys Ala Gly Cys Cys Gly Gly Ala Ala Gly Ala Cys
660 665 670

Thr Thr Thr Gly Cys Ala Ala Cys Gly Thr Ala Cys Thr Ala Cys Thr
675 680 685

Gly Cys Gly Gly Thr Gly Gly Thr Gly Gly Thr Thr Ala Cys Thr Cys
690 695 700

Thr Thr Cys Cys Ala Thr Cys Thr Cys Thr Gly Ala Cys Ala Cys Cys
705 710 715 720

Ala Cys Gly Thr Thr Cys Gly Gly Thr Gly Gly Ala Gly Gly Cys Ala
725 730 735

Cys Cys Ala Ala Ala Gly Thr Thr Gly Ala Ala Ala Thr Cys Ala Ala
740 745 750

Ala Cys Gly Thr Ala Cys Gly Cys Ala Thr Cys Ala Cys Cys Ala Thr
755 760 765

Cys Ala Cys Cys Ala Thr Cys Ala Cys Cys Ala Thr Cys Ala Cys Cys
770 775 780

Ala Thr Cys Ala Cys
785

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

eolf-seql

<213> Artificial Sequence

<220>

<223> 645 gH5gL4 specific to albumin

<400> 36

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

eolf-seql

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> PRT

<213> Artificial Sequence

<220>

<223> 645 gH5gL4ds specific to albumin

<400> 37

Gly Ala Gly Gly Thr Thr Cys Ala Gly Cys Thr Gly Cys Thr Gly Gly
1 5 10 15

Ala Gly Thr Cys Thr Gly Gly Ala Gly Gly Cys Gly Gly Gly Cys Thr
20 25 30

Thr Gly Thr Cys Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Gly Gly
35 40 45

eolf-seql

Ala Gly Cys Cys Thr Gly Cys Gly Thr Cys Thr Cys Thr Cys Thr Thr
50 55 60

Gly Thr Gly Cys Ala Gly Thr Ala Ala Gly Cys Gly Gly Cys Ala Thr
65 70 75 80

Cys Gly Ala Cys Cys Thr Gly Thr Cys Cys Ala Ala Cys Thr Ala Cys
85 90 95

Gly Cys Gly Ala Thr Thr Ala Ala Cys Thr Gly Gly Gly Thr Ala Cys
100 105 110

Gly Thr Cys Ala Gly Gly Cys Ala Cys Cys Gly Gly Gly Thr Ala Ala
115 120 125

Ala Thr Gly Cys Cys Thr Gly Gly Ala Ala Thr Gly Gly Ala Thr Cys
130 135 140

Gly Gly Cys Ala Thr Cys Ala Thr Cys Thr Gly Gly Gly Cys Cys Thr
145 150 155 160

Cys Thr Gly Gly Thr Ala Cys Gly Ala Cys Cys Thr Thr Cys Thr Ala
165 170 175

Cys Gly Cys Thr Ala Cys Thr Thr Gly Gly Gly Cys Cys Ala Ala Ala
180 185 190

Gly Gly Thr Cys Gly Thr Thr Thr Cys Ala Cys Cys Ala Thr Cys Thr
195 200 205

Cys Cys Cys Gly Thr Gly Ala Cys Ala Ala Cys Thr Cys Thr Ala Ala
210 215 220

Ala Ala Ala Cys Ala Cys Cys Gly Thr Gly Thr Ala Cys Cys Thr Gly
225 230 235 240

eolf-seql

Cys Ala Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr Cys Thr Gly Cys
245 250 255

Gly Thr Gly Cys Gly Gly Ala Ala Gly Ala Cys Ala Cys Thr Gly Cys
260 265 270

Gly Gly Thr Thr Thr Ala Cys Thr Ala Thr Thr Gly Cys Gly Cys Gly
275 280 285

Cys Gly Thr Ala Cys Cys Gly Thr Thr Cys Cys Gly Gly Gly Cys Thr
290 295 300

Ala Thr Thr Cys Thr Ala Cys Thr Gly Cys Ala Cys Cys Gly Thr Ala
305 310 315 320

Cys Thr Thr Cys Gly Ala Cys Cys Thr Gly Thr Gly Gly Gly Gly Thr
325 330 335

Cys Ala Gly Gly Gly Thr Ala Cys Thr Cys Thr Gly Gly Thr Thr Ala
340 345 350

Cys Cys Gly Thr Cys Thr Cys Gly Ala Gly Thr Gly Gly Ala Gly Gly
355 360 365

Thr Gly Gly Cys Gly Gly Thr Thr Cys Thr Gly Gly Cys Gly Gly Thr
370 375 380

Gly Gly Cys Gly Gly Thr Thr Cys Cys Gly Gly Thr Gly Gly Cys Gly
385 390 395 400

Gly Thr Gly Gly Ala Thr Cys Gly Gly Gly Ala Gly Gly Thr Gly Gly
405 410 415

Cys Gly Gly Thr Thr Cys Thr Gly Ala Thr Ala Thr Cys Cys Ala Gly
420 425 430

eolf-seql

Ala Thr Gly Ala Cys Cys Cys Ala Gly Ala Gly Thr Cys Cys Ala Ala
435 440 445

Gly Cys Ala Gly Thr Gly Thr Thr Thr Cys Cys Gly Cys Cys Ala Gly
450 455 460

Cys Gly Thr Ala Gly Gly Cys Gly Ala Thr Cys Gly Thr Gly Thr Gly
465 470 475 480

Ala Cys Thr Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Ala Gly Thr
485 490 495

Cys Cys Thr Cys Thr Cys Cys Gly Ala Gly Cys Gly Thr Thr Thr Gly
500 505 510

Gly Thr Cys Cys Ala Ala Cys Thr Thr Cys Cys Thr Gly Ala Gly Cys
515 520 525

Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys Ala Gly Ala Ala Ala Cys
530 535 540

Cys Gly Gly Gly Thr Ala Ala Ala Gly Cys Cys Cys Cys Gly Ala Ala
545 550 555 560

Ala Cys Thr Gly Cys Thr Gly Ala Thr Cys Thr Ala Cys Gly Ala Gly
565 570 575

Gly Cys Gly Thr Cys Thr Ala Ala Ala Cys Thr Gly Ala Cys Cys Thr
580 585 590

Cys Thr Gly Gly Thr Gly Thr Ala Cys Cys Gly Thr Cys Cys Cys Gly
595 600 605

Thr Thr Thr Cys Thr Cys Thr Gly Gly Cys Thr Cys Thr Gly Gly Cys
610 615 620

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Thr Cys Thr Gly Gly Thr Ala Cys Gly Gly Ala Cys Thr Thr Cys Ala
625 630 635 640

Cys Thr Cys Thr Gly Ala Cys Cys Ala Thr Cys Thr Cys Cys Thr Cys
645 650 655

Thr Cys Thr Gly Cys Ala Gly Cys Cys Gly Gly Ala Ala Gly Ala Cys
660 665 670

Thr Thr Thr Gly Cys Ala Ala Cys Gly Thr Ala Cys Thr Ala Cys Thr
675 680 685

Gly Cys Gly Gly Thr Gly Gly Thr Gly Gly Thr Thr Ala Cys Thr Cys
690 695 700

Thr Thr Cys Cys Ala Thr Cys Thr Cys Thr Gly Ala Cys Ala Cys Cys
705 710 715 720

Ala Cys Gly Thr Thr Cys Gly Gly Thr Thr Gly Thr Gly Gly Cys Ala
725 730 735

Cys Cys Ala Ala Ala Gly Thr Thr Gly Ala Ala Ala Thr Cys Ala Ala
740 745 750

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Ala Thr Cys Ala Cys
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<400> 38

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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

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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