

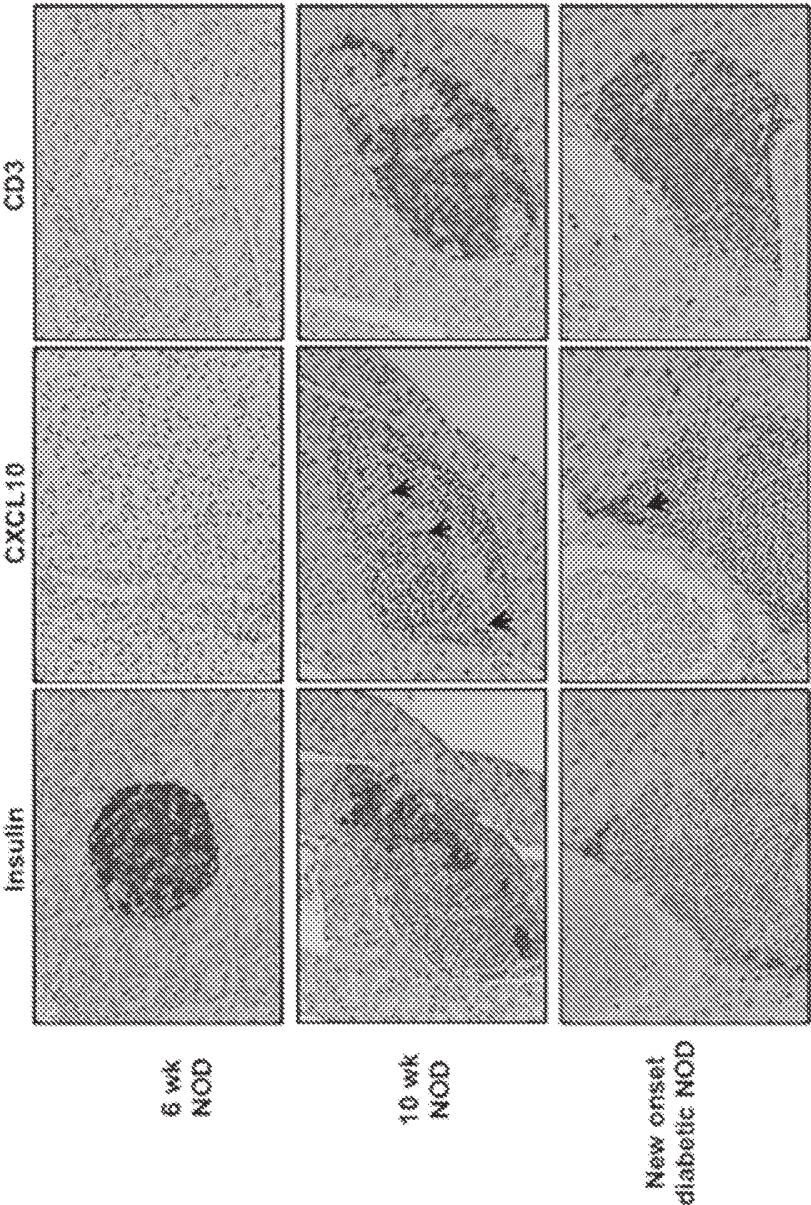


Fig. 1

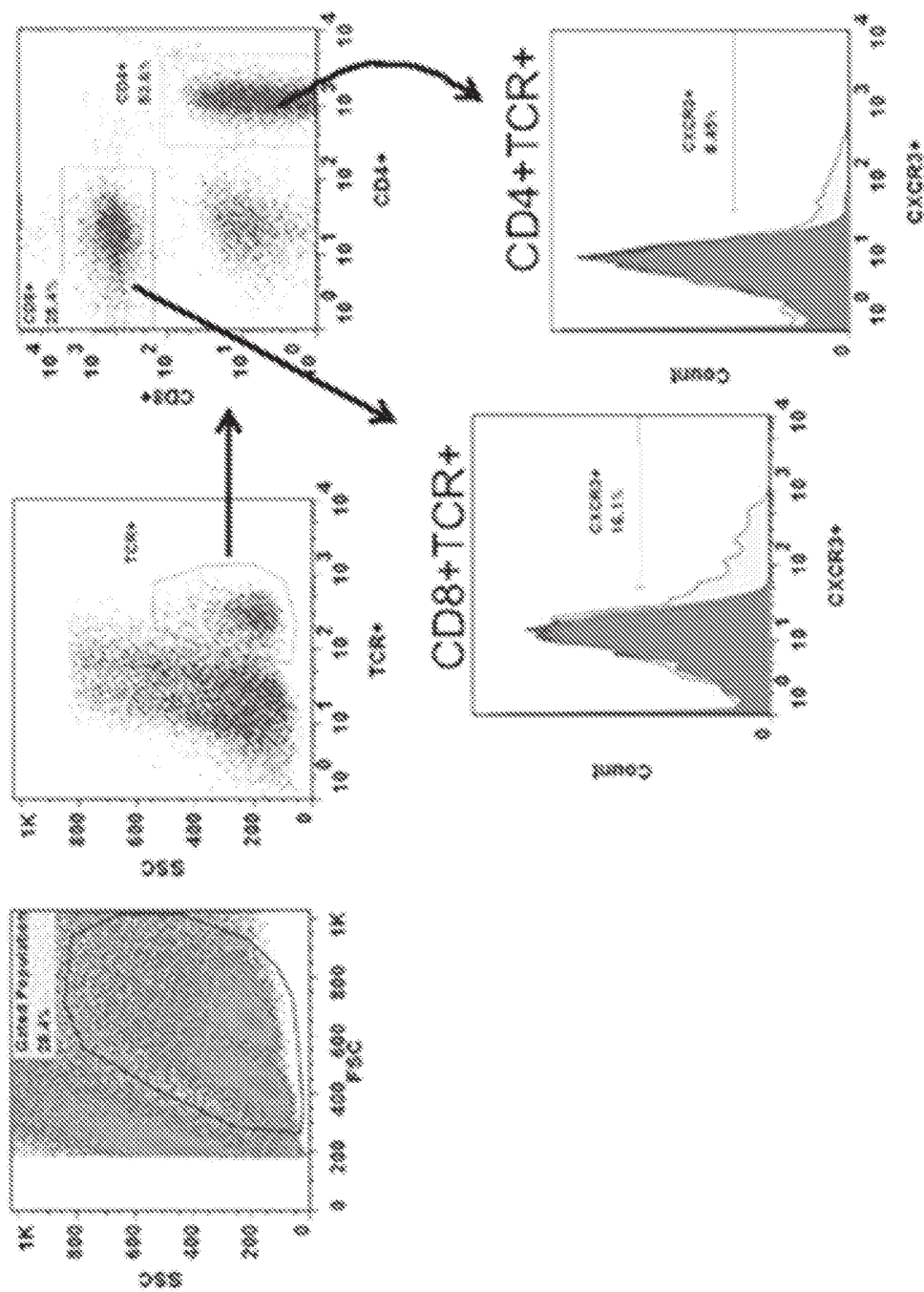


Fig. 2

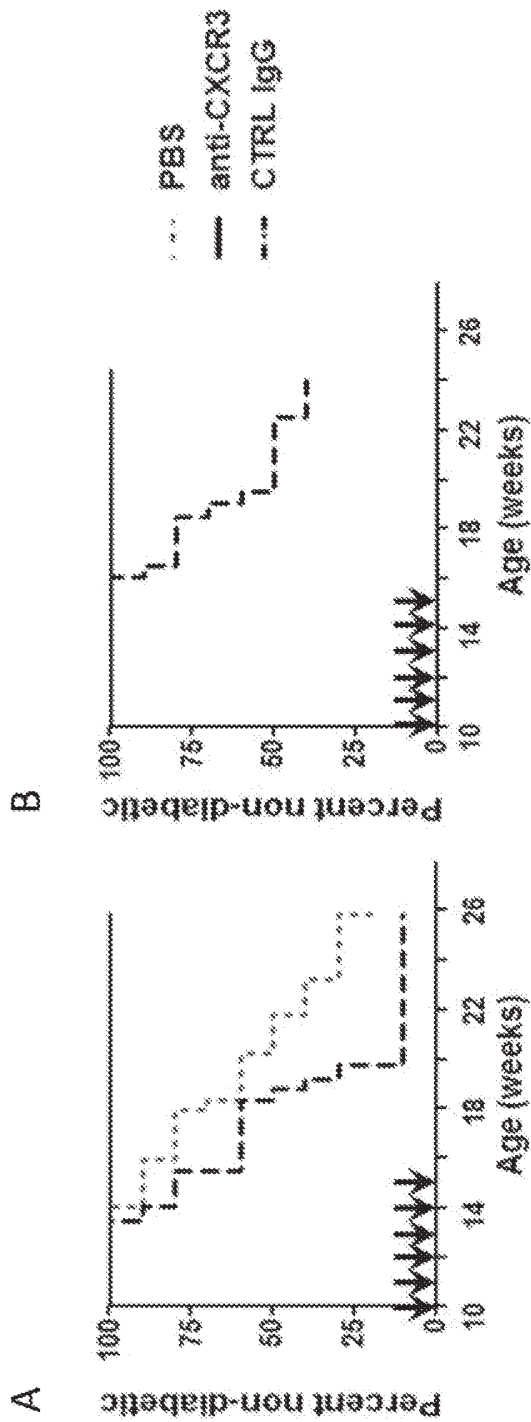


Fig. 3

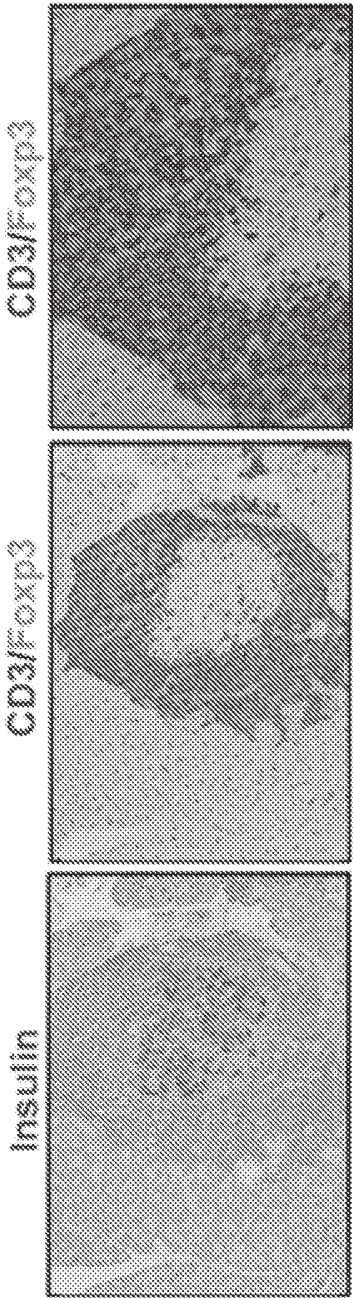


Fig. 4

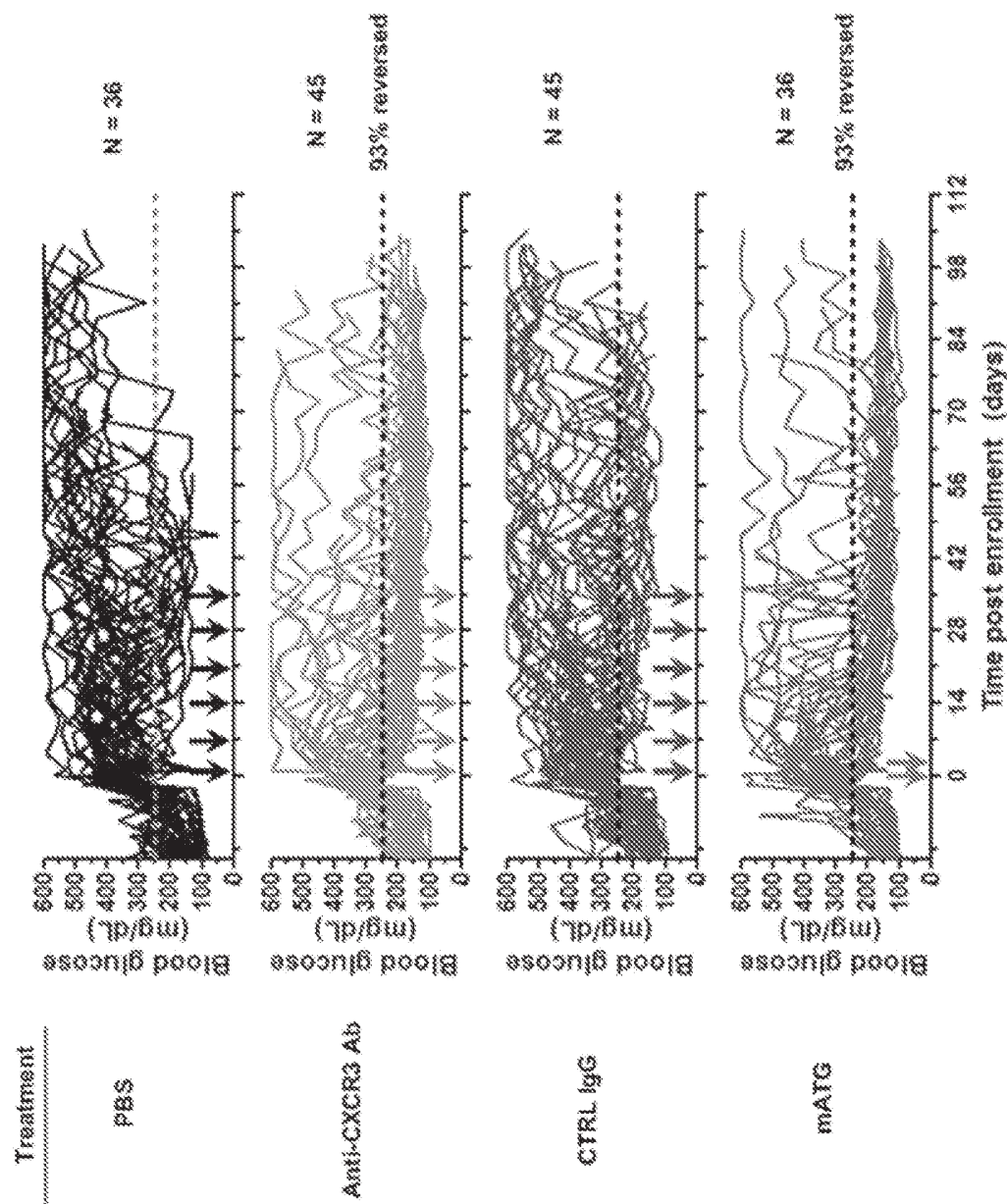


Fig. 5

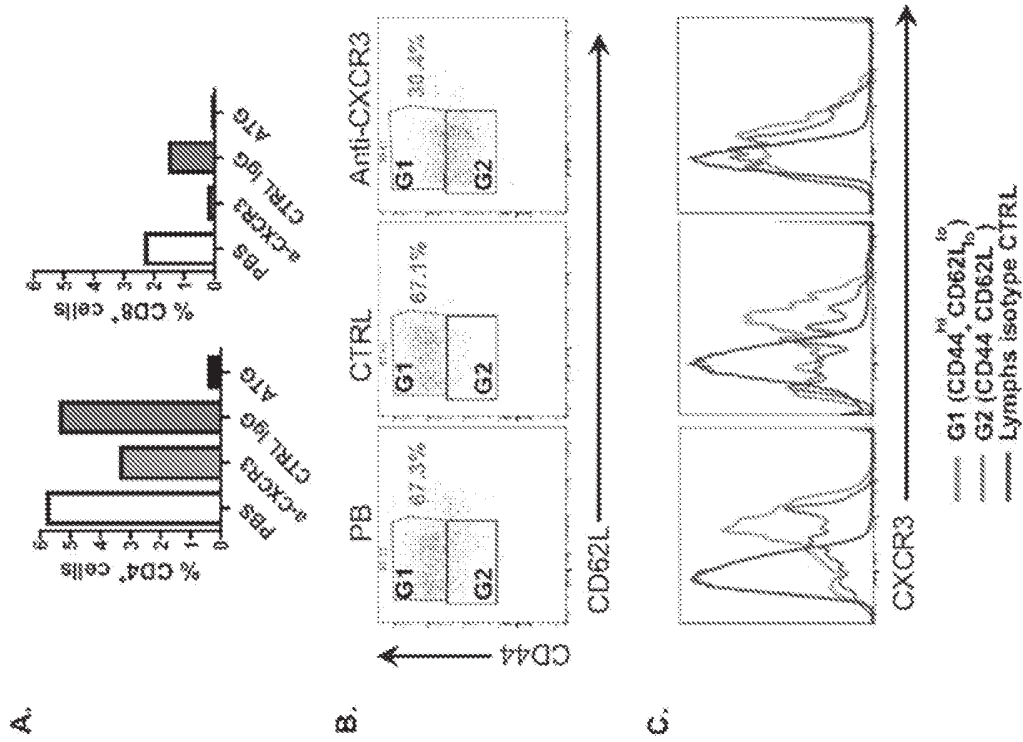


Fig. 6

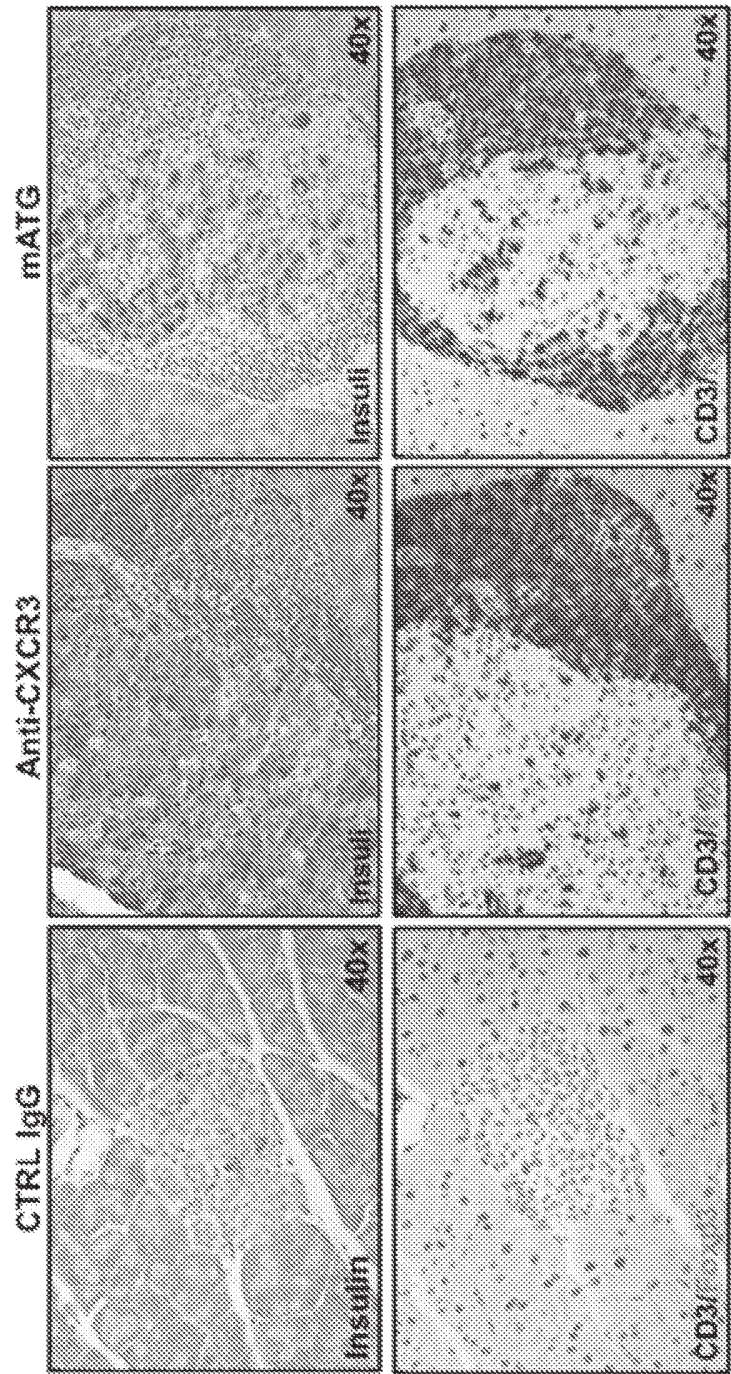


Fig. 7

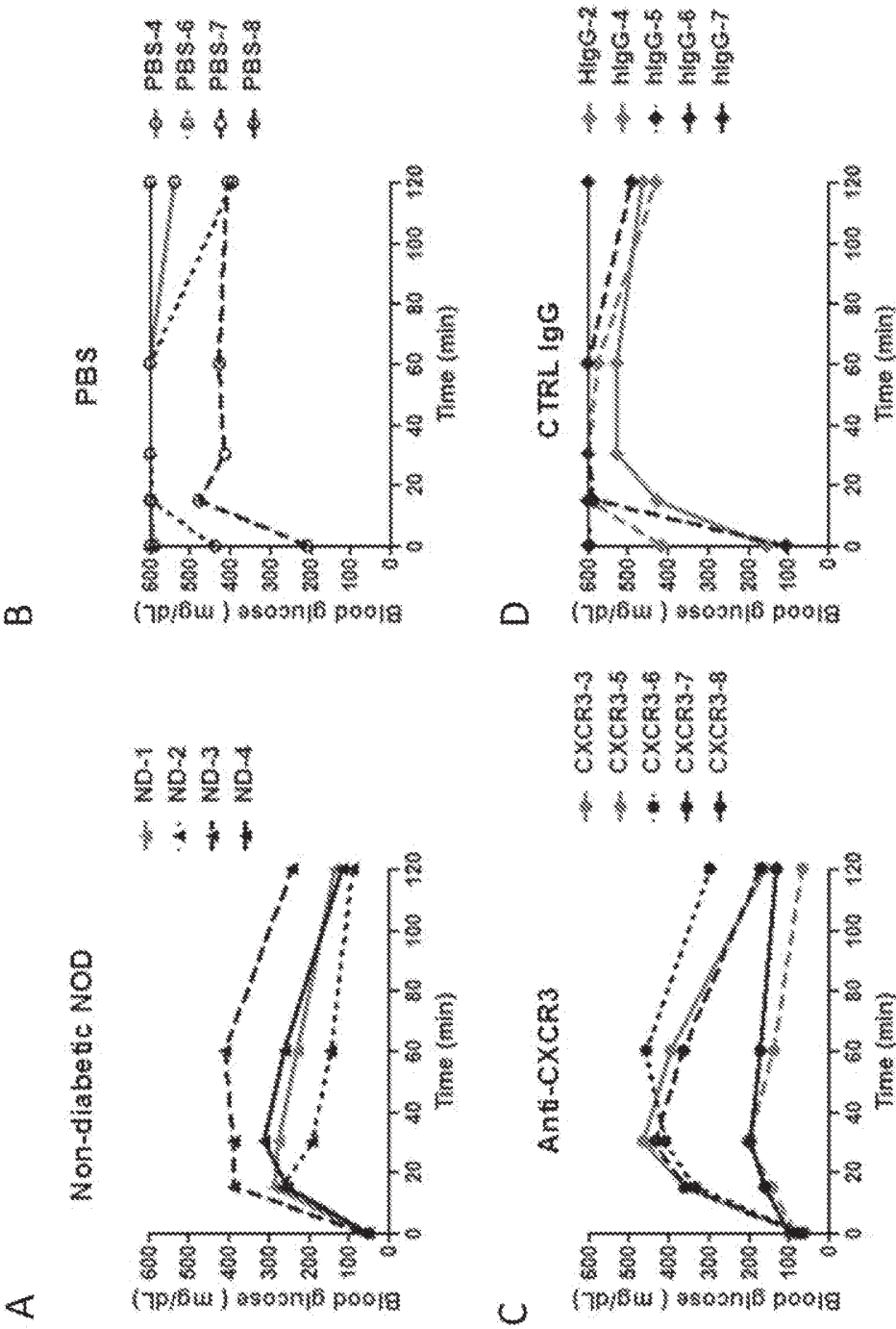


Fig. 8

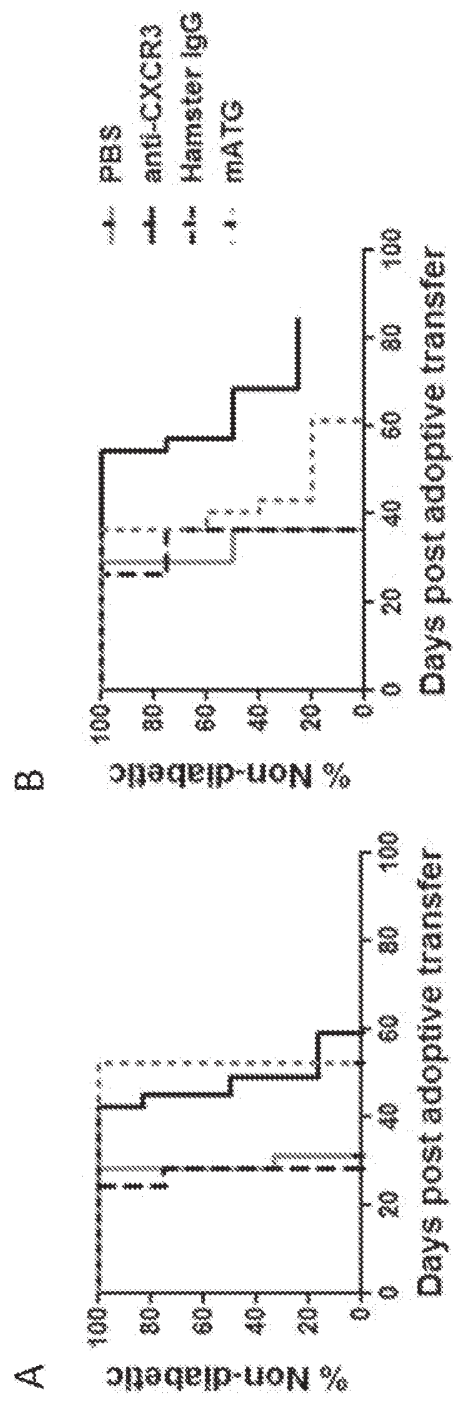


Fig. 9

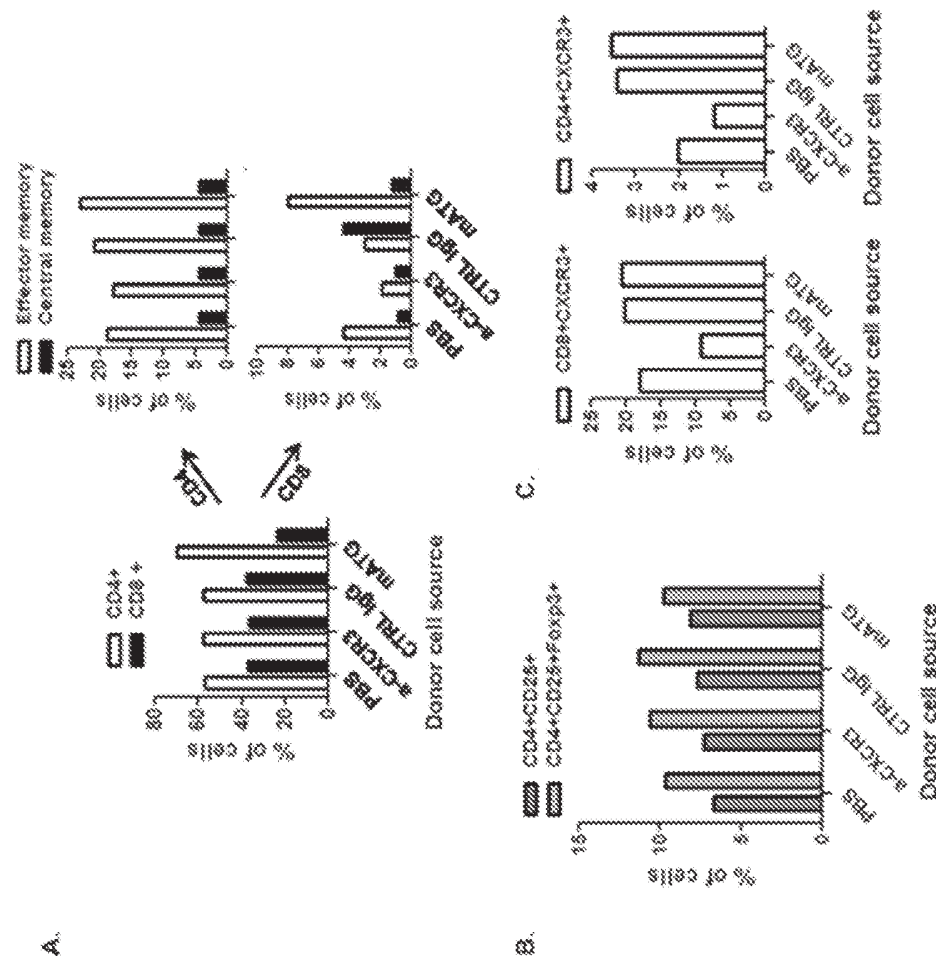


Fig. 10

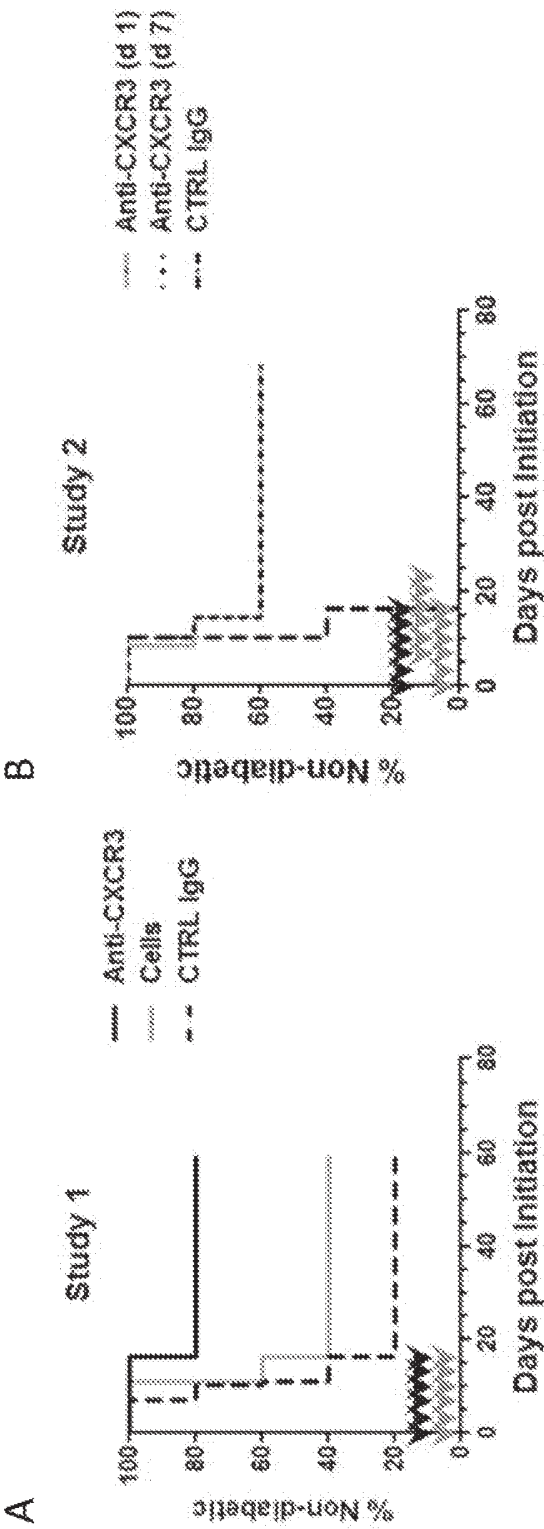


Fig. 11

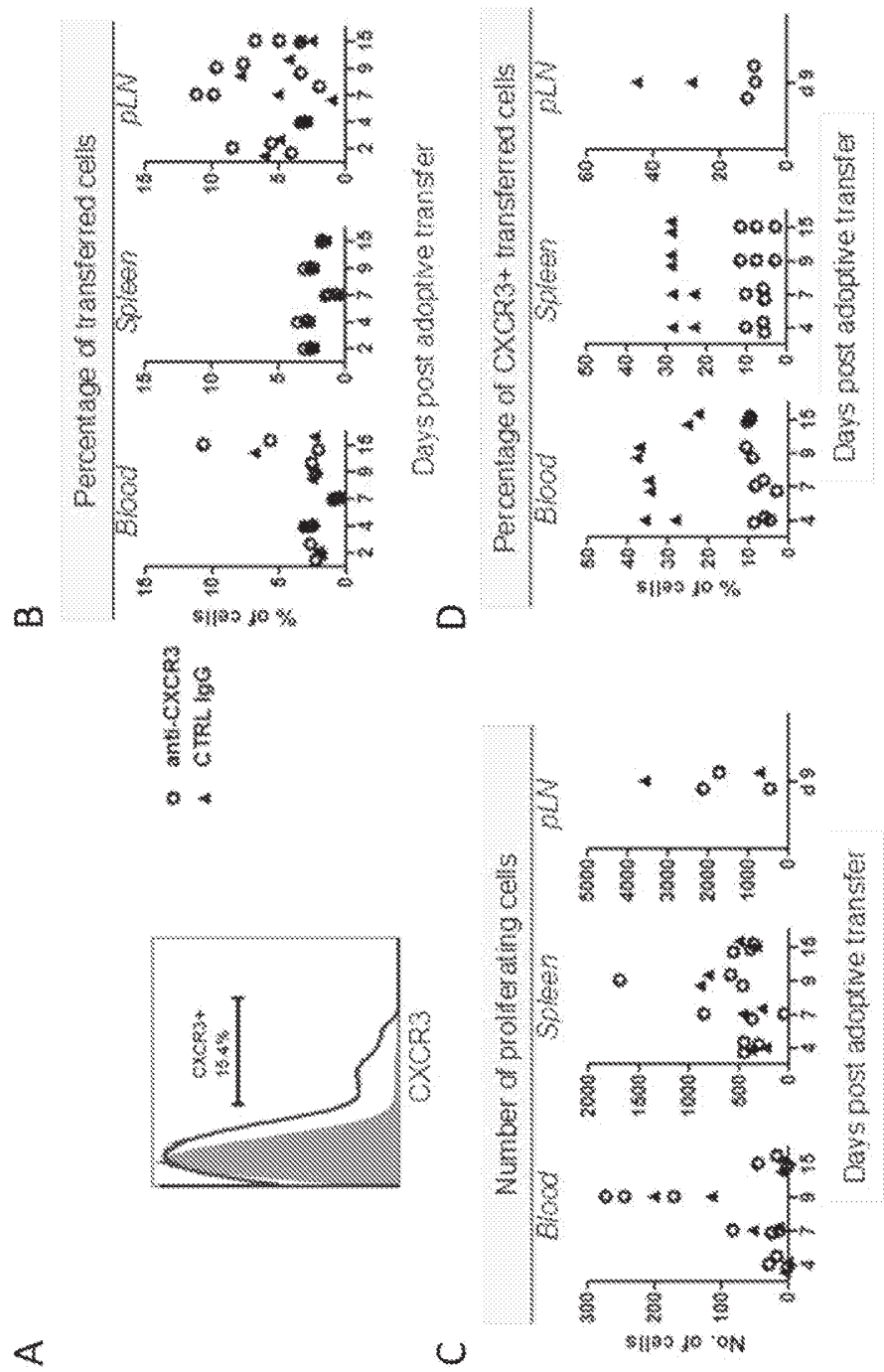


Fig. 12

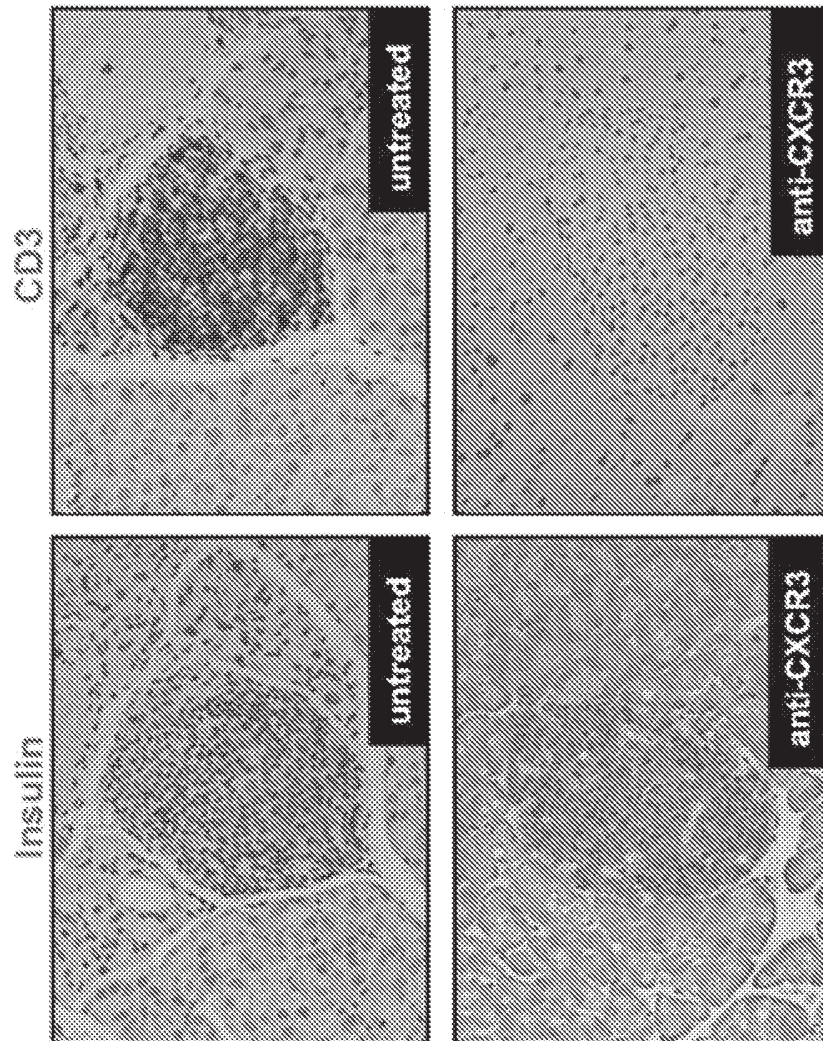


Fig. 13

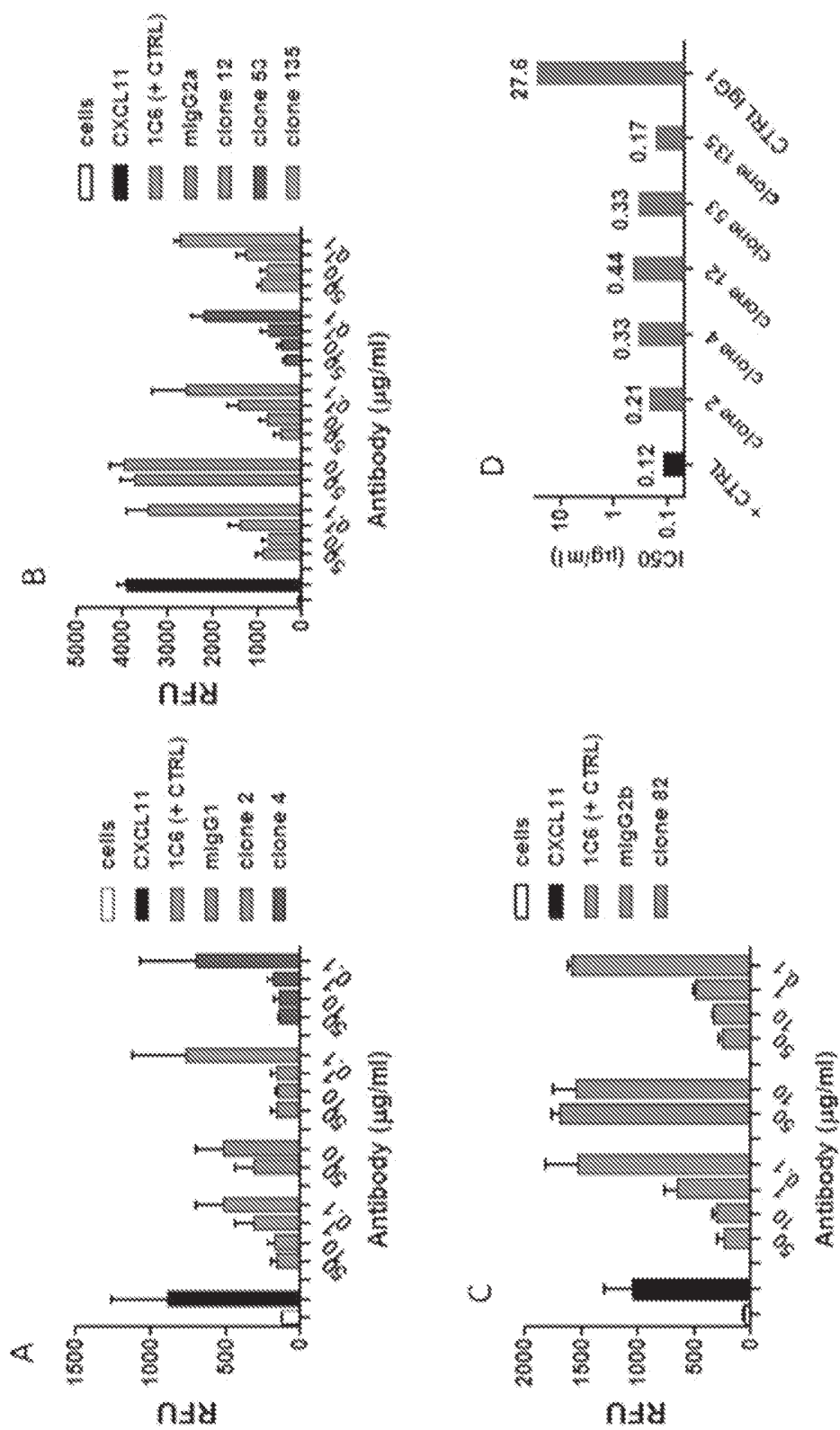


Fig. 14

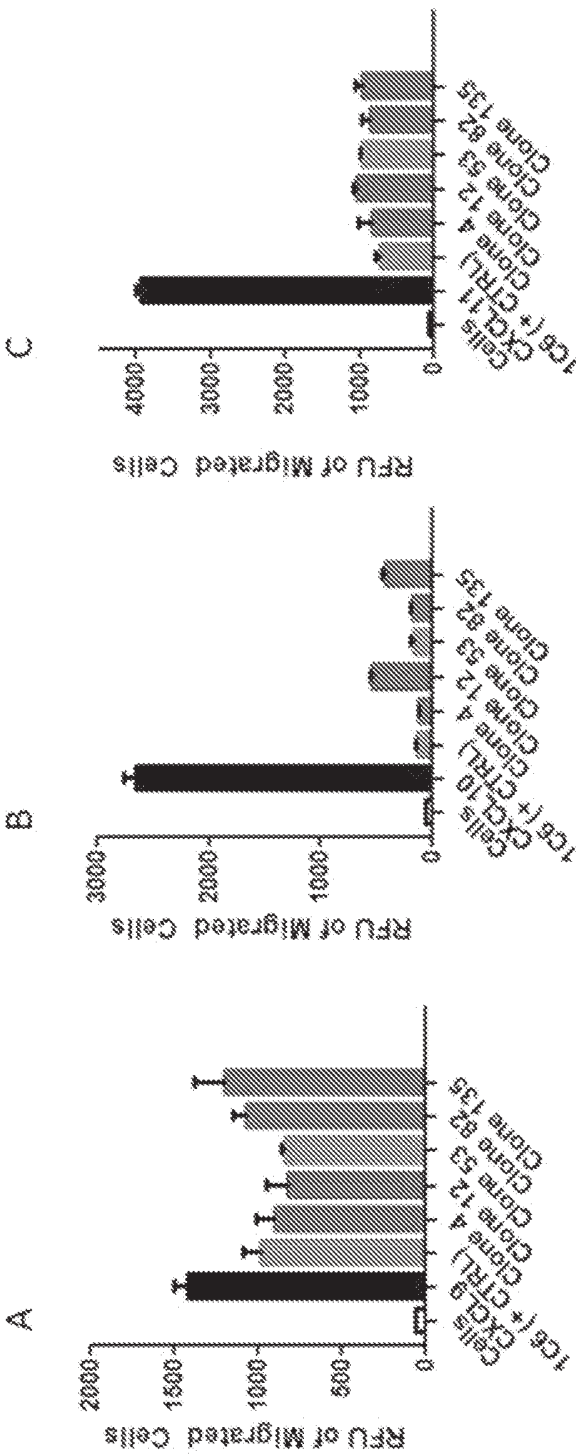


Fig. 15

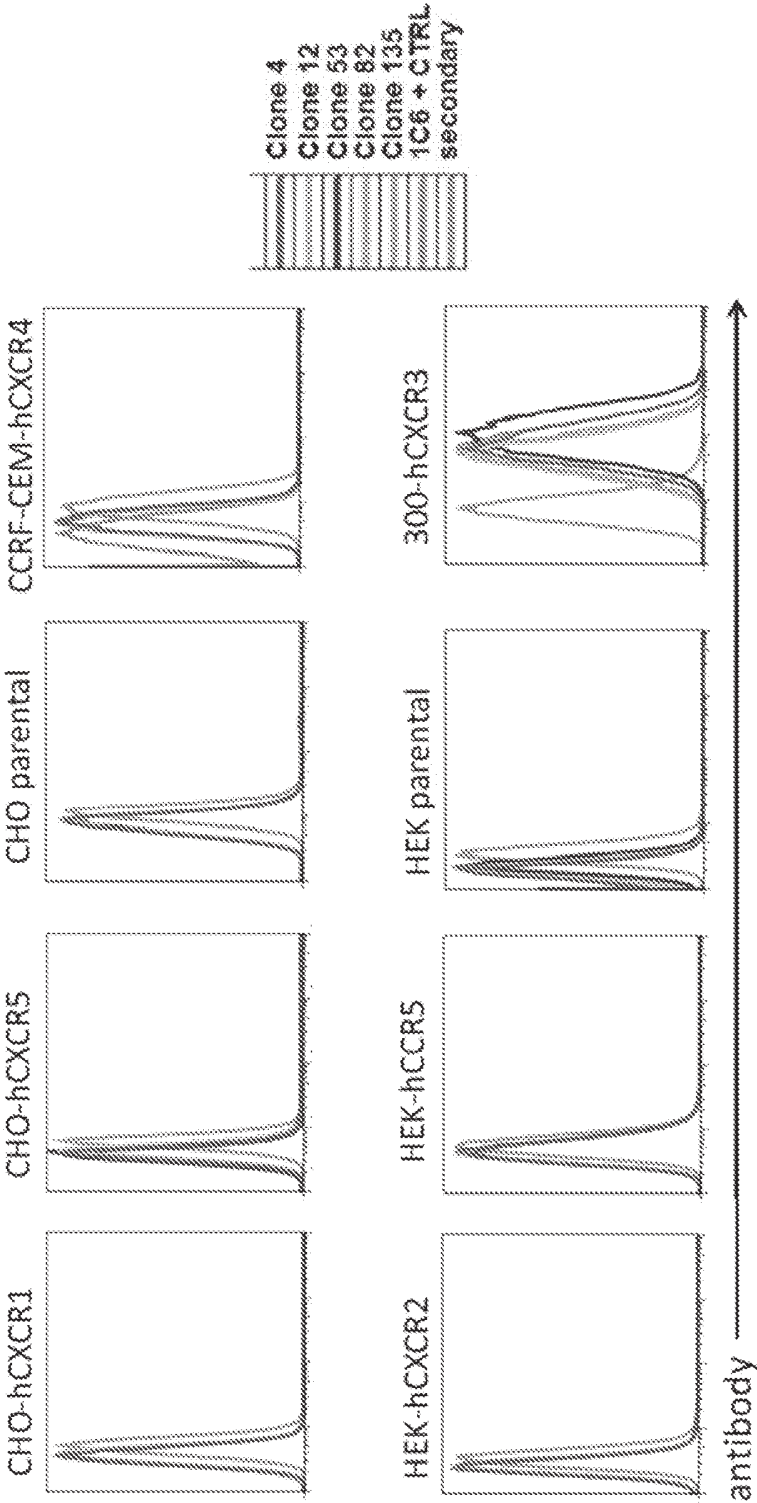


Fig. 16

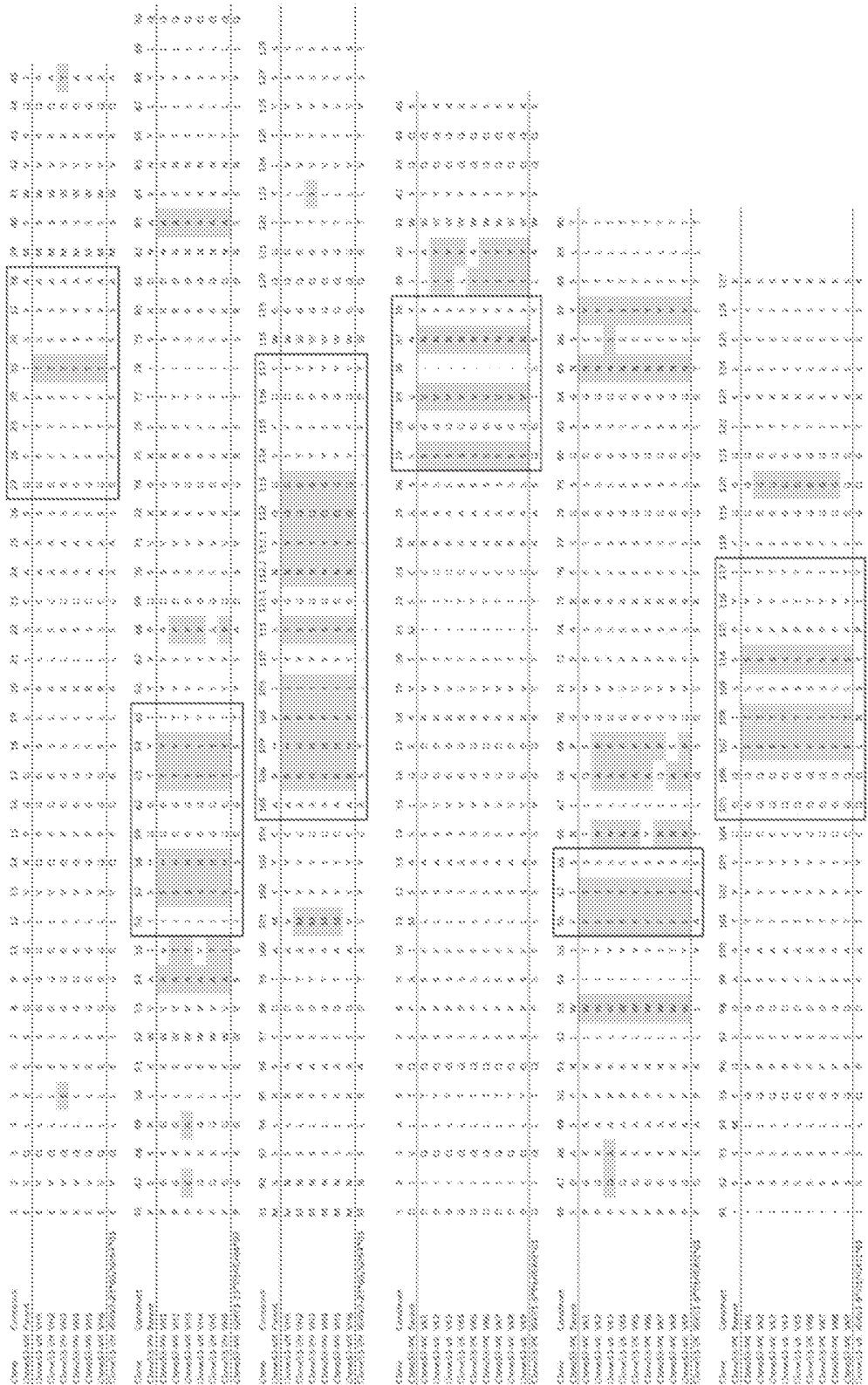


Fig. 17C

[illegible]

Fig. 17D

[illegible]

Fig. 17E

Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
Class	Constraint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
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Class	Constraint	1	2	3																																

Fig. 17F

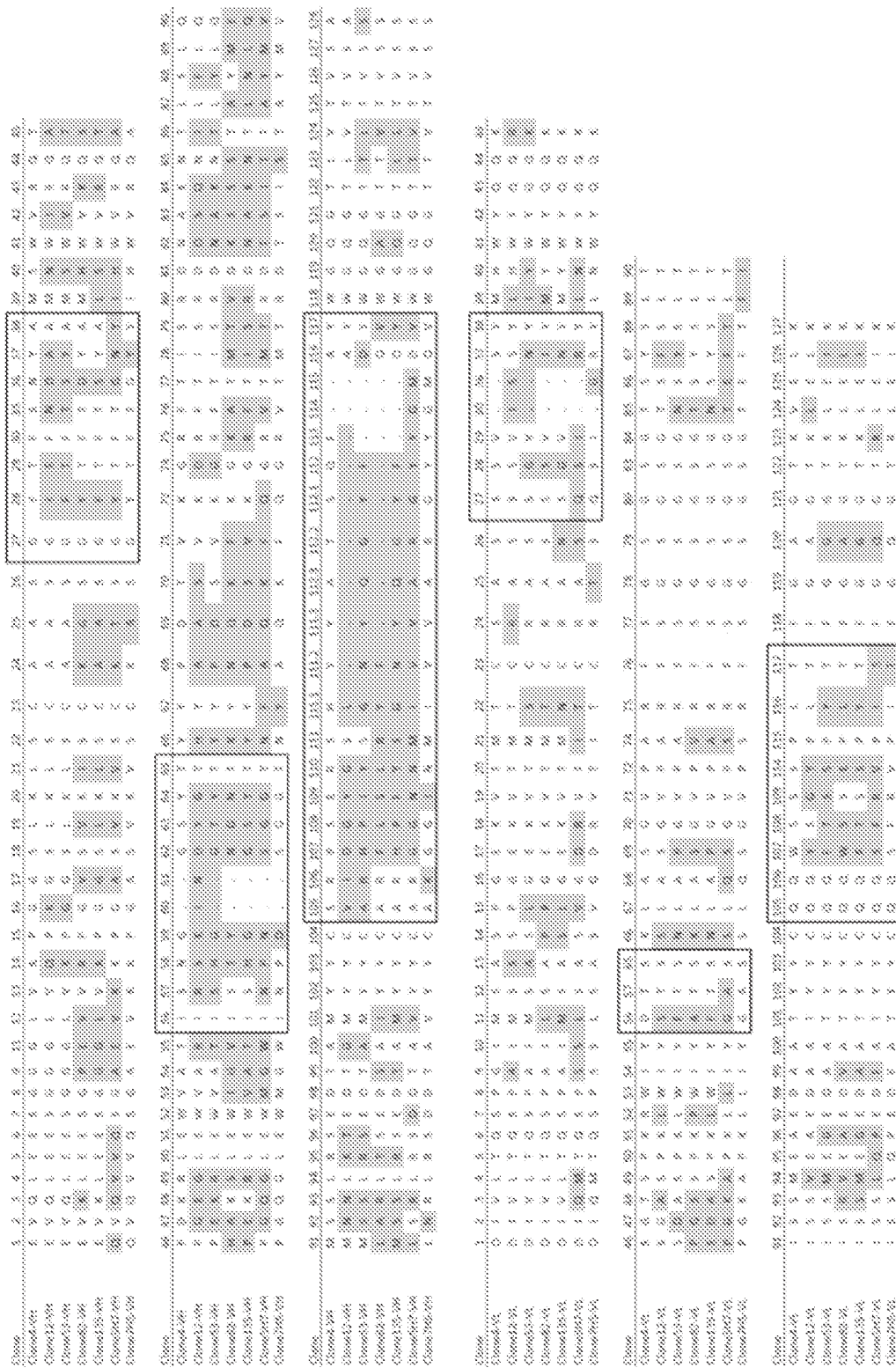


Fig. 17H



Fig. 18

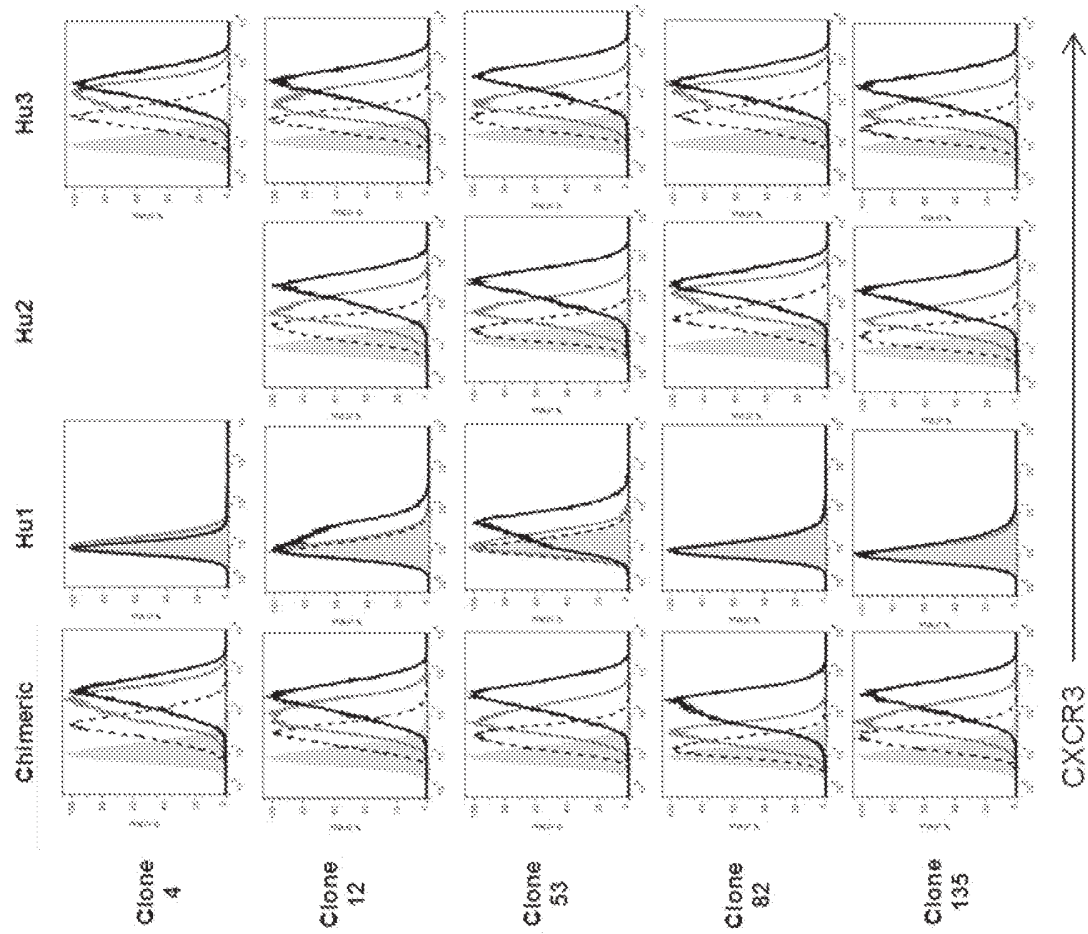


Fig. 19

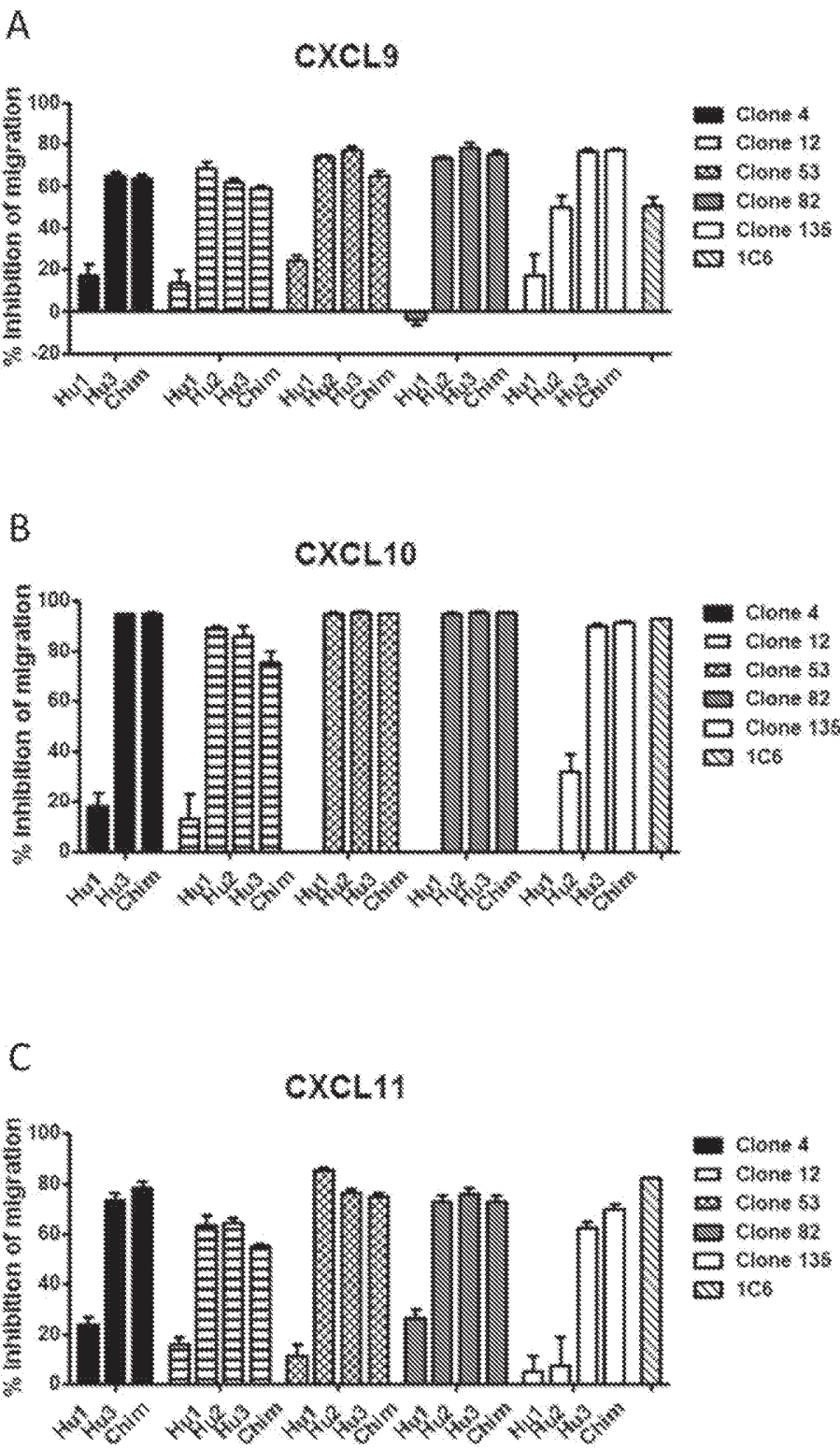


Fig. 20

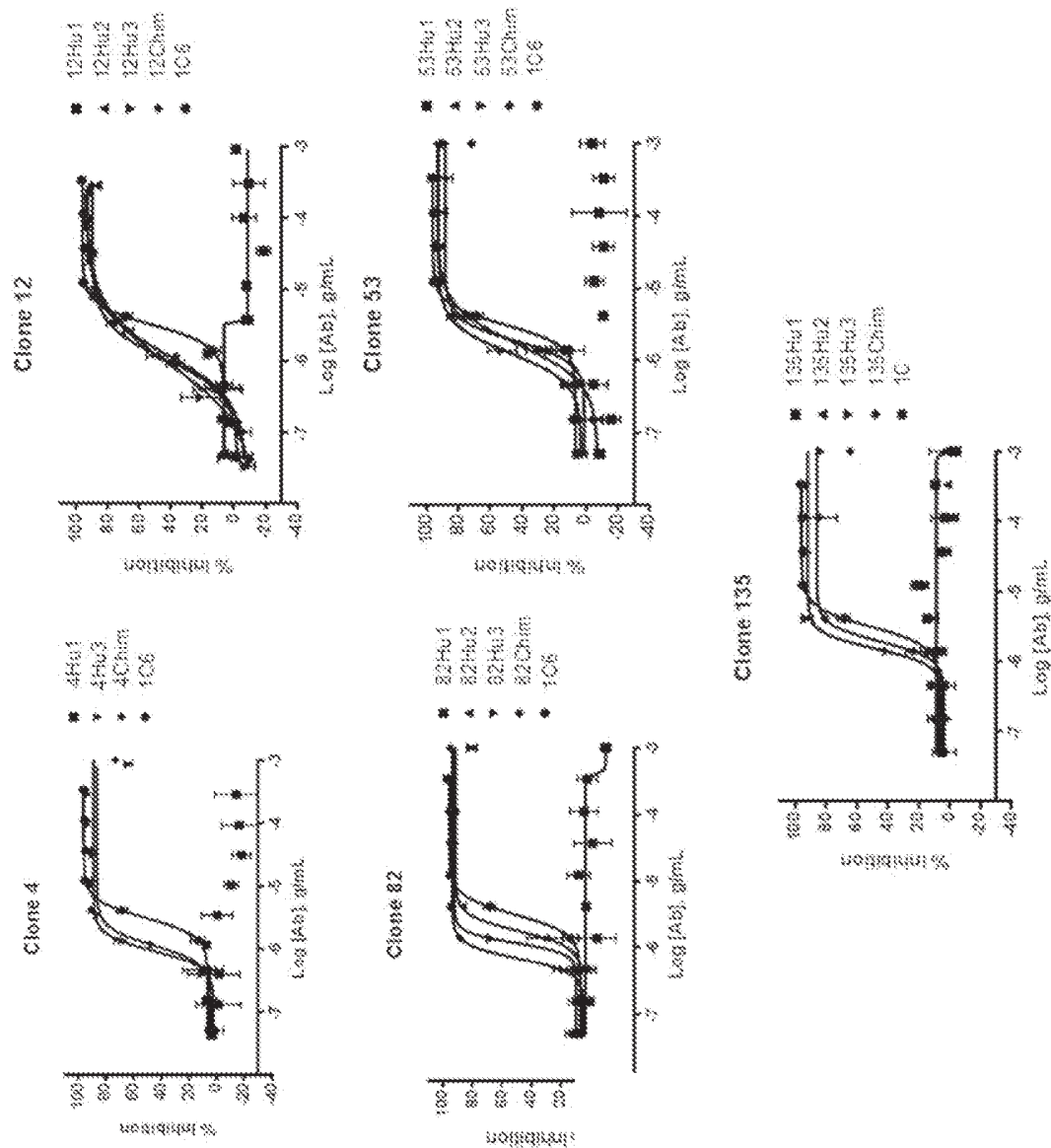
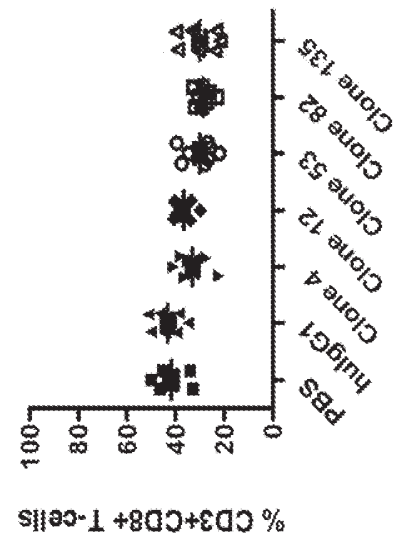
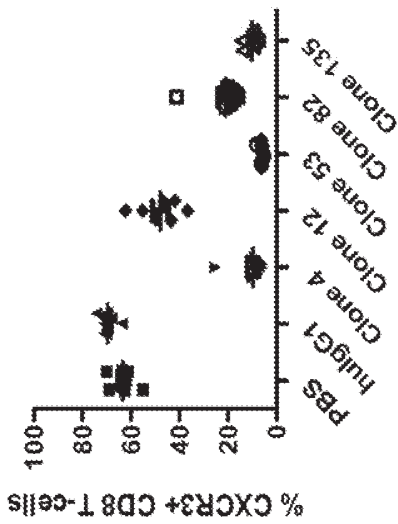


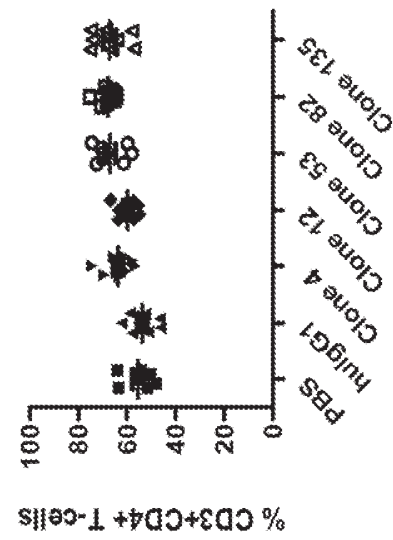
Fig. 21



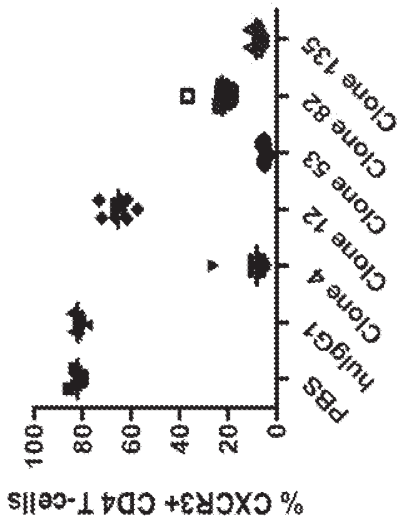
A.



B.



C.



D.

Fig. 22

Clone 12.0 - VH amino acid sequence
 - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLEESGGGLVQPKGSLKLSCAAS**GISFNDA**AMNWIRQAPGEGLEWVAR
 60 70 80 90 100
IRSKINDYGTHYAASVKDRFTISRDDSQNILFLQMNNLKTEDTGMYYC**VI**
 110
DGYGSLAYWGQGTlVTVSA (SEQ ID NO: 2)

Clone 12.0 - VL amino acid sequence
 - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPAIMSSSPGEEKVTMTCRAS**SSVISSY**LHWYQQRSGASPKLWIY
 60 70 80 90 100
STSSLASGVPARFSGSGSGTSFSLTISSVEAEDAATYYC**QQYSGYPLT**FG
 AGTKLELK (SEQ ID NO: 3)

SEQ ID NO	Region	Sequence
Heavy Chain		
115	FR1	EVQLEESGGGLVQPKGSLKLSCAAS
116	CDR1	<u>GISFNDA</u>
117	FR2	MNWIRQAPGEGLEWVAR
118	CDR2	<u>IRSKINDYGT</u>
119	FR3	HYAASVKDRFTISRDDSQNILFLQMNNLKTEDTGMYYC
120	CDR3	<u>VIDGYGSLAY</u>
121	FR4	WGQGTlVTVSA
Light Chain		
122	FR1	DIVLTQSPAIMSSSPGEEKVTMTCRAS
123	CDR1	<u>SSVISSY</u>
124	FR2	LHWYQQRSGASPKLWIY
125	CDR2	<u>STS</u>
126	FR3	SLASGVPARFSGSGSGTSFSLTISSVEAEDAATYYC
127	CDR3	<u>QQYSGYPLT</u>
128	FR4	FGAGTKLELK

Fig. 23A

Clone 12.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLVESGGGLVQPGGSLKLSKAASGISFNDAAMHWVRQASGKGLEWVAR

           60           70           80           90           100
IRSKINDYGTAYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAVYYCVI

           110
DGYGSLAYWGQGLTVTVSS (SEQ ID NO: 4)

```

Clone 12.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCRASSSVISSYLAWYQQKPGQAPRLWIY

           60           70           80           90           100
STSNRATGIPARFSGSGSGTDFTLTISSELEPEDFATYYCQQYSGYPLTFG

GGTKVEIK (SEQ ID NO: 5)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
129	FR1	EVQLVESGGGLVQPGGSLKLSKAAS
130	CDR1	<u>GISFNDA</u>
131	FR2	MHWVRQASGKGLEWVAR
132	CDR2	<u>IRSKINDYGT</u>
133	FR3	AYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAVYYC
134	CDR3	<u>VIDGYGSLAY</u>
135	FR4	WGQGLTVTVSS
Light Chain		
136	FR1	EIVLTQSPATLSLSPGERATLSCRAS
137	CDR1	<u>SSVISSY</u>
138	FR2	LAWYQQKPGQAPRLWIY
139	CDR2	<u>STS</u>
140	FR3	NRATGIPARFSGSGSGTDFTLTISSELEPEDFATYYC
141	CDR3	<u>QQYSGYPLT</u>
142	FR4	FGGGTKVEIK

Fig. 23B

Clone 12.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLVESGGGLVQPGGSLKLSCAASGISFNDAAMNWIRQASGKGLEWVAR

           60           70           80           90           100
IRSKINDYGTHYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAMYYCVI

           110
DGYGSLAYWGQGTLLVTVSS  (SEQ ID NO: 6)

```

Clone 12.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCRASSSVISSYLHWYQQKPGQAPRLWIY

           60           70           80           90           100
STSSLASGIPARFSGSGSGTDFTLTISSELPEDFATYYCQQYSGYPLTFG

AGTKVEIK  (SEQ ID NO: 7)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
143	FR1	EVQLVESGGGLVQPGGSLKLSCAAS
144	CDR1	<u>GISFNDA</u>
145	FR2	MNWIRQASGKGLEWVAR
146	CDR2	<u>IRSKINDYGT</u>
147	FR3	HYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAMYYC
148	CDR3	<u>VIDGYGSLAY</u>
149	FR4	WGQGTLLVTVSS
Light Chain		
150	FR1	EIVLTQSPATLSLSPGERATLSCRAS
151	CDR1	<u>SSVISSY</u>
152	FR2	LHWYQQKPGQAPRLWIY
153	CDR2	<u>STS</u>
154	FR3	SLASGIPARFSGSGSGTDFTLTISSELPEDFATYYC
155	CDR3	<u>QQYSGYPLT</u>
156	FR4	FGAGTKVEIK

Fig. 23C

Clone 12.3 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGLVQPKGSLKLSCAAS**GISFNDAAM**NWIRQASGKGLEWVAR
 60 70 80 90 100
IRSKINDYGTHYAASVKDRFTISRDDSQNILYLQMNNLKTEDTAMYYC**VI**
 110
DGYGSLAYWGQGLTVTVSS (SEQ ID NO: 8)

Clone 12.3 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EIVLTQSPAILSSSPGERATLSCRAS**SSVISSY**LHWYQQKPGAAPRLWIY
 60 70 80 90 100
STSSLASGIPARFSGSGSGTSFTLTISSELEAEDFATYYC**QQYSGYPLT**FG
 AGTKVEIK (SEQ ID NO: 9)

SEQ ID NO	Region	Sequence
Heavy Chain		
157	FR1	EVQLVESGGGLVQPKGSLKLSCAAS
158	CDR1	<u>GISFNDAAM</u>
159	FR2	MNWIRQASGKGLEWVAR
160	CDR2	<u>IRSKINDYGT</u>
161	FR3	HYAASVKDRFTISRDDSQNILYLQMNNLKTEDTAMYYC
162	CDR3	<u>VIDGYGSLAY</u>
163	FR4	WGQGLTVTVSS
Light Chain		
164	FR1	EIVLTQSPAILSSSPGERATLSCRAS
165	CDR1	<u>SSVISSY</u>
166	FR2	LHWYQQKPGAAPRLWIY
167	CDR2	<u>STS</u>
168	FR3	SLASGIPARFSGSGSGTSFTLTISSELEAEDFATYYC
169	CDR3	<u>QQYSGYPLT</u>
170	FR4	FGAGTKVEIK

Fig. 23D

Clone 135.0 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVKLEESGGGLVLPKPGGSLKLSAAS**GFTFTSYA**LSWVRQTPEKRLEWVAT
 60 70 80 90 100
ISHGGSYTYYPDSVKGRFTISRDNKNTLNLQMSSLRSEDAMYYC**ARHP**
 110 120
FYSGNYQGYFDYWGQGTLLTVSS (SEQ ID NO: 10)

Clone 135.0 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPAISASLGEKVTMNCRA**SGVNY**MYWYQQKSDASPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISMEGEDAATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 11)

SEQ ID NO	Region	Sequence
Heavy Chain		
171	FR1	EVKLEESGGGLVLPKPGGSLKLSAAS
172	CDR1	<u>GFTFTSYA</u>
173	FR2	LSWVRQTPEKRLEWVAT
174	CDR2	<u>ISHGGSYT</u>
175	FR3	YYPDSVKGRFTISRDNKNTLNLQMSSLRSEDAMYYC
176	CDR3	<u>ARHPFYSGNYQGYFDY</u>
177	FR4	WGQGTLLTVSS
Light Chain		
178	FR1	DIVLTQSPAISASLGEKVTMNCRA
179	CDR1	<u>SGVNY</u>
180	FR2	MYWYQQKSDASPKLWIY
181	CDR2	<u>FTS</u>
182	FR3	NLAPGV <u>PARFSGSGSGNSYSLTISMEGEDAATYYC</u>
183	CDR3	<u>QQFTSSPYT</u>
184	FR4	FGGGTKLEIK

Fig. 24A

Clone 135.1 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLEESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAV
 60 70 80 90 100
ISHGGSYTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC**ARHP**
 110 120
FYSGNYQGYFDYWGQGLTVTVSS (SEQ ID NO: 12)

Clone 135.1 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVITITCRAS**SGVNY**LAWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
STLQSGVPSRFSSGSGSGNEYTLTISSLQFEDFATYYC**QQFTSSPYT**FGQG
 TKLEIK (SEQ ID NO: 13)

SEQ ID NO	Region	Sequence
Heavy Chain		
185	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
186	CDR1	GFTFTSYA
187	FR2	MSWVRQAPGKGLEWVAV
188	CDR2	ISHGGSYT
189	FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
190	CDR3	ARHPFYSGNYQGYFDY
191	FR4	WGQGLTVTVSS
Light Chain		
192	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
193	CDR1	SGVNY
194	FR2	LAWYQQKPGKAPKLWIY
195	CDR2	FTS
196	FR3	TLQSGVPSRFS
197	CDR3	QQFTSSPYT
198	FR4	FGQGTKLEIK

Fig. 24B

Clone 135.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFTSYALSWVRQAPGKGLEWVAT

           60           70           80           90           100
ISHGGSYTYYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHP

           110          120
FYSGNYQGYFDYWGQGLTVTVSS    (SEQ ID NO: 14)

```

Clone 135.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFLSASVGDRVITTCRANSGVNYMYWYQQKPGKAPKLWIYFT

           60           70           80           90           100
SNLAPGVPSRFSGSGSGNEYTTLTISSLQFEDFATYYCQQFTSSPYTFGGG

TKLEIK    (SEQ ID NO: 15)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
199	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
200	CDR1	<u>GFTFTSYA</u>
201	FR2	LSWVRQAPGKGLEWVAT
202	CDR2	<u>ISHGGSYT</u>
203	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
204	CDR3	<u>ARHPFYSGNYQGYFDY</u>
205	FR4	WGQGLTVTVSS
Light Chain		
206	FR1	DIQLTQSPSFLSASVGDRVITTCRAN
207	CDR1	<u>SGVNY</u>
208	FR2	MYWYQQKPGKAPKLWIY
209	CDR2	<u>FTS</u>
210	FR3	<u>N</u> LAPGVPSRFSGSGSGNEYTTLTISSLQFEDFATYYC
211	CDR3	<u>QQFTSSPYT</u>
212	FR4	FGGGTKLEIK

Fig. 24C

Clone 135.3 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**LSWVRQTPEKRLEWVAT
 60 70 80 90 100
ISHGGSYTYYPDSVKGRFTISRDNSKNTLNLQMSSSLRAEDTAVYYC**ARHP**
 110 120
FYSGNYQGYFDYWGQGTLVTVSS (SEQ ID NO: 16)

Clone 135.3 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTITCRAN**SGVNY**MYWYQQKPDAAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNSYTLTISSLQFEDFATYYC**QQFTSSPYT**FGGG
 TKLEIK (SEQ ID NO: 17)

SEQ ID NO	Region	Sequence
Heavy Chain		
213	FR1	EVQLLES GGGLVQ PGGSLRLSCAAS
214	CDR1	<u>GFTFTSYA</u>
215	FR2	LSWVRQTPEKRLEWVAT
216	CDR2	<u>ISHGGSYT</u>
217	FR3	YYPDSVKGRFTISRDN SKNTLNLQ MSSSLRAEDTAVYYC
218	CDR3	<u>ARHPFYSGNYQGYFDY</u>
219	FR4	WGQGT LVT VSS
Light Chain		
220	FR1	DIQLTQSPSFLSASVGDRV TITCRAN
221	CDR1	<u>SGVNY</u>
222	FR2	MYWYQQKPDAA PKLWIY
223	CDR2	<u>FTS</u>
224	FR3	<u>N</u> LAPGVPSRFS GSGSGNSYTLT IS SLQ FEDFATYYC
225	CDR3	<u>QQFTSSPYT</u>
226	FR4	FGGGTKLEIK

Fig. 24D

Clone 4.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVLPKPGGSLKLSKAASGFTFSNYAMSWVRQTPDKRLEWVAT

           60           70           80           90           100
ISNGGSYTYYPDTVKGRFTISRDNKNTLSLQMSLRSEDTAMYCYSRPS

           110          120
ERSHYYATSQFAYWGQGLTVTVSA    (SEQ ID NO: 18)

```

Clone 4.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPGIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDT

           60           70           80           90           100
SKLASGVPARFSGSGSGTSYSLTISSEAEADAATYYCQQWSSSPLTFGAG

TKVELK    (SEQ ID NO: 19)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
227	FR1	EVQLEESGGGLVLPKPGGSLKLSKAAS
228	CDR1	<u>GFTFSNYA</u>
229	FR2	MSWVRQTPDKRLEWVAT
230	CDR2	<u>ISNGGSYT</u>
231	FR3	YYPDTVKGRFTISRDNKNTLSLQMSLRSEDTAMYCY
232	CDR3	<u>SRPSERSHYYATSQFAY</u>
233	FR4	WGQGLTVTVSA
Light Chain		
234	FR1	DIVLTQSPGIMSASPGEKVTMTCSAS
235	CDR1	<u>SSVSY</u>
236	FR2	MHWYQQKSGTSPKRWIY
237	CDR2	<u>DTS</u>
238	FR3	KLASGVPARFSGSGSGTSYSLTISSEAEADAATYYC
239	CDR3	<u>QQWSSSPLT</u>
240	FR4	FGAGTKVELK

Fig. 25A

Clone 4.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVAV

           60           70           80           90           100
ISNGGSYTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCSRPS

           110          120
ERSHYYATSQFAYWGQGTLTVVSS      (SEQ ID NO: 20)

```

Clone 4.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCRASSSVSYLAWYQQKPGQAPRRWIYDT

           60           70           80           90           100
SNRATGIPARFSGSGSGTDYTLTISSLEPEDFAVYYCQQWSSSPLTFGGG

TKVEIK      (SEQ ID NO: 21)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
241	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
242	CDR1	<u>GFTFSNYA</u>
243	FR2	MSWVRQAPGKGLEWVAV
244	CDR2	<u>ISNGGSYT</u>
245	FR3	YYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
246	CDR3	<u>SRPSERSHYYATSQFAY</u>
247	FR4	<u>WGQGT</u> LTVSS
Light Chain		
248	FR1	EIVLTQSPATLSLSPGERATLSCRAS
249	CDR1	<u>SSVSY</u>
250	FR2	LAWYQQKPGQAPRRWIY
251	CDR2	<u>DTS</u>
252	FR3	<u>NRATGIPARFSGSGSGTDYTLTIS</u> SLEPEDFAVYYC
253	CDR3	<u>QQWSSSPLT</u>
254	FR4	<u>FGGGT</u> KVEIK

Fig. 25B

Clone 4.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVAT

           60           70           80           90           100
ISNGGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCSRPS

           110          120
ERSHYYATSQFAYWGQGTLVTVSS   (SEQ ID NO: 22)

```

Clone 4.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGTAPRRWIYDT

           60           70           80           90           100
SKLASGIPARFSGSGSGTDYTLTISSLEPEDFATYYCQQWSSSPLTFGAG

TKVEIK   (SEQ ID NO: 23)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
255	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
256	CDR1	<u>GFTFSNYA</u>
257	FR2	MSWVRQAPGKGLEWVAT
258	CDR2	<u>ISNGGSYT</u>
259	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYC
260	CDR3	<u>SRPSERSHYYATSQFAY</u>
261	FR4	<u>WGQGT</u> LVTVSS
Light Chain		
262	FR1	EIVLTQSPATLSLSPGERATLSCSAS
263	CDR1	<u>SSVSY</u>
264	FR2	MHWYQQKPGTAPRRWIY
265	CDR2	<u>DTS</u>
266	FR3	<u>KL</u> ASGIPARFSGSGSGTDYTLTIS SLEPED FATYYC
267	CDR3	<u>QQWSSSPLT</u>
268	FR4	<u>FGAG</u> TKVEIK

Fig. 25C

Clone 4.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQTPDKRLEWVAT

           60           70           80           90           100
ISNGGSYTYYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYCSRPS

           110          120
ERSHYYATSQFAYWGQGLTVTVSS    (SEQ ID NO: 24)

```

Clone 4.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPAILSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRRWIYDT

           60           70           80           90           100
SKLASGIPARFSGSGSGTSYTLTISSLEAEDFATYYCQQWSSSPLTFGAG

TKVEIK    (SEQ ID NO: 25)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
269	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
270	CDR1	<u>GFTFSNYA</u>
271	FR2	MSWVRQTPDKRLEWVAT
272	CDR2	<u>ISNGGSYT</u>
273	FR3	YYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYC
274	CDR3	<u>SRPSERSHYYATSQFAY</u>
275	FR4	WGQGLTVTVSS
Light Chain		
276	FR1	EIVLTQSPAILSLSPGERATLSCSAS
277	CDR1	<u>SSVSY</u>
278	FR2	MHWYQQKPGQAPRRWIY
279	CDR2	<u>DTS</u>
280	FR3	KLASGIPARFSGSGSGTSYTLTIS <u>SLEA</u> EDFATYYC
281	CDR3	<u>QQWSSSPLT</u>
282	FR4	FGAGTKVEIK

Fig. 25D

Clone 4.4 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT
 60 70 80 90 100
ISNGGSYTYYPDSFQGRFTISRDNASTLSLQMSLKSEDTAMYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLLTVSA (SEQ ID NO: 26)

SEQ ID NO	Region	Sequence
Heavy Chain		
283	FR1	EVQLVESGGGVKKPGGSLKLSCAAS
284	CDR1	<u>GFTFSNYA</u>
285	FR2	MSWVRQTPGKGLEWVAT
286	CDR2	<u>ISNGGSYT</u>
287	FR3	YYPDSFQGRFTISRDNASTLSLQMSLKSEDTAMYYC
288	CDR3	<u>ERSHYATSQFAY</u>
289	FR4	WGQGTLLTVSA

Fig. 25E

Clone 4.5 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT
 60 70 80 90 100
ISNGGSYTYYPDSFQGRFTISRDNASTLSLQMSLKAEDTAMYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLLVTVSS (SEQ ID NO: 27)

SEQ ID NO	Region	Sequence
Heavy Chain		
290	FR1	EVQLVESGGGVKKPGGSLKLSCAAS
291	CDR1	GFTFSNYA
292	FR2	MSWVRQTPGKGLEWVAT
293	CDR2	ISNGGSYT
294	FR3	YYPDSFQGRFTISRDNASTLSLQMSLKAEDTAMYYC
295	CDR3	SRPSERSHYATSQFAY
296	FR4	WGQGTLLVTVSS

Fig. 25F

Clone 4.6 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT

60 70 80 90 100
ISQGGSYTYYPESFQGRFTISRDKAKSTLSLQMSLKSSEDAMYYC**SRPS**

110 120
ERSHYATSQFAYWGQGTLLTVSA (SEQ ID NO: 28)

SEQ ID NO	Region	Sequence
Heavy Chain		
297	FR1	EVQLVESGGGVKKPGGSLKLSCAAS
298	CDR1	GFTFSNYA
299	FR2	MSWVRQTPGKGLEWVAT
300	CDR2	ISQGGSYT
301	FR3	YYPESFQGRFTISRDKAKSTLSLQMSLKSSEDAMYYC
302	CDR3	SRPSERSHYATSQFAY
303	FR4	WGQGTLLTVSA

Fig. 25G

Clone 4.7 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISQGGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYYATSQFAYWGQGTLVTVSS (SEQ ID NO: 29)

SEQ ID NO	Region	Sequence
Heavy Chain		
304	FR1	EVQLLES GGGLVQPGGSLRLS CAAS
305	CDR1	<u>GFTFSNYA</u>
306	FR2	MSWVRQAPGKGLEWVAT
307	CDR2	<u>ISQGGSYT</u>
308	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
309	CDR3	<u>ERSHYYATSQFAY</u>
310	FR4	WGQGT LVT VSS

Fig. 25H

Clone 4.8 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT

 60 70 80 90 100
ISNLGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**SRPS**

 110 120
ERSHYYATSQFAYWGQGTLVTVSS (SEQ ID NO: 30)

SEQ ID NO	Region	Sequence
Heavy Chain		
311	FR1	EVQLLES GGGLVQPGGSLRLSCAAS
312	CDR1	<u>GFTFSNYA</u>
313	FR2	MSWVRQAPGKGLEWVAT
314	CDR2	<u>ISNLGSYT</u>
315	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
316	CDR3	<u>ERSHYYATSQFAY</u>
317	FR4	WGQGT LVT VSS

Fig. 25I

Clone 4.9 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISNSGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYYATSQFAYWGQGTLVTVSS (SEQ ID NO: 31)

SEQ ID NO	Region	Sequence
Heavy Chain		
318	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
319	CDR1	<u>GFTFSNYA</u>
320	FR2	MSWVRQAPGKGLEWVAT
321	CDR2	<u>ISNSGSYT</u>
322	FR3	YYPDSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
323	CDR3	<u>ERSHYYATSQFAY</u>
324	FR4	WGQGT LVT VSS

Fig. 25J

Clone 4.10 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISDGGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYYATSQFAYWGQGTLVTVSS (SEQ ID NO: 32)

SEQ ID NO	Region	Sequence
Heavy Chain		
325	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
326	CDR1	<u>GFTFSNYA</u>
327	FR2	MSWVRQAPGKGLEWVAT
328	CDR2	<u>ISDGGSYT</u>
329	FR3	YYPDSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
330	CDR3	<u>ERSHYYATSQFAY</u>
331	FR4	WGQGT LVT VSS

Fig. 25K

Clone 4.11 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT

 60 70 80 90 100
ISNVGSYTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**SRPS**

 110 120
ERSHYATSQFAYWGQGTLVTVSS (SEQ ID NO: 33)

SEQ ID NO	Region	Sequence
Heavy Chain		
332	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
333	CDR1	<u>GFTFSNYA</u>
334	FR2	MSWVRQAPGKGLEWVAT
335	CDR2	<u>ISNVGSYT</u>
336	FR3	YYPDSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
337	CDR3	<u>ERSHYATSQFAY</u>
338	FR4	WGQGT LVT VSS

Fig. 25L

Clone 4.4 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPGSLASVGDRVMTCSAS**SSVSY**MHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVELK (SEQ ID NO: 34)

SEQ ID NO	Region	Sequence
Light Chain		
339	FR1	DIVLTQSPGSLASVGDRVMTCSAS
340	CDR1	<u>SSVSY</u>
341	FR2	MHWYQQKPGTSPKRWIY
342	CDR2	<u>DTS</u>
343	FR3	KLASGVPARFSGSGSGTSYSLTISSSLQPEDAATYYC
344	CDR3	<u>QQWSSSPLT</u>
345	FR4	FGAGTKVELK

Fig. 25M

Clone 4.5 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPSSLSASVGDRVTITCSAS**SSVSY**MHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVEIK (SEQ ID NO: 35)

SEQ ID NO	Region	Sequence
Light Chain		
346	FR1	DIVLTQSPSSLSASVGDRVTITCSAS
347	CDR1	<u>SSVSY</u>
348	FR2	MHWYQQKPGTSPKRWIY
349	CDR2	<u>DTS</u>
350	FR3	KLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC
351	CDR3	<u>QQWSSSPLT</u>
352	FR4	FGAGTKVEIK

Fig. 25N

Clone 4.6 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPSSLSASVGDRVTITCSAS**SSVSY**MHWYQQKPGQSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVEIK (SEQ ID NO: 36)

SEQ ID NO	Region	Sequence
Light Chain		
353	FR1	DIVLTQSPSSLSASVGDRVTITCSAS
354	CDR1	<u>SSVSY</u>
355	FR2	MHWYQQKPGQSPKRWIY
356	CDR2	<u>DTS</u>
357	FR3	KLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC
358	CDR3	<u>QQWSSSPLT</u>
359	FR4	FGAGTKVEIK

Fig. 25O

Clone 4.7 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPGSLASVGDRVTMTCSAS**SSVSY**MHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVELK (SEQ ID NO: 37)

SEQ ID NO	Region	Sequence
Light Chain		
360	FR1	DIQLTQSPGSLASVGDRVTMTCSAS
361	CDR1	SSVSY
362	FR2	MHWYQQKPGTSPKRWIY
363	CDR2	DTS
364	FR3	KLASGVPARFSGSGSGTSYSLTISSSLQPEDAATYYC
365	CDR3	QQWSSSPLT
366	FR4	FGAGTKVELK

Fig. 25P

Clone 53.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVKPGGSLKLSCAASGFTFTSYAMSWVRQTPEKRLEWVAT

           60           70           80           90           100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDAMYYCCARHP

           110          120
IYSGNYQGIFYDYWGQGTTLTVSS  (SEQ ID NO: 38)

```

Clone 53.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPAISASLGEKVTMSCRASSGVNYIYWYQQKSDASPKLWIYFT

           60           70           80           90           100
SNLAPGVPARFSGSGSGNSYSLTISMEGEDAATYYCQQFTSSPYTFGGG

TKLEIK  (SEQ ID NO: 39)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
367	FR1	EVQLEESGGGLVKPGGSLKLSCAAS
368	CDR1	<u>GFTFTSYA</u>
369	FR2	MSWVRQTPEKRLEWVAT
370	CDR2	<u>ISHGGTYT</u>
371	FR3	YYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDAMYYC
372	CDR3	<u>ARHPIYSGNYQGIFYDY</u>
373	FR4	WGQGTTLTVSS
Light Chain		
374	FR1	DIVLTQSPAISASLGEKVTMSCRAS
375	CDR1	<u>SGVNY</u>
376	FR2	IYWYQQKSDASPKLWIY
377	CDR2	<u>FTS</u>
378	FR3	NLAPGVPARFSGSGSGNSYSLTISMEGEDAATYYC
379	CDR3	<u>QQFTSSPYT</u>
380	FR4	FGGGTKLEIK

Fig. 26A

Clone 53.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVAV

           60           70           80           90           100
ISHGGTYTYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARHP

           110          120
IYSGNYQGYFDYWGQGLTVTVSS  (SEQ ID NO: 40)

```

Clone 53.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFLSASVGDRVITITCRASSGVNYLAWYQQKPGKAPKLWIYFT

           60           70           80           90           100
STLQSGVPSRFSSGSGSGNEYTLTISSLQPEDFATYYCQQFTSSPYTFGQG

TKLEIK  (SEQ ID NO: 41)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
381	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
382	CDR1	<u>GFTFTSYA</u>
383	FR2	MSWVRQAPGKGLEWVAV
384	CDR2	<u>ISHGGTYT</u>
385	FR3	YYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC
386	CDR3	<u>ARHP</u> IYSGNYQGYFDY
387	FR4	WGQGLTVTVSS
Light Chain		
388	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
389	CDR1	<u>SGVNY</u>
390	FR2	LAWYQQKPGKAPKLWIY
391	CDR2	<u>FTS</u>
392	FR3	<u>STLQSGVPSRFS</u> SGSGSGNE YTLTISS LQPEDFATYYC
393	CDR3	<u>QQFTSSPYT</u>
394	FR4	FGQG <u>TKLEIK</u>

Fig. 26B

Clone 53.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVAT

           60           70           80           90           100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYCARHP

           110          120
IYSGNYQGYFDYWGQGLTVTVSS    (SEQ ID NO: 42)

```

Clone 53.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFLSASVGDRVITITCRASSGVNYIYWYQQKPGKAPKLWIYFT

           60           70           80           90           100
SNLAPGVPSRFSGSGSGNEYTTLTISLQPEDFATYYCQQFTSSPYTFGGG

TKLEIK    (SEQ ID NO: 43)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
395	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
396	CDR1	<u>GFTFTSYA</u>
397	FR2	MSWVRQAPGKGLEWVAT
398	CDR2	<u>ISHGGTYT</u>
399	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
400	CDR3	<u>ARHP</u> IYSGNYQGYFDY
401	FR4	WGQGLTVTVSS
Light Chain		
402	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
403	CDR1	<u>SGVNY</u>
404	FR2	IYWYQQKPGKAPKLWIY
405	CDR2	<u>FTS</u>
406	FR3	<u>SN</u> LAPGVPSRFSGSGSGNEYTTLTISLQPEDFATYYC
407	CDR3	<u>QQFTSSPYT</u>
408	FR4	FGGGTKLEIK

Fig. 26C

Clone 53.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQTPEKRLEWVAT

           60           70           80           90           100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYCARHP

           110          120
IYSGNYQGYFDYWGQGTTVTVSS  (SEQ ID NO: 44)

```

Clone 53.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFLSASVGDRVITTCRASSGVNYIYWYQQKPDAAAPKLWIYFT

           60           70           80           90           100
SNLAPGVPSRFSGSGSGNSYTLTISSLQPEDFATYYCQQFTSSPYTFGGG

TKLEIK  (SEQ ID NO: 45)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
409	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
410	CDR1	<u>GFTFTSYA</u>
411	FR2	MSWVRQTPEKRLEWVAT
412	CDR2	<u>ISHGGTYT</u>
413	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
414	CDR3	<u>ARHP</u> IYSGNYQGYFDY
415	FR4	WGQGTTVTVSS
Light Chain		
416	FR1	DIQLTQSPSFLSASVGDRVITTCRAS
417	CDR1	<u>SGVNY</u>
418	FR2	IYWYQQKPDAAAPKLWIY
419	CDR2	<u>FTS</u>
420	FR3	<u>SN</u> LAPGVPSRFSGSGSGNSYTLTISSLQPEDFATYYC
421	CDR3	<u>QQFTSSPYT</u>
422	FR4	FGGGTKLEIK

Fig. 26D

Clone 53.4 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAV
 60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGLTVTVSS (SEQ ID NO: 46)

SEQ ID NO	Region	Sequence
Heavy Chain		
423	FR1	EVQLLES GGGLVQ PGGSLRLSCAAS
424	CDR1	<u>GFTFTSYA</u>
425	FR2	MSWVRQAPGKGLEWVAV
426	CDR2	<u>ISHGGTYT</u>
427	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
428	CDR3	<u>ARHPIYSGNYQGYFDY</u>
429	FR4	WGQGLTVTVSS

Fig. 26E

Clone 53.5 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTLVTVSS (SEQ ID NO: 47)

SEQ ID NO	Region	Sequence
Heavy Chain		
430	FR1	EVQLLES GGGLVQPGGSLRLS CAAS
431	CDR1	<u>GFTFTSYA</u>
432	FR2	MSWVRQAPGKGLEWVAT
433	CDR2	<u>ISHGGTYT</u>
434	FR3	YYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
435	CDR3	<u>ARHPIYSGNYQGYFDY</u>
436	FR4	WGQGT LVT VSS

Fig. 26F

Clone 53.6 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT

60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC**ARHP**

110 120
IYSGNYQGYFDYWGQGTLTVTVSS (SEQ ID NO: 48)

SEQ ID NO	Region	Sequence
Heavy Chain		
437	FR1	EVQLLES GGGLVQPGGSLRL SCAAS
438	CDR1	<u>GFTFTSYA</u>
439	FR2	MSWVRQAPGKGLEWVAT
440	CDR2	<u>ISHGGTYT</u>
441	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC
442	CDR3	<u>ARHPIYSGNYQGYFDY</u>
443	FR4	WGQGT L TVTVSS

Fig. 26G

Clone 53.4 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTTTCRAS**SGVNY**LYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGGG

TKLEIK (**SEQ ID NO: 49**)

SEQ ID NO	Region	Sequence
Light Chain		
444	FR1	DIQLTQSPSFLSASVGDRVTTTCRAS
445	CDR1	<u>SGVNY</u>
446	FR2	LYWYQQKPGKAPKLWIY
447	CDR2	<u>FTS</u>
448	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
449	CDR3	<u>QQFTSSPYT</u>
450	FR4	FGGGTKLEIK

Fig. 26H

Clone 53.5 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTTTCRAS**SGVNY**IAWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 50)

SEQ ID NO	Region	Sequence
Light Chain		
451	FR1	DIQLTQSPSFLSASVGDRVTTTCRAS
452	CDR1	SGVNY
453	FR2	IAWYQQKPGKAPKLWIY
454	CDR2	FTS
455	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
456	CDR3	QQFTSSPYT
457	FR4	FGGGTKLEIK

Fig. 26I

Clone 53.6 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTTTCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
STLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 51)

SEQ ID NO	Region	Sequence
Light Chain		
458	FR1	DIQLTQSPSFLSASVGDRVTTTCRAS
459	CDR1	SGVNY
460	FR2	IYWYQQKPGKAPKLWIY
461	CDR2	FTS
462	FR3	TLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
463	CDR3	QQFTSSPYT
464	FR4	FGGGTKLEIK

Fig. 26J

Clone 53.7 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVITITCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLQPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 52)

SEQ ID NO	Region	Sequence
Light Chain		
465	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
466	CDR1	SGVNY
467	FR2	IYWYQQKPGKAPKLWIY
468	CDR2	FTS
469	FR3	NLQPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
470	CDR3	QQFTSSPYT
471	FR4	FGGGTKLEIK

Fig. 26K

Clone 53.8 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTTTCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLASGVPSRFSGSGSGGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 53)

SEQ ID NO	Region	Sequence
Light Chain		
472	FR1	DIQLTQSPSFLSASVGDRVTTTCRAS
473	CDR1	SGVNY
474	FR2	IYWYQQKPGKAPKLWIY
475	CDR2	FTS
476	FR3	NLASGVPSRFSGSGSGGNEYTLTISSLQPEDFATYYC
477	CDR3	QQFTSSPYT
478	FR4	FGGGTKLEIK

Fig. 26L

Clone 53.9 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVTTTCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPY**TFGQG

TKLEIK (SEQ ID NO: 54)

SEQ ID NO	Region	Sequence
Light Chain		
479	FR1	DIQLTQSPSFLSASVGDRVTTTCRAS
480	CDR1	SGVNY
481	FR2	IYWYQQKPGKAPKLWIY
482	CDR2	FTS
483	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
484	CDR3	QQFTSSPYT
485	FR4	FGQGTKLEIK

Fig. 26M

Clone 53.7 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES GGG LVQ PGG SLKL SCAAS **GFTFTSYA** MSWVRQTPGKRLEWVAT
 60 70 80 90 100
ISHGGTYT YYPDSVKGRFTISRDN SKNTLYLQMSSLRSEDTAMY YC **ARHP**
 110 120
IYSGNYQGYFDY WGQGTTLTVSS (SEQ ID NO: 63)

SEQ ID NO	Region	Sequence
Heavy Chain		
486	FR1	EVQLLES GGG LVQ PGG SLKL SCAAS
487	CDR1	<u>GFTFTSYA</u>
488	FR2	MSWVRQTPGKRLEWVAT
489	CDR2	<u>ISHGGTYT</u>
490	FR3	YYPDSVKGRFTISRDN SKNTLYLQMSSLRSEDTAMY YC
491	CDR3	<u>ARHPIYSGNYQGYFDY</u>
492	FR4	WGQGTTLTVSS

Fig. 26N

Clone 53.8 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLKLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTLVTVSS (SEQ ID NO: 64)

SEQ ID NO	Region	Sequence
Heavy Chain		
493	FR1	EVQLLES GGGLVQPGGSLKLSCAAS
494	CDR1	<u>GFTFTSYA</u>
495	FR2	MSWVRQAPGKGLEWVAT
496	CDR2	<u>ISHGGTYT</u>
497	FR3	YYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYC
498	CDR3	<u>ARHP</u> IYSGNYQGYFDY
499	FR4	WGQGT LVT VSS

Fig. 26O

Clone 53.9 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES GGG LVQ PGG SLKL SCAAS **GFTFTSYA** MSWVRQTPGKRLEWVAT

60 70 80 90 100
ISHGGTYT YYPESVKGRFTISR DQSKNTLYLQMSSLRSEDTAVYYC **ARHP**

110 120
IYSGNYQGYFDY WGQGTTLTVSS (SEQ ID NO: 65)

SEQ ID NO	Region	Sequence
Heavy Chain		
500	FR1	EVQLLES GGG LVQ PGG SLKL SCAAS
501	CDR1	<u>GFTFTSYA</u>
502	FR2	MSWVRQTPGKRLEWVAT
503	CDR2	<u>ISHGGTYT</u>
504	FR3	YYPESVKGRFTISR DQSKNTLYLQMSSLRSEDTAVYYC
505	CDR3	<u>ARHP</u> IYSGNYQGYFDY
506	FR4	WGQGTTLTVSS

Fig. 26P

Clone 53.10 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLKLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYPESVKGRFTISRDQSKNTLYLQMSSLRAEDTAVYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTLVTVSS (SEQ ID NO: 66)

SEQ ID NO	Region	Sequence
Heavy Chain		
507	FR1	EVQLLES GGGLVQ PGGSLKLSCAAS
508	CDR1	<u>GFTFTSYA</u>
509	FR2	MSWVRQAPGKGLEWVAT
510	CDR2	<u>ISHGGTYT</u>
511	FR3	YYPESVKGRFTISR DQSKNTLYLQ MSSLRAEDTAVYYC
512	CDR3	<u>ARHP</u> IYSGNYQGYFDY
513	FR4	<u>WGQGT</u> LVTVSS

Fig. 26Q

Clone 53.10 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAIMSASVGDRVTMSCRAS**SGVNY**IYWYQQKPGASPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 67)

SEQ ID NO	Region	Sequence
Light Chain		
514	FR1	DIQLTQSPAIMSASVGDRVTMSCRAS
515	CDR1	<u>SGVNY</u>
516	FR2	IYWYQQKPGASPKLWIY
517	CDR2	<u>FTS</u>
518	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
519	CDR3	<u>QQFTSSPYT</u>
520	FR4	FGGGTKLEIK

Fig. 26R

Clone 53.11 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTISCRAS**SGVNY**IYWYQQKPGQSPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 68)

SEQ ID NO	Region	Sequence
Light Chain		
521	FR1	DIQLTQSPAILSASVGDRVTISCRAS
522	CDR1	SGVNY
523	FR2	IYWYQQKPGQSPKLWIY
524	CDR2	FTS
525	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
526	CDR3	QQFTSSPYT
527	FR4	FGGGTKLEIK

Fig. 26S

Clone 53.12 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTMSCRAS**SGVNY**IYWYQQKPGASPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 69)

SEQ ID NO	Region	Sequence
Light Chain		
528	FR1	DIQLTQSPAILSASVGDRVTMSCRAS
529	CDR1	SGVNY
530	FR2	IYWYQQKPGASPKLWIY
531	CDR2	FTS
532	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
533	CDR3	QQFTSSPYT
534	FR4	FGGGTKLEIK

Fig. 26T

Clone 53.13 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTISCRAS**SGVNY**IYWYQQKPGQSPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPY**TFGGG

TKLEIK (SEQ ID NO: 70)

SEQ ID NO	Region	Sequence
Light Chain		
535	FR1	DIQLTQSPAILSASVGDRVTISCRAS
536	CDR1	SGVNY
537	FR2	IYWYQQKPGQSPKLWIY
538	CDR2	FTS
539	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
540	CDR3	QQFTSSPYT
541	FR4	FGGGTKLEIK

Fig. 26U

Clone 82.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVKLEESGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGV

           60           70           80           90           100
ISTYNGNTKYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARFL

           110
SLRYFDVWGAGTTVTVSS    (SEQ ID NO: 55)

```

Clone 82.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPAILSAPPGEKVTMTCRASSSVIYMYWYQQKPGSSPKPWIYAT

           60           70           80           90           100
SKLASGVPVRFSGSGSGTSYSSLTISRVEAEDVATYYCQQWSSEPLTFGAG

TKLELK    (SEQ ID NO: 56)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
542	FR1	EVKLEESGPEVVRPGVSVKISCKGS
543	CDR1	<u>GYTFTDYA</u>
544	FR2	MHWVKQSHAKSLEWIGV
545	CDR2	<u>ISTYNGNT</u>
546	FR3	KYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYC
547	CDR3	<u>ARFLSLRYFDV</u>
548	FR4	WGAGTTVTVSS
Light Chain		
549	FR1	DIVLTQSPAILSAPPGEKVTMTCRAS
550	CDR1	<u>SSVIY</u>
551	FR2	MYWYQQKPGSSPKPWIY
552	CDR2	<u>ATS</u>
553	FR3	KLASGVPVRFSGSGSGTSYS <u>SLTISR</u> VEAEDVATYYC
554	CDR3	<u>QQWSSEPLT</u>
555	FR4	FGAGTKLELK

Fig. 27A

Clone 82.1 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 QVKLVQSGAEVKKPGASVKVSCKAS**GYTFTDYA**MHWVRQAPGQRLEWIGW
 60 70 80 90 100
ISTYNGNTKYSQKFQGRATMTVDKSASTAYMELSSLRSEDVAVYYC**ARFL**
 110
SLRYFDVWGKGTTVTVSS (SEQ ID NO: 57)

Clone 82.1 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVITTCRAS**SSVIY**LAWYQQKPGKAPKRWIY**AT**
 60 70 80 90 100
STLQSGVPSRFSSGSGSGTEYTLTISSLQPEDFATYYC**QQWSSEPLT**FGGG
 TKVEIK (SEQ ID NO: 58)

SEQ ID NO	Region	Sequence
Heavy Chain		
556	FR1	QVKLVQSGAEVKKPGASVKVSCKAS
557	CDR1	<u>GYTFTDYA</u>
558	FR2	MHWVRQAPGQRLEWIGW
559	CDR2	<u>ISTYNGNT</u>
560	FR3	KYSQKFQGRATMTVDKSASTAYMELSSLRSEDVAVYYC
561	CDR3	<u>ARFLSLRYFDV</u>
562	FR4	WGKGTTVTVSS
Light Chain		
563	FR1	DIQLTQSPSFLSASVGDRVITTCRAS
564	CDR1	<u>SSVIY</u>
565	FR2	LAWYQQKPGKAPKRWIY
566	CDR2	<u>ATS</u>
567	FR3	<u>TLQSGVPSRFS</u> SGSGSGTEYTLTISSLQPEDFATYYC
568	CDR3	<u>QQWSSEPLT</u>
569	FR4	FGGGTKVEIK

Fig. 27B

Clone 82.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
QVKLVQSGAEVKKPGASVKVSCKGSGYTFTDYAMHWVRQAPGQRLEWIGV

           60           70           80           90           100
ISTYNGNTKYNQKFQGRATMTVDKSASTAYMELSSLRSEDTAIYYCARFL

           110
SLRYFDVWGAGTTVTVSS      (SEQ ID NO: 59)

```

Clone 82.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFLSASVGDRVITITCRASSSVIYMYWYQQKPGKAPKRWIYAT

           60           70           80           90           100
SKLASGVPSRFSGSGSGTEYTLTISSLQPEDFATYYCQQWSSEPLTFGAG

TKVEIK      (SEQ ID NO: 60)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
570	FR1	QVKLVQSGAEVKKPGASVKVSCKGS
571	CDR1	<u>GYTFTDYA</u>
572	FR2	MHWVRQAPGQRLEWIGV
573	CDR2	<u>ISTYNGNT</u>
574	FR3	KYNQKFQGRATMTVDKSASTAYMELSSLRSEDTAIYYC
575	CDR3	<u>ARFLSLRYFDV</u>
576	FR4	WGAGTTVTVSS
Light Chain		
577	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
578	CDR1	<u>SSVIY</u>
579	FR2	MYWYQQKPGKAPKRWIY
580	CDR2	<u>ATS</u>
581	FR3	KLASGVPSRFSGSGSGTEYTLTISSLQPEDFATYYC
582	CDR3	<u>QQWSSEPLT</u>
583	FR4	FGAGTKVEIK

Fig. 27C

Clone 82.3 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 QVKLVQSGPEVKVPGASVKVSCKGS**GYTFTDYA**MHWVRQAPGQSLEWIGV
 60 70 80 90 100
ISTYNGNTKYNQKFQGRATMTVDKSASTAYMELSRLRSEDTAIYYC**ARFL**
 110
SLRYFDVWGAGTTVTVSS (SEQ ID NO: 61)

Clone 82.3 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASPGDRVITTCRAS**SSVIY**MYWYQQKPGSAPKPWIY**AT**
 60 70 80 90 100
SKLASGVPVRFSGSGSGTSYTLTISRLQAEDFATYYC**QQWSSEPLT**FGAG
 TKVEIK (SEQ ID NO: 62)

SEQ ID NO	Region	Sequence
Heavy Chain		
584	FR1	QVKLVQSGPEVKVPGASVKVSCKGS
585	CDR1	<u>GYTFTDYA</u>
586	FR2	MHWVRQAPGQSLEWIGV
587	CDR2	<u>ISTYNGNT</u>
588	FR3	KYNQKFQGRATMTVDKSASTAYMELSRLRSEDTAIYYC
589	CDR3	<u>ARFLSLRYFDV</u>
590	FR4	WGAGTTVTVSS
Light Chain		
591	FR1	DIQLTQSPSFLSASPGDRVITTCRAS
592	CDR1	<u>SSVIY</u>
593	FR2	MYWYQQKPGSAPKPWIY
594	CDR2	<u>ATS</u>
595	FR3	KLASGVPVRFSGSGSGTSYTLTISRLQAEDFATYYC
596	CDR3	<u>QQWSSEPLT</u>
597	FR4	FGAGTKVEIK

Fig. 27D

SEQ ID NO	Antibody	Sequence
598	12.0 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGCCTGGTGCAGCCCAAGGGCAGCCTGAAGCTGAGCTGTGCCGCCAGCGGCATCAGCTTCAACGACGCCGCCATGAACTGGATCCGGCAGGCCCTGGCGAGGGCCTGGAATGGGTGGCCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTACGCCGCCAGCGTGAAGGACCGGTTTACCATCAGCCGGGACGACAGCCA GAATATCCTGTTTCTGCAGATGAACAACCTGAAAACCGAGGACACCGGCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGGGGCCAGGGAACCCTGGTGACAGTGTCCGCC3'
599	12.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCATGAGCAGCAGCCCTGGCGAGAAAGTGACCATGACCTGCCGGGCCAGCAGCAGCGTGATCAGCAGCTACCTGCACTGGTATCAGCAGCGGAGCGGCCAGCCCCAAGCTGTGGATCTACAGCACCAGCAGCCTGGCCAGCGGCGTGCCAGCCAGATTTTCTGGCAGCGGCAGCGGCACCTCCTTCAGCCTGACCATCAGCAGCGTGGAAGCCGAGGACGCCGCCACCTACTACTGCCAGCAGTACAGCGGCTACCCCCCTGACCTTCGGAGCCGGCACCAAGCTGGAAGTGAAG3'
600	12.1 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCAGCCTGAAGCTGTCTTGTGCCGCCAGCGGCATCAGCTTCAACGACGCCGCCATGCACTGGGTGCGCCAGGCCTCTGGCAAGGGCCTGGAATGGGTGGCCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCGCTACGCCGCCAGCGTGAAGGGCAGATTACCATCAGCCGGGACGACAGCCA GAACACCCTGTACCTGCAGATGAACAGCCTGAAAACCGAGGACACCGCCGTGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGGGGCCAGGGAACCCTGGTGACAGTGTCCAGC3'
601	12.1 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAGCAGCTACCTGGCCTGGTATCAGCAGAAGCCCCGGCCAGGCCCCCAGACTGTGGATCTACAGCACCAGCAACCGGGCCACCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCAGCCTGGAACCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCGGCTACCCCCCTGACCTTCGGCGGAGGCACCAAGGTGGAATCAAG3'

Fig. 28A

SEQ ID NO	Antibody	Sequence
602	12.2 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGC GGCAGCCTGAAGCTGTCTTGTGCCGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGAACTGGATCCGGCAGGCCAGCGGCAAGGGCCTGGAAT GGGTGGCCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTAC GCCGCCAGCGTGAAGGGCCGGTTTACCATCAGCCGGGACGACAGCCA GAACACCCTGTACCTGCAGATGAACAGCCTGAAAACCGAGGACACCG CCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCTGGTGACAGTGTCCAGC3'
603	12.2 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCT GGCGAGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAG CAGCTACCTGCACTGGTATCAGCAGAAGCCCGGCCAGGCCCCCAGAC TGTGGATCTACAGCACCAGCAGCCTGGCCAGCGGCATCCCCGCCAGA TTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCTC CCTGGAACCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCCTGACCTTCGGAGCCGGCACCAAGGTGGAAATCAAG3'
604	12.3 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCCTGGTGCAGCCCAAG GGCAGCCTGAAGCTGAGCTGTGCCGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGAACTGGATCCGGCAGGCCAGCGGCAAGGGCCTGGAAT GGGTGGCCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTAC GCCGCCAGCGTGAAGGACCGGTTTACCATCAGCCGGGACGACAGCCA GAACATCCTGTACCTGCAGATGAACAACCTGAAAACCGAGGACACCG CCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCTGGTGACAGTGTCCAGC3'
605	12.3 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCATCCTGAGCAGCTCTCCA GGCGAGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAG CAGCTACCTGCACTGGTATCAGCAGAAGCCTGGCGCCGCTCCCCGGC TGTGGATCTACAGCACAAGCAGCCTGGCCAGCGGCATCCCCGCCAGA TTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCAG CCTGGAAGCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCCTGACCTTCGGAGCCGGCACCAAGGTGGAAATCAAG3'

Fig. 28B

SEQ ID NO	Antibody	Sequence
606	135.0 VH	5'GAAGTGAAGCTGGAAGAGTCCGGCGGAGGCCTGGTGAAACCTGGCGGCA GCCTGAAGCTGAGCTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGACCCCCGAGAAGAGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACGCCAAGAACACCCTGAACCTGCAGATGAGCA GCCTGCGGAGCGAGGACACCGCCATGTACTACTGCGCCAGGCACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGC TGACCGTGTCTCT3'
607	135.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCATGAGCGCCAGCCTGGGCG AGAAAGTGACCATGAACTGCCGGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGTCCGACGCCAGCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACAGCCTGACCATCAGCAGCATGGAAGGCGAGGACGCCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
608	135.1 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCCACGGCGGCAGCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
609	135.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACCTGGCCT GGTATCAGCAGAAGCCCGGCAAGGGCCCCCAAGCTGTGGATCTACTTCACCA GCACCCTGCAGAGCGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCCAGGGCACCA AGCTGGAAATCAAG3'

Fig. 28C

SEQ ID NO	Antibody	Sequence
610	135.2 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGGCCCCCTGGCAAAGGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
611	135.2 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGCCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
612	135.3 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGACCCCCGAGAAGAGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACAGCAAGAACACCCTGAACCTGCAGATGAGCA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGGCACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
613	135.3 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGCCCCGACGCCGCTCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACACCCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'

Fig. 28D

SEQ ID NO	Antibody	Sequence
614	4.0 VH	5'GAAGTGCAGCTGGAGGAGTCAGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTAAACTCTCCTGTGCAGCCTCTGGATTCACTTTTCAGTAATTATGCCATGTCTTGGGTTCGCCAGACTCCGGATAAGCGGCTGGAGTGGGTCGCAACCA TTAGTAATGGTGGTAGTTACACCTACTATCCAGACACTGTGAAGGGTCGCT TCACCATCTCCAGAGACAATGCCAAGAACACCCTGTCTCTGCAAATGAGCA GTCTGAGGTCTGAGGACACGGCCATGTATTACTGTTCAAGACCCTCTGAGA GATCCCATTACTACGCTACTAGCCAGTTTGCTTACTG GGGCCAAGGGACTCTGGTCACTGTCTCTGCA3'
615	4.0 VL	5'GACATTGTGCTGACCCAGTCTCCAGGAATCATGTCTGCATCTCCAGGGG AGAAAGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGCATT GGTACCAGCAGAAGTCAGGCACCTCCCCCAAAGATGGATTTATGACACAT CCAAAGTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGA CCTCTTACTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTT ATTACTGCCAGCAGTGGAGTAGTAGCCCGCTCACGTTTCGGTGCTGGGACCA AGGTGGAGCTGAAA3'
616	4.1 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCAACGGCGGCAGCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
617	4.1 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCTGGCG AGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGTCTTACCTGGCCT GGTATCAGCAGAAGCCCCGGCCAGGCCCCCAGACGGTGGATCTACGACACCA GCAACCGGGCCACCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCGACTACACCCTGACCATCAGCAGCCTGGAACCCGAGGACTTCGCCGTGT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGCGGAGGCACCA AGGTGGAAATCAAG3'

Fig. 28E

SEQ ID NO	Antibody	Sequence
618	4.2 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
619	4.2 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCTGGCG AGAGAGCCACCCTGAGCTGTAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCCGGCACCGCCCCCAGACGGTGGATCTACGATACCA GCAAGCTGGCCAGCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCGACTACACCCTGACCATCAGCAGCCTGGAACCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'
620	4.3 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGACCCCCGACAAGCGGCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAGCA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
621	4.3 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCATCCTGAGCCTGTCTCCAGGCG AGAGAGCCACCCTGAGCTGCAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCCGGCCAGGCCCCCAGACGGTGGATCTACGATACCA GCAAGCTGGCCAGCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACACCCTGACCATCAGCAGCCTGGAAGCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'

Fig. 28F

SEQ ID NO	Antibody	Sequence
622	4.4 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGTCCGAGGACACCGCCATGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTGCT3'
623	4.5 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGGCCGAGGACACCGCCATGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTCT3'
624	4.6 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCACAA TCAGCCAGGGCGGCAGCTACACCTACTACCCCGAGAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACCAGGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGTCCGAGGACACCGCCATGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTGCT3'
625	4.7 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCCAGGGTGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'

Fig. 28G

SEQ ID NO	Antibody	Sequence
626	4.8 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATCTGGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
627	4.9 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATTCAGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
628	4.10 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCGACGGTGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
629	4.11 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATGTCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGCCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'

Fig. 28H

SEQ ID NO	Antibody	Sequence
630	4.4 VL	5 'GACATCGTGCTGACCCAGAGCCCCGGCAGCCTGTCTGCCAGCGTGGGCG ACAGAGTGACCATGACCTGCAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCACCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAACTGAAG3 '
631	4.5 VL	5 'GACATCGTGCTGACCCAGAGCCCCAGCAGCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCACCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAAATCAAG3 '
632	4.6 VL	5 'GACATCGTGCTGACCCAGAGCCCCAGCAGCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCCAGTCCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAAATCAAG3 '
633	4.7 VL	5 'GACATCCAGCTGACCCAGAGCCCCGGCAGCCTGTCTGCCAGCGTGGGCG ACAGAGTGACCATGACCTGCAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCACCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAACTGAAG3 '

Fig. 28I

SEQ ID NO	Antibody	Sequence
634	53.0 VH	5'GAGGTTTCAGCTGGAGGAGTCAGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCACTAGCTATGCCATGTCTTGGGTTCGCCAGACTCCGGAGAAGAGGCTGGAGTGGGTCGCAACCA TTAGTCATGGTGGTACTTACACCTACTATCCAGACAGTGTGAAGGGACGAT TCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAAATGAGCA GTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGACATCCTATCT ACTCTGGTAACTACCAGGGATACTTTGACTACTGG GGCCAAGGCACCCTCTCACAGTCTCCTCA3'
635	53.0 VL	5'GACATTGTGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGG AGAAGGTCACCATGAGCTGCAGGGCCAGCTCAGGTGTAAATTACATATACT GGTACCAGCAGAAGTCAGATGCCTCCCCCAAACCTATGGATTTATTTACAT CCAACCTGGCTCCTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGA ACTCTTATTCTCTCACAATCAGCAGCATGGAGGGTGAAGATGCTGCCACTT ATTACTGCCAGCAGTTTACTAGTTCCCCGTACACGTTCCGGAGGGGGGACCA AGCTGGAAATAAAA3'
636	53.1 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCCACGGCGGCACCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
637	53.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGGCCAGCAGCGGCGTGAACCTACCTGGCCT GGTATCAGCAGAAGCCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCACCCTGCAGAGCGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCCAGGGCACCA AGCTGGAAATCAAG3'

Fig. 28J

SEQ ID NO	Antibody	Sequence
638	53.2 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
639	53.2 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
640	53.3 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGACCCCCGAGAAGCGGCTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGGCACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCACCG TGACCGTGTCTCTCT3'
641	53.3 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCCGACGCCGCTCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'

Fig. 28K

SEQ ID NO	Antibody	Sequence
642	53.4 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCGTAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
643	53.5 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
644	53.6 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCCCTGGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGGTGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'

Fig. 28L

SEQ ID NO	Antibody	Sequence
645	53.4 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACCTCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '
646	53.5 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCGCCT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '
647	53.6 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCACCCCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '
648	53.7 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGCAACCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '

Fig. 28M

SEQ ID NO	Antibody	Sequence
649	53.8 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCTCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '
650	53.9 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCTACACCTTCGGCCAAGGCACCA AGCTGGAAATCAAG3 '

Fig. 28N

SEQ ID NO	Antibody	Sequence
651	82.0 VH	5'GAAGTGAAGCTGGAAGAGTCCGGCCCTGAGGTGGTGCGCCCTGGCGTGTCCGTGAAGATCAGCTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCATGCACTGGGTGAAACAGAGCCACGCCAAGAGCCTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCAAGGGCAAGGCCACCATGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAAGTGGCCC GGCTGACCAGCGAGGACAGCGCCATCTACTACTGCGCCCCGGTTCCTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCACCGTGACCGTGTCTAGC3'
652	82.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCCTGTCTGCCCCCCTGGCG AGAAAGTGACCATGACCTGCCGGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCCGGCAGCAGCCCCAAGCCCTGGATCTACGCCACCA GCAAGCTGGCCAGCGGCGTGCCAGTGCGGTTTAGCGGCAGCGGCTCTGGCA CCAGCTACAGCCTGACCATCAGCCGGGTGGAAGCCGAGGACGTGGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCCTGACCTTCGGAGCCGGCACCA AGCTGGAAGTGAAG3'
653	82.1 VH	5'CAGGTGAAACTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCA GCGTGAAGGTGTCTCTGCAAGGCCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCCCTGGCCAGAGACTGGAATGGATCGGCTGGA TCAGCACCTACAACGGCAACACCAAGTACAGCCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAGTGGAGCA GCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCCCGGTTCCTGAGCC TGCGGTACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGTCCAGC3'
654	82.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGGCCAGCAGCAGCGTGATCTACCTGGCCT GGTATCAGCAGAAGCCCCGGCAAGGGCCCCCAAGCCCTGGATCTACGCCACCA GCACACTGCAGAGCGGCGTGCCAGCAGATTAGCGGCAGCGGCTCTGGCA CCGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCCTGACCTTCGGCGGAGGCACCA AAGTGGAAATCAAG3'

Fig. 280

SEQ ID NO	Antibody	Sequence
655	82.2 VH	5' CAGGTGAAACTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCA GCGTGAAGGTGTCCTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCCTGGCCAGAGACTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAGTGAAGCA GCCTGCGGAGCGAGGACACCGCCATCTACTACTGCGCCCCGGTTCCTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCACCGTGACCGTGTCTAGC3'
656	82.2 VL	5' GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCGGGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCCGGCAAGGCCCCCAAGCCCTGGATCTACGCCACCA GCAAGCTGGCCAGCGGCGTGCCCGAGCAGATTTTCTGGCAGCGGCAGCGGCA CCGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'
657	82.3 VH	5' CAGGTGAAACTGGTGCAGAGCGGCCCTGAAGTGAAGGTGCCAGGCGCCA GCGTGAAGGTGTCCTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCCTGGCCAGAGCCTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAGTGAAGCA GGCTGCGGAGCGAGGACACCGCCATCTACTACTGCGCCCCGGTTCCTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCACCGTGACCGTGTCTAGC3'
658	82.3 VL	5' GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCCCTGGCG ACAGAGTGACCATCACCTGTCGGGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCCGGCAGCGCCCCCAAGCCCTGGATCTACGCCACAA GCAAGCTGGCCAGCGGCGTGCCCGTGCGGTTTAGCGGCTCTGGCAGCGGCA CCAGCTACACCCTGACCATCAGCCGGCTGCAGGCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'

Fig. 28P