

Target (informal name)	mAb	Conc. mg/ml	Visc. cP	HC Type (including allotypes)	LC Type	VL Germline	VH Germline	pI	HC SEQ ID NO	LC SEQ ID NO
anti-amyloid	A	142.2	5.0	IgG1 (f) (R;EM)	Kappa	VK2 A23	VH2 2-26	9.0	168	166
GMCSF (247)	B	139.7	5.6	IgG2	Kappa	VK3 A27	VH1 1-02	8.7	4	2
CGRPR	C	136.6	6.3	IgG2	Lambda	VL1 1g	VH3 3-15	8.6	180	178
RANKL	D	152.7	6.6	IgG2	Kappa	VK3 A27	VH3 3-23	8.6	172	170
Sclerostin (27H6)	E	145.0	6.7	IgG2	Kappa	VK2 O1	VH3 3-48	6.6	8	6
IL-1R1	F	153.9	6.7	IgG2	Kappa	VK6 A10	VH5 5-51	7.4	12	10
Myostatin	G	141.0	6.8	IgG1 (z) (K;EM)	Kappa	VK1 O18	VH3 3-07	8.7	16	14
B7RP1	H	137.5	7.7	IgG2	Kappa	VK1 L15	VH3 3-07	7.7	20	18
Amyloid	I	140.6	8.2	IgG1 (za) (K;DL)	Kappa	VK2 A17	VH2 2-70	8.7	24	22
GMCSF (3.112)	J	156.0	8.2	IgG2	Kappa	VK3 A27	VH1 1-02	8.8	28	26
CGRP (32H7)	K	159.5	8.3	IgG2	Kappa	VK3 A27	VH3 3-33	8.7	32	30
CGRP (3B6.2)	L	161.1	8.4	IgG2	Lambda	VL3 3l	VH1 1-02	8.6	36	34
PCSK9 (8A3.1)	M	150.0	9.1	IgG2	Kappa	VK2 A19	VH3 3-07	6.7	40	38
PCSK9 (492)	N	150.0	9.2	IgG2	Kappa	VK2 A19	VH3 3-07	6.9	44	42
CGRP	O	155.2	9.6	IgG2	Lambda	VL1 1b	VH3 3-33	8.8	48	46
Hepcidin	P	147.1	9.9	IgG2	Lambda	VL3 3r	VH3 3-33	7.3	52	50
TNFR p55)	Q	157.0	10.0	IgG2	Kappa	VK3 A27	VH3 3-23	8.2	56	54
OX40L	R	144.5	10.0	IgG2	Kappa	VK2 A23	VH3 3-33	8.7	60	58
HGF	S	155.8	10.6	IgG2	Kappa	VK3 L16	VH4 4-59	8.1	64	62
GMCSF	T	162.5	11.0	IgG2	Kappa	VK4 B3	VH1 1-02	8.1	68	66
Glucagon R	V	146.0	12.1	IgG2	Kappa	VK1 A30	VH3 3-33	8.4	72	70
GMCSF (4.381)	U	144.5	12.1	IgG2	Kappa	VK3 A27	VH1 1-02	8.4	76	74

FIGURE 1A

Target (Informal name)	mAb	Conc. mg/ml	Visc. cP	HC Type (including allotypes)	LC Type	VL Germline	VH Germline	pI	HC SEQ ID NO	LC SEQ ID NO
Sclerostin (13F3)	W	155.0	12.1	IgG2	Kappa	VK1 L19	VH1 1-46	7.8	80	78
CD-22	X	143.7	12.2	IgG1 (f) (R;EM)	Kappa	VK1 O18	VH1 1-69	8.8	84	82
INFgR	Y	154.2	12.2	IgG1 (za) (K;DL)	Kappa	VK3 A27	VH5 5-51	8.8	88	86
Ang2	Z	151.5	12.4	IgG2	Kappa	VK2 A19	VH3 3-48	7.4	92	90
TRAILR2	AA	158.3	12.5	IgG1 (f) (R;EM)	Kappa	VK3 A27	VH4 4-30	8.7	96	94
EGFR	AB	141.7	14.0	IgG2	Kappa	VK1 O18	VH4 4-61	6.8	100	98
IL-4R	AC	145.8	15.2	IgG2	Kappa	VK3 A27	VH3 3-48	8.6	104	102
IL-15	AD	149.0	16.3	IgG1 (f) (R;EM)	Kappa	VK3 A27	VH5 5-51	8.8	108	106
IGF1R	AE	159.2	17.3	IgG1 (za) (K;DL)	Kappa	VK2 A19	VH4 4-04	8.6	112	110
IL-17R	AF	150.9	19.1	IgG2	Kappa	VK3 L16	VH1 1-18	8.6	116	114
Dkk1 (6.37.5)	AG	159.4	19.6	IgG2	Kappa	VK2 A2	VH3 3-33	8.2	120	118
Sclerostin	AH	134.8	20.9	IgG2	Kappa	VK1 O2	VH1 1-e	7.4	124	122
TSLP	AI	134.2	21.4	IgG2	Lambda	VL3 3h	VH3 3-33	7.2	128	126
Dkk1 (11H10)	AJ	145.3	22.5	IgG2	Kappa	VK3 L6	VH3 3-48	8.2	132	130
PCSK9	AK	145.2	22.8	IgG2	Lambda	VL2 2a2	VH1 1-18	8.1	136	134
GIPR (2G10.006)	AQ	150.0	19.1	IgG1 (z) (K;EM)	Kappa	VK3 L16	VH3 3-33	8.1	160	158
Activin	AL	133.9	29.4	IgG2	Lambda	VL3 3r	VH1 1-18	7.0	140	138
Sclerostin (2B8)	AM	150.0	30.0	IgG2	Lambda	VL6 6a	VH3 3-33	6.7	144	142
Sclerostin	AN	141.4	30.4	IgG2	Kappa	VK1 O2	VH1 1-18	6.8	148	146
c-fms	AO	146.9	32.1	IgG2	Kappa	VK4 B3	VH1 1-18	6.6	152	150
$\alpha 4\beta 7$	AP	154.9	32.7	IgG2	Kappa	VK1 L19	VH1 1-24	6.5	156	154

FIGURE 1B

Target (informal name)	mAb	SEQ ID NOS							
		HC FR1	HC FR2	HC FR3	HC FR4	LC FR1	LC FR2	LC FR3	LC FR4
anti-amyloid	A	280	281	282	283	189	190	191	192
GMCSF (247)	B	300	285	301	276	197	194	198	196
CGRPR	C	316	317	318	287	257	258	259	250
RANKL	D	291	292	293	276	193	194	195	196
Sclerostin (27H6)	E	304	292	349	276	246	225	226	188
IL-1R1	F	277	278	279	276	185	186	187	188
Myostatin	G	304	289	346	287	205	206	219	231
B7RP1	H	304	289	305	276	205	229	207	196
Amyloid	I	333	281	334	276	235	236	226	237
GMCSF (3.112)	J	344	285	345	283	193	194	201	196
CGRP (32H7)	K	302	289	338	287	193	194	198	231
CGRP (3B6.2)	L	299	285	339	287	266	267	268	269
PCSK9 (8A3.1)	M	304	289	315	287	227	225	226	188
PCSK9 (492)	N	304	289	314	287	227	225	228	188
CGRP	O	302	289	306	287	254	255	256	250
Hepcidin	P	302	289	303	283	263	264	265	250
TNFR p55)	Q	291	292	293	276	193	199	198	196
OX40L	R	302	289	303	276	189	190	213	214
HGF	S	273	274	275	276	181	182	183	184
GMCSF	T	299	285	301	276	215	211	216	217
Glucagon R	V	302	289	310	287	205	222	223	188
GMCSF (4.381)	U	299	285	301	276	193	202	203	204

FIGURE 1C

Target (Informal name)	mAb	SEQ ID NOS							
		HC FR1	HC FR2	HC FR3	HC FR4	LC FR1	LC FR2	LC FR3	LC FR4
Sclerostin (13F3)	W	347	285	348	276	208	245	207	214
CD-22	X	307	308	309	287	218	206	219	220
INF γ R	Y	329	330	331	332	193	194	198	214
Ang2	Z	326	292	305	276	227	225	226	231
TRAILR2	AA	319	320	321	287	193	200	198	196
EGFR	AB	335	336	337	283	205	206	221	188
IL-4R	AC	304	292	305	276	193	194	198	196
IL-15	AD	322	323	324	276	193	194	198	230
IGF1R	AE	311	312	313	283	224	225	226	196
IL-17R	AF	299	285	328	276	181	232	233	188
Dkk1 (6.37.5)	AG	302	289	341	276	240	241	242	243
Sclerostin	AH	294	285	295	276	205	206	207	196
TSLP	AI	288	289	290	283	251	252	253	250
Dkk1 (11H10)	AJ	340	292	305	287	238	194	239	231
PCSK9	AK	284	285	286	287	247	248	249	250
GIPR (2G10.006)	AQ	302	342	303	276	181	194	234	188
Activin	AL	299	285	325	283	260	261	262	250
Sclerostin (2B8)	AM	302	289	303	287	270	271	272	250
Sclerostin	AN	327	285	328	287	205	206	207	188
c-fms	AO	299	285	328	276	210	211	212	214
α 4 β 7	AP	296	297	298	276	208	206	209	196
c-kit	BA	299	285	295	276	210	211	212	188

FIGURE 1D

Chain	High viscosity subfamily	Low viscosity subfamily	p-value	Residues in high viscosity subfamily, positions in Aho numbering, residues in low viscosity subfamily				
				FR1	CDR1	FR2	CDR2	FR3
Heavy	VH1 1-18	VH1 1-02	0.0002		S33G, G40Y, S42H		S59N, Y61N, N65S, N67G,	T82R, T86I, R94S, S95R
Heavy	VH3 3-33	VH3 3-07	0.076	Q1E, R17G	G40W, M41_, H42S		V57S/Q, W/S59K/R, Y60Q, N67E	S85A
Light	VK3 L16	VK3 A27	0.031	M4L, V13L	_33S		D58G	A76D, S95R, Q97E, S98P

FIGURE 2

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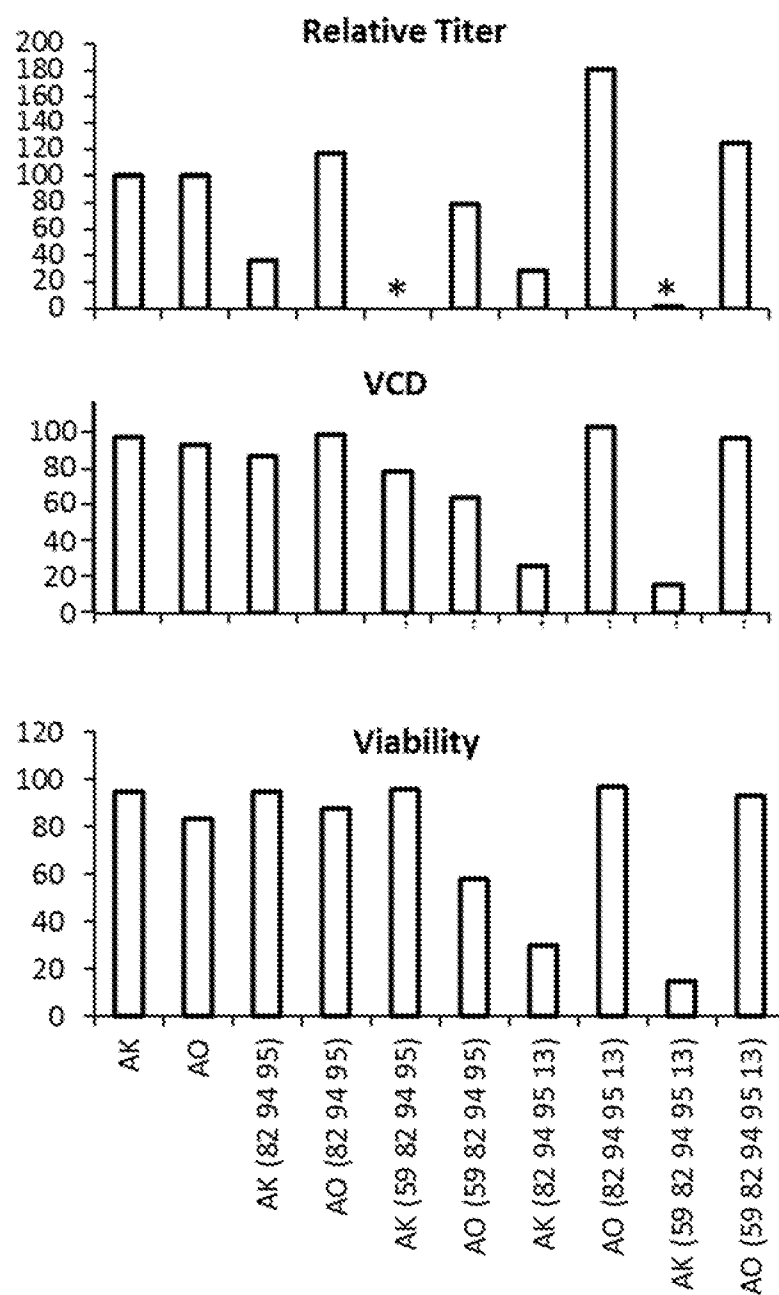


FIGURE 3

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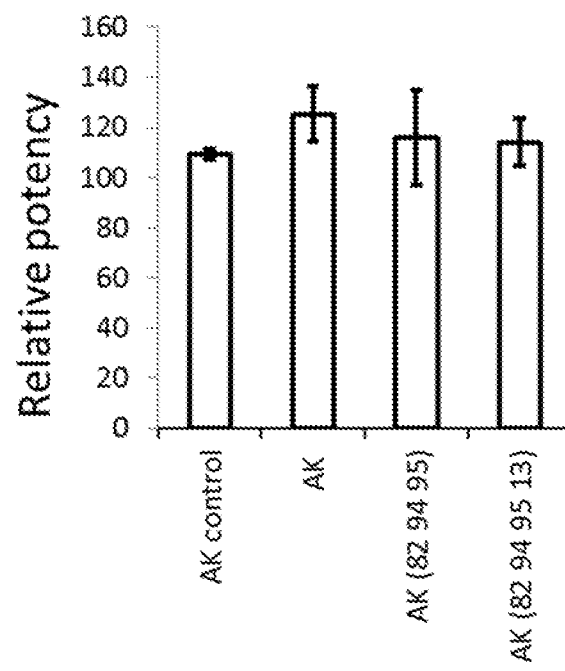


FIGURE 4

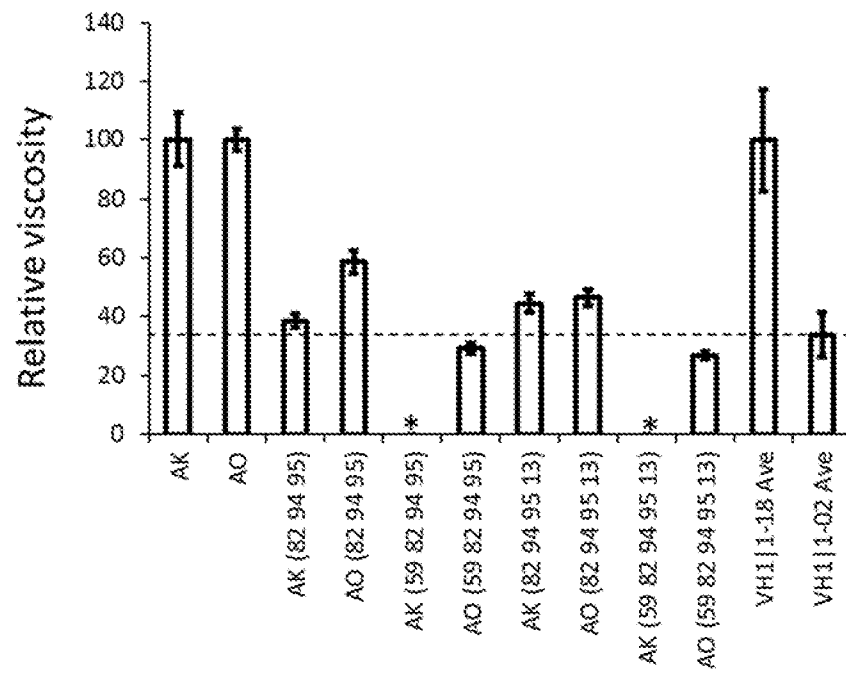


FIGURE 5

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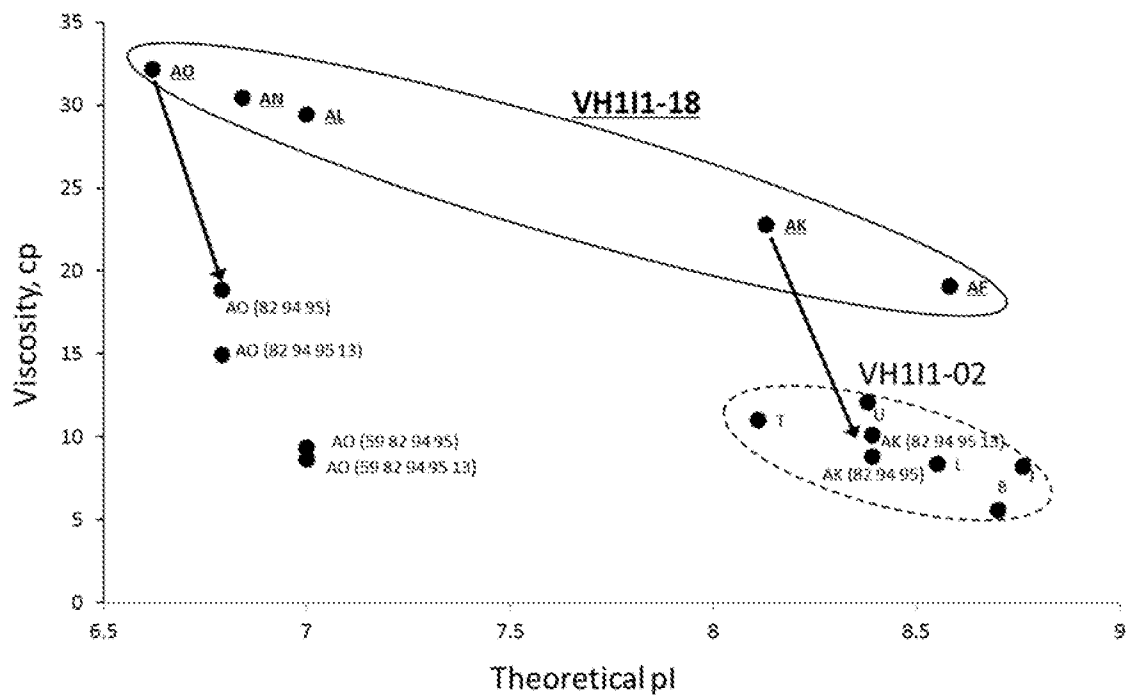


FIGURE 6

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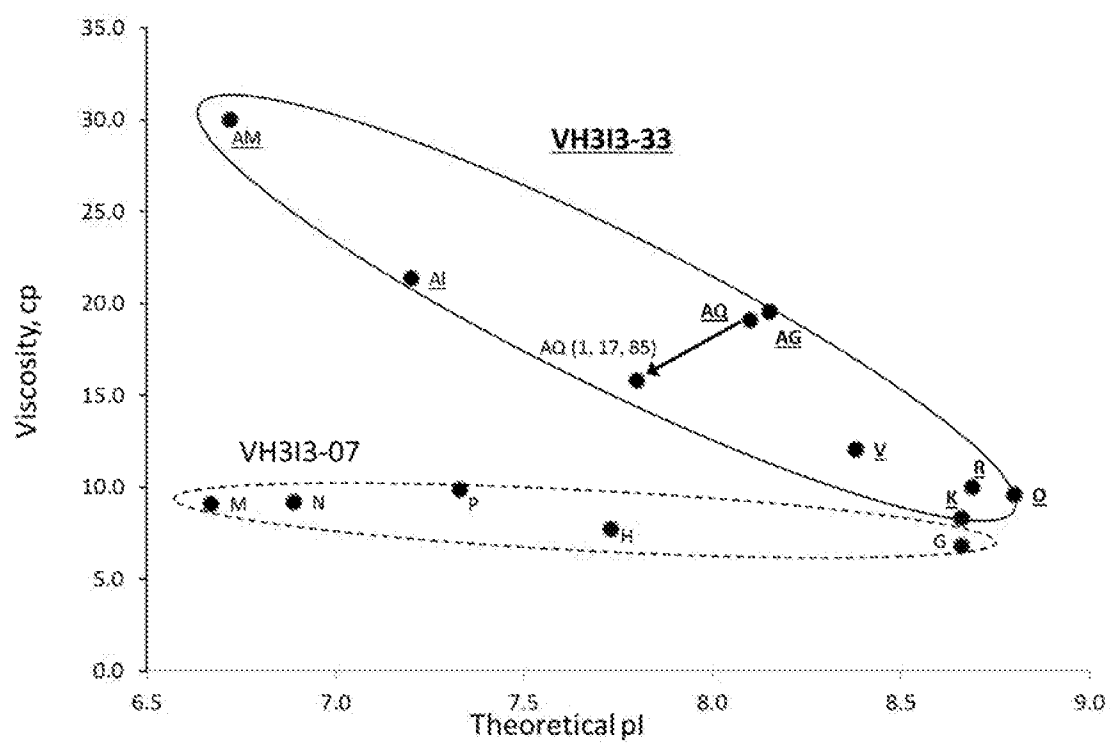


FIGURE 7

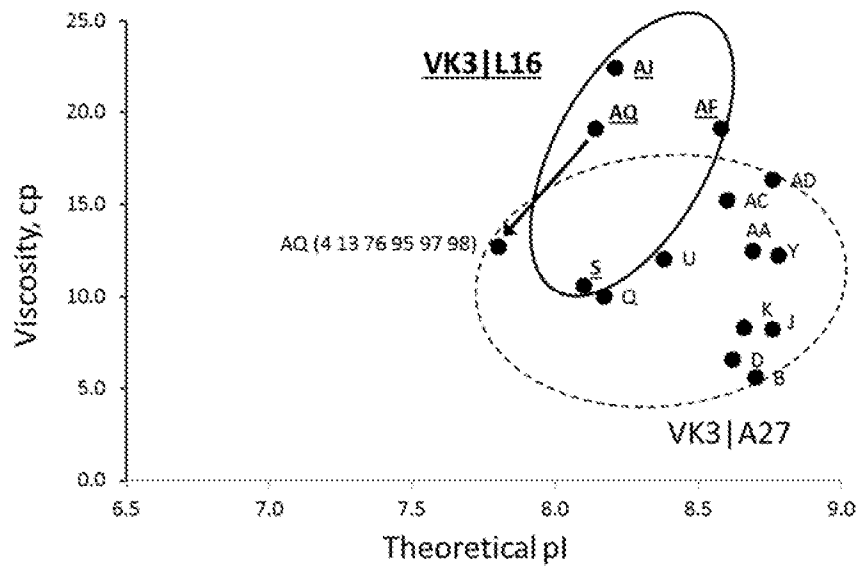


FIGURE 8

VH1 1-18 and VH1 1-02 Global sequence parameters					CDR1			CDR2					FR3									
					32	33	35	52	53	54	55	57	67	68	69	70	71	72	73	74	75	
					31	33	35	52	a	53	54	56	66	67	68	69	70	71	72	73	74	
					31	33	35	52	a	53	54	56	66	67	68	69	70	71	72	73	74	
mAbs	Visc, cP	pl	VL	VH1	33	40	42	59	60	61	65	67	77	78	79	80	81	82	83	84	85	
VBase				VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
B	5.8	8.7	VK3 A27	VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
J	8.2	8.8	VK3 A27	VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
L	8.4	8.6	VL3 3i	VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
T	11.0	8.1	VK4 B3	VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
U	12.1	8.4	VK3 A27	VH1 1-02	G	Y	H	N	P	N	S	G	R	V	T	M	T	R	D	T	S	
AF	19.1	8.6	VK3 L16	VH1 1-18	R	G	S	S	I	Y	S	N	R	V	T	M	T	I	D	T	S	
AK	22.8	8.1	VL2 2a2	VH1 1-18	S	G	S	S	F	Y	N	N	R	G	T	M	T	I	D	P	S	
AL	29.4	7.0	VL3 3r	VH1 1-18	S	G	S	I	P	Y	N	N	R	V	T	M	T	I	D	T	S	
AN	30.4	6.8	VK1 O2	VH1 1-18	D	N	H	N	P	N	S	G	R	V	T	M	T	I	D	T	S	
AO	32.1	6.6	VK4 B3	VH1 1-19	S	G	S	S	A	Y	N	N	R	V	T	M	T	I	D	T	S	
Vbase				VH1 1-19	S	G	S	S	A	Y	N	N	R	V	T	M	T	I	D	T	S	
p-value	0.0002	0.03																				

FR3																							VH	VL	Schem
76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	52	12	EU
75	76	77	78	79	80	81	82	a	b	c	83	84	85	86	87	88	89	90	91	92	93	94	50	13	Kabat
75	76	77	78	79	80	81	82	a	b	c	83	84	85	86	87	88	89	90	91	92	93	94	52	13	Chothia
86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	59	13	Aho
I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	Y	C	A	R			
I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	Y	C	A	R	N	L	
I	S	T	A	S	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	F	C	A	R	N	L	
I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	F	C	A	R	N	V	
I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	Y	C	A	R	N	V	
I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	Y	C	A	R	N	L	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R	S	V	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R	S	G	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	F	C	A	R	I	V	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R	N	A	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R	S	V	
I	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R			

FIGURE 9

mAb mutant symbols	Heavy chain mutations	Light chain mutations
AK	AK_HC	AK_LC
AK (82 94 95)	AK_HC: [T82R, R94S, S95R]	AK_LC
AK (59 82 94 95)	AK_HC: [S59K, T82R, R94S, S95R]	AK_LC
AK (82 94 95 13)	AK_HC: [T82R, R94S, S95R]	AK_LC: [G13L]
AK (59 82 94 95 13)	AK_HC: [S59K, T82R, R94S, S95R]	AK_LC: [G13L]
AO	AO_HC	AO_LC
AO (82 94 95)	AO_HC: [T82R, R94S, S95R]	AO_LC
AO (59 82 94 95)	AO_HC: [S59K, T82R, R94S, S95R]	AO_LC
AO (82 94 95 13)	AO_HC: [T82R, R94S, S95R]	AO_LC: [V13L]
AO (59 82 94 95 13)	AO_HC: [S59K, T82R, R94S, S95R]	AO_LC: [V13L]

FIGURE 10

VH3 3-07 and VH3 3-33 Global Sequence Parameters					FR1		CDR1			CDR2				FR3	Scheme
					1	16	33	34	35	50	52	53	57	75	EU
					1	16	33	34	35	50	52	52a	56	74	Kabat
					1	16	33	34	35	50	52	52a	56	74	Chothia
mAb	Visc, cP	pI	VL	VH3	1	17	40	41	42	57	59	60	67	85	Aho
VBase				VH3 3-07	E	G	W	M	S	N	K	Q	E	A	
G	6.8	8.7	VK1 O18	VH3 3-07	E	G	W		N	Q	R	L	A	A	
H	7.7	7.7	VK1 L15	VH3 3-07	E	G	W		S	Y	K	Q	E	A	
<u>K</u>	8.3	8.7	VK3 A27	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
M	9.1	6.7	VK2 A19	VH3 3-07	E	G	W		S	S	K	Q	E	A	
N	9.2	6.9	VK2 A19	VH3 3-07	E	G	W		S	S	K	Q	E	A	
<u>O</u>	9.6	8.8	VL1 1b	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>S</u>	<u>F</u>	<u>I</u>	<u>S</u>	
<u>P</u>	9.9	7.3	VL3 3r	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
<u>R</u>	10.0	8.7	VK2 A23	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
<u>V</u>	12.1	8.4	VK1 A30	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
<u>AG</u>	19.6	8.2	VK2 A2	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>S</u>	<u>Y</u>	<u>D</u>	<u>A</u>	
<u>AI</u>	21.4	7.2	VL3 3h	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
<u>AQ</u>	19.1	8.1	VK3 L16	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>A</u>	<u>W</u>	<u>F</u>	<u>D</u>	<u>S</u>	
<u>AM</u>	30.0	6.7	VL6 6a	<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>A</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
<u>VBase</u>				<u>VH3 3-33</u>	<u>Q</u>	<u>R</u>	<u>G</u>	<u>M</u>	<u>H</u>	<u>V</u>	<u>W</u>	<u>Y</u>	<u>N</u>	<u>S</u>	
p-value	0.076	0.300													

FIGURE 11

VK3 A27 and VK3 L Global Sequence Parameters					FR1		CDR1		CDR2	FR3				Scheme
					4	12	31	33	51	66	85	87	88	EU
					4	12	31	33	51	65	82b	83	84	Kabat
					4	12	31	33	51	65	82b	83	84	Chothia
mAb	Visc, cP	pI	VH	VK3	4	13	33	40	58	76	95	97	98	Aho
VBase				VK3 A27	L	L	S	Y	G	D	R	E	P	
B	5.6	8.7	VH1 1-02	VK3 A27	L	L	S	Y	G	D	R	E	P	
D	6.6	8.6	VH3 3-23	VK3 A27	L	L	G	Y	G	D	R	E	P	
J	8.2	8.8	VH1 1-02	VK3 A27	L	L	S	Y	G	D	R	E	P	
K	8.3	8.7	VH3 3-33	VK3 A27	L	L	S	Y	G	D	R	E	P	
Q	10.0	8.2	VH3 3-23	VK3 A27	L	L	S	Y	G	D	R	E	P	
<u>S</u>	10.6	8.1	VH4 4-59	<u>VK3 L16</u>	<u>M</u>	<u>V</u>	-	<u>N</u>	<u>G</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	
U	12.1	8.4	VH1 1-02	VK3 A27	L	L	N	Y	G	D	R	E	P	
Y	12.2	8.8	VH5 5-51	VK3 A27	L	L	S	Y	G	D	R	E	P	
AA	12.5	8.7	VH4 4-30	VK3 A27	L	L	R	Y	G	D	R	E	P	
AC	15.2	8.6	VH3 3-48	VK3 A27	L	L	N	Y	G	D	R	E	P	
AD	16.3	8.8	VH5 5-51	VK3 A27	L	L	S	Y	G	D	R	E	P	
<u>AF</u>	19.1	8.6	VH1 1-18	<u>VK3 L16</u>	<u>M</u>	<u>V</u>	-	<u>N</u>	<u>D</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	
<u>AJ</u>	22.5	8.2	VH3 3-48	<u>VK3 L6</u>	<u>L</u>	<u>L</u>	-	<u>Y</u>	<u>D</u>	<u>A</u>	<u>S</u>	<u>E</u>	<u>P</u>	
<u>AQ</u>	19.1	8.1	VH3 3-33	<u>VK3 L16</u>	<u>M</u>	<u>V</u>	-	<u>N</u>	<u>G</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	
<u>Vbase</u>				<u>VK3 L16</u>	<u>M</u>	<u>V</u>	-	<u>N</u>	<u>G</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	
p-value	0.007	0.011												

FIGURE 12

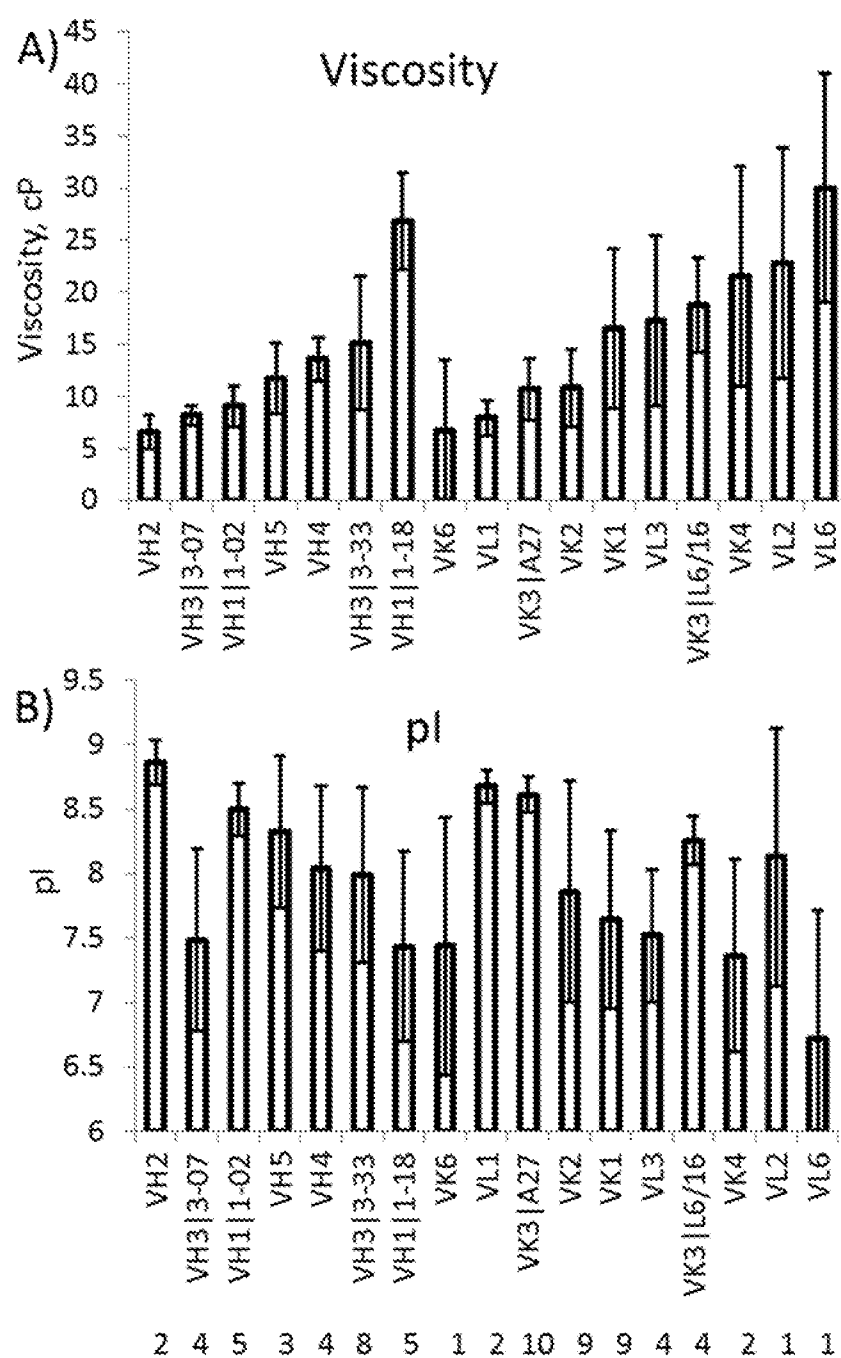


FIGURE 13

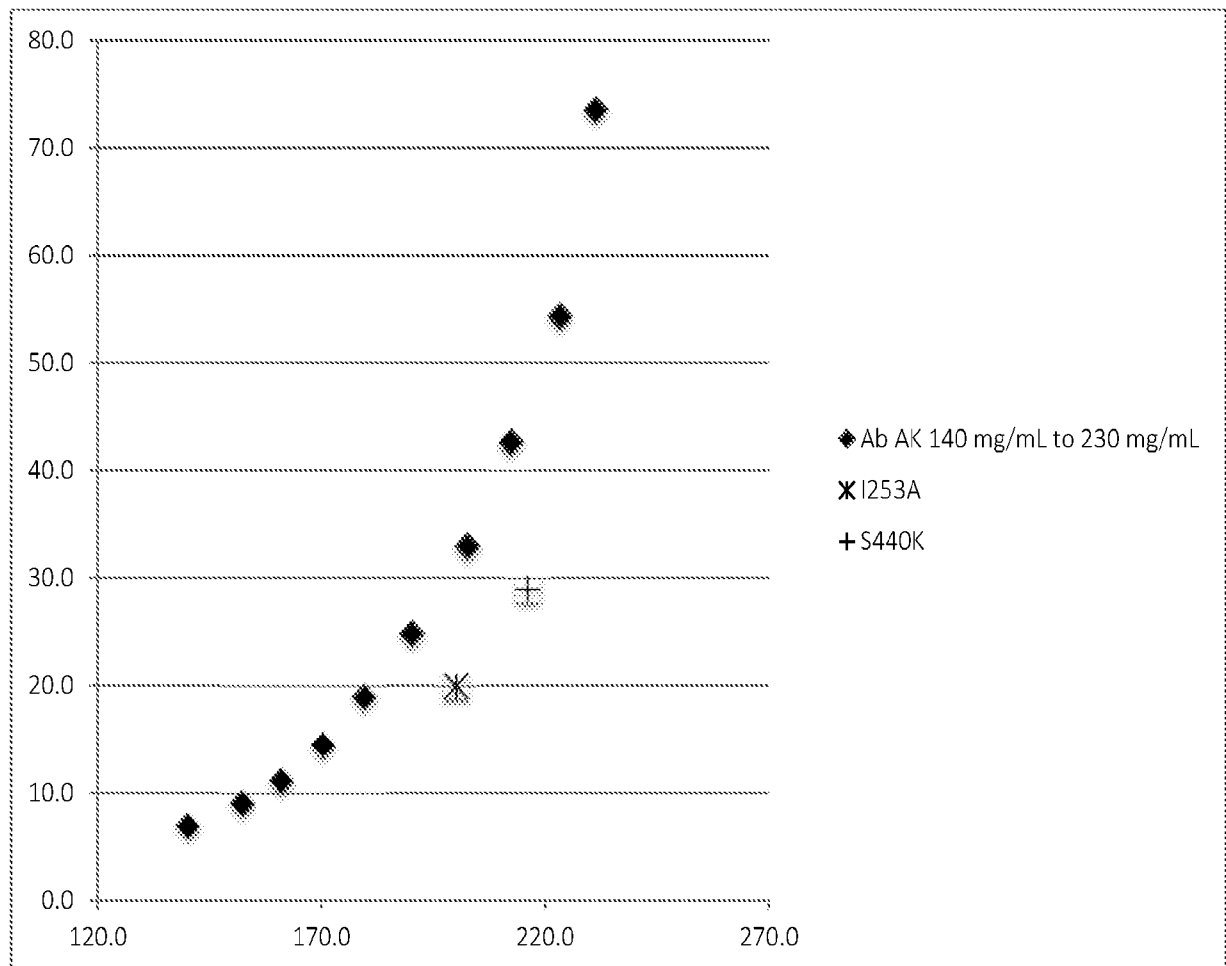


FIGURE 14A

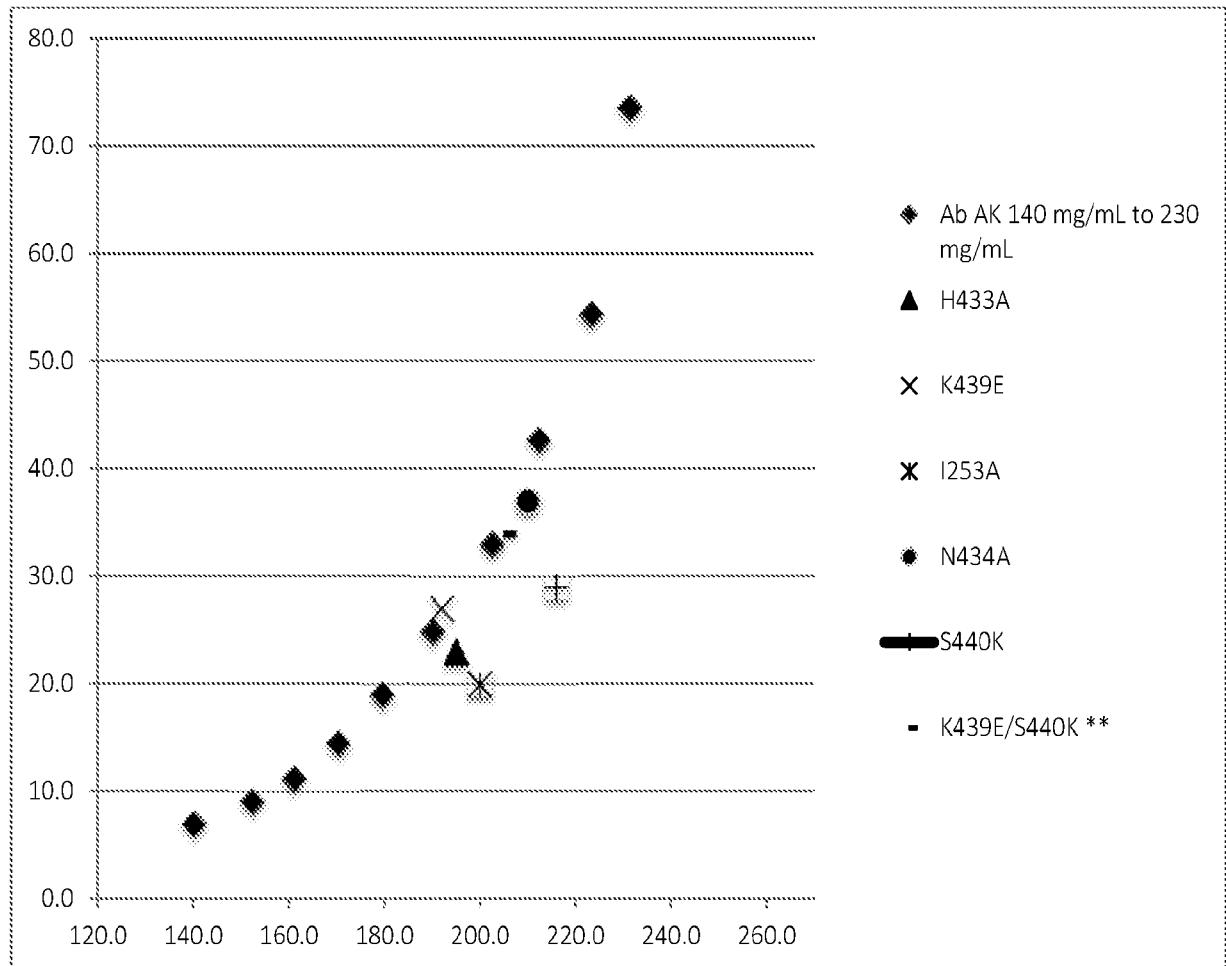


FIGURE 14B

Sample	Viscosity (cP) @ 1000s-1 @ 25C	Relative viscosity
Antibody AK	43.7	100%
Fab Mutant	25.6	59%
Fc Mutant	34.8	80%
Double Mutant	22.6	52%

FIGURE 15

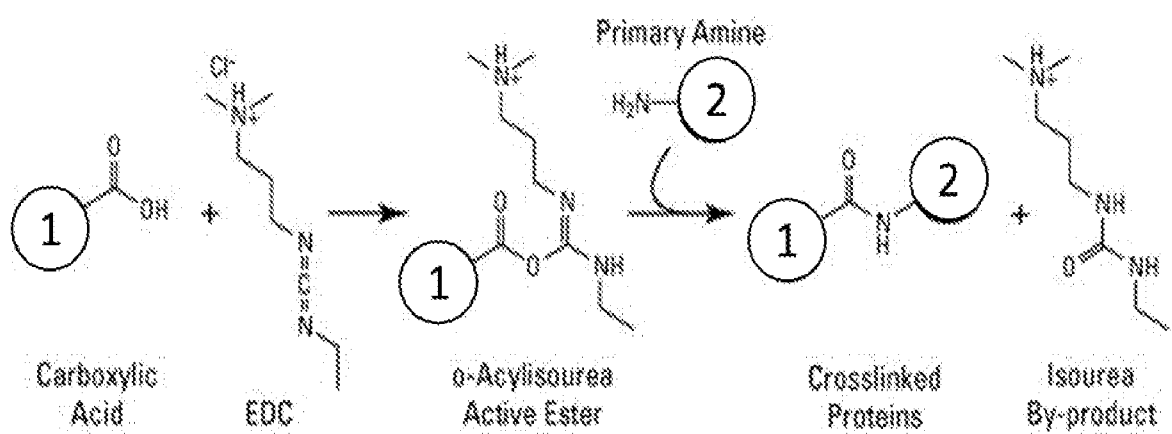


FIGURE 16

Protein	Target	Monomer	Dimer	Other	Viscosity at 150 mg/mL at 25°C
ASA1		Yes	Yes	No	~ 2-4 cP in A5
ASA2		Yes	Yes	No	~ 2-4 cP in A5
Ab BA	C-kit	Yes	Yes	Yes	~50 cP in A52Su
Ab AH	sclerostin	Yes	Yes	Yes	~22 cP in A52Su
Ab AN	sclerostin	Yes	Yes	Yes	~30 cP in A52Su

FIGURE 17

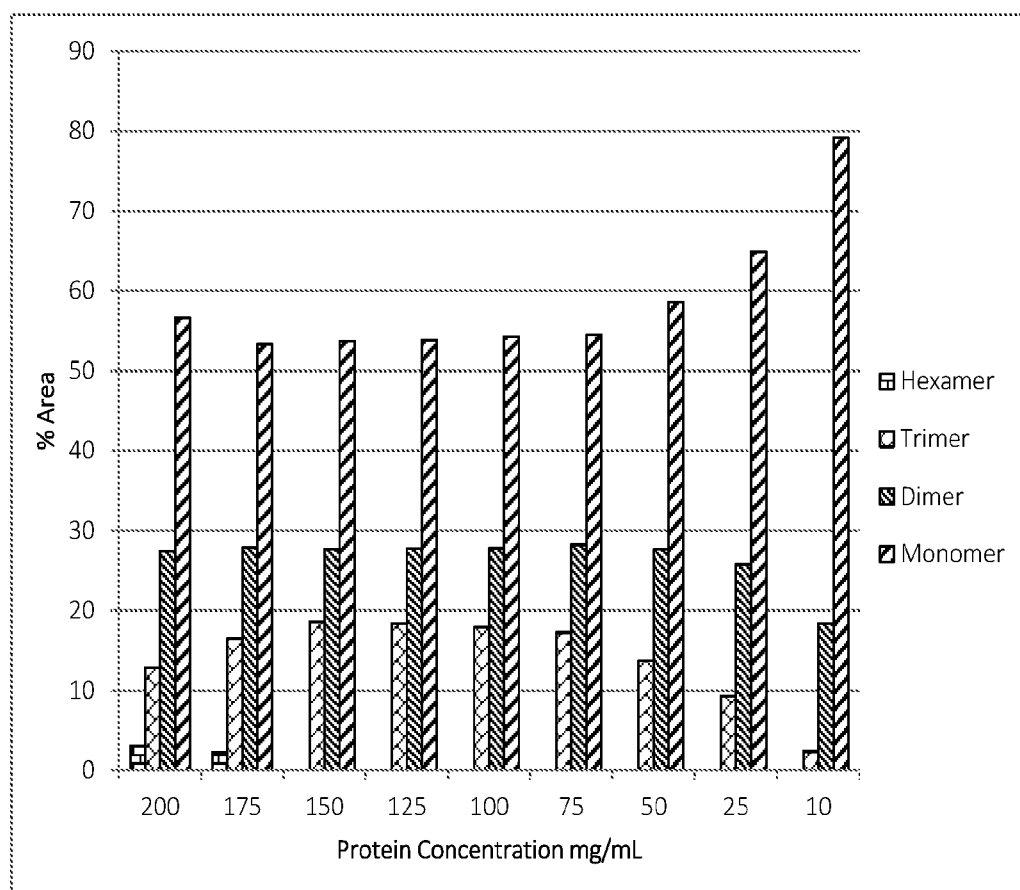


FIGURE 18

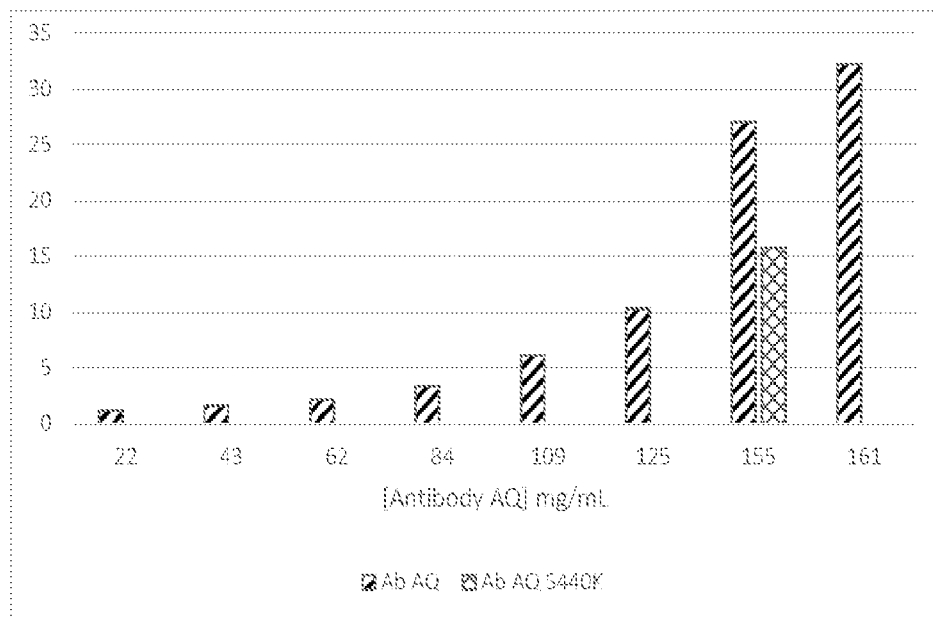


FIGURE 19A

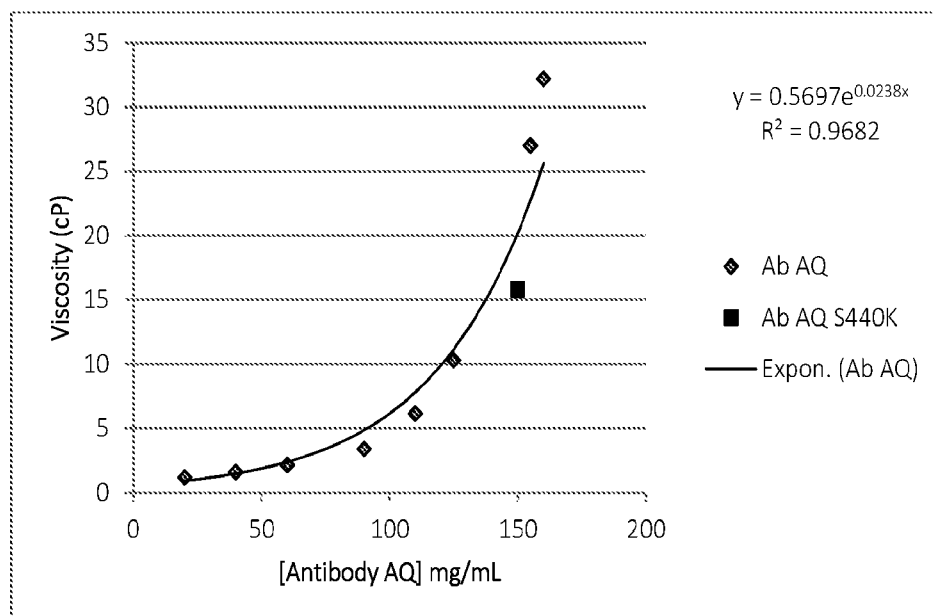


FIGURE 19B

AQ mutant symbols	AQ HC mutations in Aho (Linear) numbering	AQ LC mutations in Aho (Linear) numbering	Conc, mg/mL	Visc, cP	STDEV, cP	Visc Rel to AQ
AQ	AQ_HC	AQ_LC	151.1	19.1	0.6	1
AQ (HC 1, 17, 85)	AQ_HC: Q1(1)E, R17(16)G, S85(75)A	AQ_LC	151.7	15.8	0.8	0.87
AQ (LC 4 13 76 95 97 98)	AQ_HC:	AQ_LC: M4(4)L, V13(13)L, A76(60)D, S95(77)R, Q97(79)E, S98(80)P	149.1	12.7	0.4	0.67
AQ (HC 1, 17, 85) (LC 4 13 76 95 97 98)	AQ_HC: Q1(1)E, R17(16)G, S85(75)A	AQ_LC: M4(4)L, V13(13)L, A76(60)D, S95(77)R, Q97(79)E, S98(80)P	152.6	24.2	1	1.26

FIGURE 20A

4 Abs cAMP assay in 293/huGIPR#10

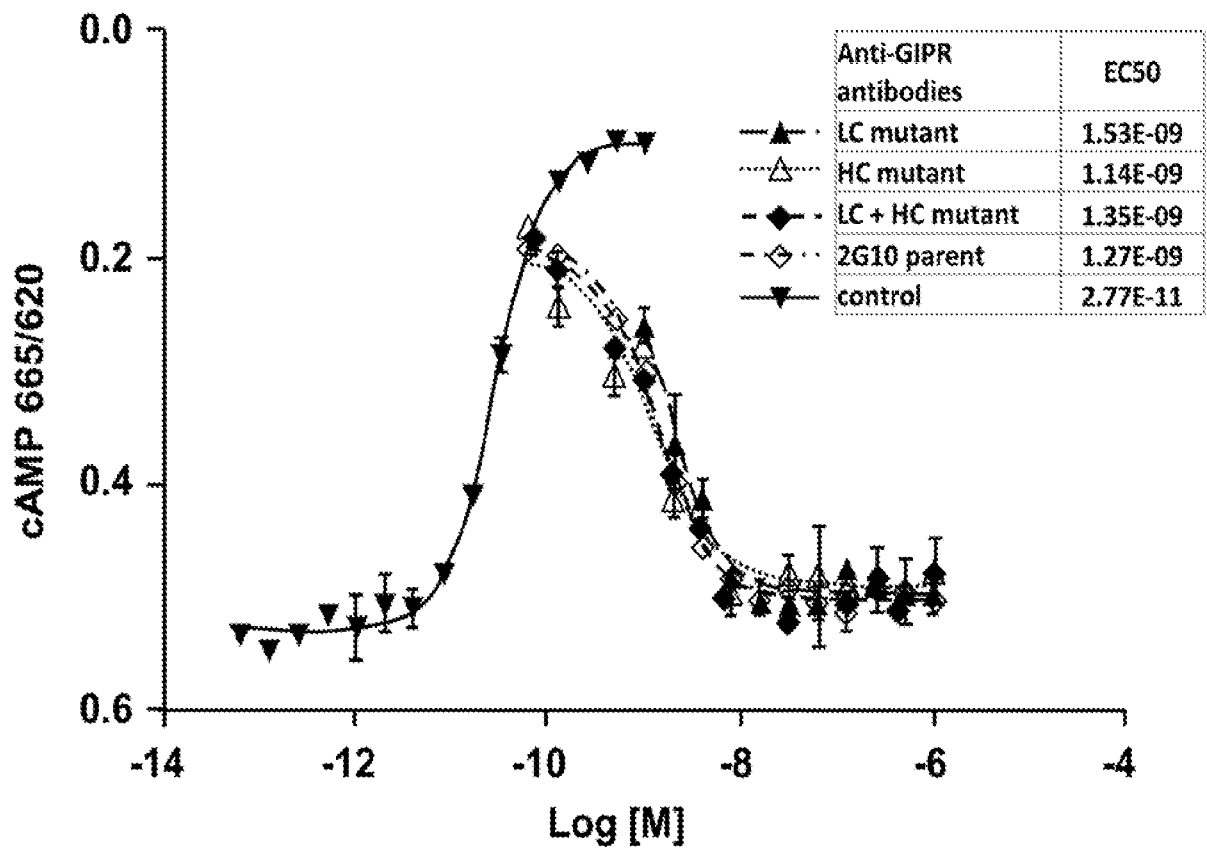


FIGURE 20B

Group #	Test Material	Dose Level (mg/kg)	Dose Volume (mL/kg)	Dose Concentration (mg/mL)	# Animals
1	Antibody AK (control)	10	0.071	140	4
	Diluent (procedural control)	0	0.071	0	
2	Antibody AK (Fab mutation)	10	0.048	210	4
	Diluent (procedural control)	0	0.048	0	
3	Antibody AK (Fc mutation)	10	0.048	210	4
4	Antibody AK (Fab and Fc double mutation)	10	0.048	210	4

FIGURE 21

Dose Group and Level	T _{max} (Day)	C _{max} (µg/mL)	AUC _{last} (day*µg/mL)	AUC _{last/D} (day*kg*µg/mL*mg)
Antibody AK 10 mg/kg	2.5	87.8	923	92.3
Antibody AK (Fab mutation) 10 mg/kg	2.5	91.1	807	80.7
Antibody AK (Fc mutation) 10 mg/kg	0.81	125	1020	102
Antibody AK (Fab + Fc mutation) 10 mg/kg	1	112	740	74.0

FIGURE 22

LDL-C% pretest *															
Days post dose															
Animal #	pretest (Day 1 CLAB)	1.02	2	3	4	6	8	11	15	18	22	25	29	36	43
1001	100.00%	101.75%	66.67%	40.35%	36.84%	29.82%	33.33%	29.82%	15.79%	24.56%	21.05%	22.81%	31.58%	57.89%	59.65%
1002	100.00%	95.00%	52.50%	45.00%	37.50%	37.50%	47.50%	20.00%	7.50%	50.00%	32.50%	30.00%	42.50%	60.00%	70.00%
1003	100.00%	111.11%	58.33%	27.78%	27.78%	22.22%	22.22%	36.11%	8.33%	25.00%	22.22%	19.44%	61.11%	97.22%	97.22%
1004	100.00%	105.97%	52.24%	35.82%	32.84%	29.85%	19.40%	14.93%	4.48%	4.48%	19.40%	19.40%	83.58%	98.51%	100.00%
mean	100.00%	103.50%	57.50%	37.50%	34.00%	30.00%	29.50%	24.00%	9.00%	23.00%	23.00%	22.50%	56.50%	79.00%	82.00%
2001	100.00%	106.52%	58.70%	34.78%	26.09%	28.26%	30.43%	28.26%	21.74%	52.17%	32.61%	39.13%	39.13%	54.35%	69.57%
2002	100.00%	100.00%	48.57%	34.29%	31.43%	28.57%	25.71%	8.57%	8.57%	25.71%	28.57%	42.86%	65.71%	120.00%	102.86%
2003	100.00%	110.34%	63.79%	32.76%	32.76%	24.14%	13.79%	18.97%	5.17%	15.52%	18.97%	24.14%	41.38%	60.34%	67.24%
2004	100.00%	114.29%	62.86%	37.14%	31.43%	25.71%	22.86%	28.57%	20.00%	22.86%	31.43%	31.43%	48.57%	65.71%	77.14%
mean	100.00%	108.05%	59.20%	34.48%	30.46%	26.44%	22.41%	21.26%	13.22%	28.74%	27.01%	33.33%	47.13%	71.84%	77.01%
3001	102.63%	63.16%	42.11%	31.58%	28.95%	23.68%	18.42%	7.89%	23.68%	28.95%	76.32%	113.16%	126.32%	97.37%	94.87%
3002	104.17%	50.00%	29.17%	27.08%	29.17%	18.75%	14.58%	6.25%	16.67%	25.00%	52.08%	81.25%	89.58%	79.17%	76.00%
3003	100.00%	37.21%	18.60%	18.60%	6.98%	6.98%	6.98%	6.98%	6.98%	39.53%	67.44%	116.28%	95.35%	102.33%	102.33%
3004	100.00%	55.00%	40.00%	32.50%	27.50%	25.00%	27.50%	20.00%	22.50%	25.00%	22.50%	32.50%	37.50%	50.00%	50.00%
mean	100.00%	101.78%	50.89%	31.95%	27.22%	23.08%	18.34%	16.57%	10.06%	17.16%	29.59%	54.44%	85.80%	86.98%	82.25%
4001	100.00%	105.88%	76.47%	56.86%	47.06%	45.10%	35.29%	39.22%	25.49%	31.37%	31.37%	37.25%	64.71%	92.16%	96.08%
4002	100.00%	102.17%	54.35%	39.13%	32.61%	30.43%	21.74%	28.26%	15.22%	28.26%	28.26%	34.78%	34.78%	67.39%	82.61%
4003	100.00%	94.92%	54.24%	35.59%	30.51%	20.34%	22.03%	27.12%	15.25%	23.73%	57.63%	45.76%	67.80%	74.58%	81.36%
4104	100.00%	102.99%	56.72%	32.84%	34.33%	35.82%	28.36%	29.85%	31.34%	25.37%	28.36%	26.87%	44.78%	55.22%	59.70%
mean	100.00%	101.35%	60.09%	40.36%	35.87%	32.74%	26.91%	30.94%	22.42%	26.91%	36.77%	35.87%	53.36%	71.30%	78.48%

FIGURE 23

Pharmacokinetics

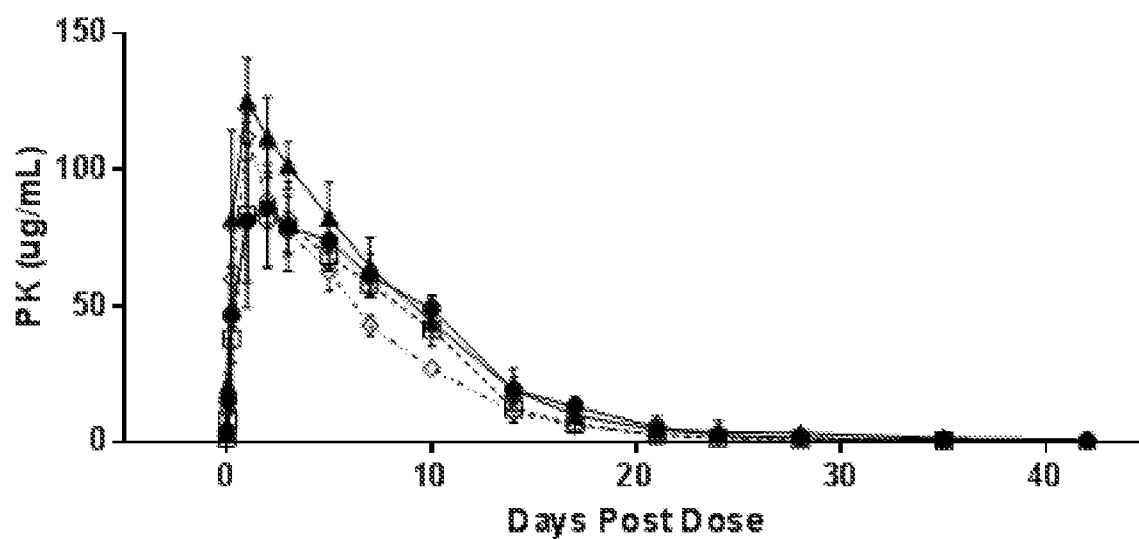


FIGURE 24A

LDL-C (% difference from baseline)

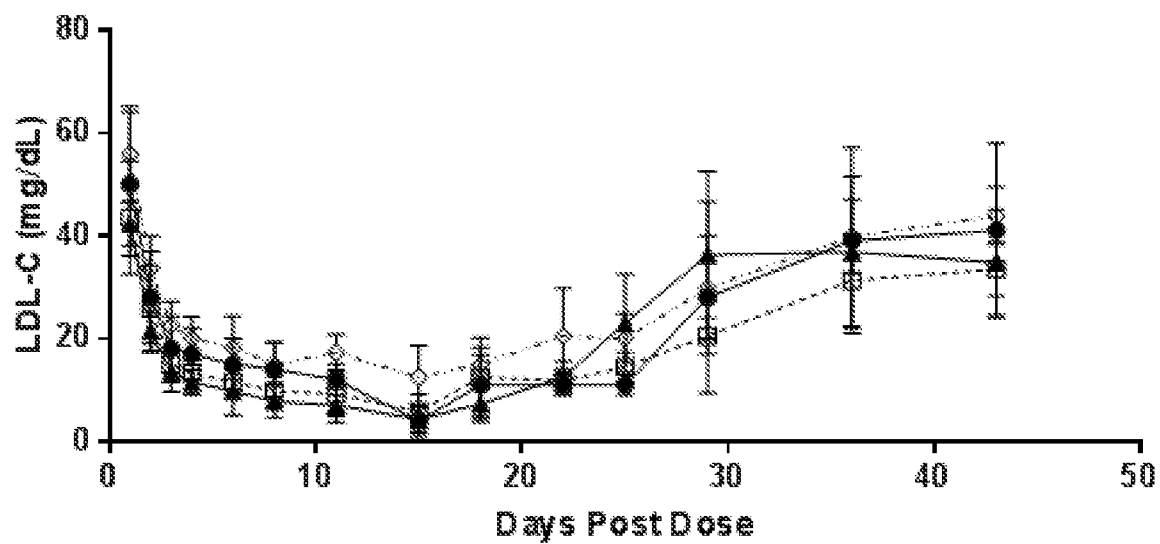


FIGURE 24B