

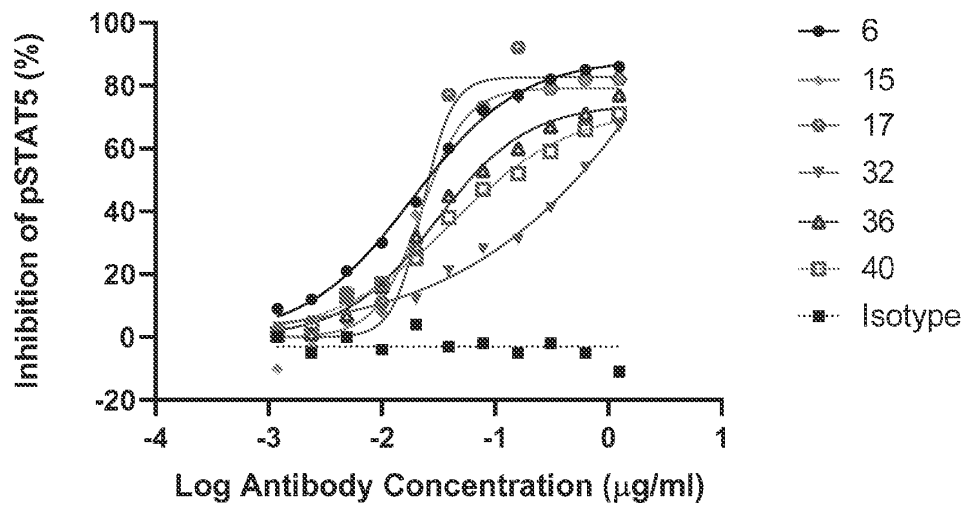


FIG. 1

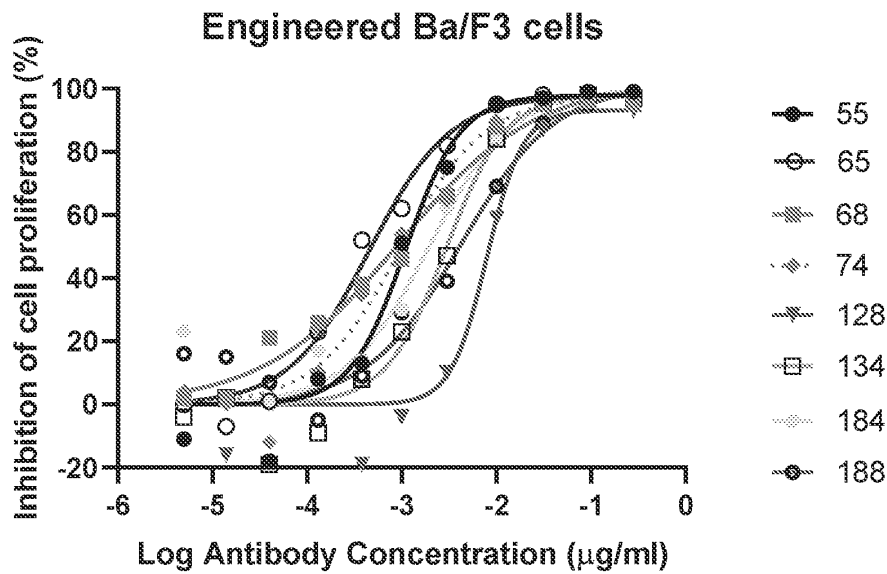


FIG. 2

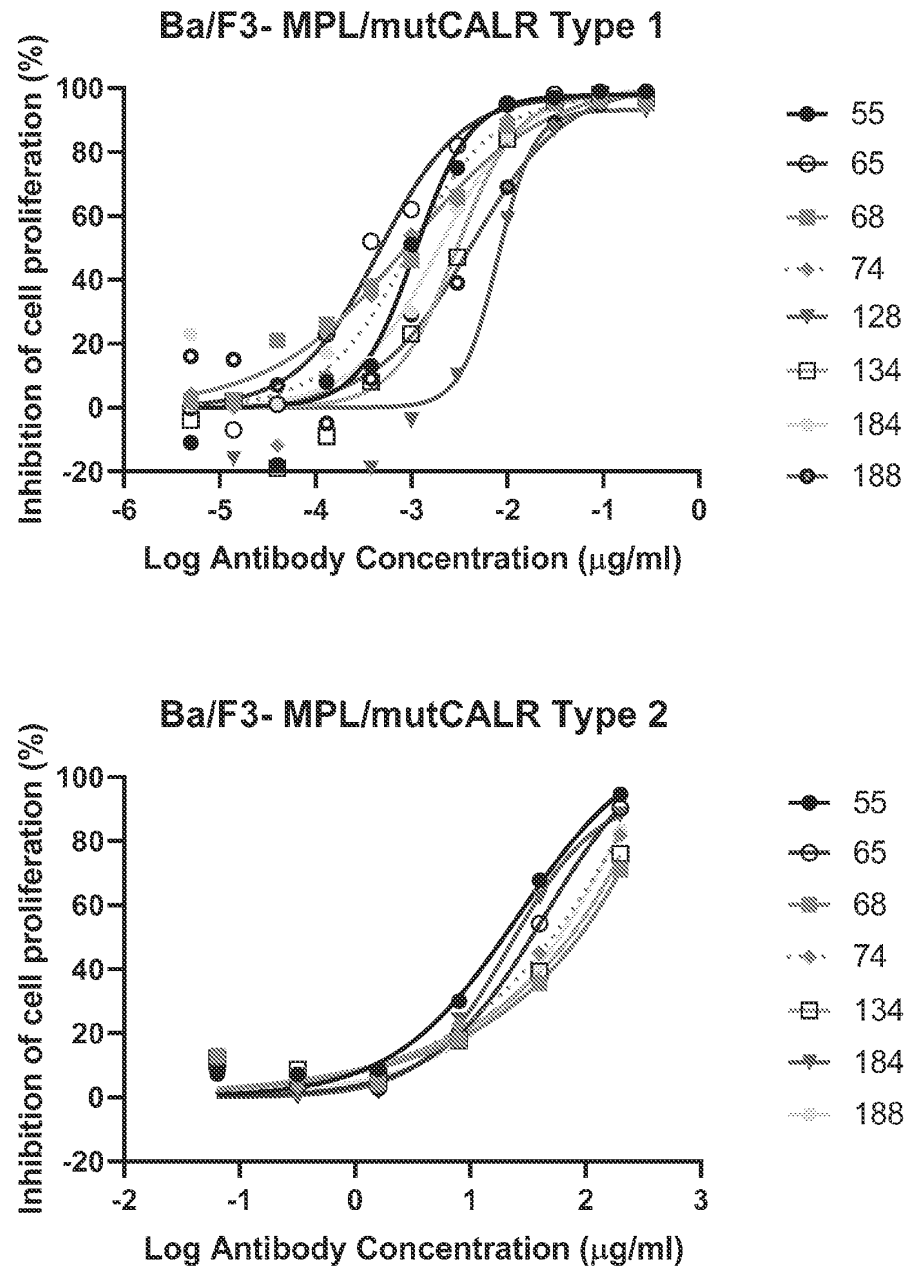


FIG. 3

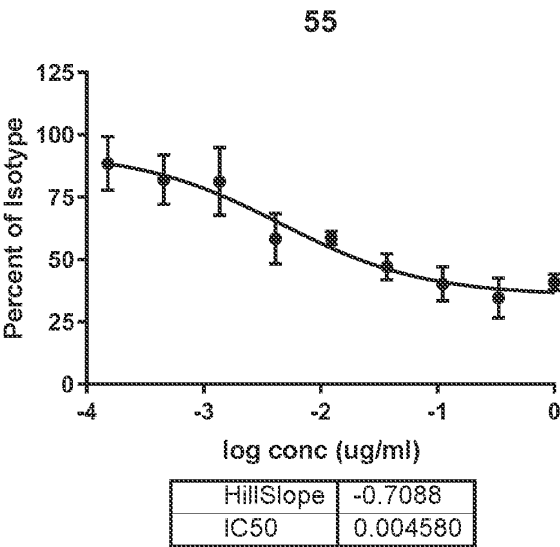


FIG. 4A

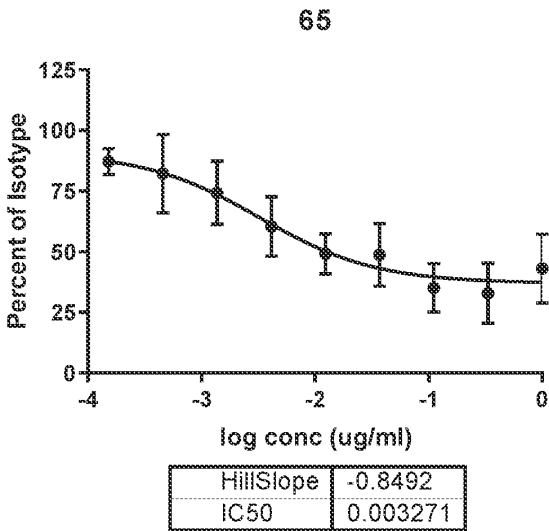


FIG. 4B

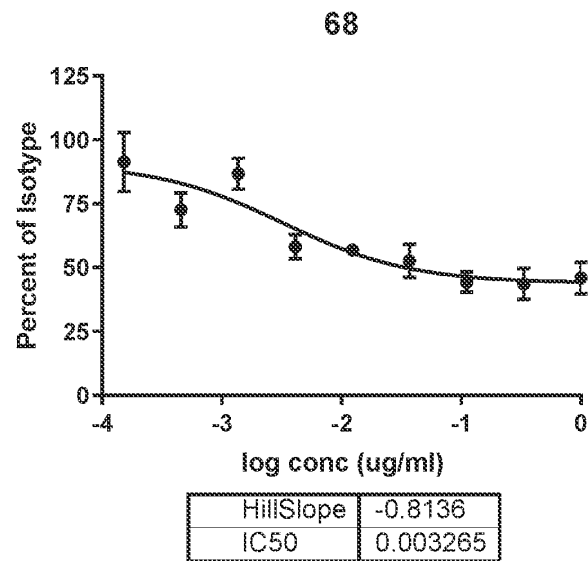


FIG. 4C

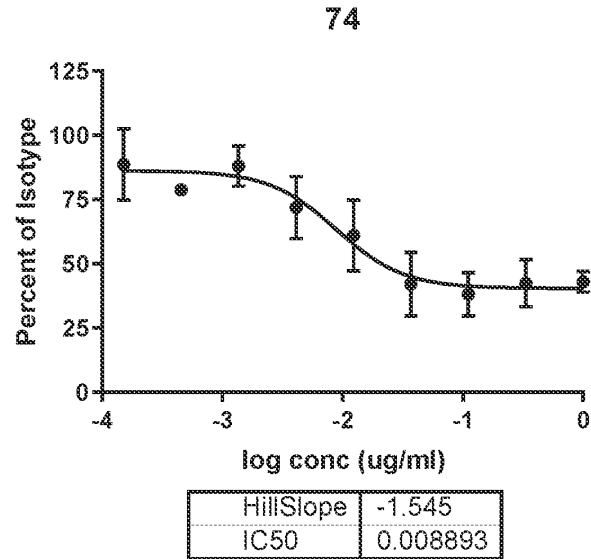


FIG. 4D

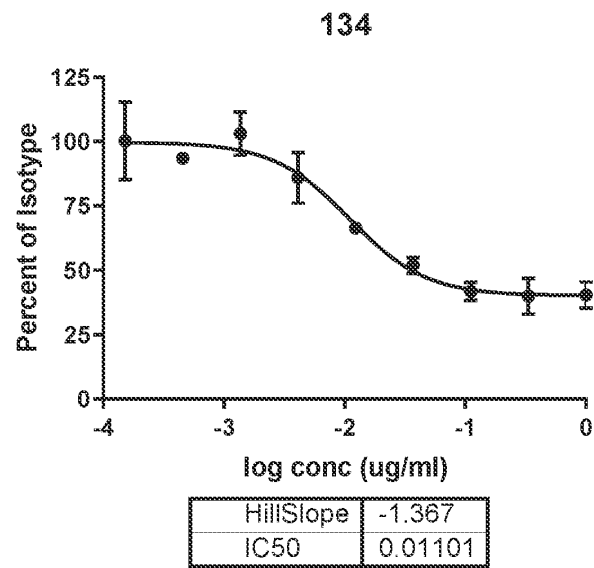


FIG. 4E

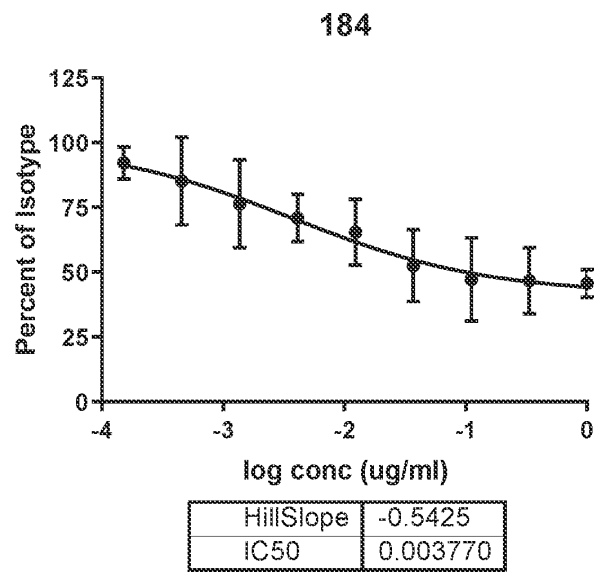


FIG. 4F

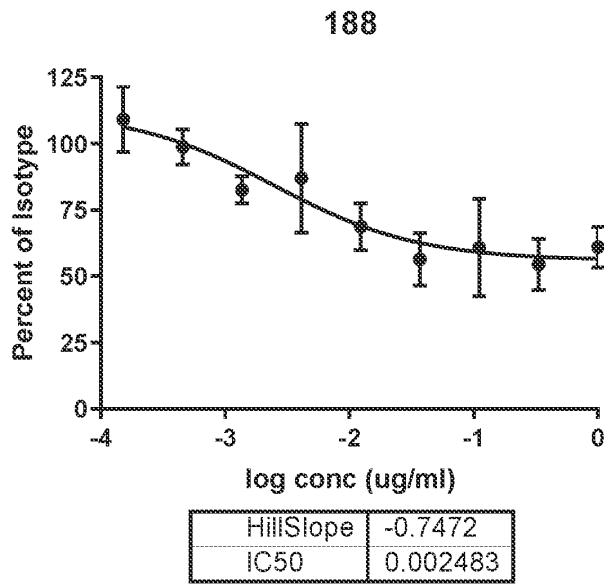


FIG. 4G

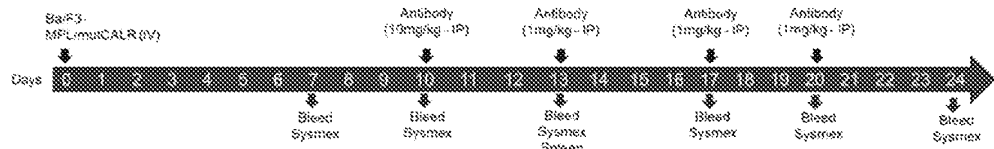


FIG. 5

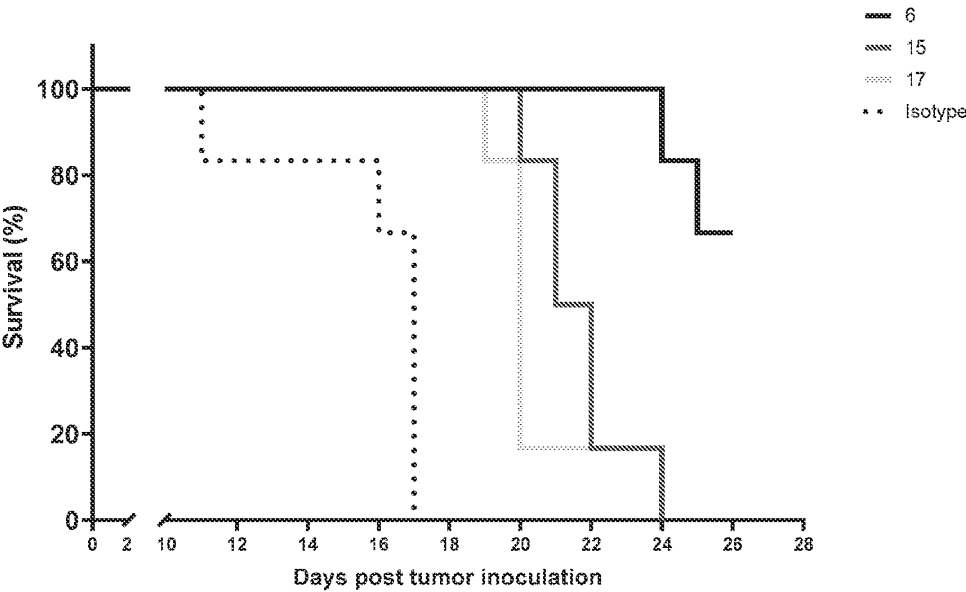


FIG. 6

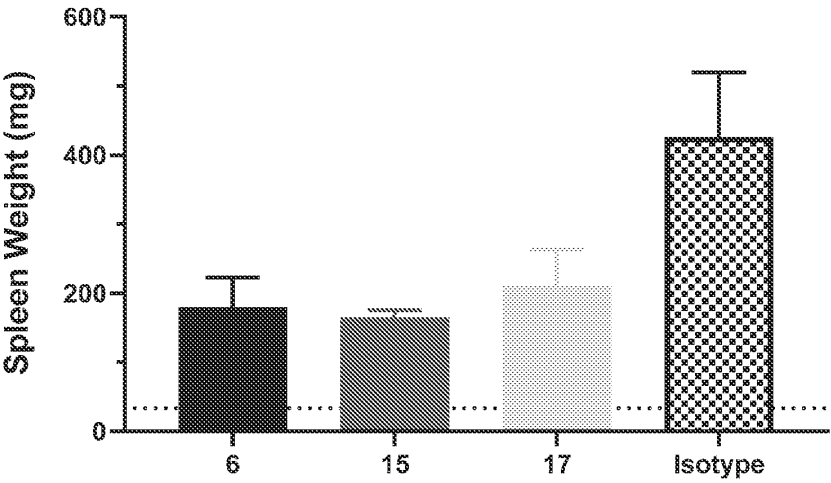


FIG. 7

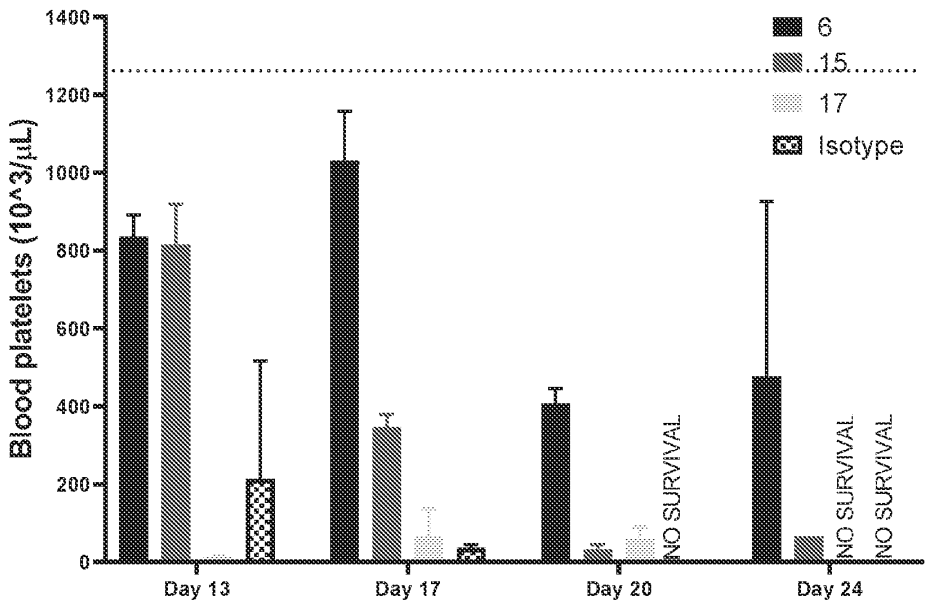


FIG. 8

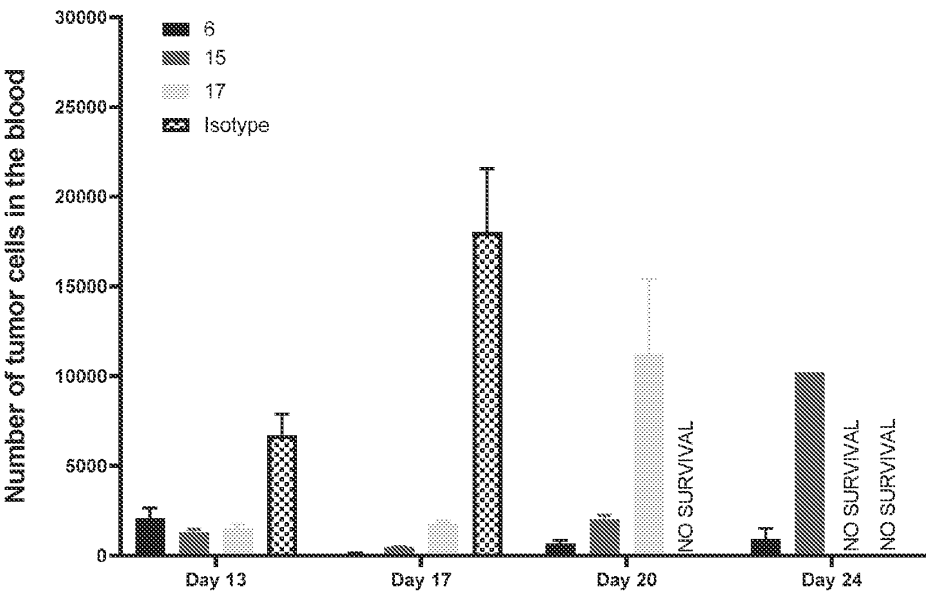


FIG. 9

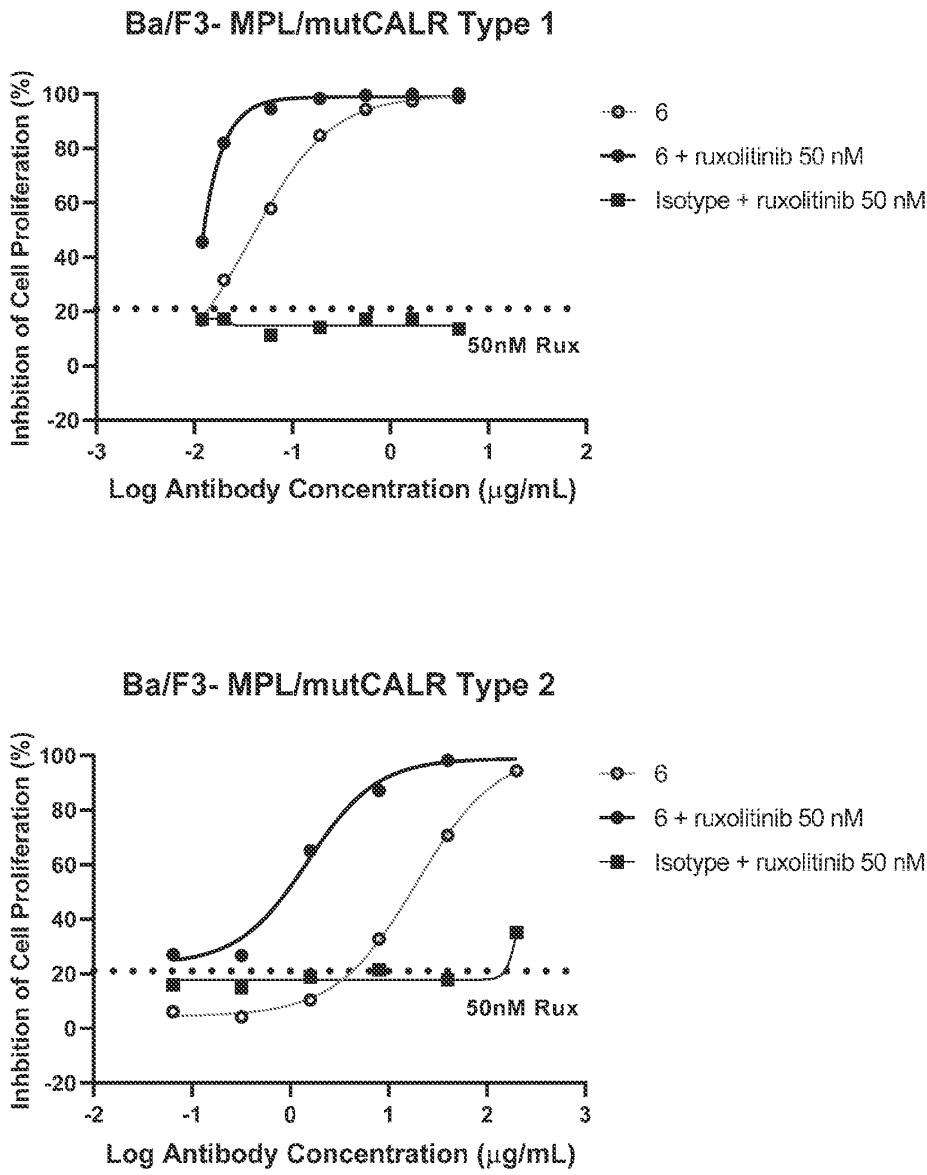


FIG. 10

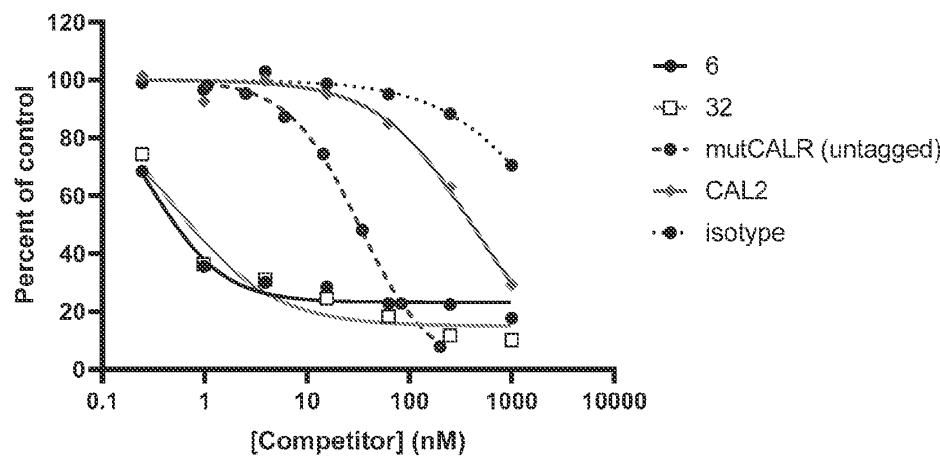


FIG. 11

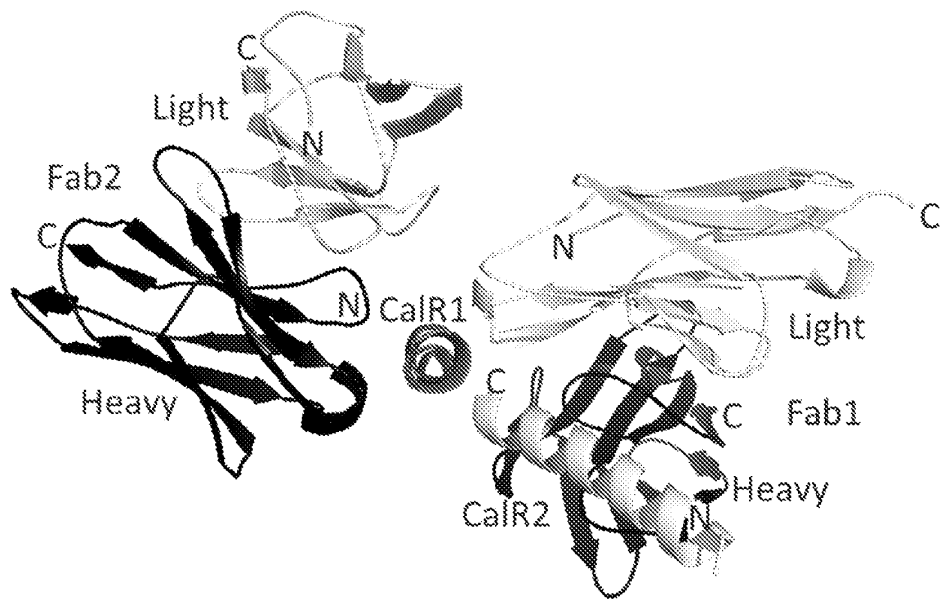


FIG. 12A

CDR	Amino Acids	CDR Length	SEQ ID NO:
L1	THR23, GLY24, THR25, SER26, SER27, ASP28, VAL29, GLY30, GLY31, <u>TYR32</u> , ASN33, TYR34, VAL35, SER36	14	30
L2	<u>GLU52</u> , VAL53, SER54, ASN55, ARG56, PRO57, SER58	7	55
L3	GLN91, VAL92, TRP93, ASP94, SER95, SER96, ASN97, <u>ASP98*</u> , LEU99, LEU100, ILE101	11	71
H1	<u>GLY26</u> , TYR27, THR28, LEU29, THR30, <u>GLU31</u> , LEU32, SER33, MET34, GLN35	10	329
H2	GLY50, PHE51, <u>ASP52*</u> , PRO53, <u>ASP54</u> , ASP55, GLY56, GLU57, THR58, <u>MET59</u> , TYR60, ALA61, GLU62, LYS63, PHE64, GLN65, GLY66	17	7
H3	SER99, PRO100, GLY101, TYR102, <u>ASP103</u> , PHE104, PHE105, <u>ASP106</u> , TYR107	9	18

FIG. 12B

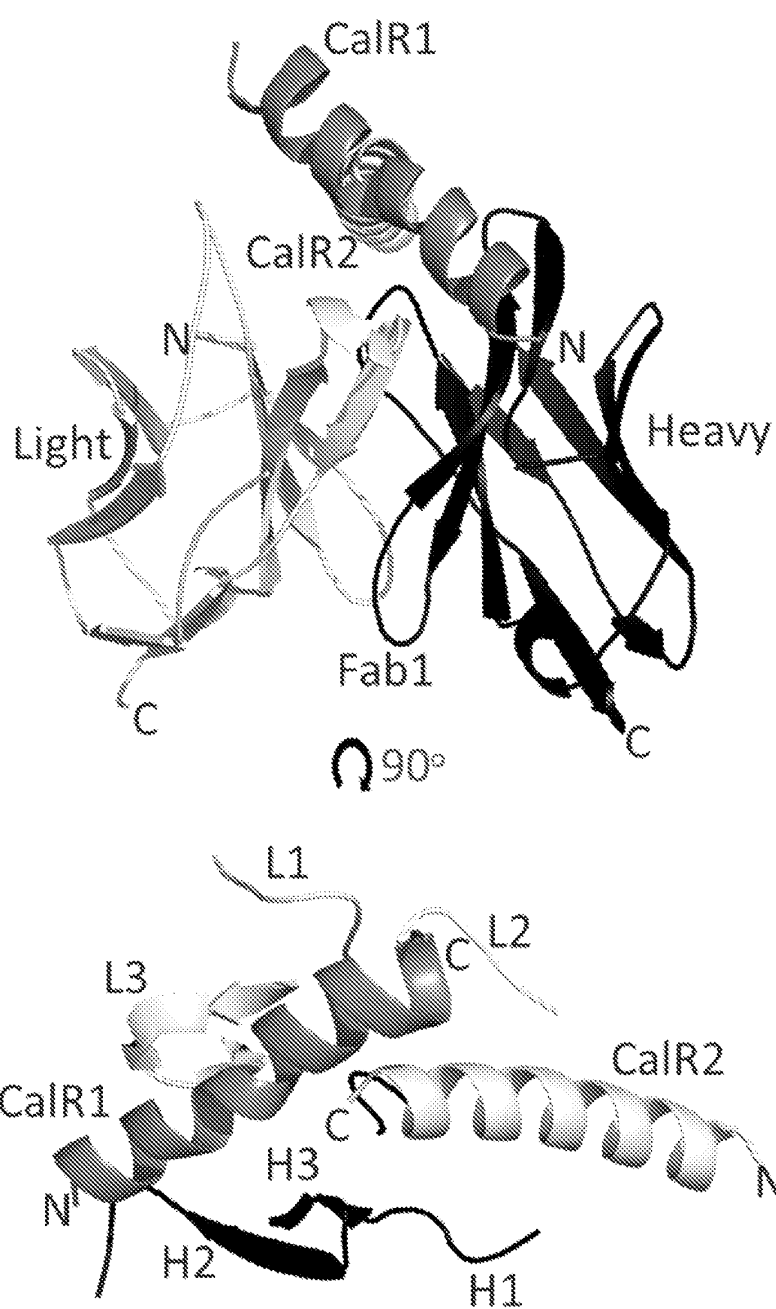


FIG. 12C

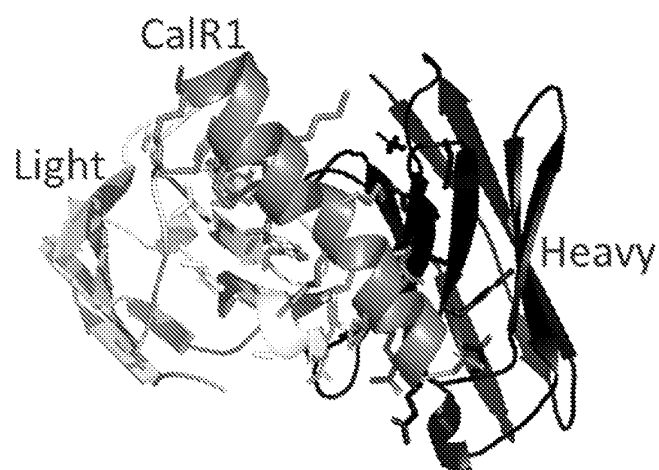
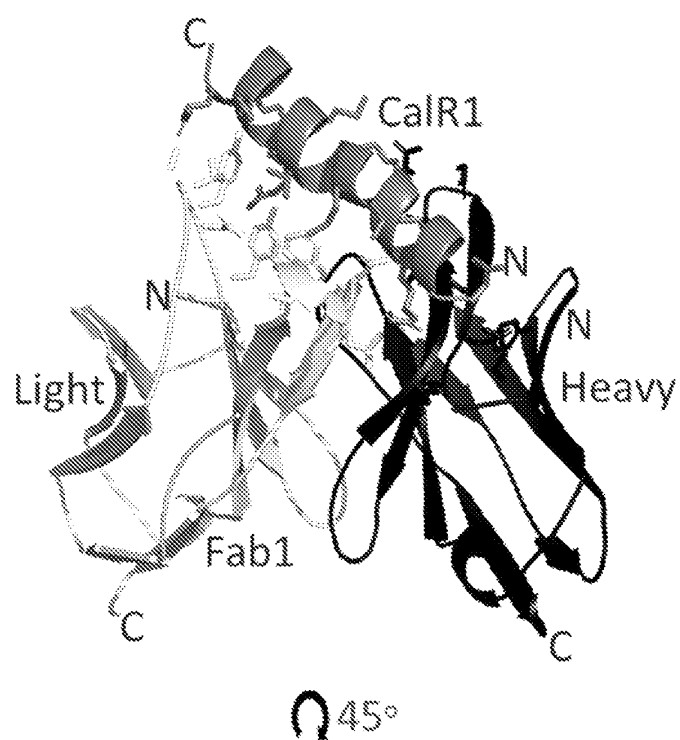


FIG. 13A

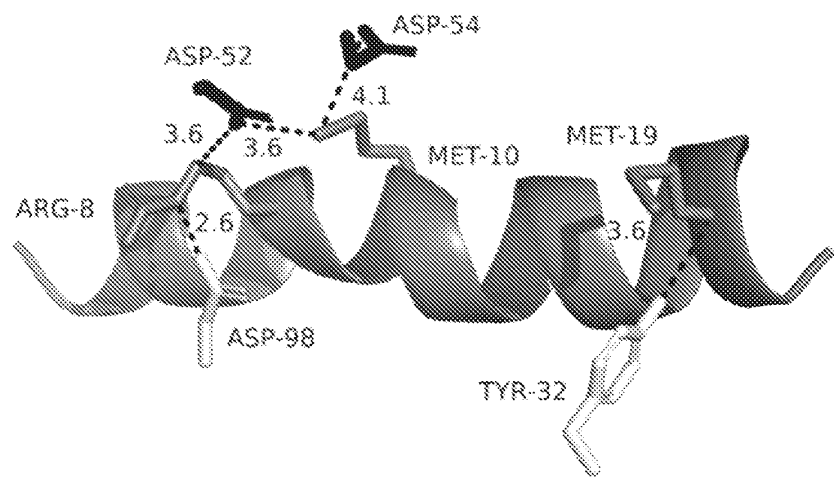


FIG. 13B

CalR1 Amino acid	Fab1 Amino acid	Light or Heavy Chain	Distance (Å)	Specific Interactions
Arg 8	Asp 52	H	3.6	1x hydrogen bond
Arg 8	Asp 98	L	2.6	2x hydrogen bond, 1x salt bridge
Met 10	Asp 52	H	3.6	3x van der waals
Met 10	Asp 54	H	4.1	7x van der waals
Met 19	Tyr 32	L	3.6	9x van der waals

FIG. 13C

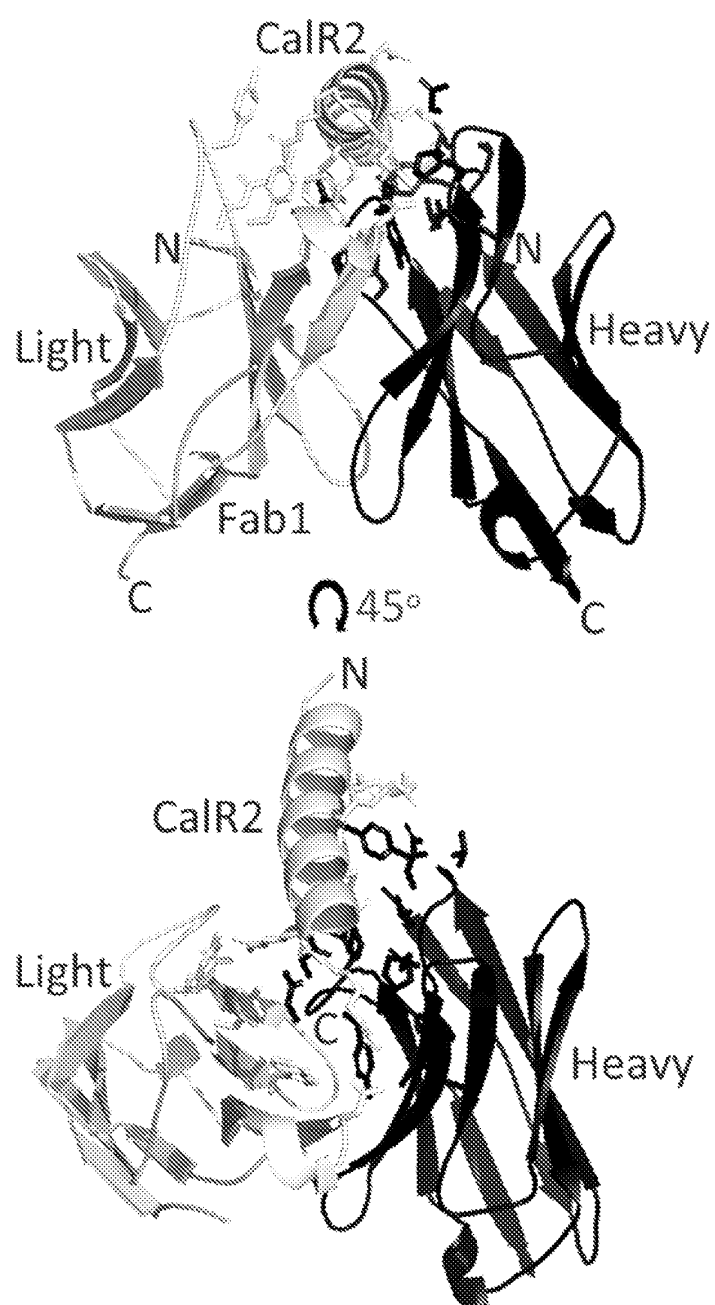


FIG. 14A

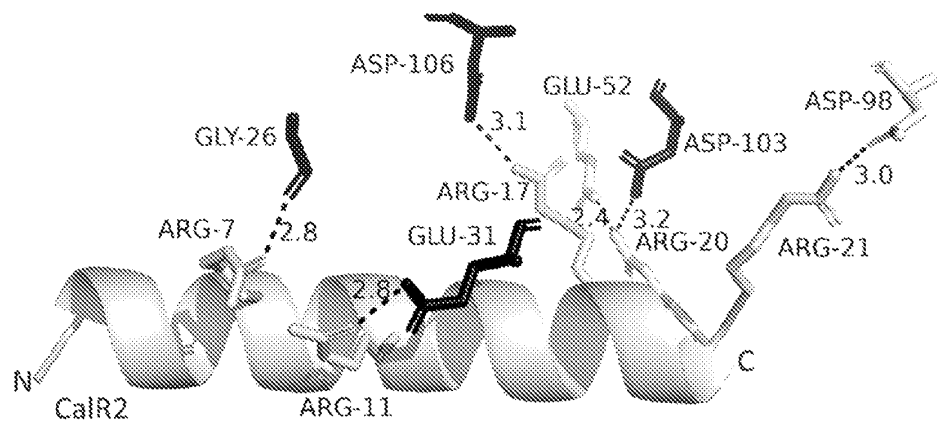


FIG. 14B

CalR2 Amino acid	Fab1 Amino acid	Light or Heavy Chain	Distance (A)	Specific Interactions
Arg 7	Gly 26	H	2.8	1x hydrogen bond
Arg 11	Glu 31	H	2.8	1x hydrogen bond
Arg 17	Asp 106	H	3.1	1x hydrogen bond, 1x salt bridge
Arg 20	Glu 52	L	2.4	1x hydrogen bond, 1x salt bridge
Arg 20	Asp 103	H	3.2	1x hydrogen bond, 1x salt bridge
Arg 21	Asp 98	L	3.0	1x hydrogen bond, 1x salt bridge

FIG. 14C

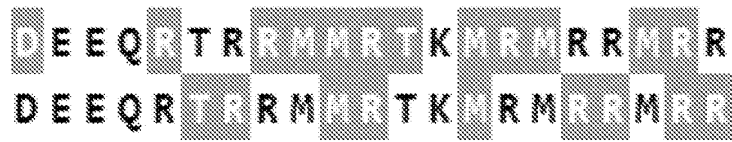


FIG. 15

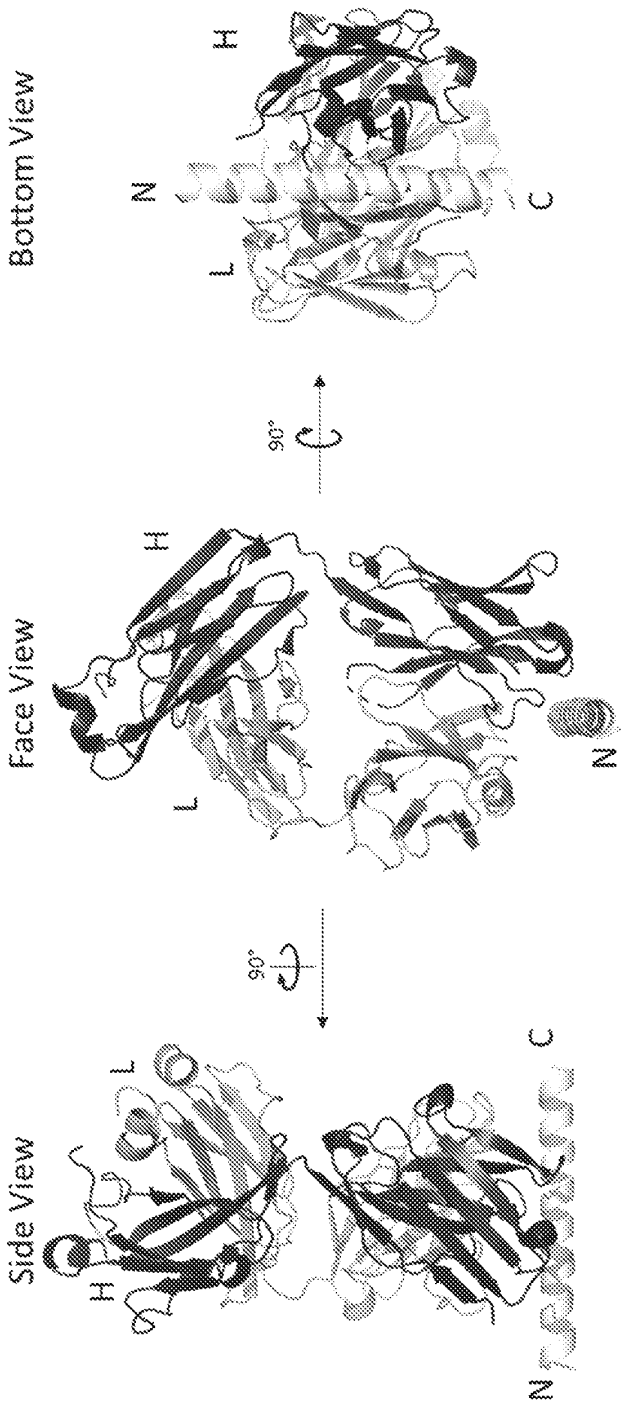


FIG. 16A

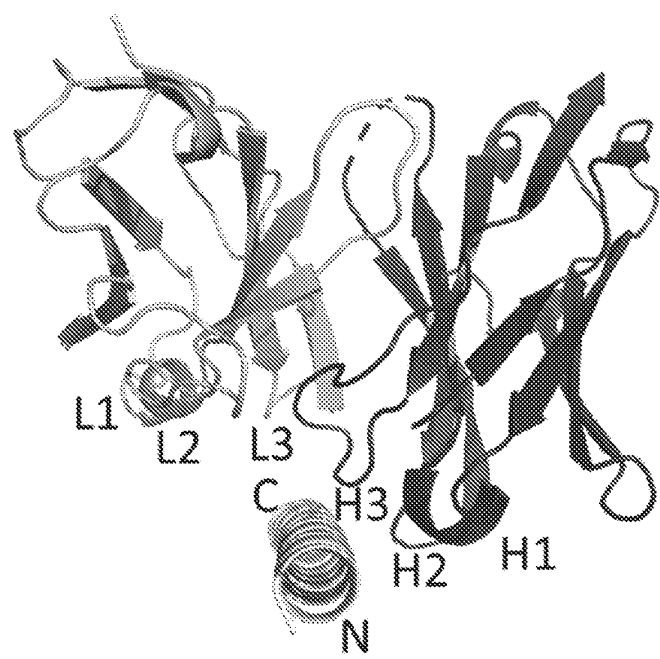


FIG. 16B

CDR	Amino Acids	CDR Length	SEQ ID NO:
L1	THR23, GLY24, THR25, SER26, SER27, ASP28, VAL29, GLY30, GLY31, TYR32, ASN33, TYR34, VAL35, SER36	14	30
L2	GLU52, VAL53, SER54, ASN55, ARG56, PRO57, SER58	7	55
L3	GLN91, VAL92, TRP93, ASP94, SER95, SER96, ASN97, ASP98, LEU99, LEU100, ILE101	11	71
H1	GLY26, TYR27, THR28, LEU29, THR30, GLU31, LEU32, SER33, MET34, GLN35	10	329
H2	GLY50, PHE51, ASP52, PRO53, ASP54, ASP55, GLY56, GLU57, THR58, MET59, TYR60, ALA61, GLU62, LYS63, PHE64, GLN65, GLY66	17	7
H3	SER99, PRO100, GLY101, TYR102, ASP103, PHE104, PHE105, ASP106, TYR107	9	18

FIG. 16C

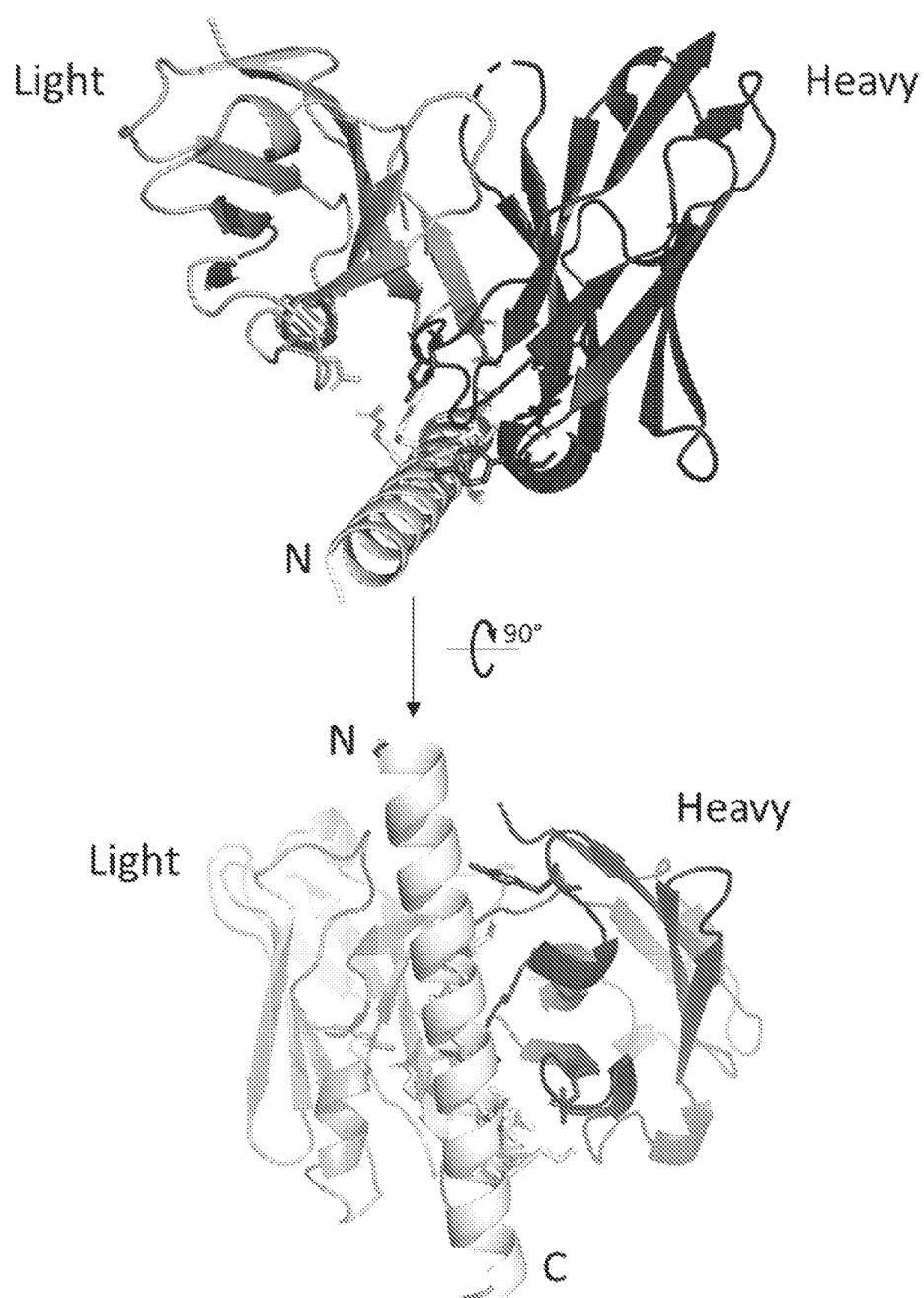


FIG. 17A

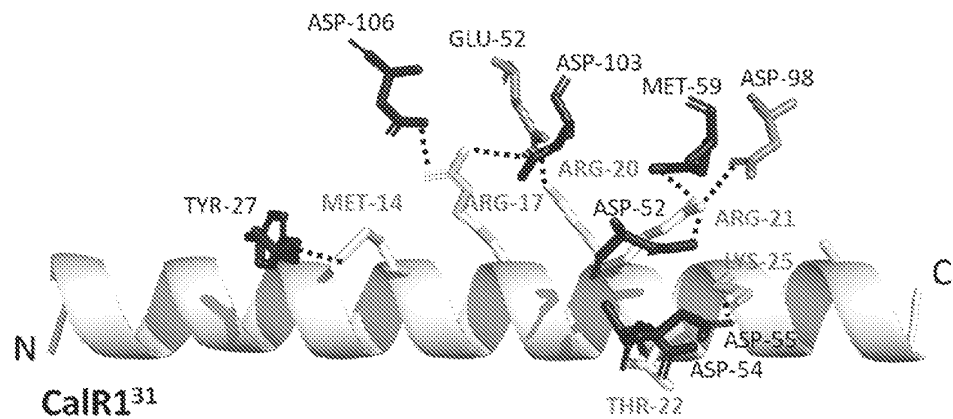


FIG. 17B

CalR1 ³¹ Amino acid	Fab Amino acid	Chain	CDR	Interaction Type	Distance (Å)
Met14	Tyr27	H	H1	arene	3.65
Arg17	Asp106	H	H3	ionic and H bond	3.04
Arg17	Asp103	H	H3	ionic and H bond	3.29
Arg20	Glu52	L	L2	ionic and H bond	3.03
Arg20	Asp103	H	H3	ionic and H bond	2.72
Arg21	Asp98	L	L3	ionic and H bond	3.13
Arg21	Asp52	H	H2	ionic and H bond	3.26
Arg21	Met59	H	H2	ionic and H bond	3.62
Thr22	Asp54	H	H2	H bond	3.16
Lys25	Asp54	H	H2	ionic and H bond	3.18
Lys25	Asp52	H	H2	ionic and H bond	3.24
Lys25	Asp55	H	H2	ionic bond	2.89

FIG. 17C

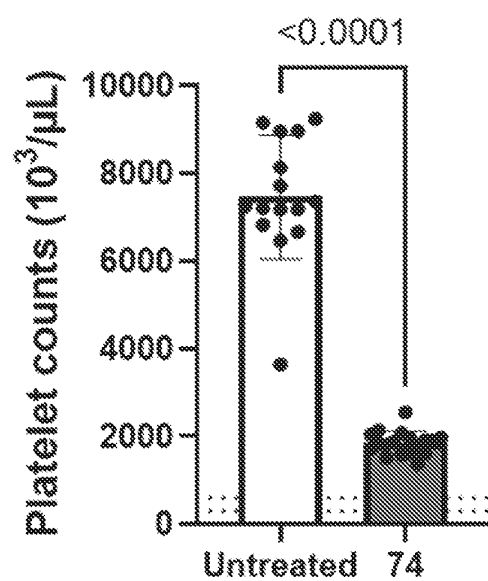


FIG. 18A

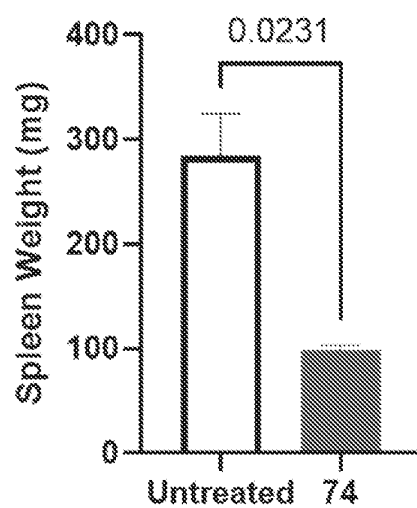


FIG. 18B

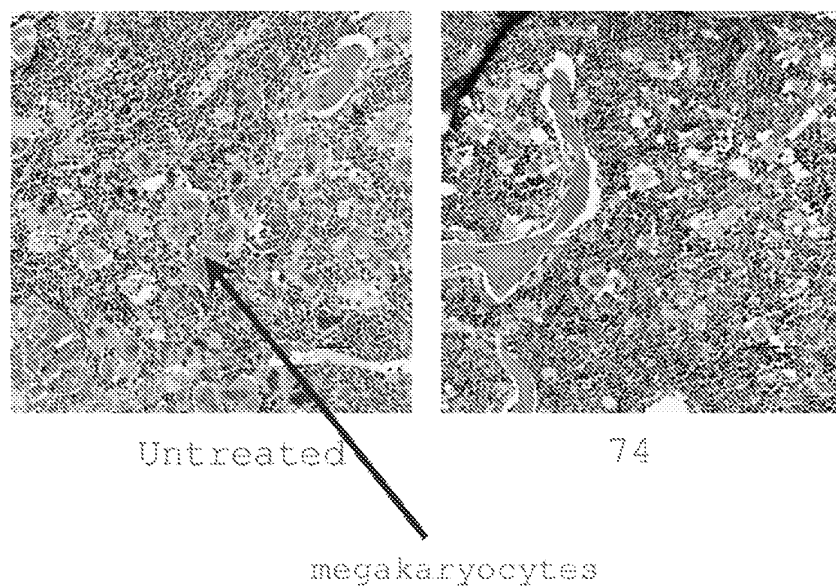


FIG. 18C

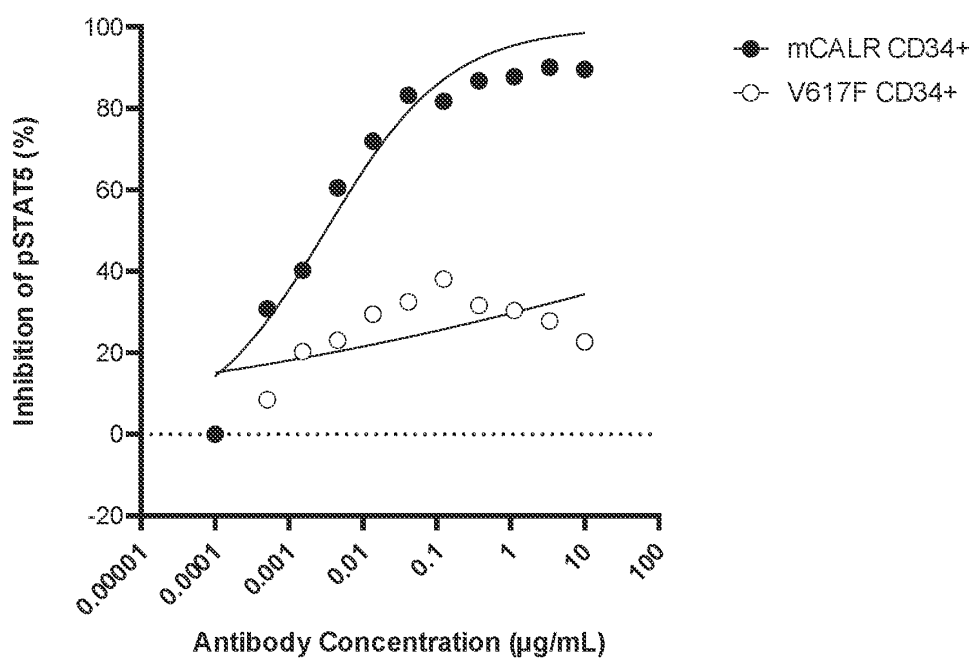


FIG. 19A

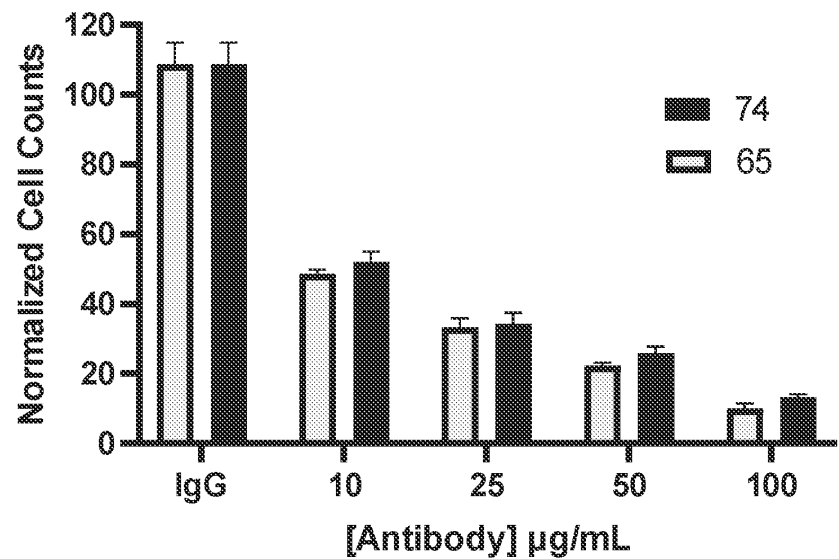


FIG. 19B

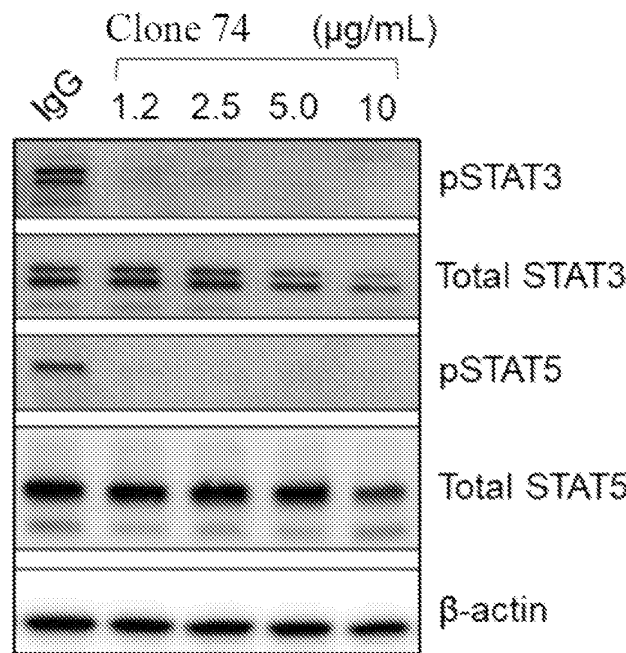


FIG. 19C

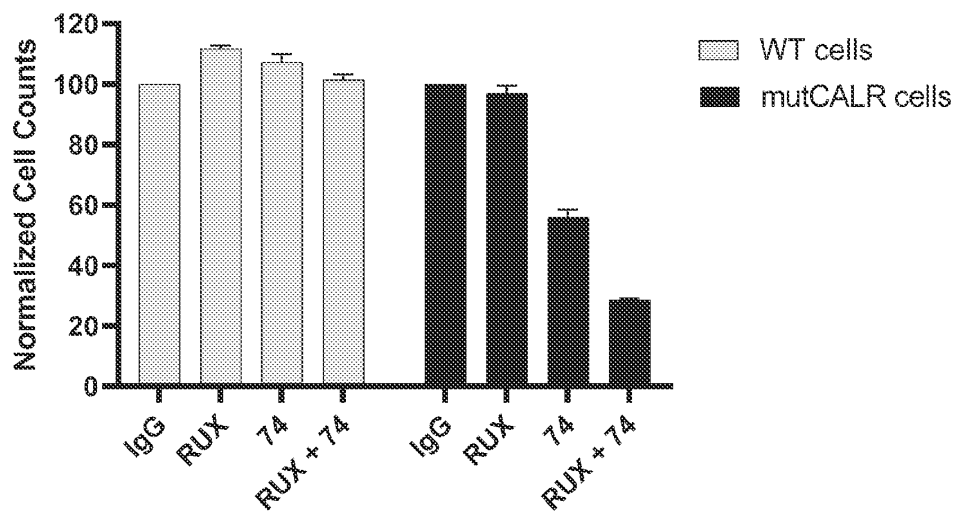


FIG. 19D

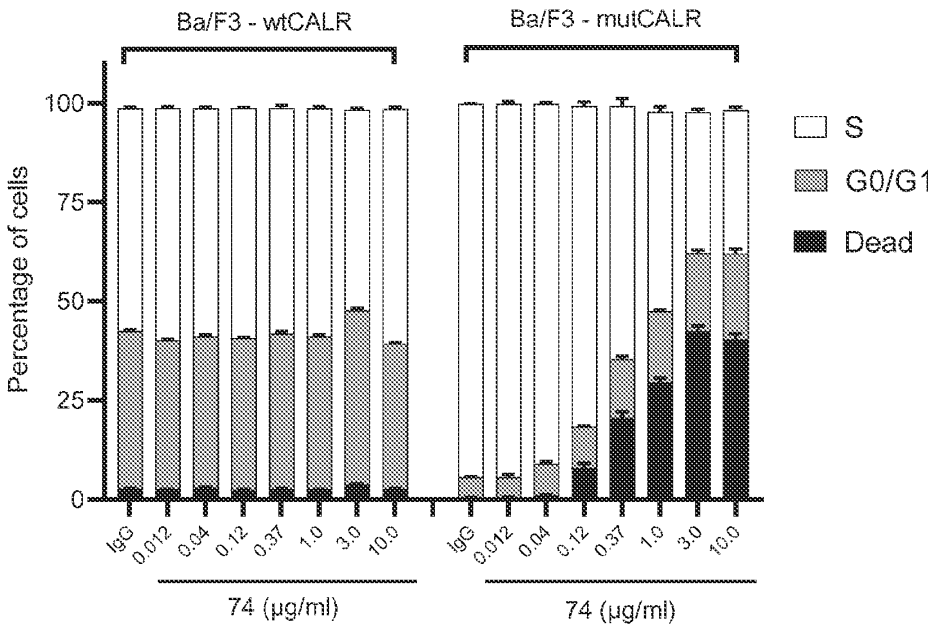


FIG. 20

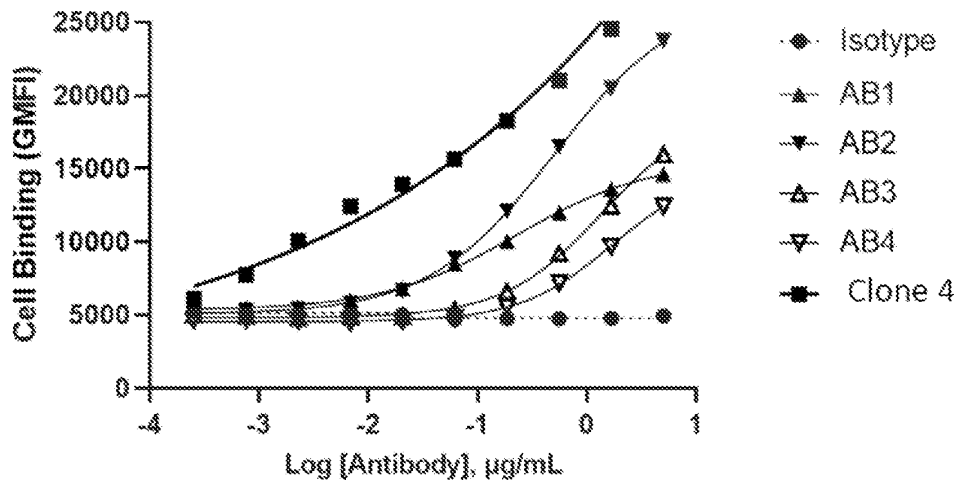


FIG. 21A

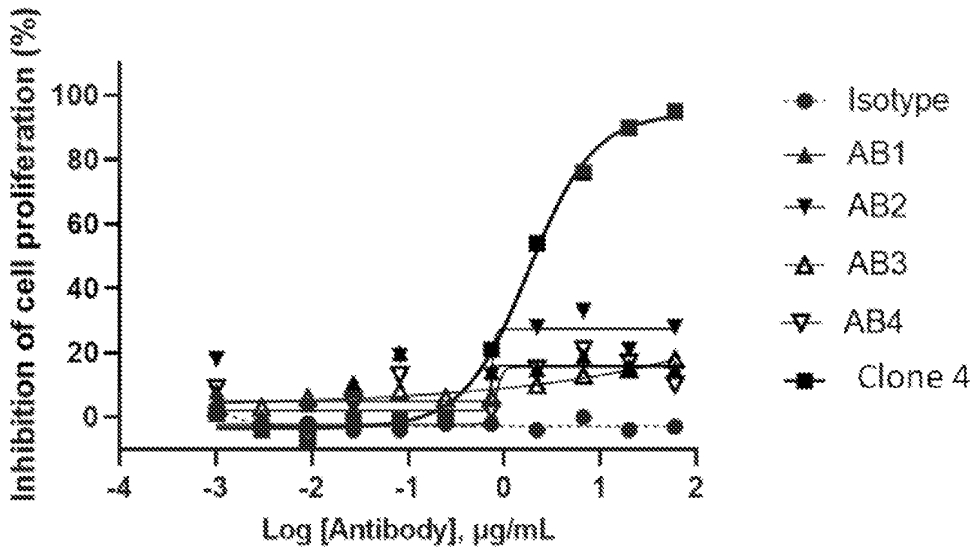


FIG. 21B