

eolf-seq1
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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

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

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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
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Phe Asn Arg Gly Glu Cys
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Ala Ser Ile Ser Pro Ser Gly Gly Leu Thr Tyr Tyr Arg Asp Ser Val

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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
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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
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Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
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Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
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Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly
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Gln Gly Thr Leu Val Thr Val Ser Ser
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<223> Light chain of anti-albumin Fv component

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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
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<223> Linker 1

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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

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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
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Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu
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Val Thr Val Ser Ser
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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
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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
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Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val
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Glu Ile Lys Arg Thr
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<223> 645gH1 heavy chain variable domain

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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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
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<210> 18
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<223> 645gL1 light chain variable domain

<400> 18

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
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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

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

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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

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

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eo1f-seq1

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Leu	Ala	Trp	Tyr	Gln	Gln	Lys
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Tyr	Asn	Ala	Asn	Thr	Leu	His
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Thr	Gly	Val	Pro	Ser	Arg	Phe
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Ser	Gly	Ser	Gly	Thr	Asp	Ser
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Thr	Leu	Thr	Ile	Ser	Ser	Leu
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Gln	Pro	Leu	Gln	Pro	Leu	
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Glu	Asp	Phe	Ala	Thr	Tyr	Tyr
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Cys	Gln	Gln	Tyr	Tyr	Asp	Tyr
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Thr	Phe	Gly	Gly	Gly	Thr	Lys
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Pro	Ser	Val	Phe	Ile	Phe	Pro
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Glu	Ala					
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Lys	Val	Gln	Trp	Lys	Val	Asp
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Asn	Ala	Leu	Gln	Ser	Gly	Asn
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Ser	Gly	Asn	Ser	Gln	Asp	Ser
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Glu	Ser	Val	Thr	Glu	Gln	Asp
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Ser	Lys	Asp	Ser	Thr	Tyr	Ser
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Leu	Ser					
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Ser	Thr	Leu	Thr	Leu	Ser	Lys
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Ala	Asp	Tyr	Glu	Lys	His	Lys
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Ser	Gly					
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275

280

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Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
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Val Glu Ile Lys
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<212> DNA
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caggaatctg	tgaccgaaca	ggactccaaa	gactccacct	actctctgtc	tagcaccctg		600
actctgtcca	aagcagacta	cgagaaacac	aaagtgtacg	cttgcggaagt	tacccatcag		660
ggtctgagct	ctccggttac	caaatccttt	aatagagggg	agtgtggtgg	cgggtggcagt		720
ggtggtggag	gttccggagg	tggcggttca	gacatacaaa	tgaccagag	tccttcatcg		780
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agcaattttc	tatcctggta	tcaacagaaa	ccggggaagg	ctccaaaact	tctgatttat		900
gaagcctcga	aactcaccag	tggagttccg	tcaagattca	gtggctctgg	atcagggaca		960
gacttcacgt	tgacaatcag	ttcgtgcaa	ccagaggact	ttgcgaccta	ctattgtggt		1020
ggaggttaca	gtagcataag	tgatacgaca	tttgggtgcg	gtactaaggt	ggaaatcaaa		1080
cgtaacctaa							1089

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

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

<400> 24							
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cgtttctctg	cgtctggttc	tggtagcgac	tctactctga	ccatctcctc	tctccagccg		240
gaagatttcg	cgacctacta	ctgccagcag	tactacgatt	accactgac	gtttggtggt		300
ggtaccaaag	ttgagatcaa	acgtacggtt	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
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ctgagctctc	cggttaccaa	atcctttaat	agaggggagt	gtggtggcgg	tggcagtggt		660
ggtggagggt	ccggagggtg	cggttcagac	atacaaatga	cccagagtc	ttcatcggtg		720
tccgcgtccg	ttggcgatag	ggtgactatt	acatgtcaaa	gctctcctag	cgtctggagc		780
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gcctcgaaac	tcaccagtgg	agttccgtca	agattcagtg	gctctggatc	agggacagac		900
ttcacgttga	caatcagttc	gctgcaacca	gaggactttg	cgacctacta	ttgtggtgga		960
ggttacagta	gcataagtga	tacgacattt	gggtgcggta	ctaagggtga	aatcaaaccg		1020

acctaa

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

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

<400> 25
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 gtgcagctcg tcgagtctgg aggcgggctt gtccagcctg gagggagcct 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 cccagaccta catctgcaac 660
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttggtcc 720
 ggaggtggcg gttccggagg tggcgggtacc ggtggcgggtg 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
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 tcttgtgcag caagcggttt cacgttcacc aactacggtg tccactggat tcgtcaggca 120
 ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctgggtggtct gacgtactac 180
 cgtgactctg tcaaagggtc tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240

						eof-seq1	
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gaaggatatct	tcgactactg	gggtcaggggt	accctggtaa	ctgtctcaag	cgcttctaca		360
aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg		420
gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca		480
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	tggactctac		540
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc		600
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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

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gatatccaga	tgaccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 120
attacctgtc	gtgcaacca gagcatctac aacgctctgg cttggtatca gcagaaaccg 180
ggtaaagcgc	caaaactcct gatctacaac gcgaacactc tgcataaccgg tgttccgtct 240
cgtttctctg	cgtctggttc tggtagcgac tctactctga ccatctcctc tctgcagccg 300
gaagatttcg	cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 360
ggtaccaaag	ttgagatcaa acgtacgggt gctgcaccat ctgtcttcat cttcccccca 420
tctgatgagc	agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac 480
cctagagagg	caaagtcca gtggaagggt gataacgccc ttcaatccgg aaactcccag 540
gagagtgtca	ctgagcagga ctcaaaggac tccacctata gccttagcag cacactgaca 600
ctgagcaagg	ctgactacga gaaacacaag gtctacgcct gcgaagtgac acatcaaggc 660
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ggtggtggct	ccggaggcgg aggaagcgac atccagatga ccagagccc 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	
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ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataaccg tggtccgtct	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
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acctga	1026

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

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

<400> 1

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eo1f-seq1

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

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

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

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
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ccgggtaaatt gcctggaatg gatcggcatc atctgggcct ctggtacgac cttctacgct 180
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cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg taccgttccg 300
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cagccggaag actttgcaac gtactactgc ggtgggtgggt actcttccat ctctgacacc 720
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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

