

			1		50
v1	(1)	EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY			
v2	(1)	EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY			
v3	(1)	EEELQVIQPKSVSVAAGESAILLCTVTSLIPVGPIONFRGAGPARELIY			
v4	(1)	EEGLQVIQPKSVSVAAGESAILHCTATSLIPVGPIONFRGAGPARELIY			
v5	(1)	EEELQVIQPKFVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY			
v6	(1)	EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY			
v7	(1)	EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY			
v8	(1)	EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY			
v9	(1)	EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY			
v10	(1)	EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY			
		* * * * *			*
			51		100
v1	(51)	NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P			
v2	(51)	NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P			
v3	(51)	NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P			
v4	(51)	NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P			
v5	(51)	NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P			
v6	(51)	NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P			
v7	(51)	NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P			
v8	(51)	NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P			
v9	(51)	NOKEGHFFRVTTVSDLTKRNNMDFSIRISNITPADAGTYVCVKFRKGS-P			
v10	(51)	NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P			
		** * * * *			**
			101		119
v1	(101)	DVEFKSGAGTELSVRAKPS			
v2	(100)	DTEFKSGAGTELSVRAKPS			
v3	(100)	DTEFKSGAGTELSVRAKPS			
v4	(101)	DVEFKSGAGTELSVRAKPS			
v5	(101)	DVEFKSGAGTELSVRAKPS			
v6	(101)	DVEFKSGAGTELSVRAKPS			
v7	(100)	DTEFKSGAGTELSVRGKPS			
v8	(100)	DTEFKSGAGTELSVRAKPS			
v9	(101)	DVEFKSGAGTELSVRAKPS			
v10	(100)	DTEFKSGAGTELSVRAKPS			
		* * * * *			*

FIG. 1A

Human_v1	(1)	EEELQVIQPDKSVLVAAGETATLRC	TATSLIPVGPIQWFRGAGPCRELIY	1	50
Human_v2	(1)	EEELQVIQPDKSVVAAGESAILHCTV	TSLIPVGPIQWFRGAGPARELIY		
Cyno	(1)	EEELQVIQPEKSVVAAGESATLNC	TATSLIPVGPIQWFRGVGPARELIY		
129mouse	(1)	-KELKVTQPEKSVVAAGDSTVLNCT	LTSLLPVGPIKWYRGVGSRLLIY		
		** * * *	**** * * * * *		
	51				100
Human_v1	(51)	NQKEGHEPRVTVSDLT	KRNNMDFSIRIGNITPADAGTY		
Human_v2	(51)	NQKEGHEPRVTVSE	TKRNNMDFSISISNITPADAGTY		
Cyno	(51)	HQKEGHEPRVTPVSDPT	KRNNMDFSIRISNITPADAGTY		
129mouse	(50)	SFTGEHFRVTVNSD	ATKRNNMDFSIRISNVTPE		
		*****	* * * *		
	101				120
Human_v1	(100)	DDVEFKSGAGTELS	VRAKPS		
Human_v2	(99)	PDTEFKSGAGTELS	VRAKPS		
Cyno	(99)	PDVELKSGAGTELS	VRAKPS		
129mouse	(100)	PDTEIQSGGTEVY	VLA		
		* * * *	* * * *		

FIG. 1B

		<u>R1</u>		
		1	50	
Human_v1	(1)	EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGP	IQWFRGAGPGRELIY	
Human_v2	(1)	EEELQVIQPDKSVVAAGESAILHCTVTSLIPVGP	IQWFRGAGPARELIY	
129mouse	(1)	-KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGP	IKWYRGVGSRLLIY	
NOD	(1)	-TEVKVIQPEKSVSVAAGDSTVLNCTLTSLLPVGP	IRWYRGVGSRLLIY	
BL6	(1)	-KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGP	IRWYRGVGSRLLIY	
BALBC	(1)	-TEVKVTQPEKSVSVAAGDSTILNCTVTSLLPVGP	IRWYRGVGSRLLIY	
		** ** *	* * * *	
		51	R2	
Human_v1	(51)	NQKEGHFPRVTTVSDLT	KRNNMDFSIRIGNITPADAGTY	YCVKFKGSP-
Human_v2	(51)	NQKEGHFPRVTTVSEST	KRENMDFSISISNITPADAGTY	YCVKFKGS--
129mouse	(50)	SFTGEHFPRVTNVSDAT	KRNNMDFSIRISNVTPE	DAGTYCVKFKGPSE
NOD	(50)	SFTTEHFPRVTNVSDAT	KRSNLDIFSIRISNVTPE	DAGTYCVKFKQRS--
BL6	(50)	SFACEYVPRIRNVSDTT	KRNNMDFSIRISNVTPE	DAGTYCVKFKQSSE
BALBC	(50)	SFTGEHFPRIRNVSDTT	KRNNMDFSIRISNVTPE	DAGTYCVKFKQRSSE
		*****	*** ** *	* * *
		101	120	
Human_v1	(100)	DDVEFKSGAGTELSV	RAKPS	
Human_v2	(99)	PDTEFKSGAGTELSV	RAKPS	
129mouse	(100)	PDTEIQSGGGTEVYV	LAKPS	
NOD	(98)	PDTEIQSGGGTEVYV	LAK--	
BL6	(100)	PDTEIQSGGGTEVYV	LAK--	
BALBC	(100)	PDTEIQSGGGTEVYV	LAK-	
		* * *	* * *	** **

FIG.1C

```

Human_v1      1      50
(1) EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
Human_v2      (1) EEELQVIQPDKSVVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
      Cyno      (1) EEELQVIQPEKSVVAAGESATLNCTATSLIPVGPIQWFRGVGPGRELIY
129mouse      (1) -KELKVTQPEKSVVAAGDSTVLNCTLTSLLPVGPIKWYRGVQSRLLIY
      chicken  (1) --DFKLQQPQSSVVVIKGDTLNCTASGCPICAVKWVKWVGSDNQTVY
      **** * * * * **** * * * * ****
      51      100
Human_v1      (51) NQKEGHFPRVTVSDLTKRNNMDFESIRIGNITPADAGTYCVKFRKGS-
Human_v2      (51) NQKEGHFPRVTVSESTKRNNMDFESISINITPADAGTYCVKFRKGS--
      Cyno      (51) HQKEGHFPRVTPVSDPTKRNNMDFESIRISNITPADAGTYCVKFRKGS--
129mouse      (50) SFTGEHFPRVTNVSDATKRNNMDFESIRISNVTPEADAGTYCVKFKQGPSE
      chicken  (49) EHKGSPRVMRAVDPDN---DFTIRISNVSLDAGTYCVKLRKGIV-
      ***** * * * * **** * * * * **** * * * *
      101      120
Human_v1      (100) DDVEFKSGAGTELSVRAKPS
Human_v2      (99) PDTEFKSGAGTELSVRAKPS
      Cyno      (99) PDVELKSGAGTELSVRAKPS
129mouse      (100) PDTEIQSGGGTEVYVLAKPS
      chicken  (94) DDVVFTRGGGTEVSVHA---
      ***** * * * * ****

```

FIG. 2

S130

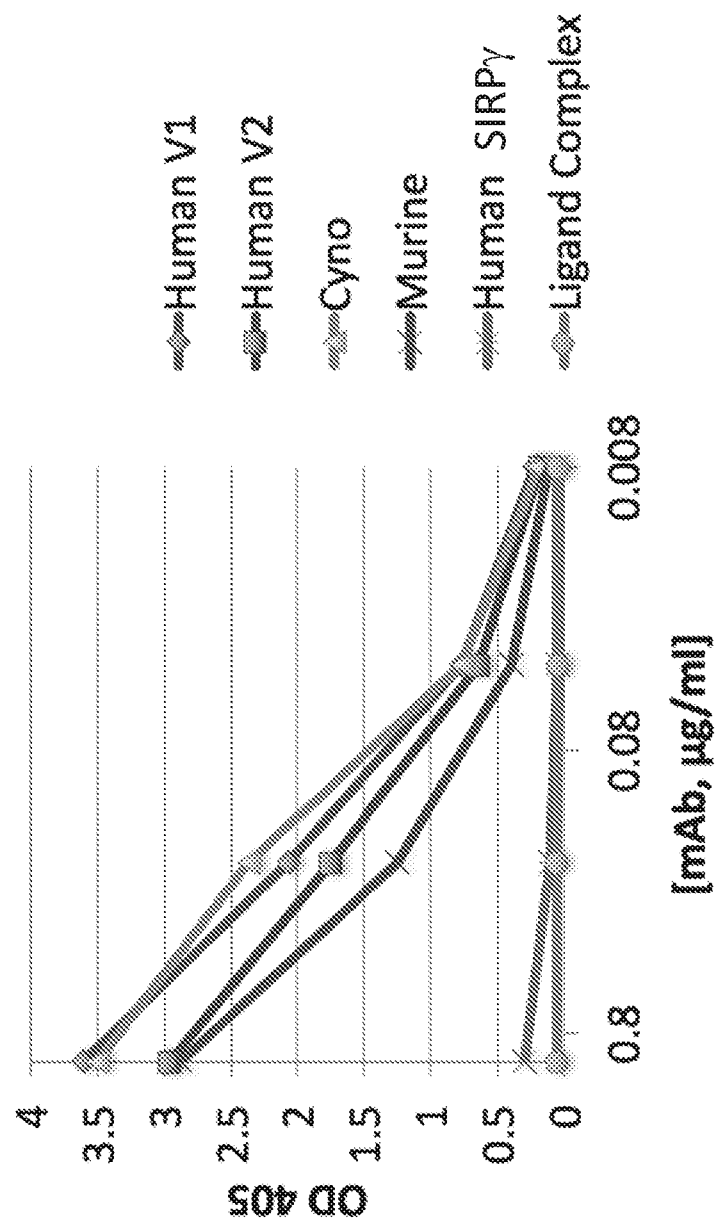


FIG. 3A

Human V1	Human V2	Cyno	Murine	Human SIRP γ	Human complex
+	+	+	+	+	-

FIG. 3B

S121

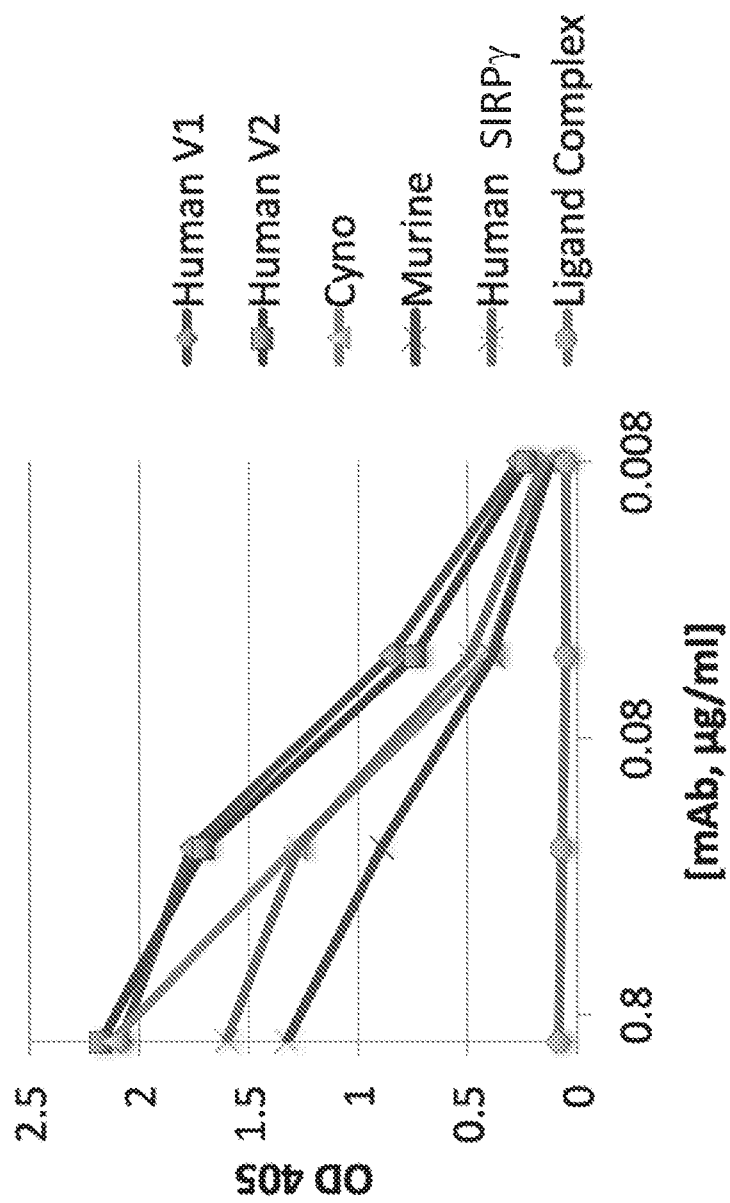


FIG. 4A

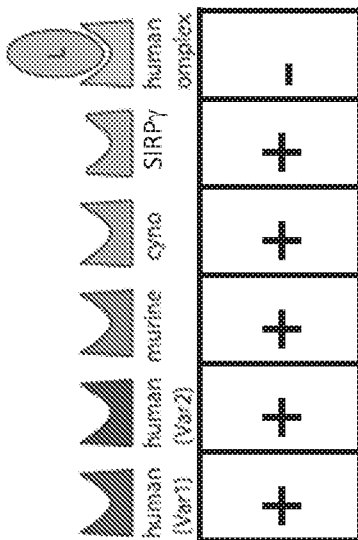


FIG. 4B

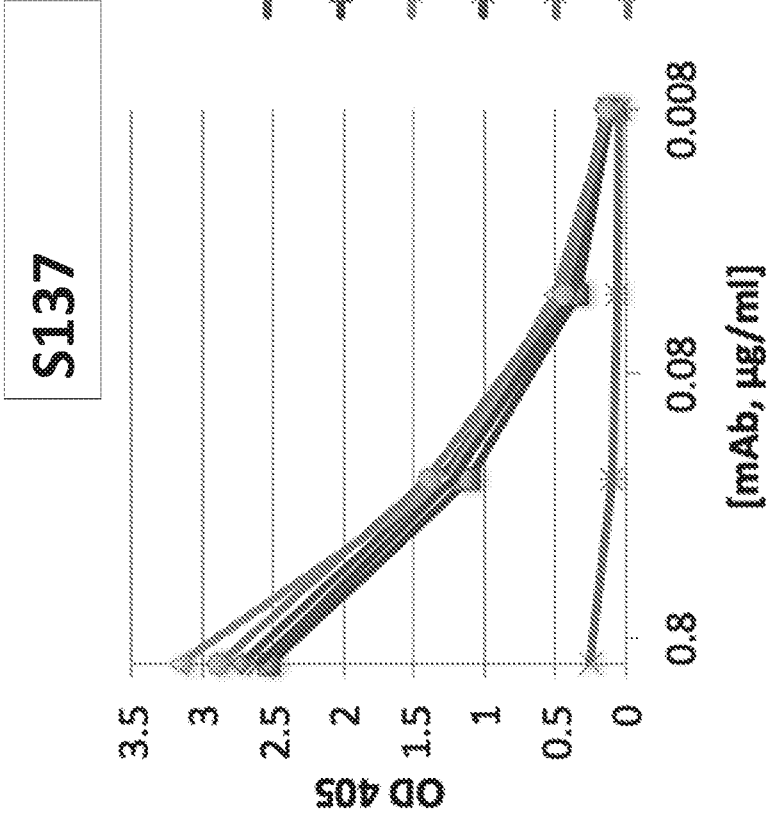


FIG. 5A

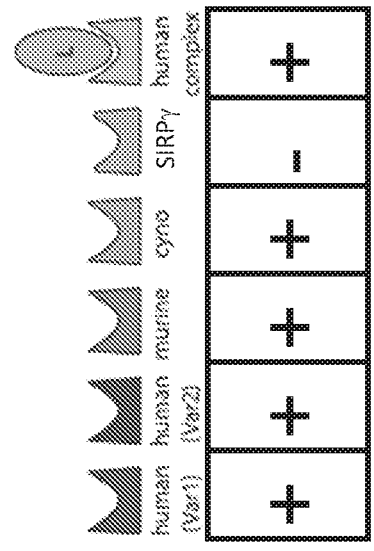


FIG. 5B

S128

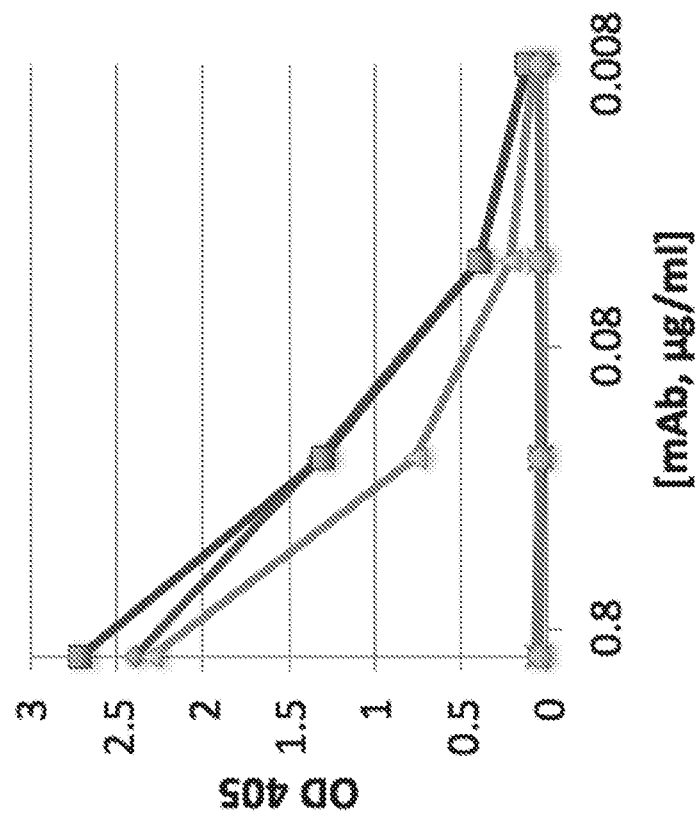


FIG. 6A

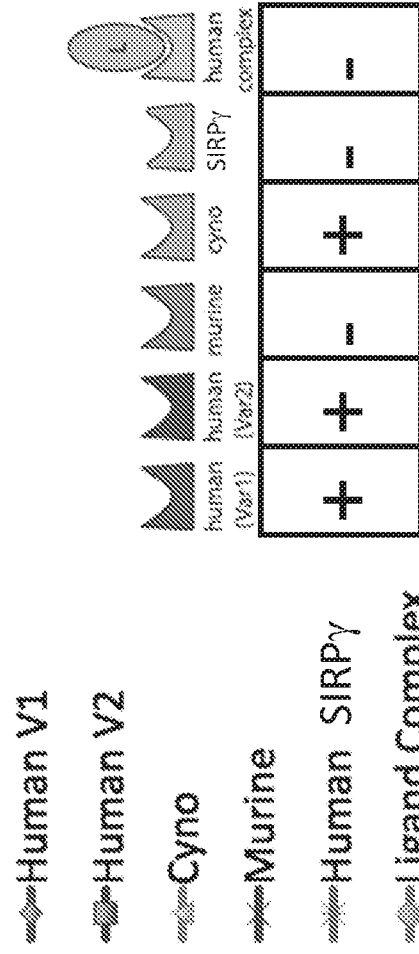


FIG. 6B

S135

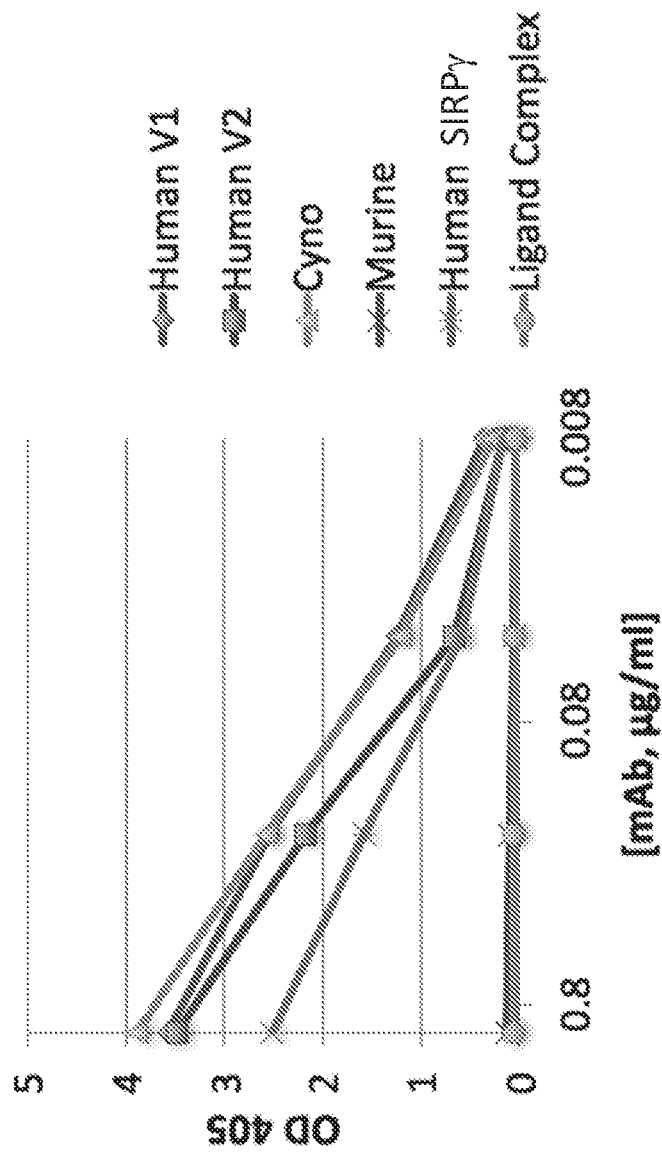


FIG. 7A

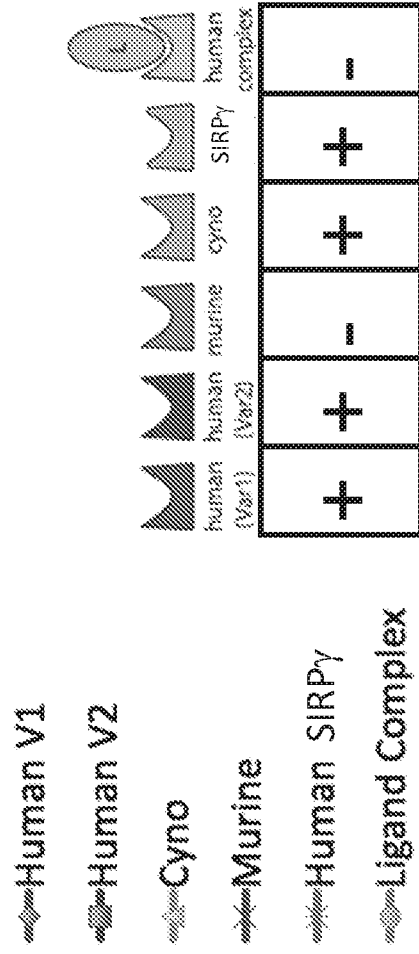


FIG. 7B

S126

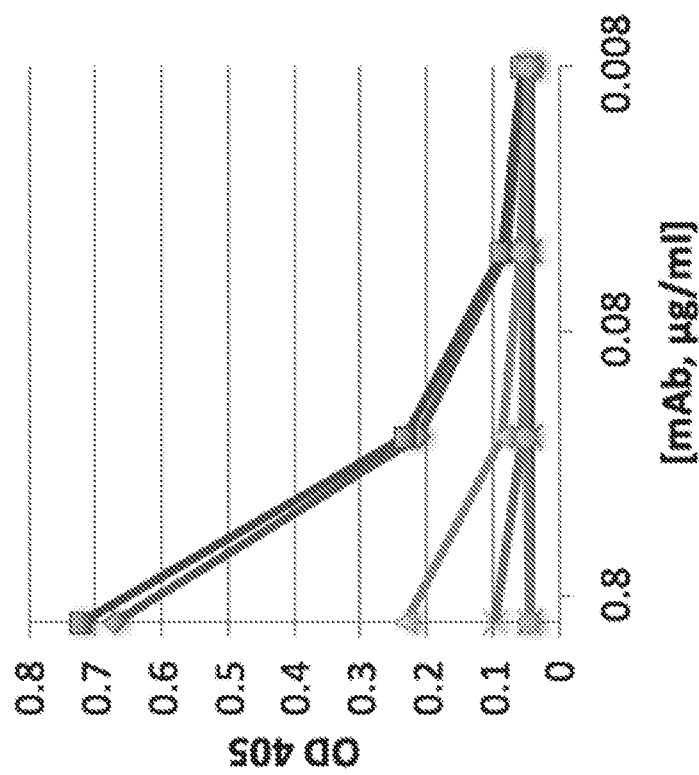


FIG. 8A

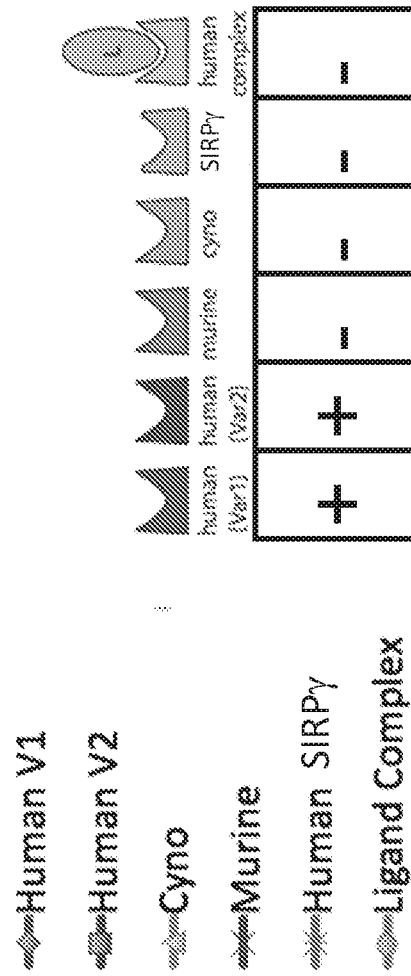


FIG. 8B

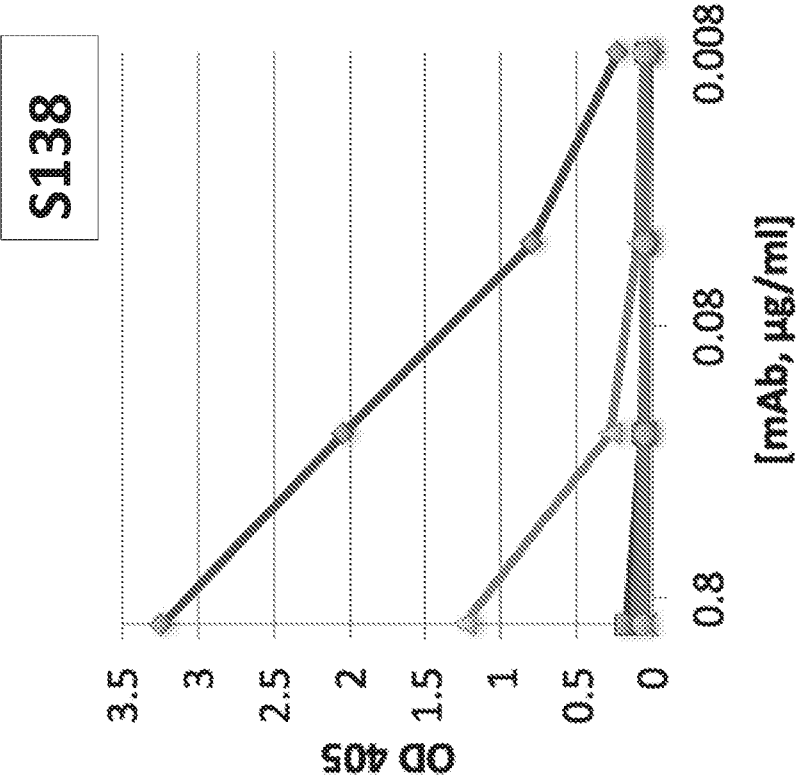


FIG. 9A

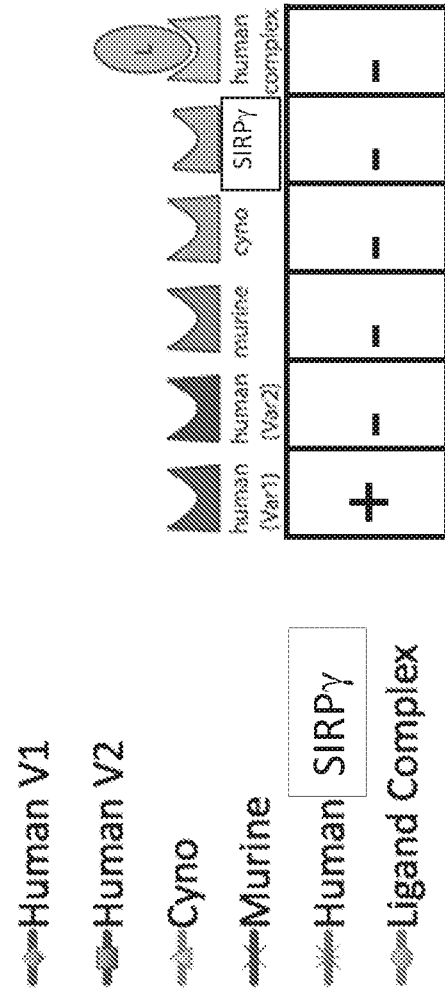


FIG. 9B

		linker	150
	101		
S1	(99)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
S2	(99)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGGLSLVCK
S8	(97)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
S9	(100)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGRALSLVCR
S11	(99)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
S12	(97)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
S13	(97)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
S14	(97)	GTTLTVLGQSSRSSGGSSGGGSMAAVTLD	ESGGGLQTPGGALSLVCK
			** *
			*
		H1	H2
	151		200
S1	(149)	GSGFTFSSHAMNWRQAPGKGLEWVAGISS---	DGRFTYYGAAVQGRAT
S2	(149)	ASGFDFSNFNMAWRQGPCKGLEVVAEISD---	TGSTPYYGSAVQGRAT
S8	(147)	ASGFTFSSYNMGWVRQAPGKGLEFVAGIYASGS	STDTDTTYGPAVAGRAT
S9	(150)	GSGFSISSYNMGWVRQAPGKGLEFIASIGS---	DGSSTHYAPAVKGRAT
S11	(149)	ASGFTFSSFNMGWVRQAPGKGLEFVAAIYS---	GNSAEYGAAVQGRAT
S12	(147)	ASGFTFSSYNMGWVRQAPGKGLEFVAGIYI--	ASGDLGTTYGAAVQGRAT
S13	(147)	ASGFTFSSYNMGWVRQAPDKGLEFVAGIYTG-	SDAGLSTTYGAAVQGRAT
S14	(147)	ASGFTFNSYNMGWVRQAPGKGLEFVAGIYS--	AGGDTSTTYGAAVNGRAT
	*	***** *	* *
		** *	***** ** *

FIG. 10A (cont.'d)

			H3	250
201				
S1	(195)	ISRDNGQSTVRLQLNNLRAEDTATYYCTKNGG-----CGSGGLDCIDAW		
S2	(195)	ISRDNGQSTVRLQLNNLRAEDTGTYFCTRN-----FGSSVSSIDAW		
S8	(197)	ISRDNGQSTVRLQLNNLRAEDTGTYCAKAAGCSTHTCTAYIADSIDAW		
S9	(196)	ITRDVGQSTVRLQLNNLRAEDTGTYFCAKDAYQCS-YATCNDYLDTIDAW		
S11	(194)	ISRDNGQSTVRLQLNNLRAEDTGTYFCAKDAG-SGCYSGVCAGTSSIDAW		
S12	(195)	ISRDDGQSTVRLQLNNLRAEDTGTYFCAKSAGGCSAHSCDTYIADSIDAW		
S13	(196)	ISRDNGQSTVRLQLNNLGAEDTGTYFCKSAGGCSDYNCDAYIADSIDAW		
S14	(195)	ISRDNGQSTVRLQLNNLRAEDTGTYFCAKAAGGCTAHNCDAYIADSIDAW		
		* * *	** *	*****
	251	261		
S1	(240)	GHGTEVIVSSS		
S2	(236)	GHGTEVIVSSS		
S8	(247)	GHGTEVIVSSS		
S9	(245)	GHGTEVIVSSS		
S11	(243)	GHGTEVIVSSS		
S12	(245)	GHGTEVIVSSS		
S13	(246)	GHGTEVIVSSS		
S14	(245)	GHGTEVIVSSS		

FIG. 10A (cont.'d)

	101	<u>linker</u>	150
S115	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S116	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S117	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S118	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S119	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S120	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S122	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S123	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCT	
S126	(101)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S128	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S130	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S135	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S137	(100)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
S138	(101)	GGGTTKVEIKQSSRSSGGGSSGGGSDVQLVESGGGVVRPGESLRLSCA	
		* * * * *	
	151	<u>H1</u>	200
S115	(150)	ASGFSFSSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR	
S116	(150)	ASGFSFSSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR	
S117	(150)	ASGFSFSSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR	
S118	(150)	ASGFSFSSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR	
S119	(150)	ASGFSFNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR	
S120	(150)	ASGFSFNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR	
S122	(150)	ASGFRFSNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR	
S123	(150)	ASGFTFRNYGMSWVRQAPGEGLEWVSASSG--SGSTYYTDSVKGRFTISR	
S126	(151)	ASGFTFSNYDMTWVRQAPGEGLEWVSGISGNGGSTYYADSVKGRFTISR	
S128	(150)	ASGFSFRSYAMNWRQAPGEGLEWVSRIDSGGGTDYADSVKGRFTISR	
S130	(150)	ASGFTFSNYAMSWVRQAPGEGLEWVSLITTNCGDAYADSVKGRFTISR	
S135	(150)	ASGFSFSIYAMSWVRQAPGEGLEWVSTIGAD--DTYYADSVKGRFTISR	
S137	(150)	ASGFTFSNYDMNWRQAPGEGLEWVSLISGSEIIYYADSVKGRFTISR	
S138	(151)	ASGFTFSNYAMNWRQAPGEGLEWVSGISGRGGDTYYADSVKGRFTISR	
		* * * * *	

		**	

FIG. 10B
(cont'd)

		H3	
	201		250
S115	(200)	NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS	
S116	(200)	NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS	
S117	(200)	NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS	
S118	(200)	NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS	
S119	(198)	NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS	
S120	(198)	NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS	
S122	(198)	NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS	
S123	(199)	NSKNTLYLQMNSLRAEDTAIYYCAKVT---WNN-FFDYWGLGTLVTVSSS	
S126	(201)	NSKNTLYLQMNSLRAEDTAVYYCAMN---RWW--FDYWGLGTLVTVSSS	
S128	(200)	NSKNTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGAPVTVSSS	
S130	(200)	NSKNTLYLQMNSLRAEDTAIYYCAKDGAHYYDIFFDYWGLGTPVTVSSS	
S135	(198)	NSKNTLYLQMNSLRAEDTAVYYCAKDSVGSWGDFFDYWGLGTLVTVSSS	
S137	(200)	NSKNTLYLQMNSLRAEDTAVYYCAKEN---NRYRFFDDWGLGTLVTVSSS	
S138	(201)	NSKNTLYLQMNSLRAEDTAIYYCAKGT---WNYGSFDYWGLGTLVTVSSS	
		* * * *	

FIG. 10B
(cont.'d)

FIG. 11A

[illegible]

FIG. 11A (cont'd)

	61	H2	H3	119
S16	(60)	VDSVKGRFTISRDN	-KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S27	(60)	VDSVKGRFTISRDN	-KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S55	(60)	VDSVKGRFTISRDN	-KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S59	(60)	VDSVKGRFTISRDN	-KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S29	(60)	VDSVKGRFTISRDN	-KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S201	(61)	ADSVKGRSTISRDN	-KNTLYLRMSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S206	(61)	ADSVKGRSTISRDN	-KNTLYLRMSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S26	(61)	GDSVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S25	(60)	GDSVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S73	(60)	GDSVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S30	(60)	GDSVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S28	(60)	SGSMKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S21	(61)	PASVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S24	(61)	PASVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S74	(61)	PASVKGRFTISRDN	-KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S23	(61)	IDSVKGRFTISRDN	-KSSLYLRMNSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S17	(61)	IDSVKGRFTISRDN	-ENSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S22	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S66	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S56	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S70	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S202	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S60	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S65	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S69	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S71	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	
S76	(61)	IDSVKGRFTISRDN	-KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGTLVTSS	

** * * * * ***** *

* *

FIG. 11A (cont'd)

		1	L1	L2	54
S16	(1)	ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDDERPS			
S59	(1)	ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDDERPS			
S27	(1)	ALTQPASVSADLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDDERPS			
S55	(1)	ALTQPASVSANLGETVEITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDDERPS			
S29	(1)	ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDDERPS			
S26	(1)	ALTQPASVSANLGGTVEITCSGGSSS--YYGWYQQKSPGSAPVTVIYSDDNQRP			
S21	(1)	ALTQPASVSANPGETVKIACSGGDYYSYYGWYQQKAPGSALVTVIYSDDDKRPS			
S24	(1)	ALTQPASVSANPGETVKIACSGGSYSYYGWYQQKSPGSALVTVIYSDDDKRPS			
S74	(1)	ALTQPASVSANPGETVKIACSGGSYSYYGWYQQKSPGSALVTVIYSDDDKRPS			
S25	(1)	ALTQPASVSANPGETVEITCSGGSYSSYYAWYQQKSPGSAPVTVIYSDDDKRPS			
S73	(1)	ALTQPASVSANPGETVKITCSGGIYSSYYAWYQQKSPGSAPVTVIYSDDDKRPS			
S30	(1)	ALTQPASVSASPGETVEITCSGGSDSSYYGWYQQKSPGSAPVTVIYSDDNKRPS			
S28	(1)	ALTQPASVSANPGETVKITCSGG--SDSYYYGWHQQKSPGSAPVTVIYSDDQRP			
S201	(1)	ALTQPASVSANPGETVKITCSGG--GTSSYYGWYQQKSPGSAPVTLIHSDDKRPS			
S206	(1)	ALTQPASVSANPGETVKITCSGG--GTSSYYGWYQQKSPGSAPVTLIHSDDKRPS			
S22	(1)	ALTQPASVSANPGETVKITCSGGDYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S60	(1)	ALTQPASVSANPGETVKITCSGGDYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S65	(1)	ALTQPASVSANPGETVKITCSGGDYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S69	(1)	ALTQPASVSANPGETVKIICSGGDYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S23	(1)	ALTQPASVSANPGETVKITCSGGDYSTYYAWYQQKSPGSAPVTVIHSDDERPS			
S66	(1)	ALTQPASVSANPGETVKITCSGGDYSTYYAWYQQKSPGSAPVTVIHSDDKRPS			
S17	(1)	ALTQPASVSANPGETVKITCSGGDWYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S70	(1)	ALTQPASVSANPGETVKITCSGGDWYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S76	(1)	ALTQPASVSANPGETVKITCSGGDWYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S202	(1)	ALTQPASVSANPGETVKITCSGGGYSTYYGWYQQRSPGSAPVTVIHSDDKRPS			
S56	(1)	ALTQPASVSANPGETVKITCSGGGYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
S71	(1)	ALTQPASVSANPGETVKITCSGGGYSTYYGWYQQKSPGSAPVTVIHSDDKRPS			
		** * * *	*****	* * *	* * *

FIG. 11A (cont'd)

	55	L3	107
S16	(55)	DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL	
S59	(55)	DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL	
S27	(55)	DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL	
S55	(55)	DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL	
S29	(55)	DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL	
S26	(53)	DIPSRFSGSASDSTATLTTITGVQVEDEAIYCCGYDSSSTYANTFCAGTTLTVL	
S21	(55)	DIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYANAFGAGTTLTVL	
S24	(55)	GIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSSYTNDGAGTTLTVL	
S74	(55)	GIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSSYTNDGAGTTLTVL	
S25	(55)	NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDQSSYTNPFCAGTTLTVL	
S73	(55)	NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDQSSYTNPFCAGTTLTVL	
S30	(55)	NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYTNPFAGTTLTVL	
S28	(54)	DIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYTNPFAGTTLTVL	
S201	(54)	DIPSRFSGSASGSTATLTTITGVQVEDEAVYCCGYDYTYVNTFCAGTTLTVL	
S206	(54)	DIPSRFSGSASGSTATLTTITGVQAEDEAVYCCGYDYTYVNTFCAGTTLTVL	
S22	(55)	DIPSRFSGSASGSAATLTTIAGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL	
S60	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL	
S65	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL	
S69	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL	
S23	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S66	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S17	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S70	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S76	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S202	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S56	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL	
S71	(55)	DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDARTYINTFCAGTTLTVL	
	*	* * * * *	*

FIG. 11B (cont'd)

		1	L1	L2	54
S136	(1)	ETVLTQSPGTLTSLPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
S137	(1)	ETVLTQSPGTLTSLPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
S175	(1)	ETVLTQSPGILSLSPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
S177	(1)	KTVLTQSPGTLTSLPGERATLTCRADQSVYTYLAWYQERPGQAPRLLIYDASSR			
S184	(1)	ETVLTQSPGTLTSLPGERATLNCRASQSVYTYLAWYQEKPGQAPRLLIYDASSR			
S185	(1)	ETVLTQSPGTLTSLPGERATLNCRASQSVYSYLAWYQERPGQAPRLLIYGASTR			
S189	(1)	ETVLTQSPGTLTSLPGERATLSCRASQSVYTYLAWYQQKPGQPPRLLIHAARNR			
S193	(1)	ETVLTQSPGTLTSLPGERATLSCRASQSVYTYLAWYQEKPGQAPRLLIYAASTR			
S178	(1)	ETVLTQSPGTLTSLPGERATLSCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
S180	(1)	ETVLTQSPGTLTSLPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
S190	(1)	ETVLTQSPGTLTSLPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSR			
		*	* * *	*	** *
S136	(55)	ATGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			108
S137	(55)	ATGIPDRFSGSGSGTVFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S175	(55)	AAGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S177	(55)	ATGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S184	(55)	ATGIPDRFSGSGSGTEFTLTISLSESEDFAVVYCCQYDRPPLTFGGGKVEIK			
S185	(55)	ATGIPDRFSGSGSGTEFTLTISLSESDDFAVVYCCQYDRPPLTFGGGKVEIK			
S189	(55)	AAGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S193	(55)	ATGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S178	(55)	ATGVPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S180	(55)	ATGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
S190	(55)	ATGIPDRFSGSGSGTEFTLTISSLQSEDFAVVYCCQYDRPPLTFGGGKVEIK			
		*	* *	*	** *

FIG. 11C

		<u>H1</u>	<u>H2</u>	<u>60</u>
	1			
S115	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S116	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S117	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S118	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S132	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S191	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY
S198	(1)	DVQLVESGGGVVRPGE	SLRLSCAASGFS	SSHAMNWWVRQAPGEGLEWVSRINSGGGGTDY
			*	*
	61		<u>H3</u>	<u>119</u>
S115	(61)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S116	(61)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S117	(60)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S118	(61)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S132	(61)	ADSVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S191	(61)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
S198	(61)	AESVKGRFTISRDNSEN	TLYLQMNSLRAED	TAVYYCAKQYDWNSEFFDYWGLGALVTVSS
			*	*

FIG. 11C (cont'd)

		<u>L1</u>	<u>L2</u>	<u>54</u>
	1			
S115	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDATNR		
S116	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDATNR		
S117	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDATNR		
S118	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDASRR		
S132	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDASNR		
S191	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDATNR		
S198	(1)	ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAHQKPGQAPRLLIYDATNR		
				**
	55		<u>L3</u>	<u>108</u>
S115	(55)	ATGISDRFSGSGGTDFTLTISSLQTEDSAVYCCQYYWPPYRFGGKVEIK		
S116	(55)	ATGISDRFSGSRSGTDFTLTISSLQTEDSAVYCCQYYWPPYRFGGKVEIK		
S117	(55)	ATGIPDRFSGSGGTDFTLTISSLQTEDSAVYCCQYYWPPYRFGGKVEIK		
S118	(55)	ATGIPDRFSGSGGTDFTLTISSLQTEDSAVYCCQYYWPPYRFGGKVEIK		
S132	(55)	ATGIPDRFSGSGGTDFTLTISSPQTEDSAVYCCQYYWPPYRFGGKVEIK		
S191	(55)	ATGIPDRFSGSGGTDFTLTISGLQTEDSAVYCCQYYWPPYRFGGKVEIK		
S198	(55)	ATGIPDRFSGSGGTDFTLTISSLQTEDSAVYCCQYYWPPYRFGGKVEIK		
		*	*	*
		*	*	*

FIG. 11D

		H1	H2	60
S173	(1)	DVQLVESGGGVVRPGESLRLSCAASGFAFSDHDMSWVRQQGPGEGLWVAGISLRGGVTWY		
S174	(1)	DVQLVESGGGVVRPGESLRLSCAASGFTFSDHDMSWVRQQGPGEGLWVAGISLRGGVTWY		
		*		
			H3	118
S173	(61)	ADSVKGRFTISRDN SKNTLYLRFLSLRTEDTAIYYCARESWNTFFDYWGGLGLTVTVSS		
S174	(61)	ADSVKGRFTISRDN SKNTLYLRFLSLRTEDTAIYYCARESWNTFFDYWGGLGLTVTVSS		
			L1	L2 55
S173	(1)	EIVLTQSPGTLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA		
S174	(1)	EIVLTQSPGTLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA		
			L3	108
S173	(56)	TGIPDRFSGSGGTDFTLTISSLSQSEDFAVYCCQQYGNQPPLTFGGGKVEIK		
S174	(56)	TGIPDRFSGSGGTDFTLTISSLSQSEDFAVYCCQQYGNQPPLTFGGGKVEIK		

FIG. 11E

		H1	H2	60	
S213	(1)	DVQLVESGGVVRPGESLRLSCEASGFTFRNYYMTWVRQAPGEGLEWVSTISDTGDTAYY			
S214	(1)	DVQLVESEGGVVRPGESLRLSCEASGFTFRNSYMTWVRQAPGEGLEWVSTISDTGDTAYY			
		*			
			H3	119	
S213	(61)	ADSVKGRFTISRDNKNSLYLQMNSLRADDTAIYYCAKSWIWWTFEDYWGLGLTVTVSS			
S214	(61)	ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIYYCAKSWIWWTFEDYWGLGLTVTVSS			
		*			
			L1	L2	55
S213	(1)	ALTQPASVSANLGGTVEITCSGNSNHYGWYQQKSPGSA	PVTLLIYADTNRPSNIP		
S214	(1)	ALTQPASVSANLGGTVEITCSGNSNHYGWYQQKSPGSA	PVTLLIYADTNRPSNIP		
			L3	103	
S213	(56)	SRFSGTSGSTTLTITGVQAEDEAVYYCGGSSTGDGIFGAGTTLTVL			
S214	(56)	SRFSGTSGSTTLTITGVQAEDEAVYYCGGSSTGDGIFGAGTTLTVL			
		*			

FIG. 11F

>209_VH
DVQLVESGAVVRPGESLRLSCKASGFTFTNFAMSWVRQAPGEGLEWVSGISGSDDTTYA
DSVKGRFTISRDNSESTLYLQMNSLRAEDTAVYYCVKDS TVSWNTFFDYWGLGLTLTVSS
>209_VL
ALTQPASVSNLGGTVKITCSGGYGSDDGSSSYYGWYQQKSPGSAFVILIYWDDKRPSDIP
SRFSGSTGTTTLTITGVQAEDEAVYFCGTYDTSSGAI FGAGTTLTVL

FIG. 11G

		<u>H1</u>	<u>H2</u>	<u>59</u>
1				
S123	(1)	DVQLVESGGGLVQPGGSLRLSCTASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY		
S194	(1)	DVQLVESGGGVVRPGESLRLSCTAASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY		
		* * *		
60			<u>H3</u>	117
S123	(60)	TDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS		
S194	(60)	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS		
		*		
			<u>L1</u>	<u>L2</u>
S123	(1)	EIVLTQSPGTLSPGERVTLTCSRASQGIAGKIAWYQQKPGQAPRLLIYDASSRATGIP		
S194	(1)	EIVLAQSPDTLSVSPGERATLTCSRASQDVAGKLAWYQQKPGQAPRLLIHATSSRADGIP		
		* * *		*
60			<u>L3</u>	108
S123	(60)	GRFSGSGSGTEFTLTITSLQSEDFAVYCCQHQHYDWSPLTFEGGGTKVEIK		
S194	(60)	ARFSGSGSGTEFTLTITGLQSEDFAVYCCQHQHYDWSPLTFEGGGTKVEIK		
		*		

FIG. 11H

	H1	H2	59
1			
S161	(1) DVQLVESGGGVVRPGESLRLSCAASGFTFSNFAMTWVRQAPGKGPENVSLVSVTATYY		
S162	(1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTYY		
S163	(1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTYY		
S164	(1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTYY		
	1	*	*
		*	*
		*	*
60			
S161	(60) ADVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKITWNNLFDYWGLGLTVTVSS	H3	117
S162	(60) ADVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKITWNNLFDYWGLGLTVTVSS		
S163	(60) ADVKGRFTISRDNKSTLYLQMNGLRAEDTAVYYCAKITWNNLFDYWGLGLTVTVSS		
S164	(60) ADVKGRFTISRDNKSTLYLQMNGLRAEDTAVYYCAKITWNNLFDYWGLGLTVTVSS		
	*	*	*
	*	*	*
	*	*	*
1			
S161	(1) EIVLTQSPGTLSPGERATLSCRASQTVGSKLAWYQQKPKGQAPRLLIYDSSSRASGIP	L1	59
S162	(1) EIVLTQSPGTLSPGERATFSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP		
S163	(1) EIVLTQSPGTLSPGERATFSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP		
S164	(1) EIVLTQSPGTLSPGERATFSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP		
	*	*	*
	*	*	*
	*	*	*
60			
S161	(60) DRFSGSGGTDFTLTISSLQSEDSAVYYCQHQNDWPPYTFGGGTKVEIK	L3	108
S162	(60) ARFSGSGGTEFTLTISSLQSEDFAVYYCQHQTDWPPYTFGGGTKVEIK		
S163	(60) ARFSGSGGTEFTLTISSLQSEDFAVYYCQHQTDWPPYTFGGGTKVEIK		
S164	(60) ARFSGSRSGTEFTLTISSLQSEDFAVYYCQHQTDWPPYTFGGGTKVEIK		
	*	*	*
	*	*	*
	*	*	*

FIG. 11I

>S149_VH
DVQLVESGGVVRPGEISRLSCAASGFTFSNFAMNWVRQAPGEGLEWVSLISVTATTYYA
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVTWNNLFDYWGLGLTLVTVSS
>S149_VL
EIVLTQSPGTLSLSPGERATLSCRASQPIDSYLAWYQQKPGQAPRLLIYNTVTRATGIPD
RFSGSGSGTDFTLTINRLEPEDFAVYYCQHQQYDWPPYIFGGGTKVEIK

>S218_VH
DVQLVESGGVVRPGEISLTLSCTASGFTFTSSTMNWVRQAPGEGLDWVSSI¹STSGVITYY
ADSVKGRATISRDNSKNTLYLRLFSLRADDTAIYYCATDTE²FDHWGPGTLVTVSS
>S218_VL
ALTQPASVSANGETVKITCFGSSGNYGWFQQKSPGSAPVTVIHYNNKRPSDIPSRFSGS
KSGSTGTLTITGVRAEDEAVYFCGAWETGSATFGAGTTLTVL

FIG. 11

	1	H1	H2	61
1119	(1)	DVQLLESGGVVQPCGSLRLSCAASGFSNFAMT	<u>WVRQAPGEGLEWVSTIGSGDTYYADS</u>	
1120	(1)	DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMT	WVRQAPGEGLEWVSTIGSGDTYYADS	
1121	(1)	DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMT	WVRQAPGEGLEWVSTIGSGDTYYADS	
1122	(1)	DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMT	WVRQAPGEGLEWVSTIGSGDTYYADS	

[illegible]

FIG. 11J (cont'd)

		L1		L2	54
119	(1)	EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR			
120	(1)	EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR			
121	(1)	EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR			
122	(1)	EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR			
			L3		
119	(55)	ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP			108
120	(55)	ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP			
121	(55)	ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP			
122	(55)	ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP			

- ▬ A1 = High affinity SIRPa (100nM)
- ▬ A2 = High affinity SIRPa (100nM) + 20nM CD47
- ▬ A3 = High affinity SIRPa (100nM) + 55nM CD47
- ▬ A4 = High affinity SIRPa (100nM) + 500 nM CD47
- ▬ A5 = High affinity SIRPa (100nM) + 1500 nM CD47
- ▬ A6 = PBST

FIG. 12A

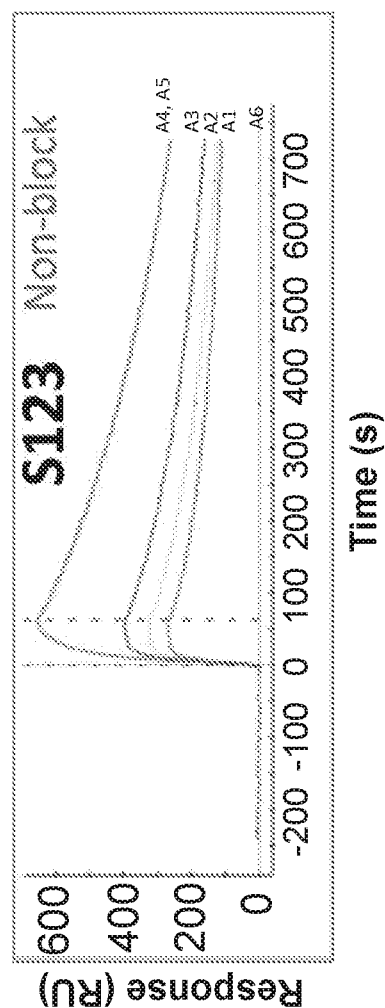
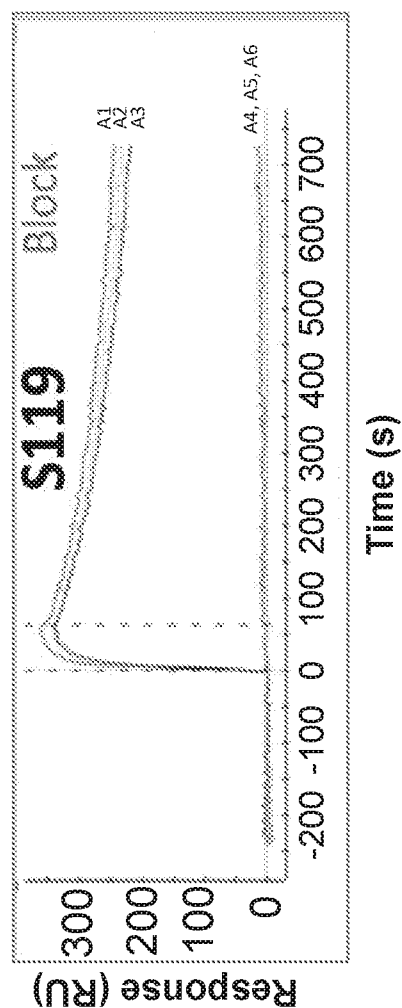


FIG. 12B

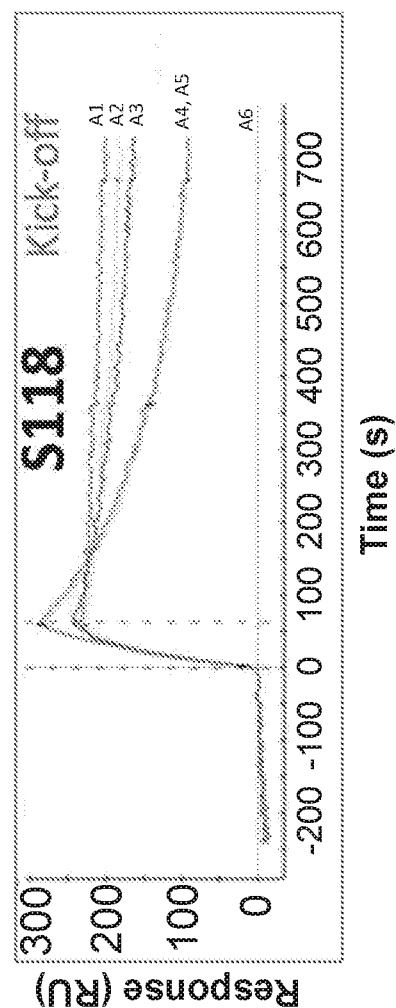


FIG. 12C

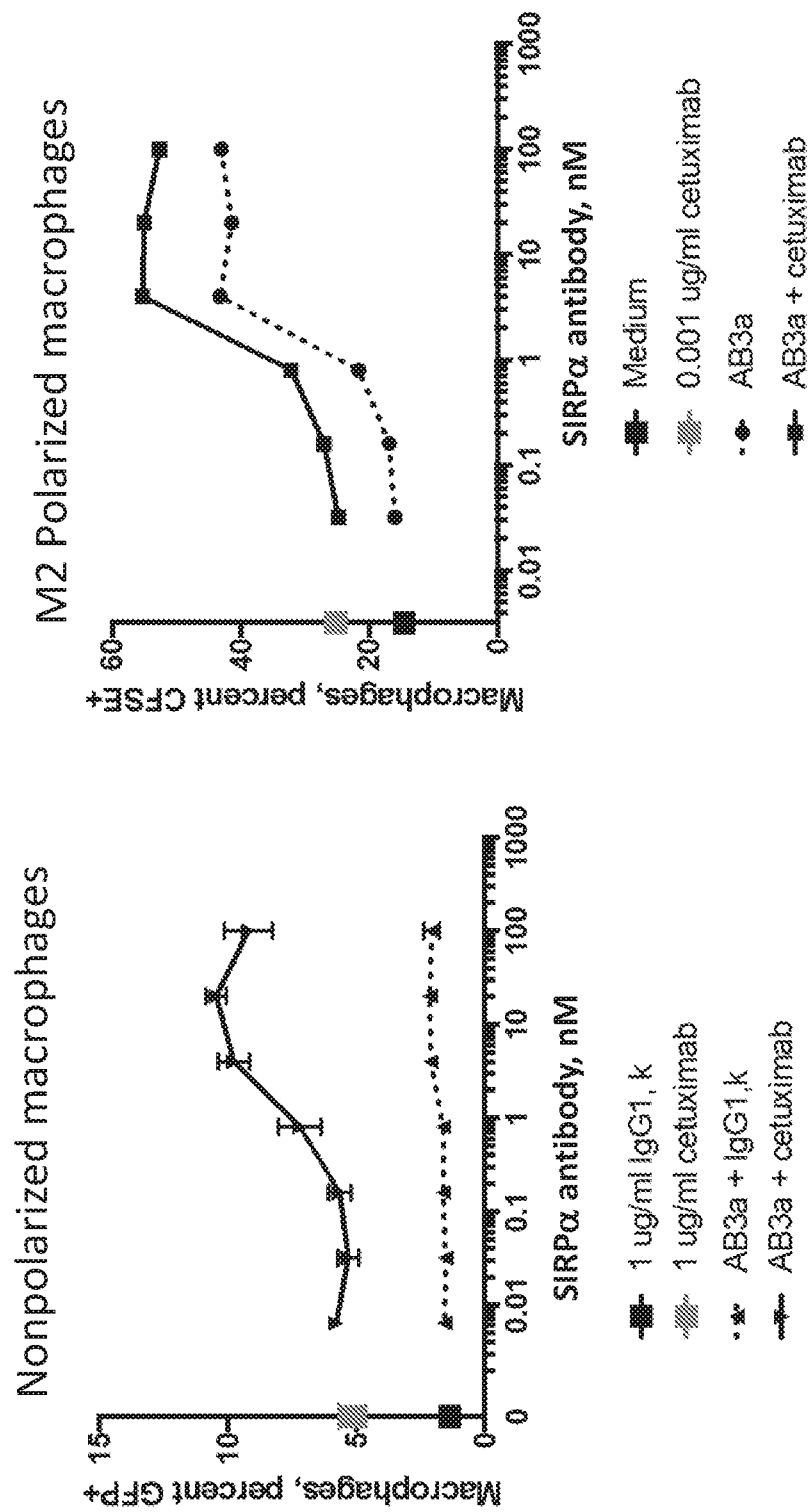


FIG. 13A

FIG. 13B

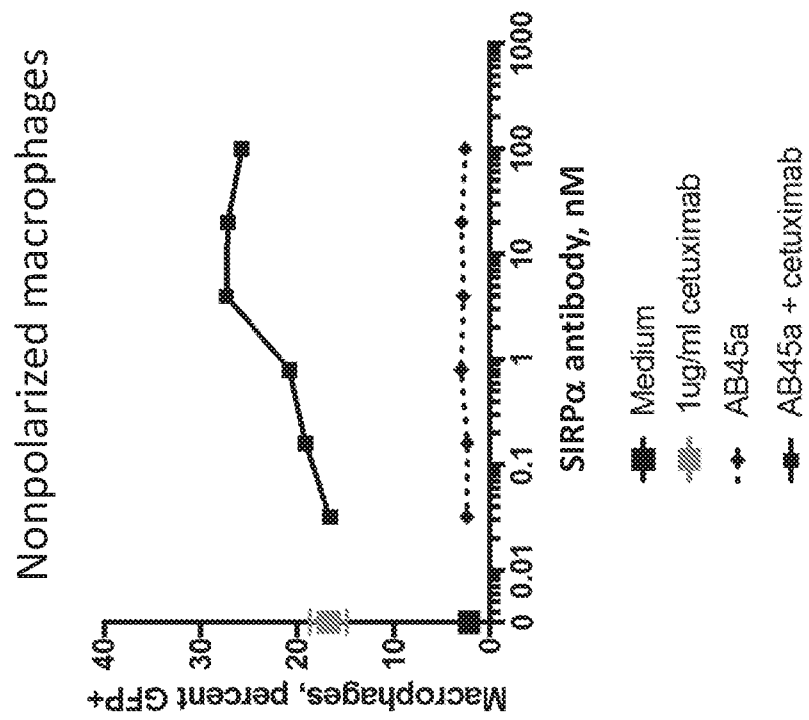


FIG. 13C

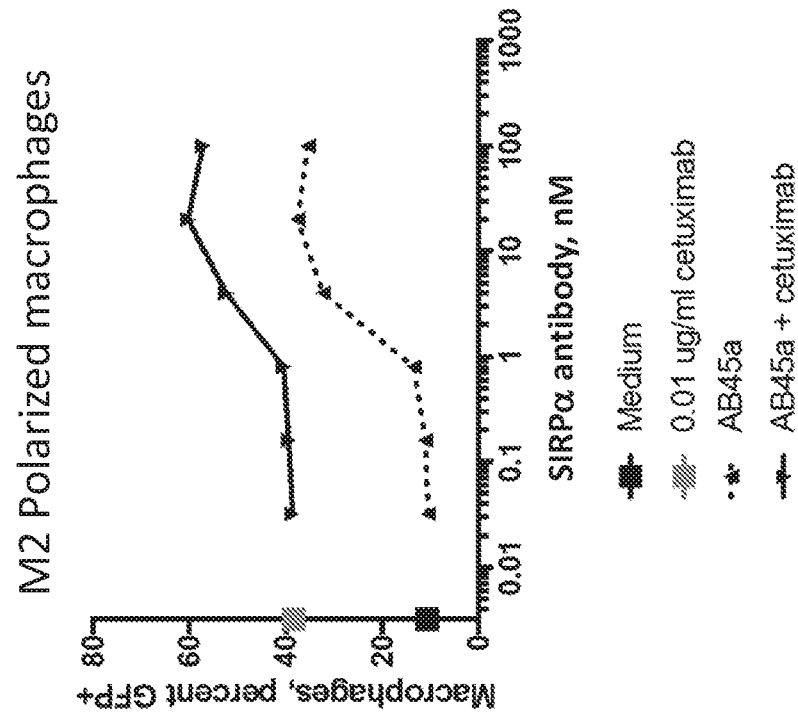


FIG. 13D

OE19 cells – Nonpolarized
macrophages

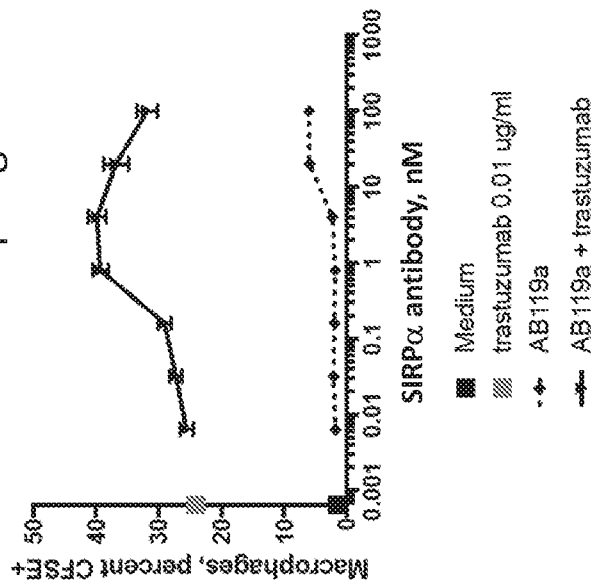


FIG. 13E

OE19 cells – Nonpolarized
macrophages

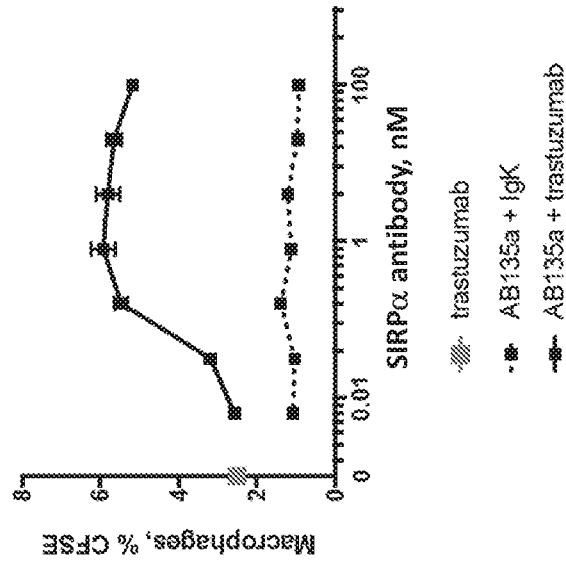


FIG. 13F

DLD-1 cells – M2
polarized macrophages

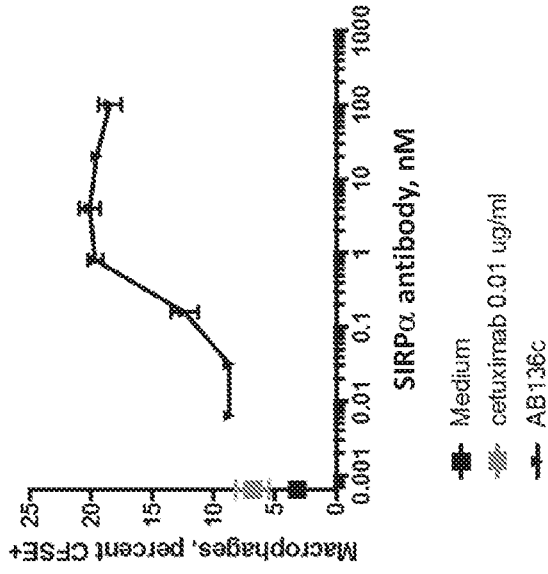
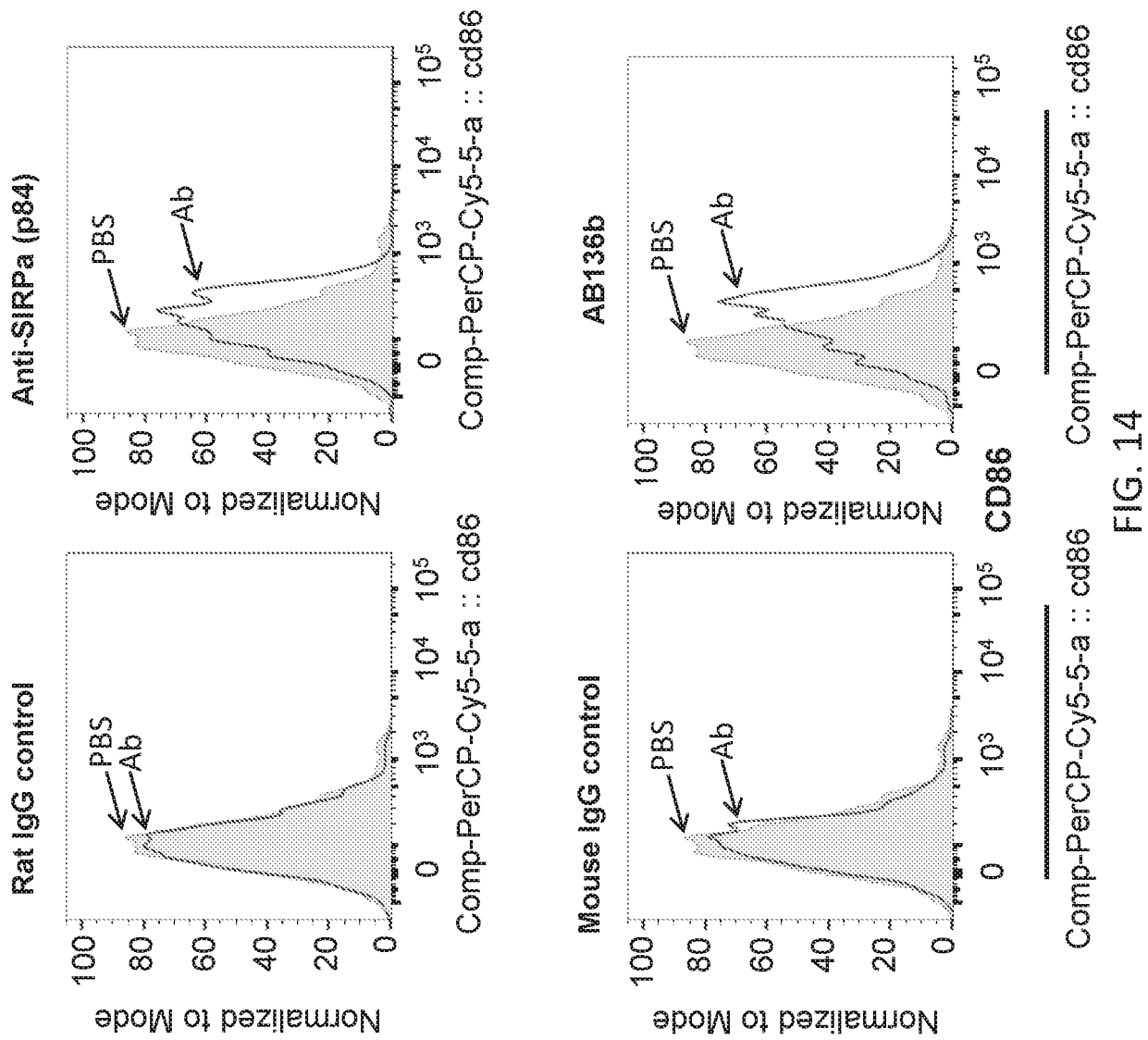
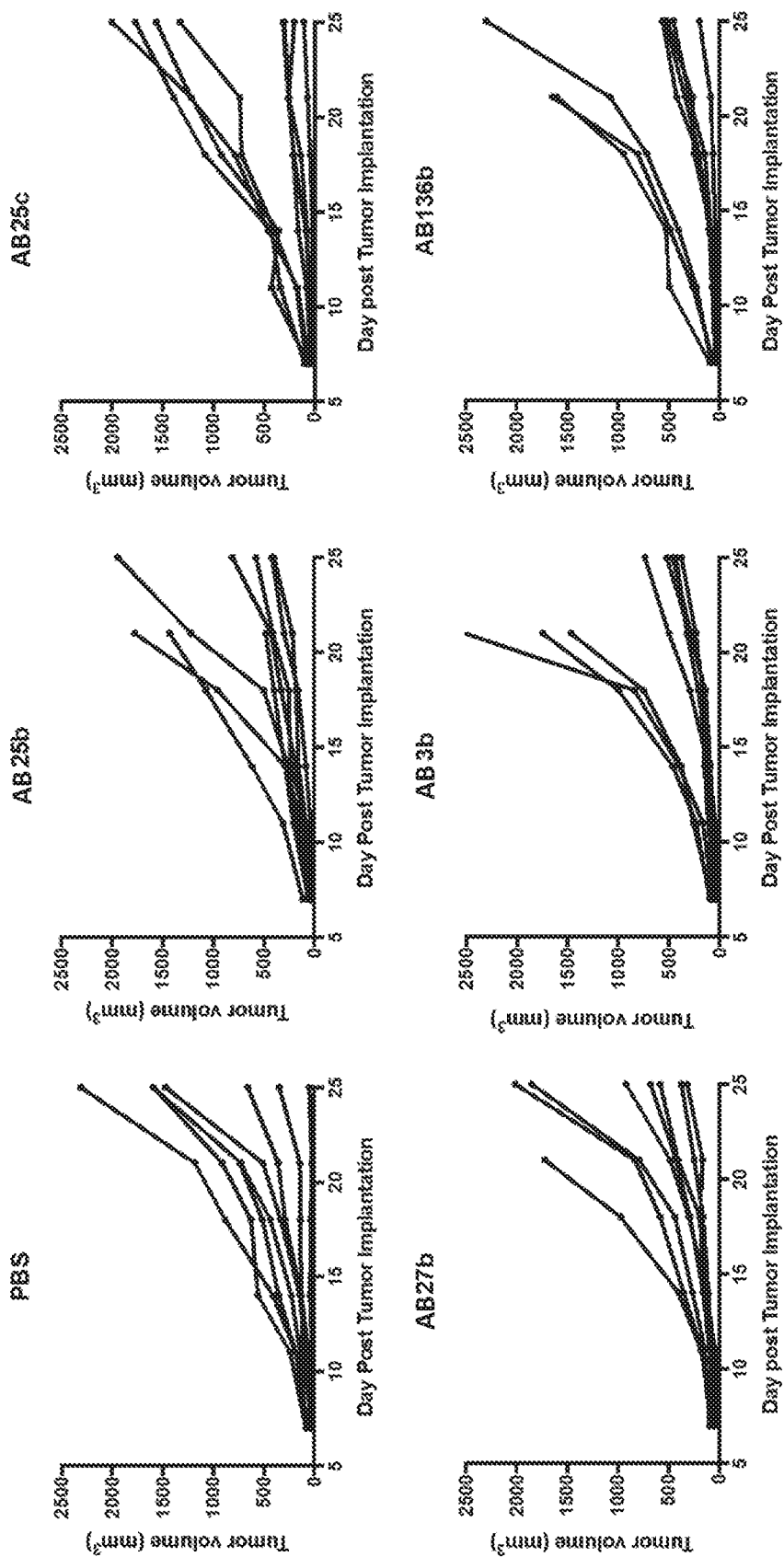


FIG. 13G





	PBS	AB25b	AB25c	AB27b	AB3b	AB136b
Mice with tumor volume <600 mm ³	2	3	4	3	4	5

FIG. 15

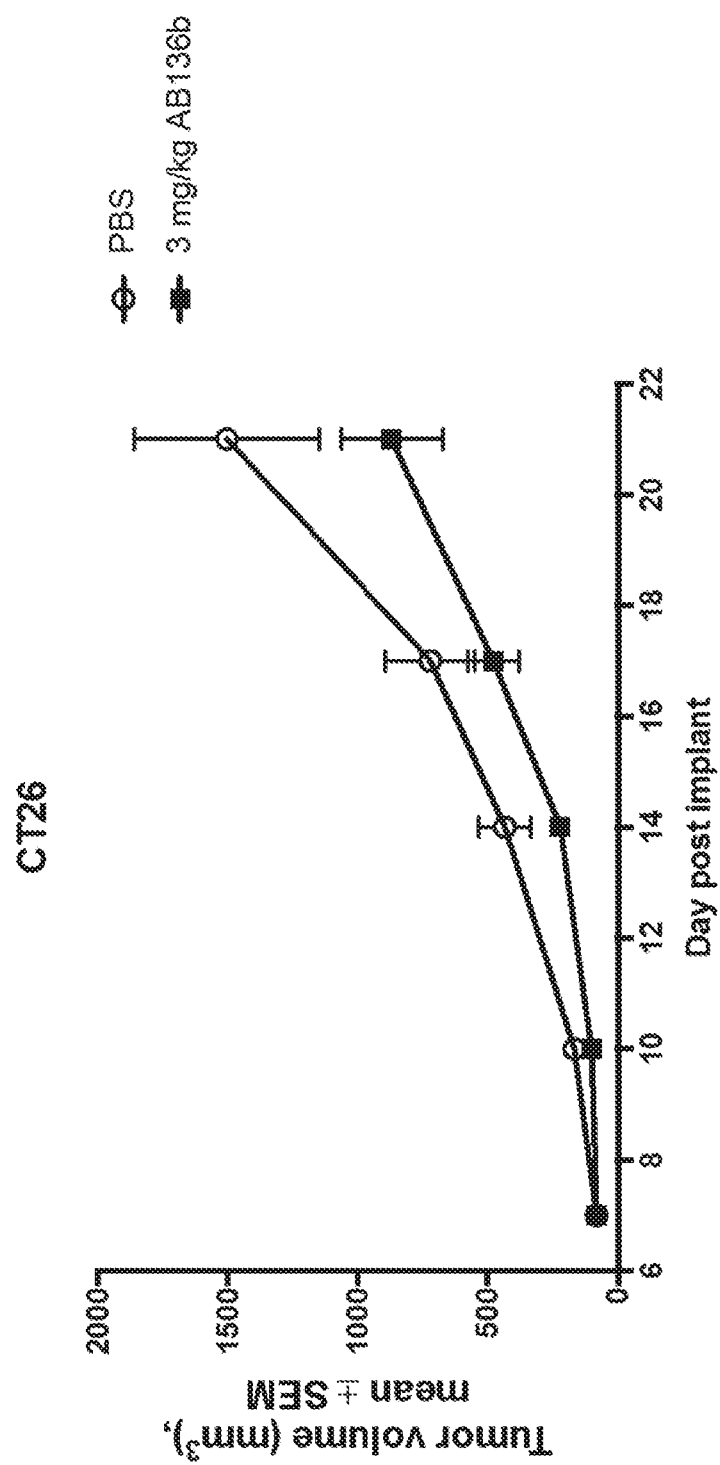


FIG. 16

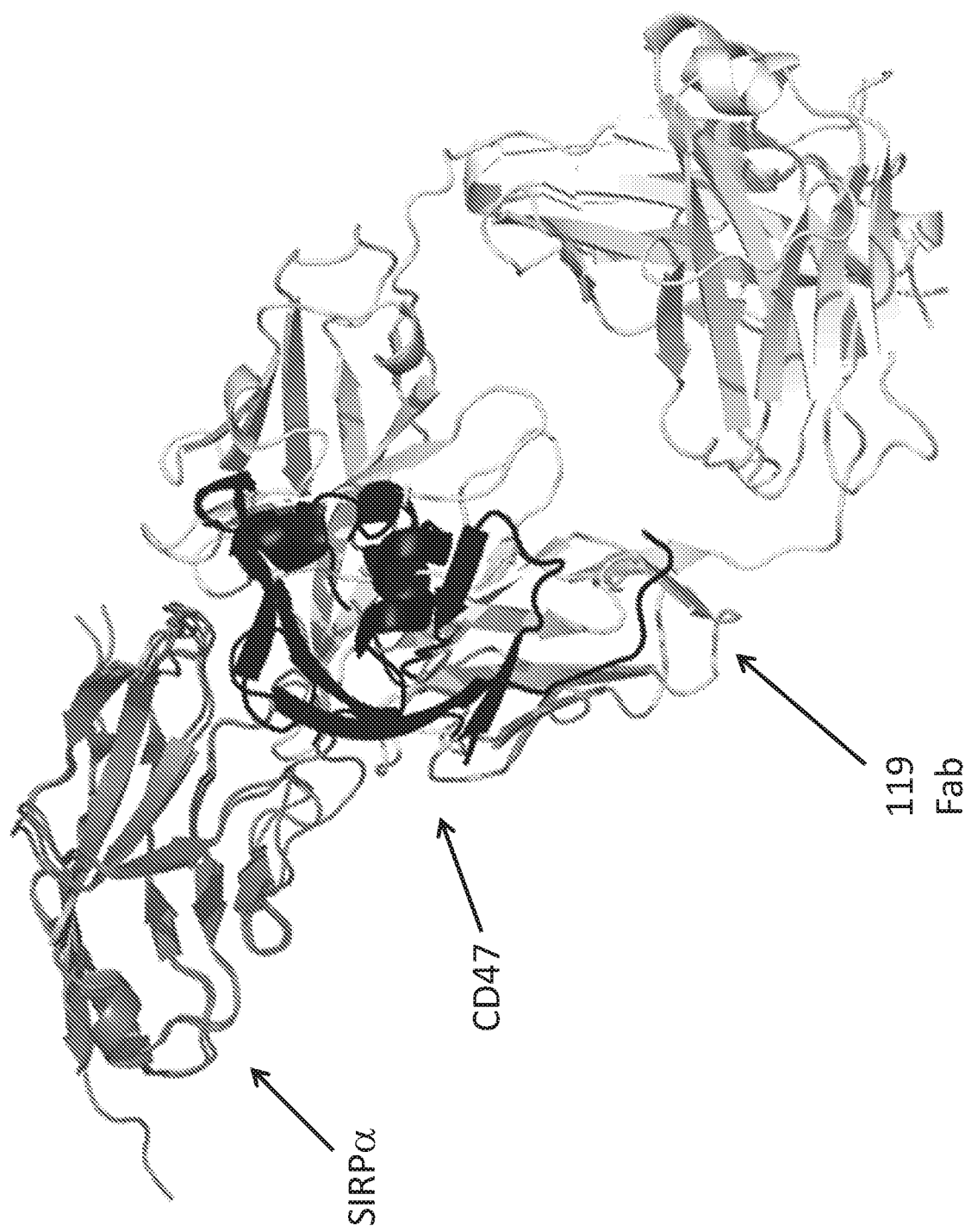


FIG. 17A

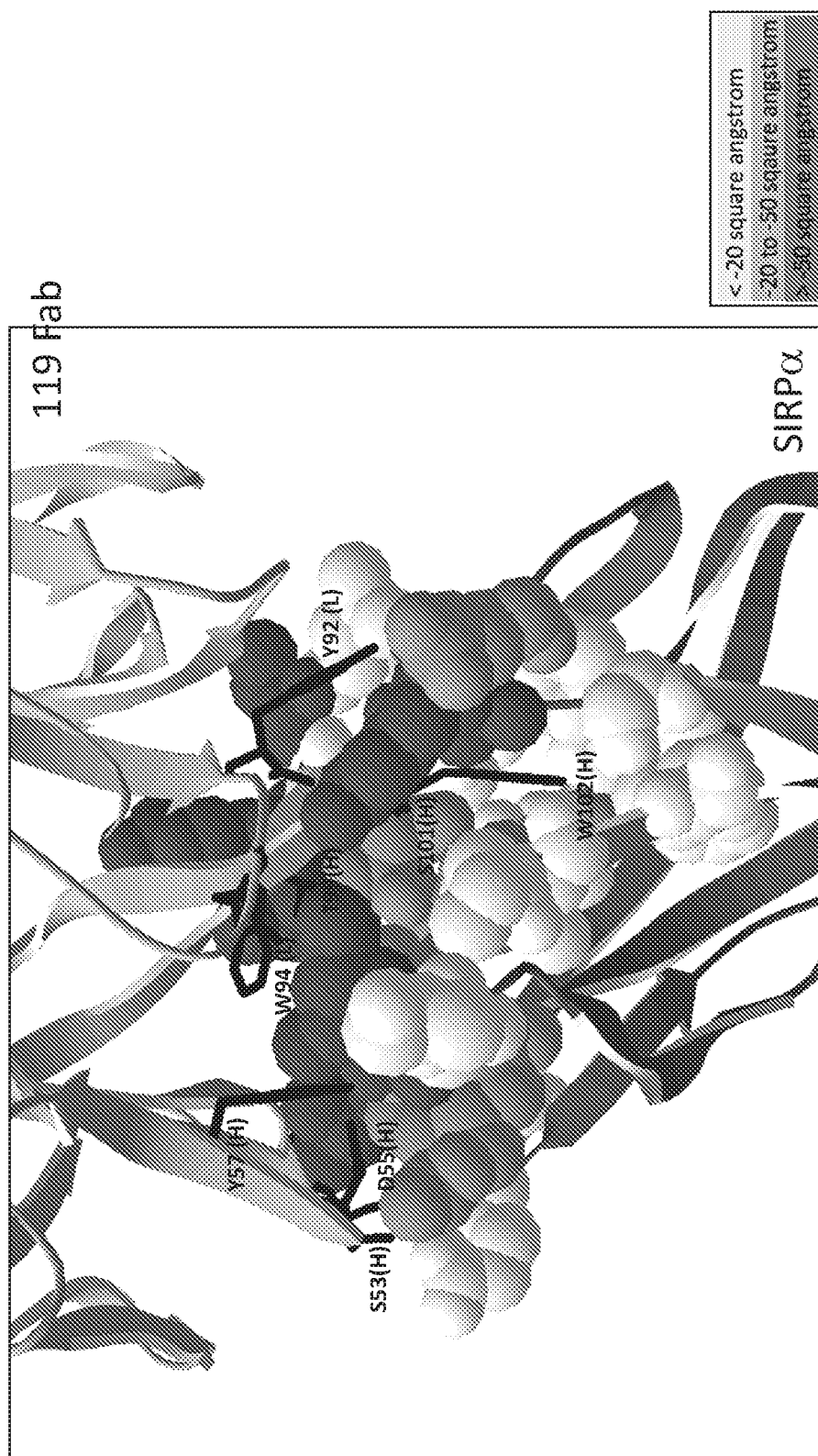


FIG. 17B

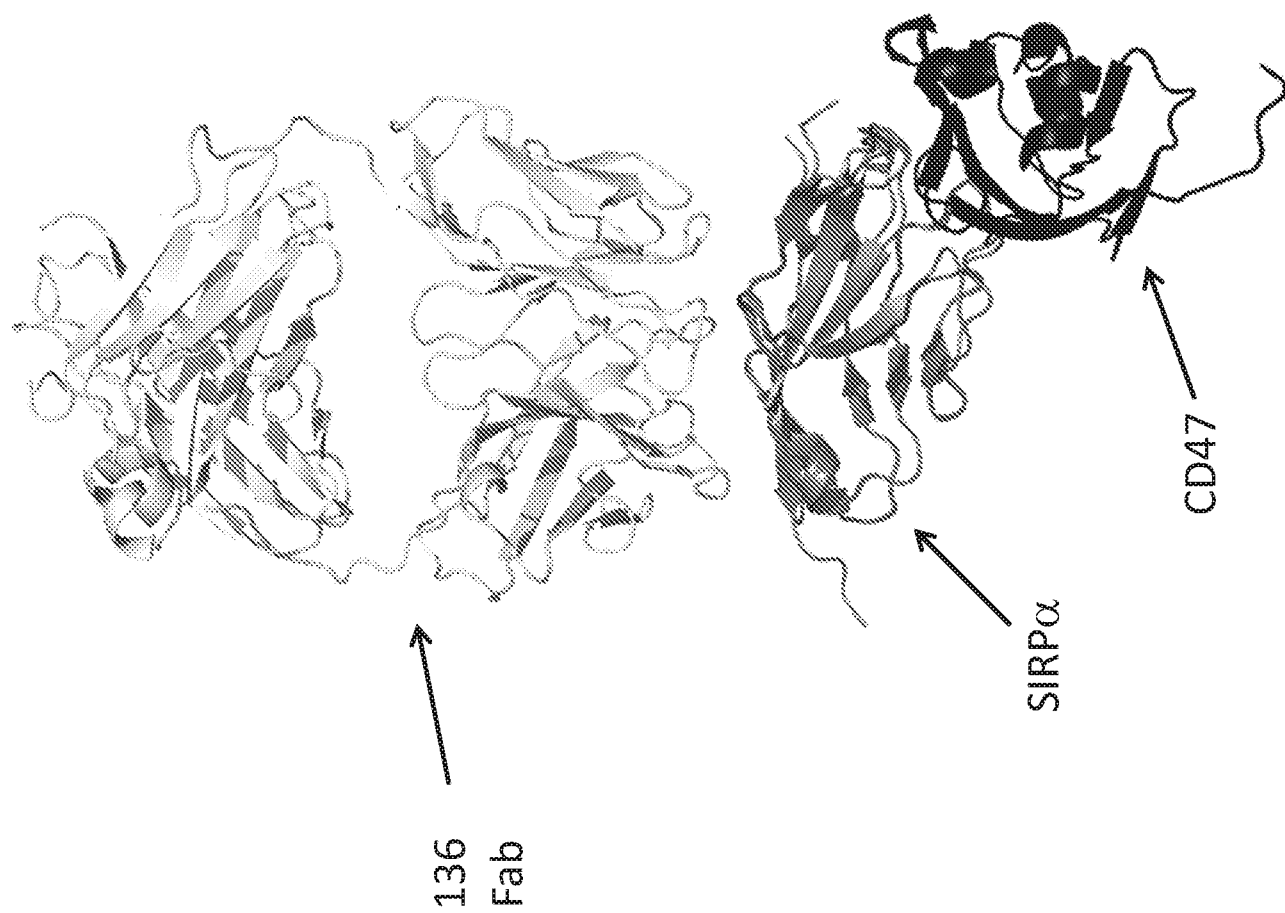


FIG. 18A

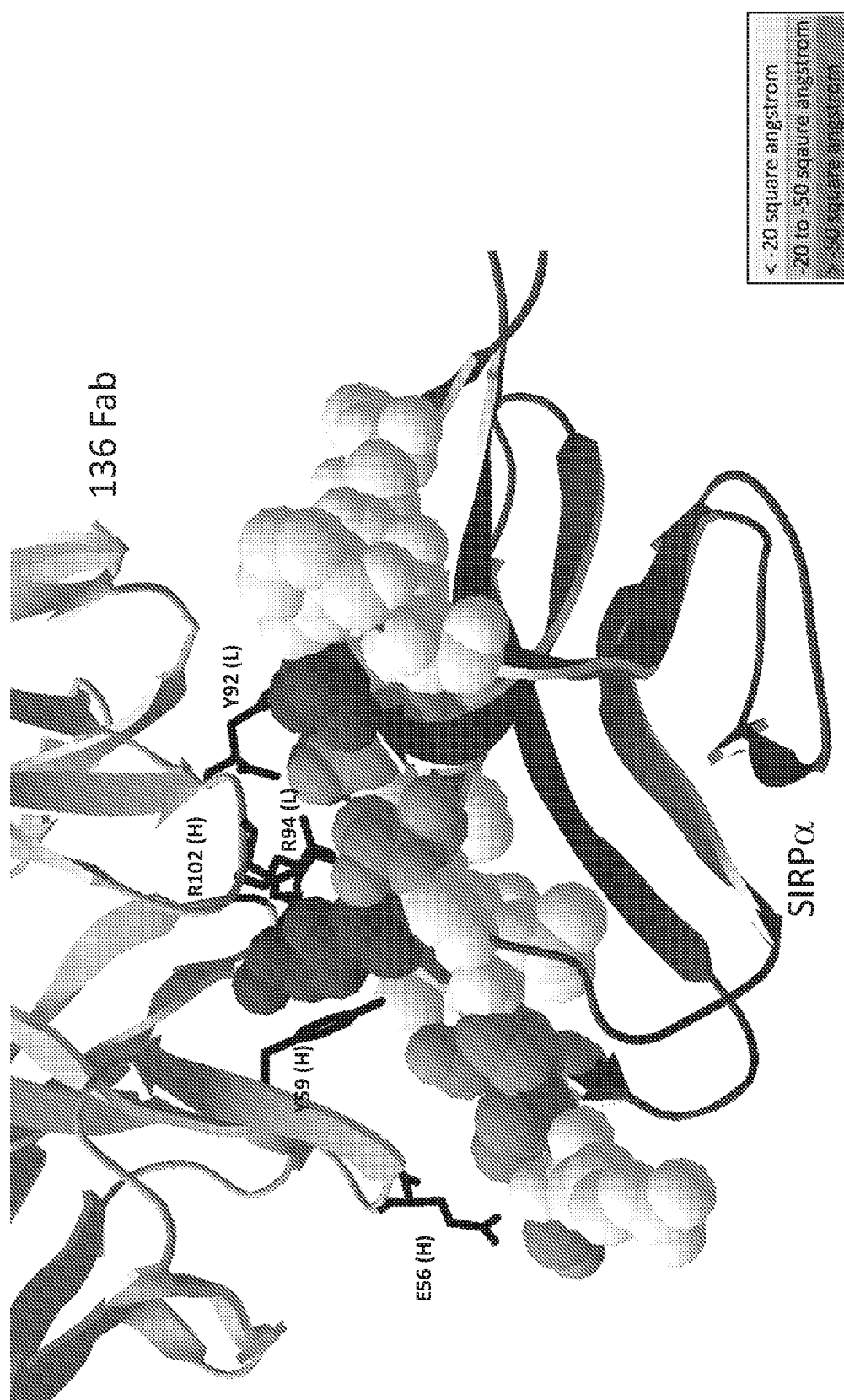


FIG. 18B

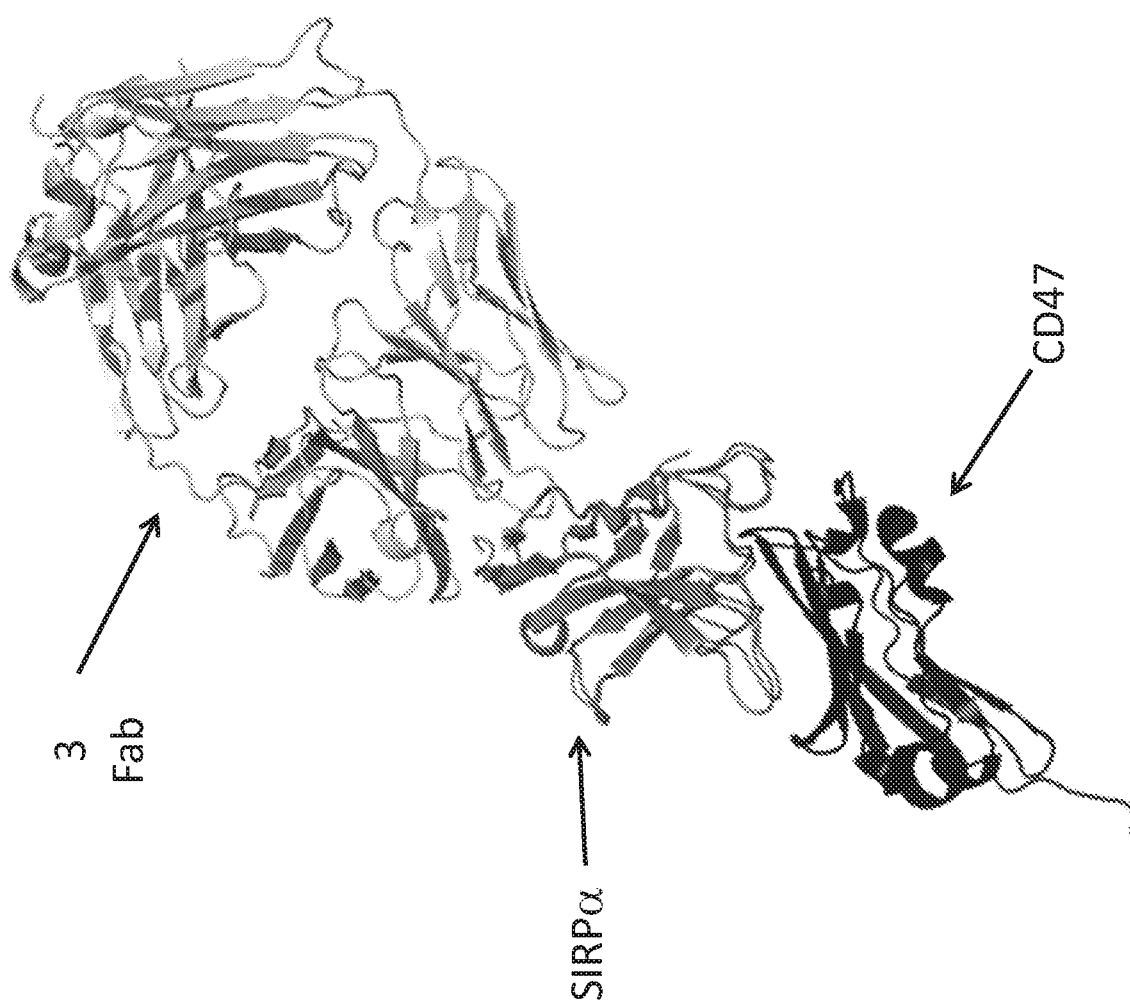


FIG. 19A

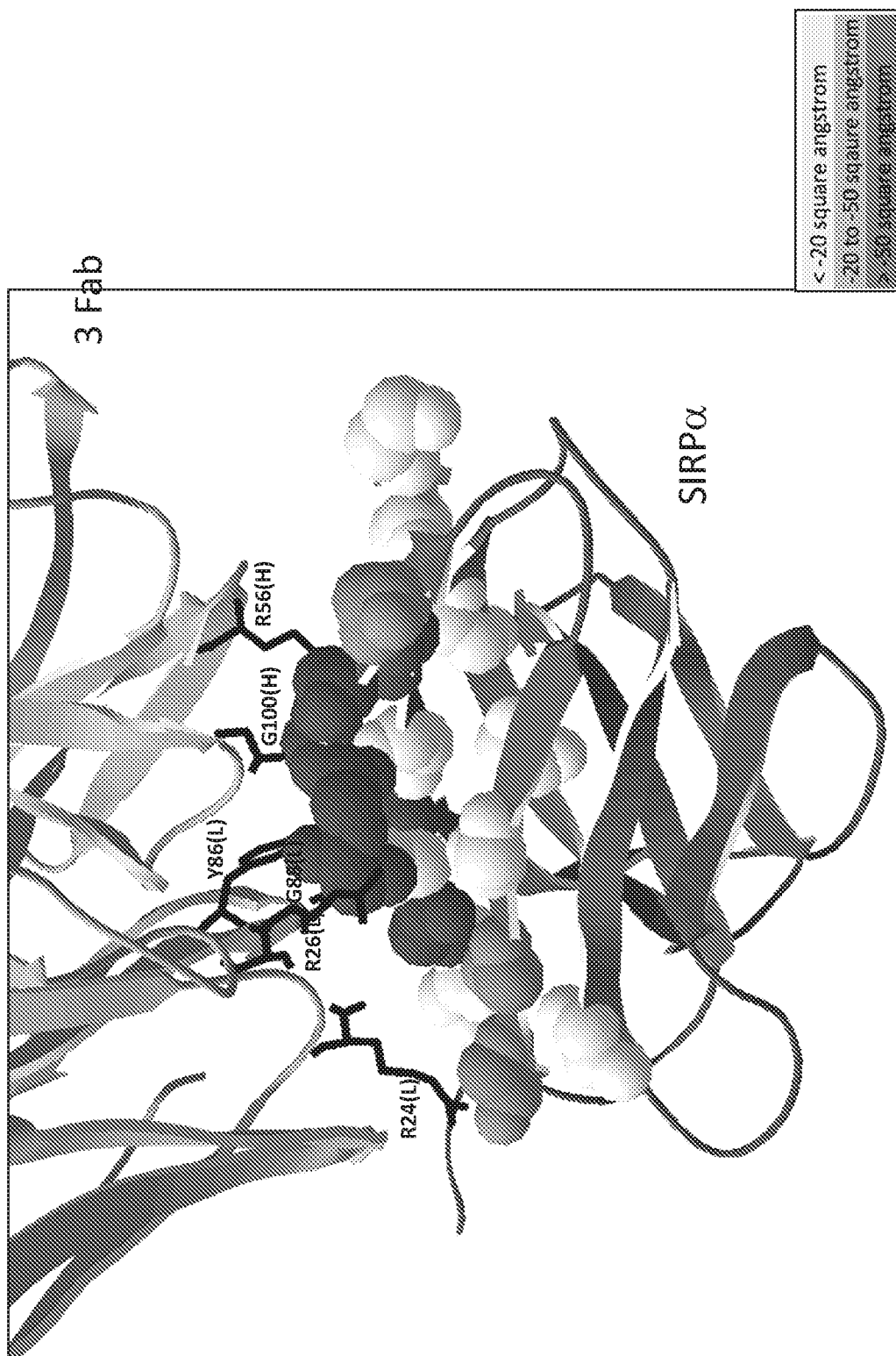


FIG. 19B

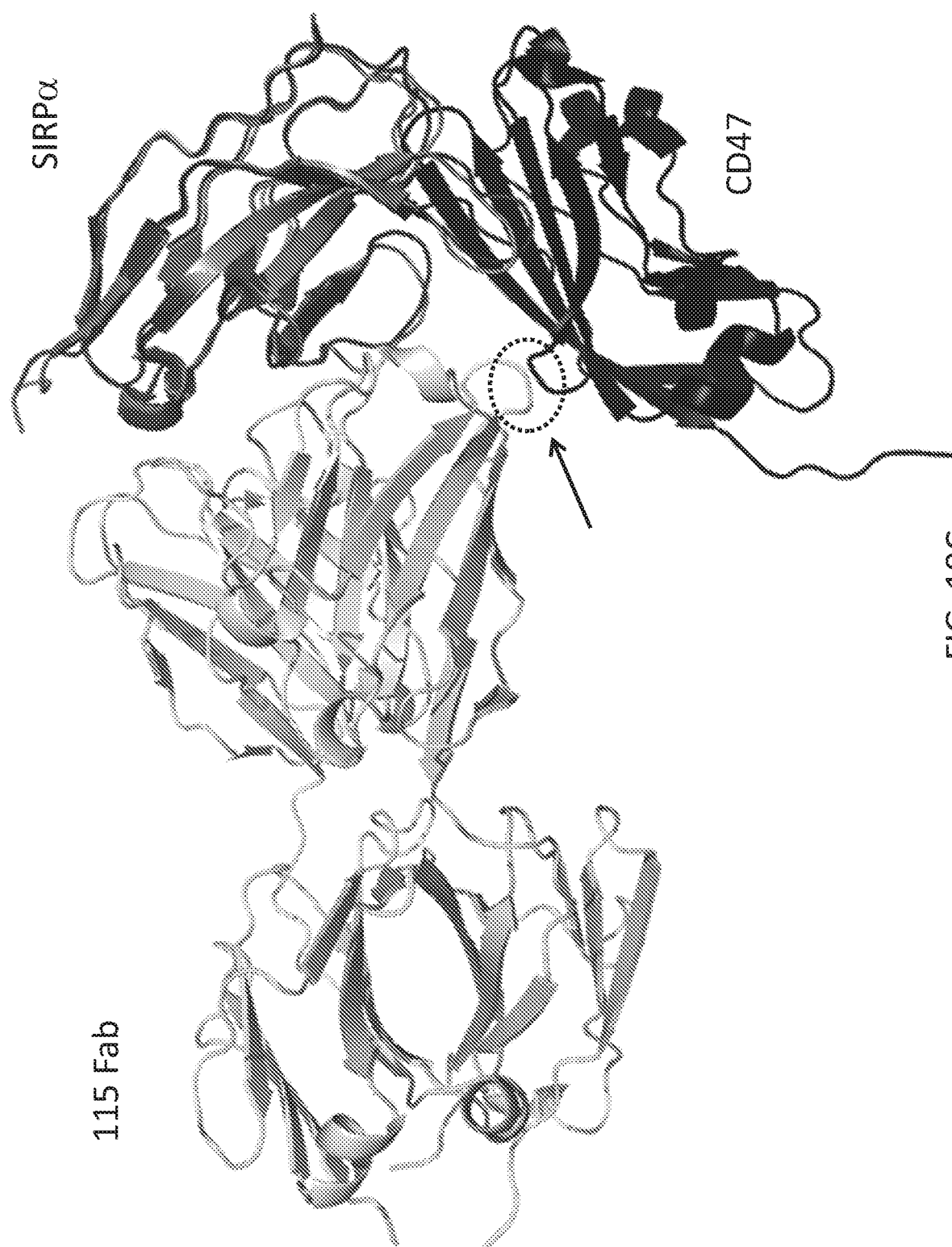


FIG. 19C

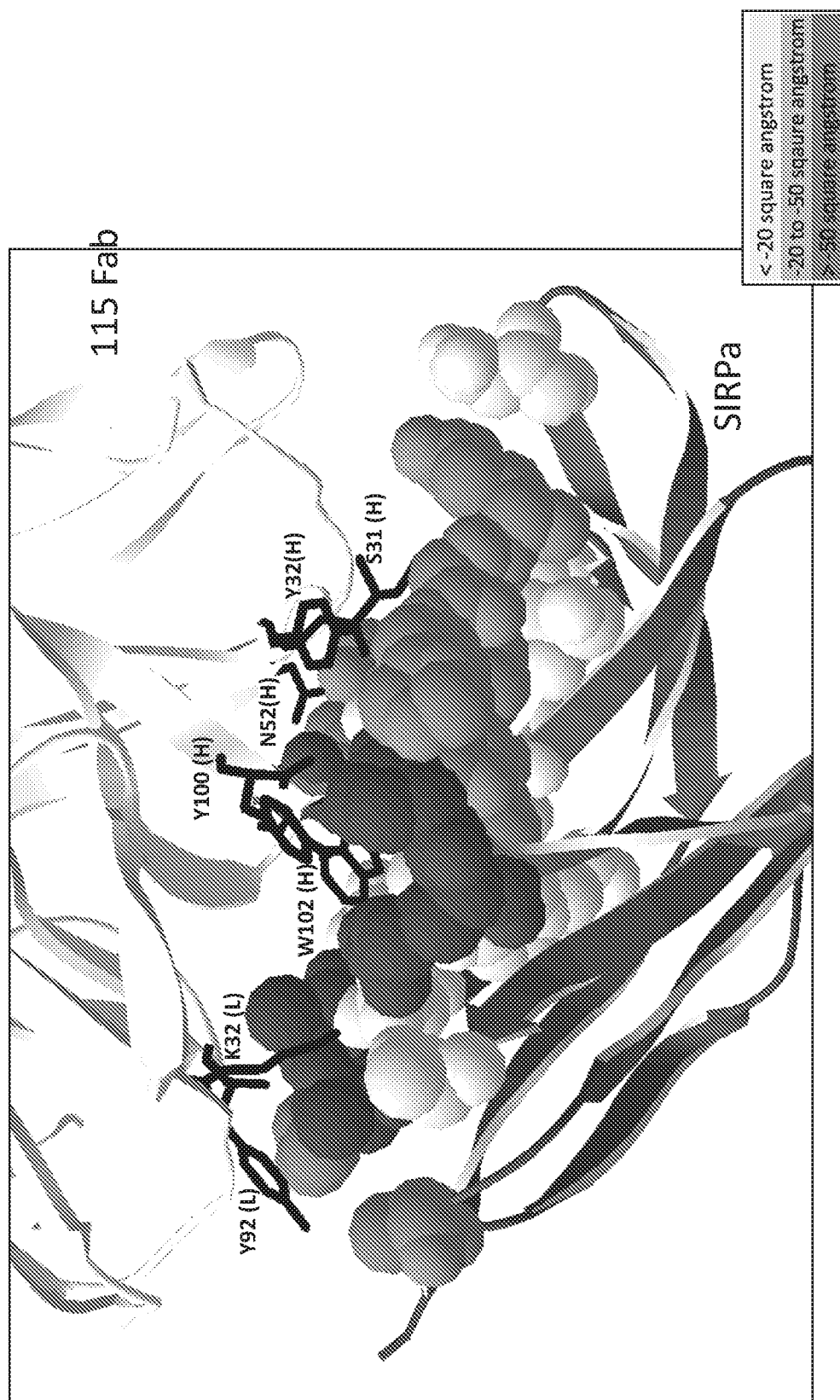


FIG. 19D

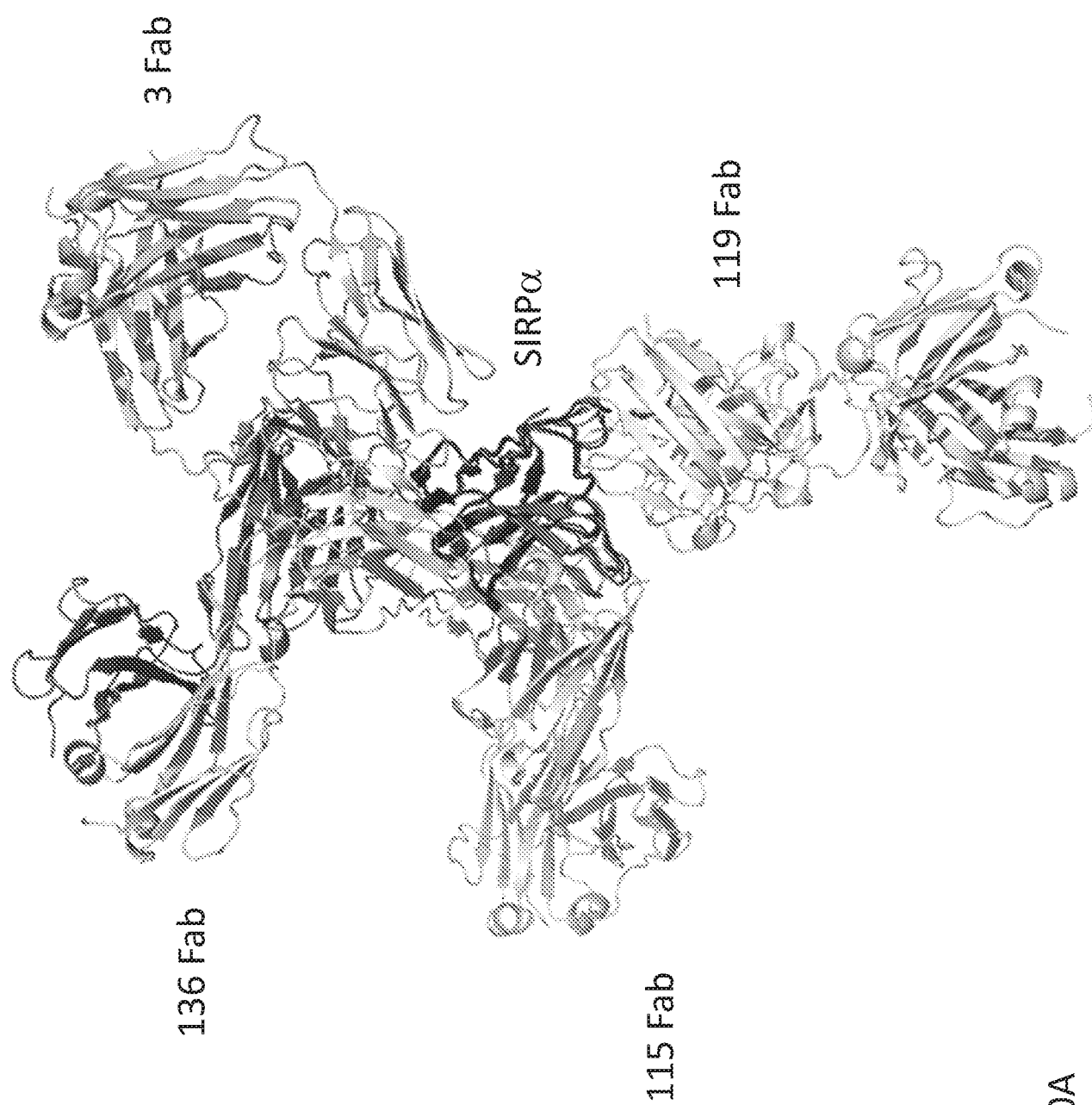


FIG. 20A

FIG. 20B

< -20 square angstrom
 -20 to -50 square angstrom
 > -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
GLU	3		-13.8			
GLN	5				-11.2	
VAL	6			-5.7	-7.2	
ILE	7				-61.9	
GLN	8			-13.2	-20.1	
PRO	9			-14.6	-7.2	
ASP	10			-1	-50.3	
LYS	11			-157.6	-159.7	
SER	12			-17.6	-54.5	
LEU	14			-42.2	-29	
ALA	17					-19.7
ARG	24				-15.1	
THR	26				-28.1	
THR	28		-5.9		-33.5	
SER	29	-1.1	-17.3			
LEU	30	-44.3	-39.8			
ILE	31	-15.2	-106.5			
PRO	32		-32.2			
VAL	33	-88.7	-81.4			
GLY	34	-25				
PRO	35	-42	-6.4			
ILE	36	-10	-13.7			

FIG. 20B (cont.'d)

< -20 square angstrom
 -20 to -50 square angstrom
 > -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
GLN	37	-1.7				
TRP	38		-2.1			
PHE	39					-2
ARG	40					-18.2
ALA	42			-52.9		
GLY	43			-16.8		
PRO	44			-10.9		-44.1
GLY	45					-21.3
ARG	46			-6.8		-15.7
GLU	47					-96.3
LEU	48					-70.3
ILE	49					-20.4
TYR	50	-5.1	-14.2			
ASN	51	-7.3				-3.3
GLN	52	-91.5	-81.9			
LYS	53	-115.8	-114.8			
GLU	54	-57.9	-35.3			-47.7
GLY	55					-19.8
HIS	56					-35.7
PHE	57					-20.6
PRO	58					-69.6
ARG	59					-69

FIG. 20B (cont.'d)

< -20 square angstrom
 -20 to -50 square angstrom
 > -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
THR	62		-21.5			
SER	64		-5.8			
ASP	65		-7.5			
LEU	66	-20.9	-11.6			
THR	67	-85.8	-62.4			
LYS	68	-24.6	-18.2			
ARG	69	-174	-134.3			
ASN	70		-73.7			
ASN	71		-28.4			
MET	72		-23.4		-12.5	
ASP	73		-1.3			
PHE	74	-11.8	-34.9			
SER	75		-2.2			
ILE	76		-4.5			
ALA	80					-11.2
THR	82					-52
PRO	83					-44.5
ALA	84					-84.6
ASP	85					-16.6
GLY	87			-4.1		
THR	88			-34.1	-12.3	
TYR	89					-1.5

FIG. 20B (cont.'d)

< -20 square angstrom
 -20 to -50 square angstrom
 > -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
TYR	90			-48.8	-4.7	
LYS	93	-5.2				
ARG	95		-44.5			
LYS	96	-96.8	-88.2			
GLY	97	-22.7	-2.9			
SER	98	-56.1	-14.2			
PRO	99	-19.7				
ASP	100					-12.4
ASP	101	-9.9				
GLU	103			-20.1		
PHE	104			-6.9		
LYS	105			-13.1		
SER	106			-49.9		
GLY	107			-6.9		
ALA	108			-83.6	-54.9	
GLY	109			-12.5	-8.5	
GLU	111			-96.8	-77	
LEU	112			-3		
SER	113			-41.5	-3.7	
ARG	115			-4.9	-4.6	
ALA	116			-23.8		

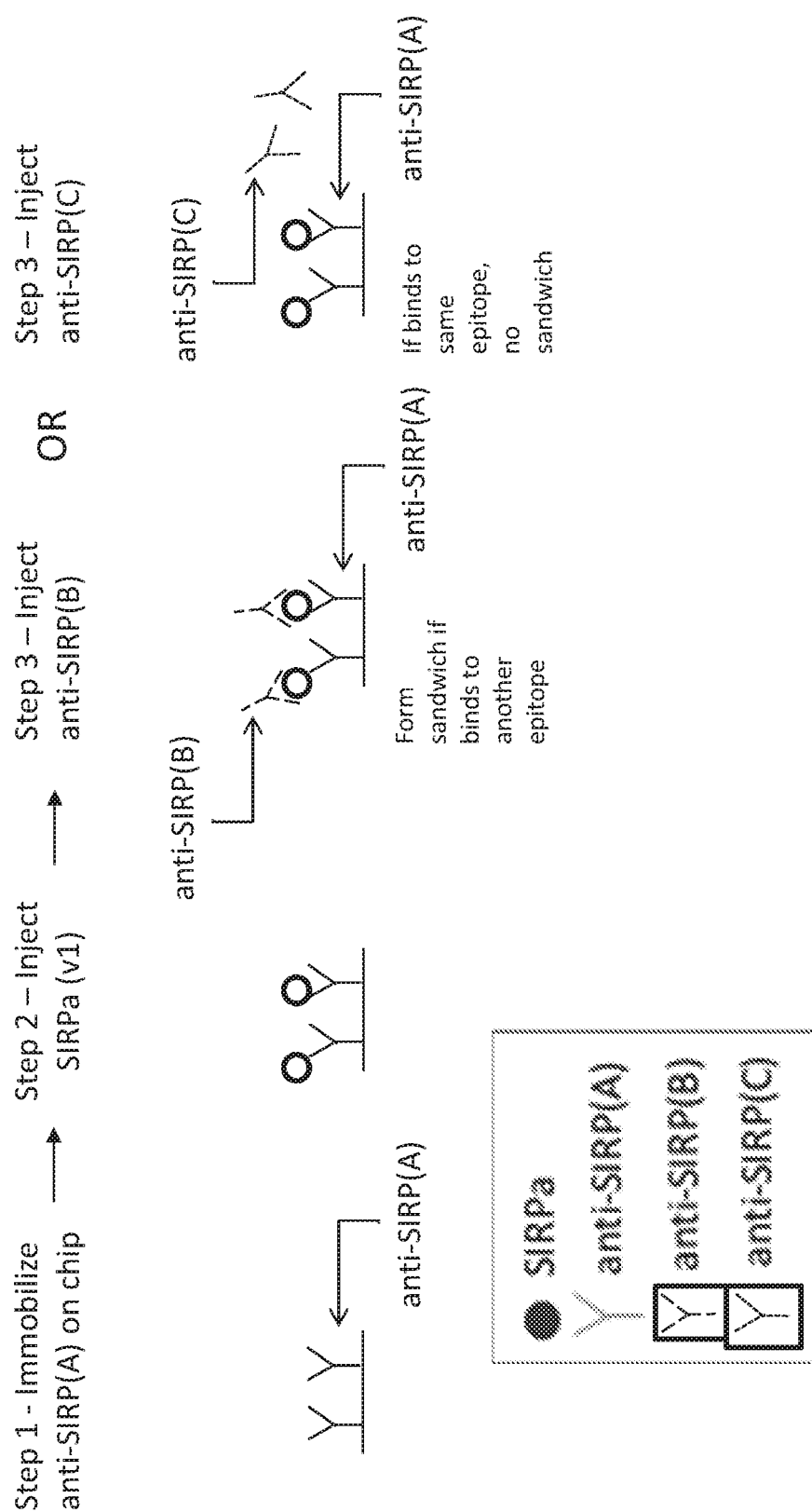


FIG. 21A

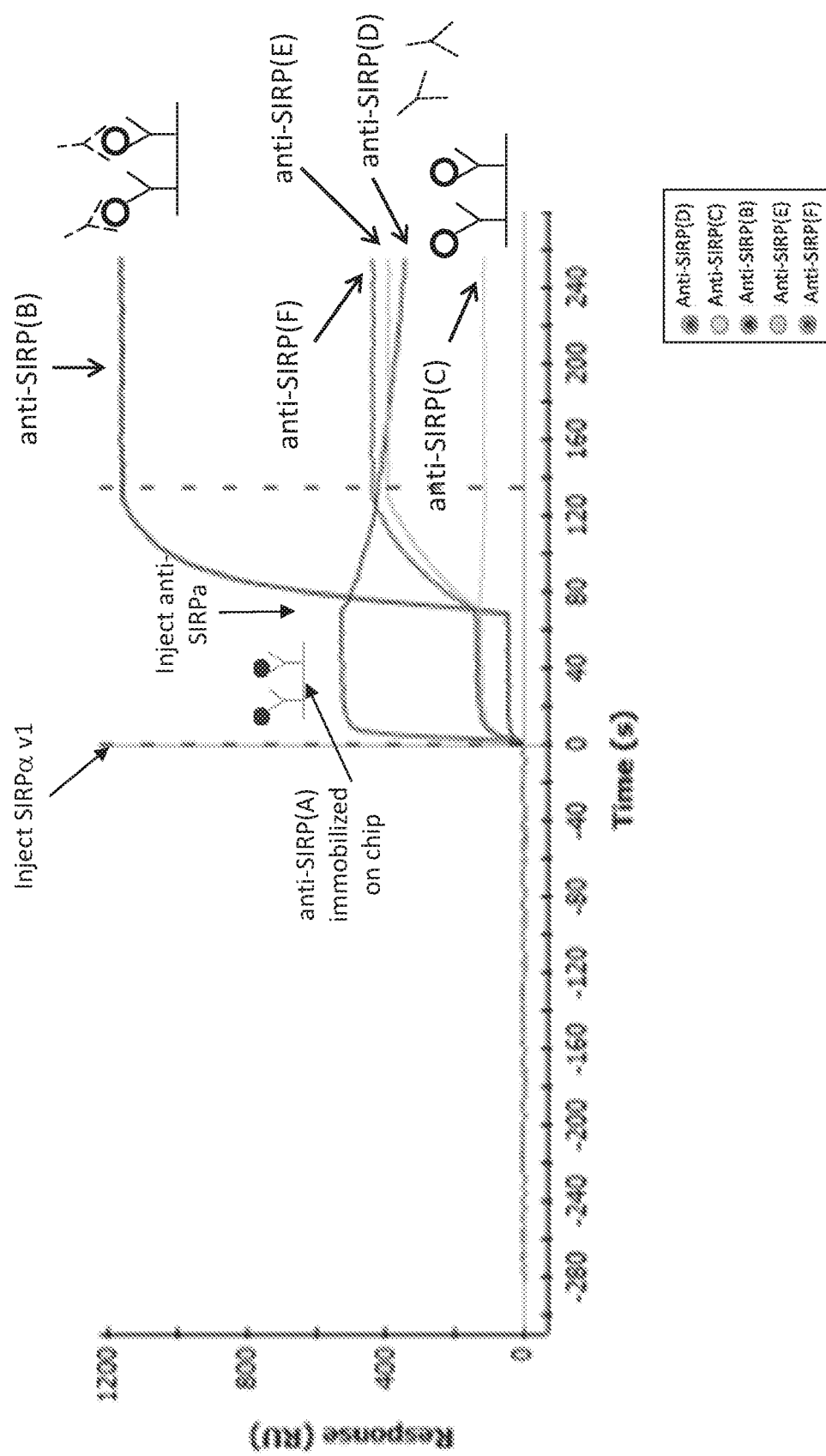
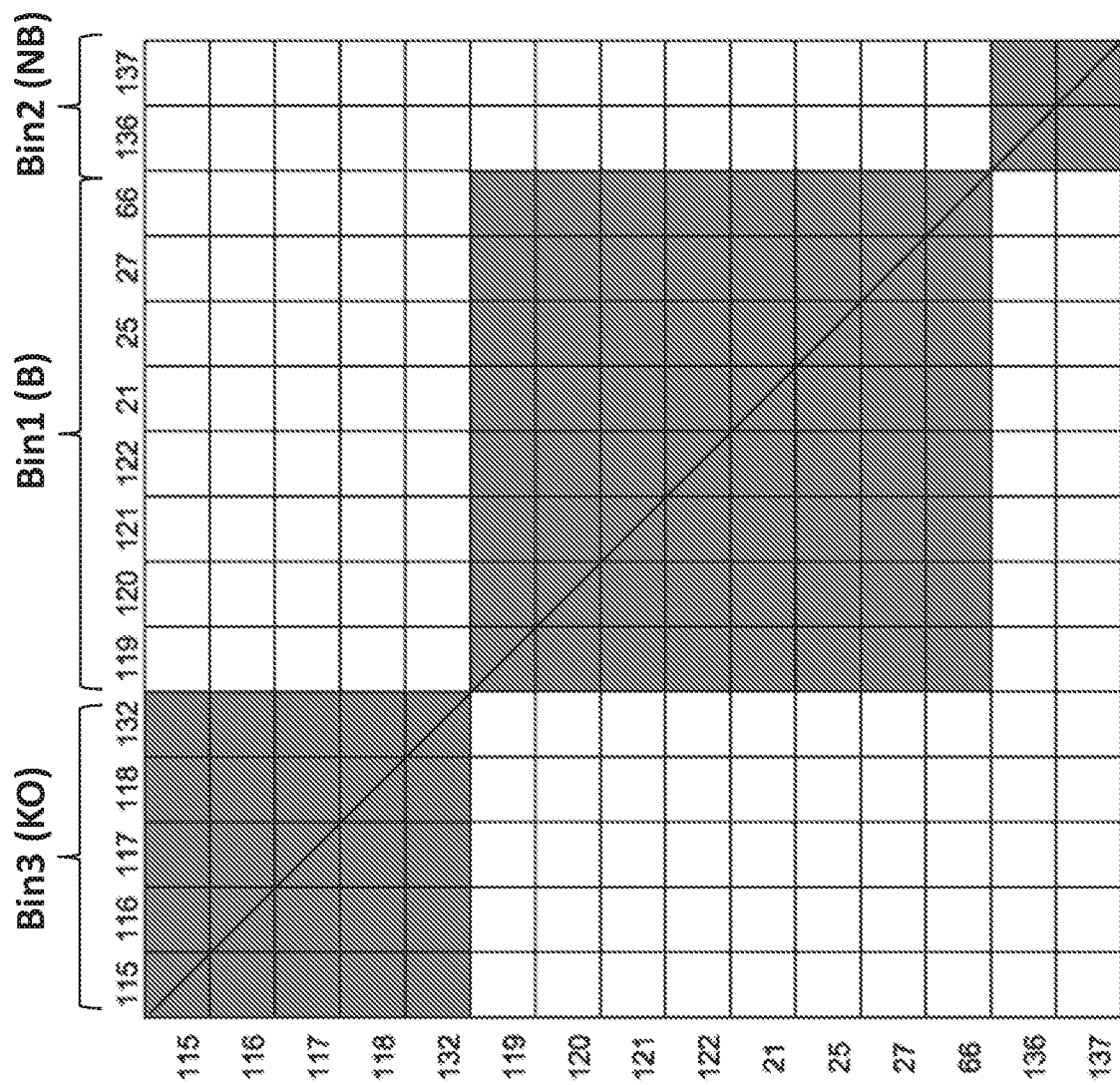


FIG. 21B



B = blockers
 NB = non-blockers
 KO = kick-off

FIG. 22A

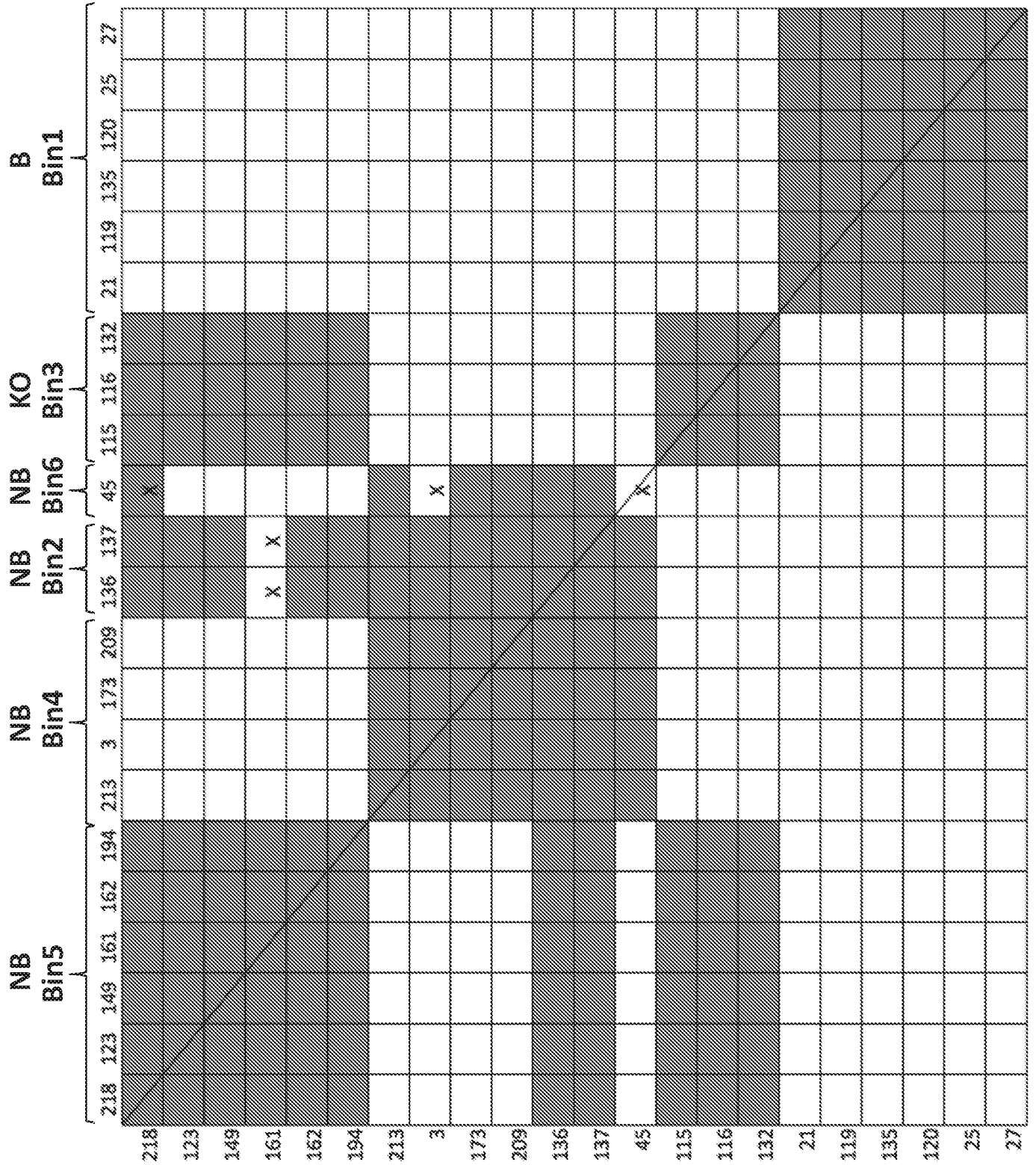


FIG. 22B

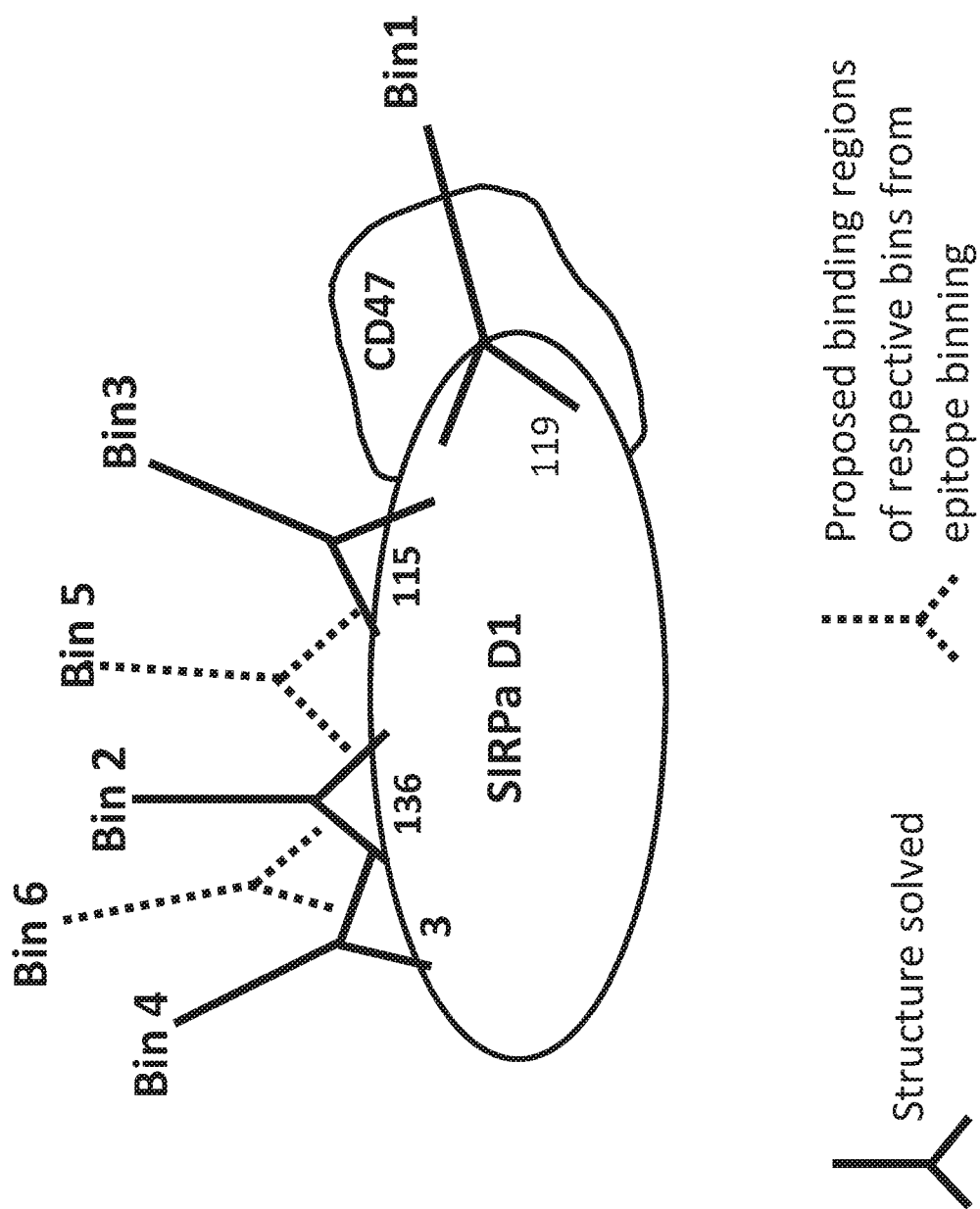


FIG. 23

			H1	40
1				
	135_VH_wt	(1)	DVQLVESGGGVVRPGESLRLSCAASGFSFIYAMSWVRQA	
	135_VH_MutAll	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFSFIYAVSWVRQA	
	135_VH_MutAll_V34M	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFSFIYAMSWVRQA	
	135_VH_MutAll_V34L	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFSFIYALSWVRQA	
		*	*	*
41				80
	135_VH_wt	(41)	PGEGLWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ	
	135_VH_MutAll	(41)	PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ	
	135_VH_MutAll_V34M	(41)	PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ	
	135_VH_MutAll_V34L	(41)	PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ	
		*		
81				120
	135_VH_wt	(81)	MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> LGTLVTVSS	
	135_VH_MutAll	(81)	MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> QGLTVTVSS	
	135_VH_MutAll_V34M	(81)	MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> QGLTVTVSS	
	135_VH_MutAll_V34L	(81)	MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> QGLTVTVSS	
		*		*

FIG. 25B

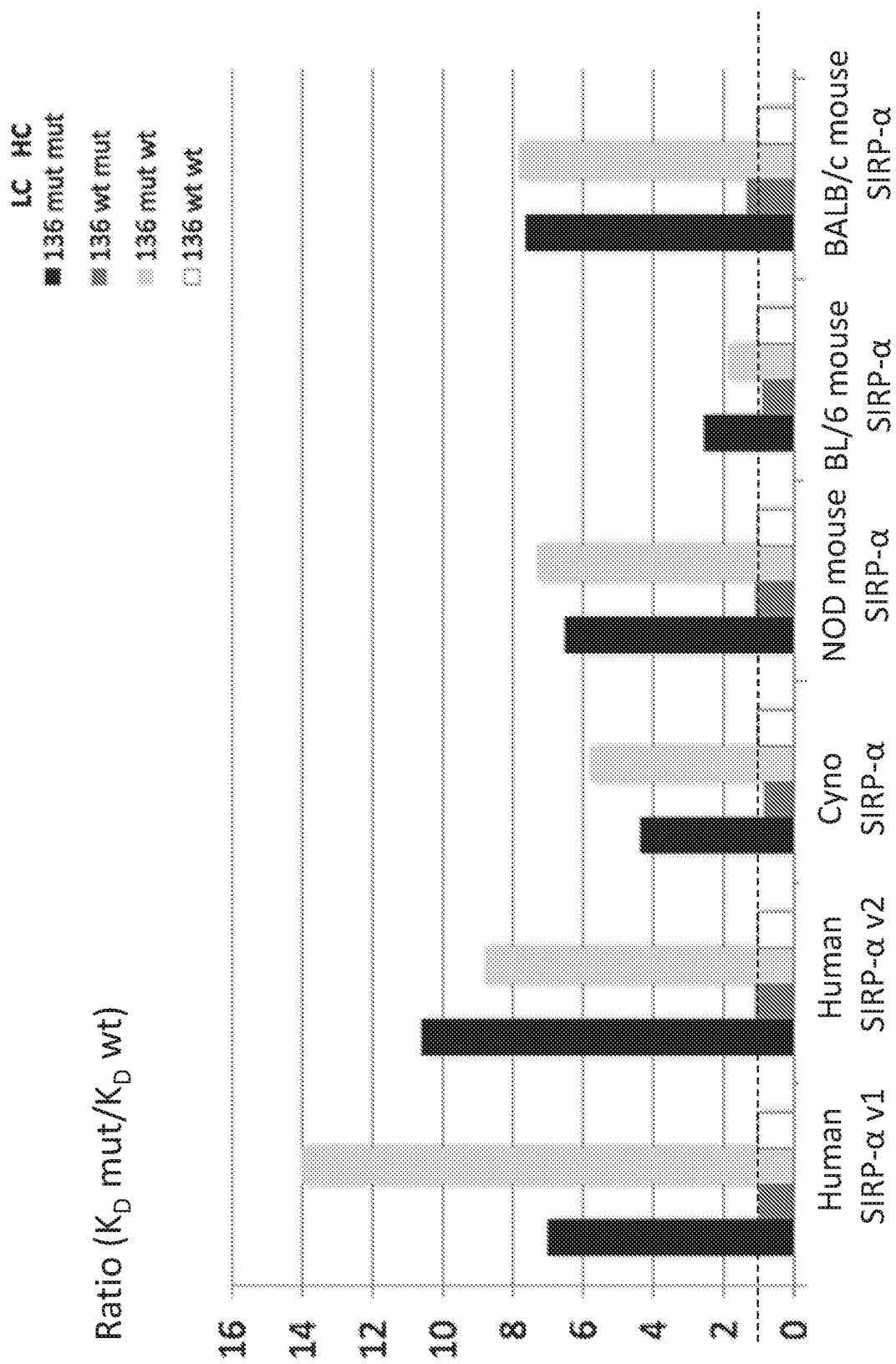
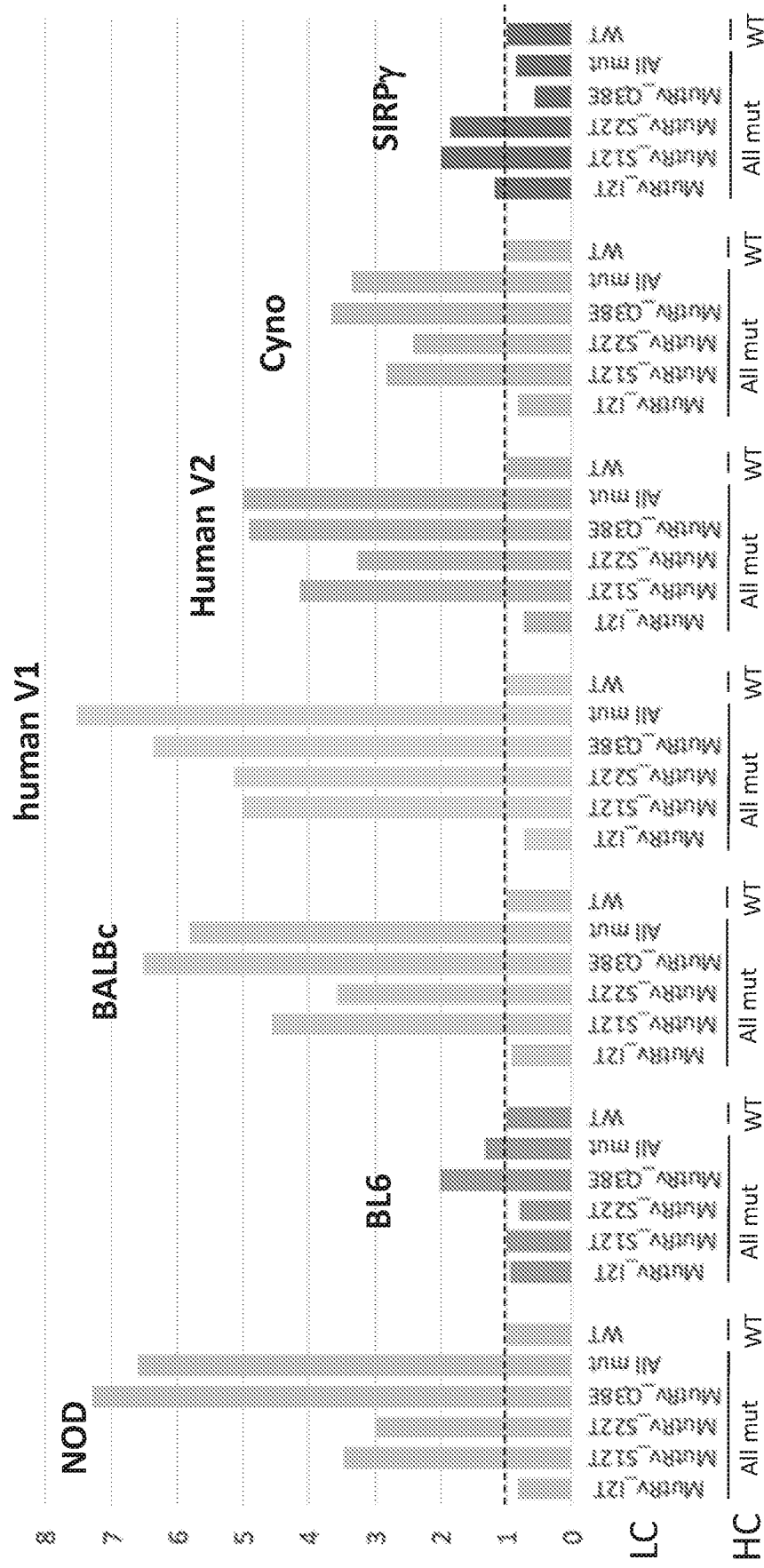


FIG. 27A



	AB21_Heavy Chain						AB25_heavy chain						AB27 Heavy Chain						AB66 Heavy Chain												
	25	25	66	66	25	21	25	66	66	25	21	25	66	66	25	21	25	66	66	25	21	25	66	66	25	21	25	66	66	25	21
Parental VL	IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1	IGLV1	IGLV3	IGLV1	IGLV1	IGLV1	IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1	IGLV3	IGLV1	IGLV3	IGLV1	IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1
Human framework	Hum1	Hum2	Hum3	Hum4	Hum5	Hum6	Hum6	Hum2	Hum3	Hum4	Hum4	Hum3	Hum3	Hum4	Hum5	Hum6	Hum6	Hum1	Hum2	Hum3	Hum4	Hum5	Hum6	Hum1	Hum2	Hum3	Hum4	Hum5	Hum6	Hum5	Hum6
Protein yield	+	-	+	-	+	<div></div>	<div></div>	+	-	-	-	+	-	-	+	-	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+
Human v1																															
Human v2																															
Cyno SIRPa																															
BALBc SIRPa																															
Human SIRPβ																															

Protein Yield (mg/mL)

“+” – no change

“-” – reduced expression

Binding affinity (Koff 1/s)

• No change

• Reduced by 1-2log

Protein Yield (mg/mL) Binding affinity (Koff 1/s)

"+" – no change • No change 

"-" – reduced expression • Reduced by 1-2log 

FIG. 28

		<u>L1</u>	<u>L2</u>	<u>54</u>
Hum1	(1)	SYELTQPPSVSVSPGQTARITCSGGSSSSYYYAWYQQKPGQAPVTLIYSDDKRP		
Hum8	(1)	SYELTQPPSVSVSPGQTARITCSGGAYSSSSYYYAWYQQKPGQAPVLVIYSDSKRP		
hum9	(1)	SYELTQPPSVSVSPGQTARITCSGGAYSSSSYYYAWYQQKPGQAPVLVIYSDDKRP		
		*	**	*
			<u>L3</u>	<u>108</u>
Hum1	(55)	SNIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL		
Hum8	(55)	SGIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL		
hum9	(55)	SGIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL		
		*		

FIG. 29

	1	H1	40
AB21_HC_MutA11	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAMS	WVRQA
AB21_HC_MutA11_M34V	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAV	SWVRQA
AB21_HC_MutA11_M34L	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAL	SWVRQA
AB27_HC_MutA11	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYAM	SWVRQA
AB27_HC_MutA11_M34V	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYAV	SWVRQA
AB27_HC_MutA11_M34L	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYAL	SWVRQA
AB25_HC_MutA11	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAMS	SWVRQA
AB25_HC_MutA11_M34V	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAV	SWVRQA
AB25_HC_MutA11_M34L	(1)	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAL	SWVRQA

	41	H2	80
AB21_HC_MutA11	(41)	PKGLEWVAGISAGGSDTYYPASVKGRFTISRDN	SKNTLY
AB21_HC_MutA11_M34V	(41)	PKGLEWVAGISAGGSDTYYPASVKGRFTISRDN	SKNTLY
AB21_HC_MutA11_M34L	(41)	PKGLEWVAGISAGGSDTYYPASVKGRFTISRDN	SKNTLY
AB27_HC_MutA11	(41)	PKGLEWVSGISSG-GDTYYVDSVKGRFTISRDN	SKNTLY
AB27_HC_MutA11_M34V	(41)	PKGLEWVSGISSG-GDTYYVDSVKGRFTISRDN	SKNTLY
AB27_HC_MutA11_M34L	(41)	PKGLEWVSGISSG-GDTYYVDSVKGRFTISRDN	SKNTLY
AB25_HC_MutA11	(41)	PKGLEWVAGISSG-SDTYYGDSVKGRFTISRDN	SKNTLY
AB25_HC_MutA11_M34V	(41)	PKGLEWVAGISSG-SDTYYGDSVKGRFTISRDN	SKNTLY
AB25_HC_MutA11_M34L	(41)	PKGLEWVAGISSG-SDTYYGDSVKGRFTISRDN	SKNTLY

	81	H3	118
AB21_HC_MutA11	(81)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB21_HC_MutA11_M34V	(81)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB21_HC_MutA11_M34L	(81)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB27_HC_MutA11	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB27_HC_MutA11_M34V	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB27_HC_MutA11_M34L	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB25_HC_MutA11	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB25_HC_MutA11_M34V	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS
AB25_HC_MutA11_M34L	(80)	LQMNSLRAEDTAVYICARETWNHLEFDYWGQGL	TVTVSS

FIG. 30

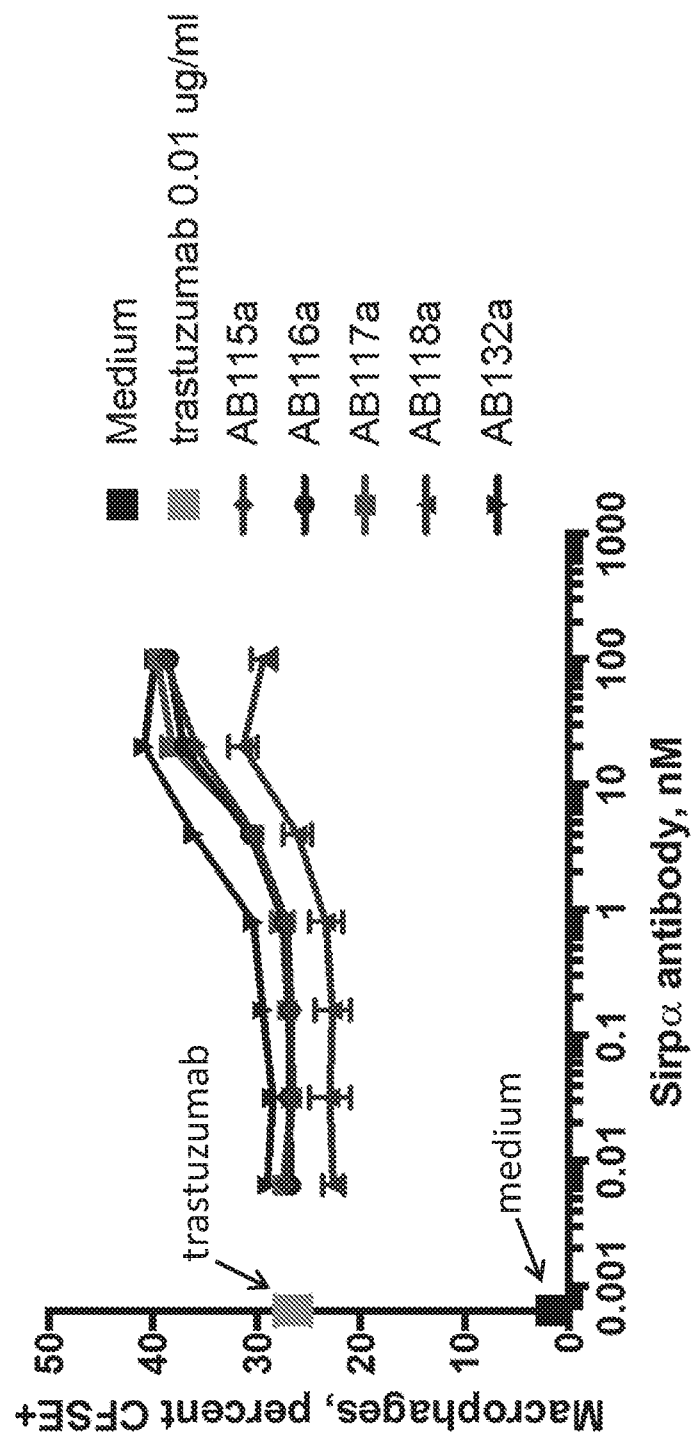


FIG. 31

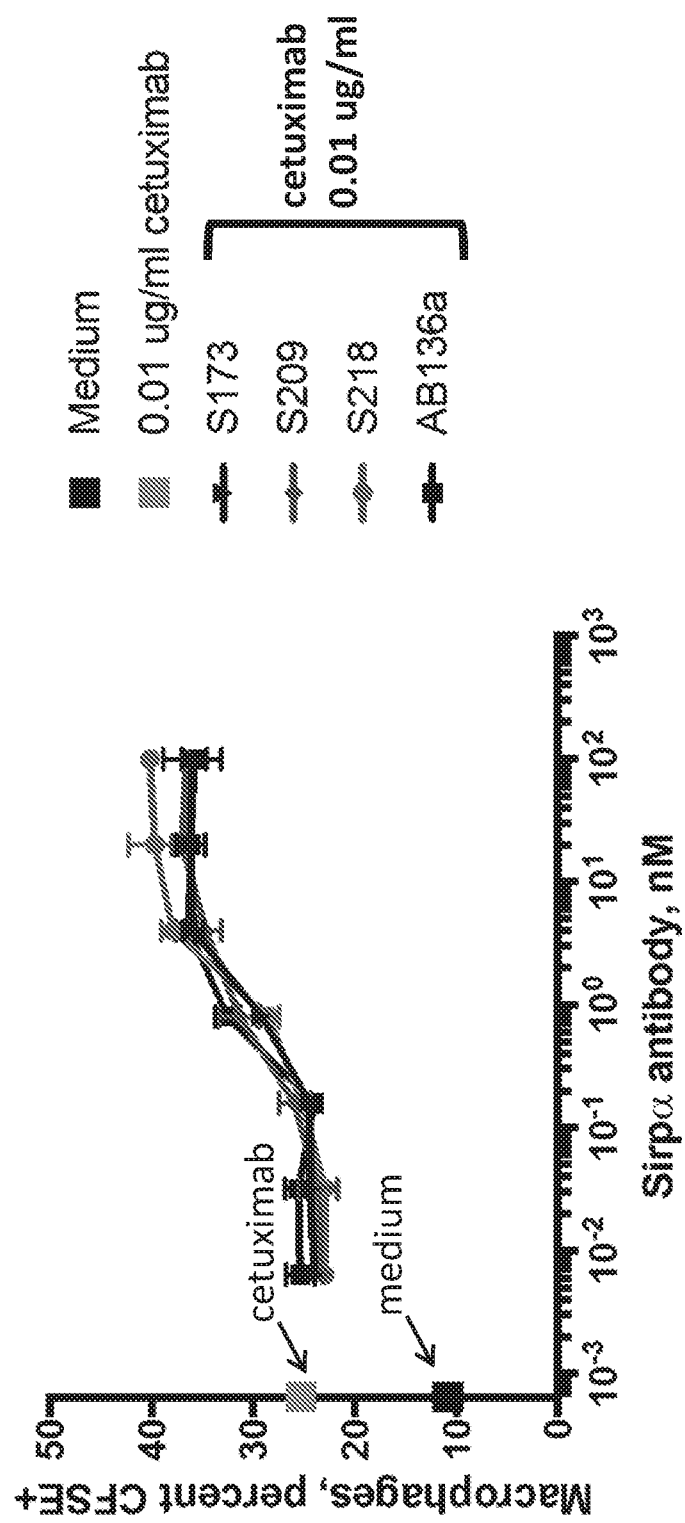


FIG. 32

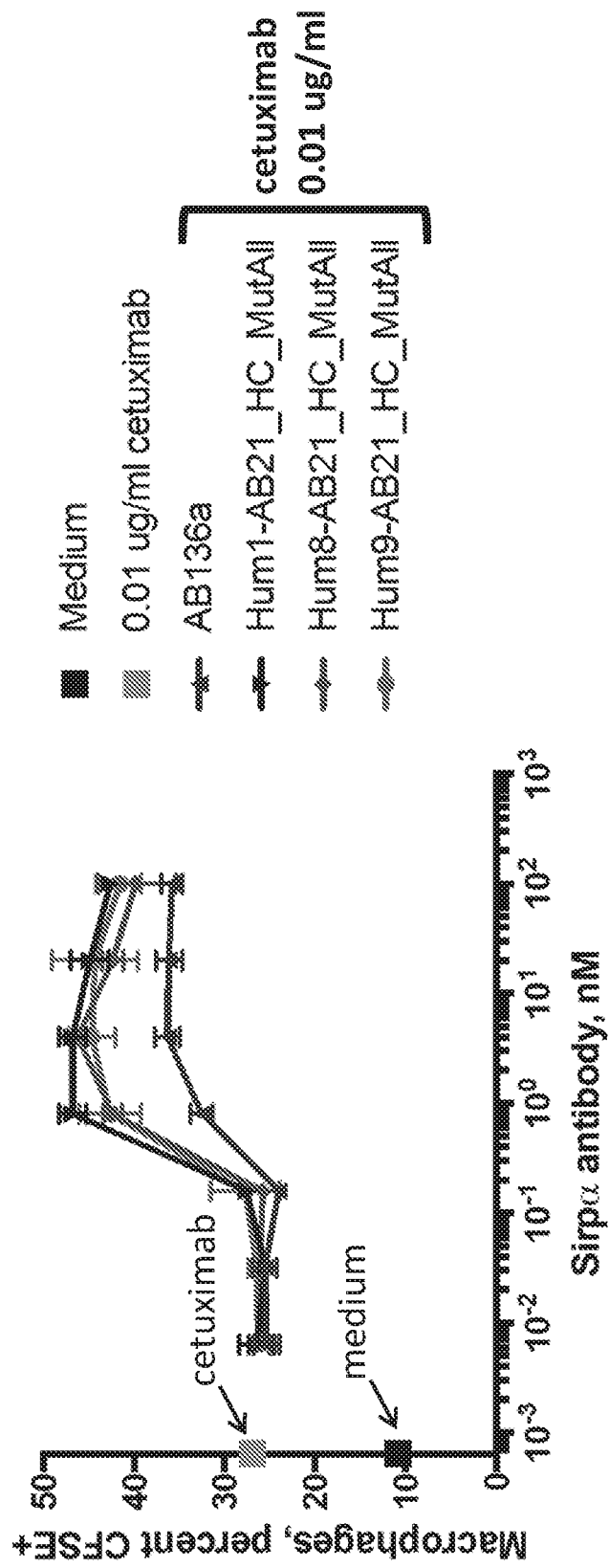


FIG. 33A

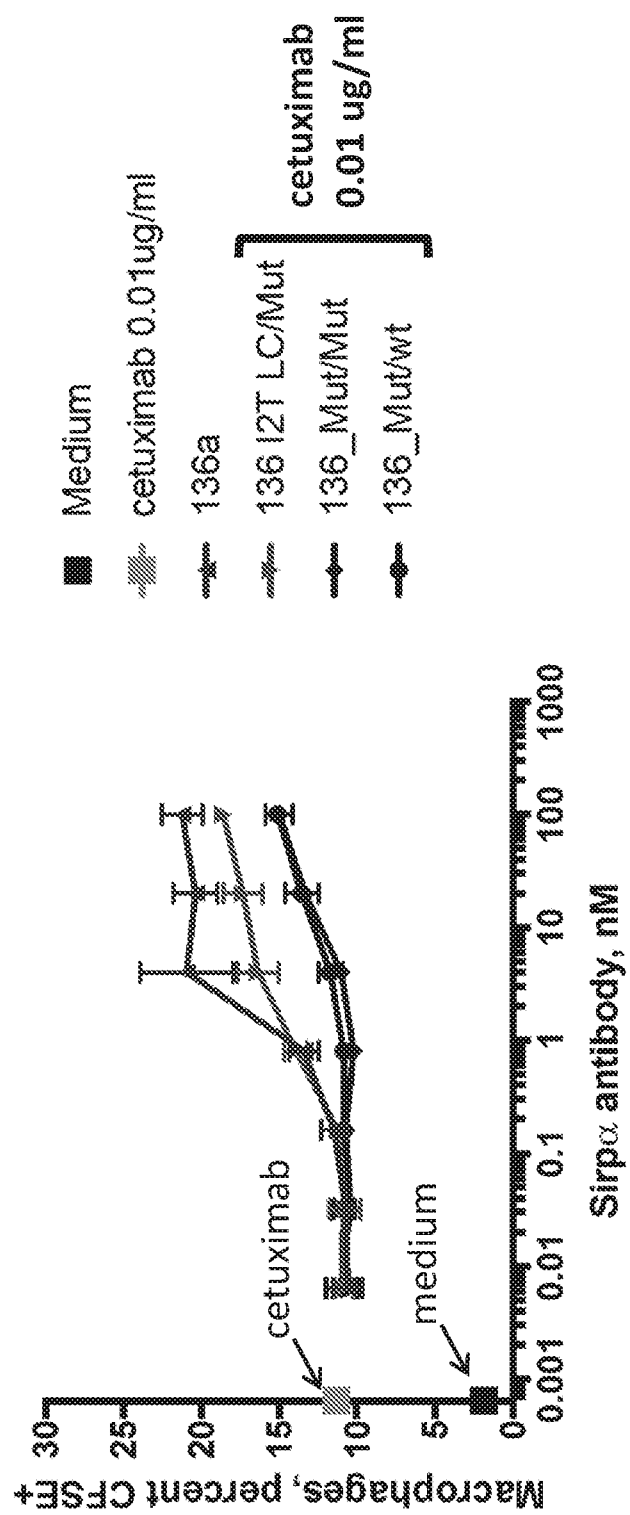


FIG. 33B

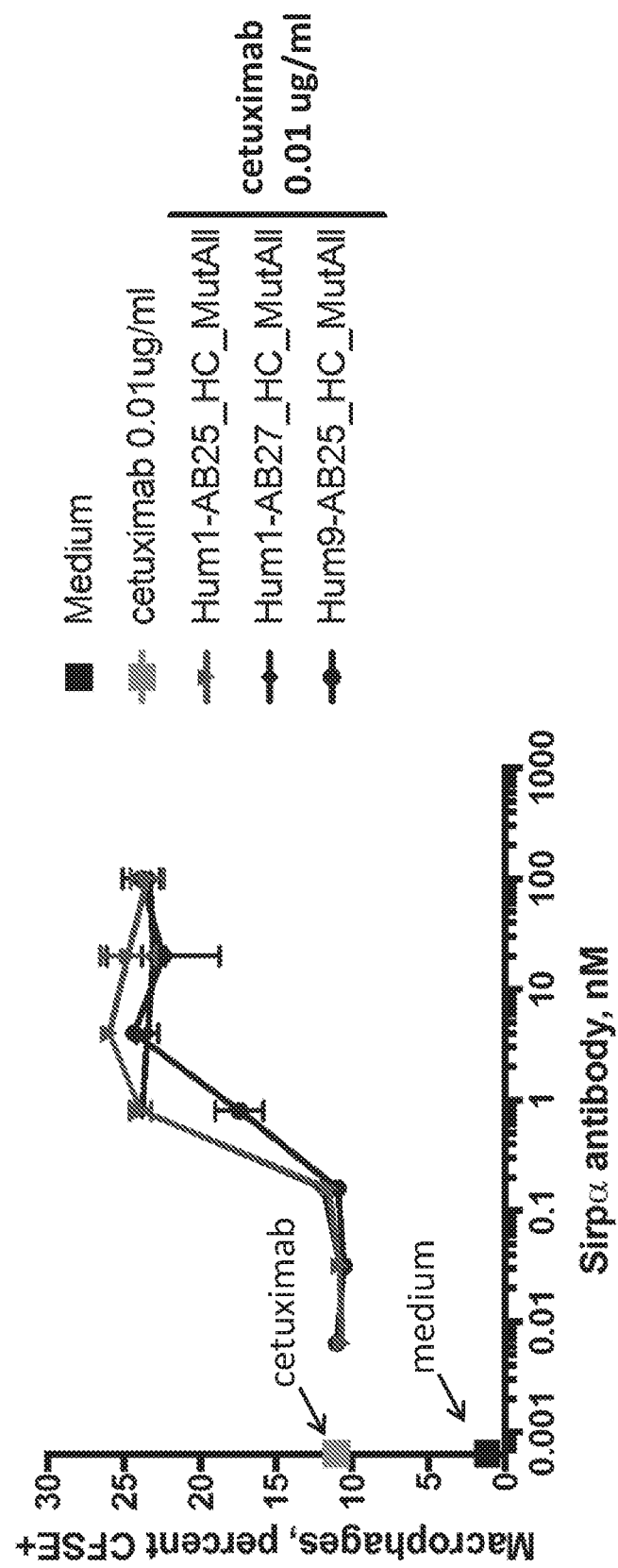


FIG. 33C

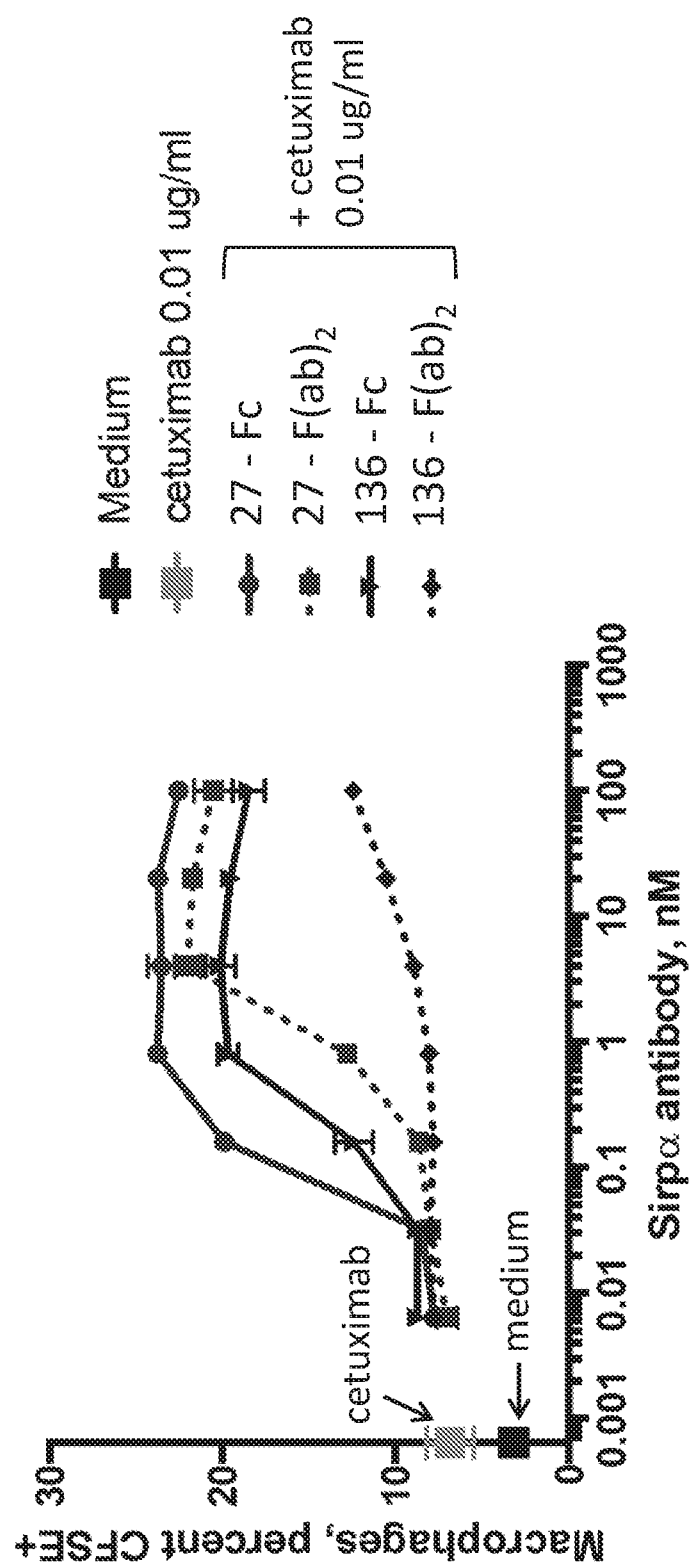


FIG. 34

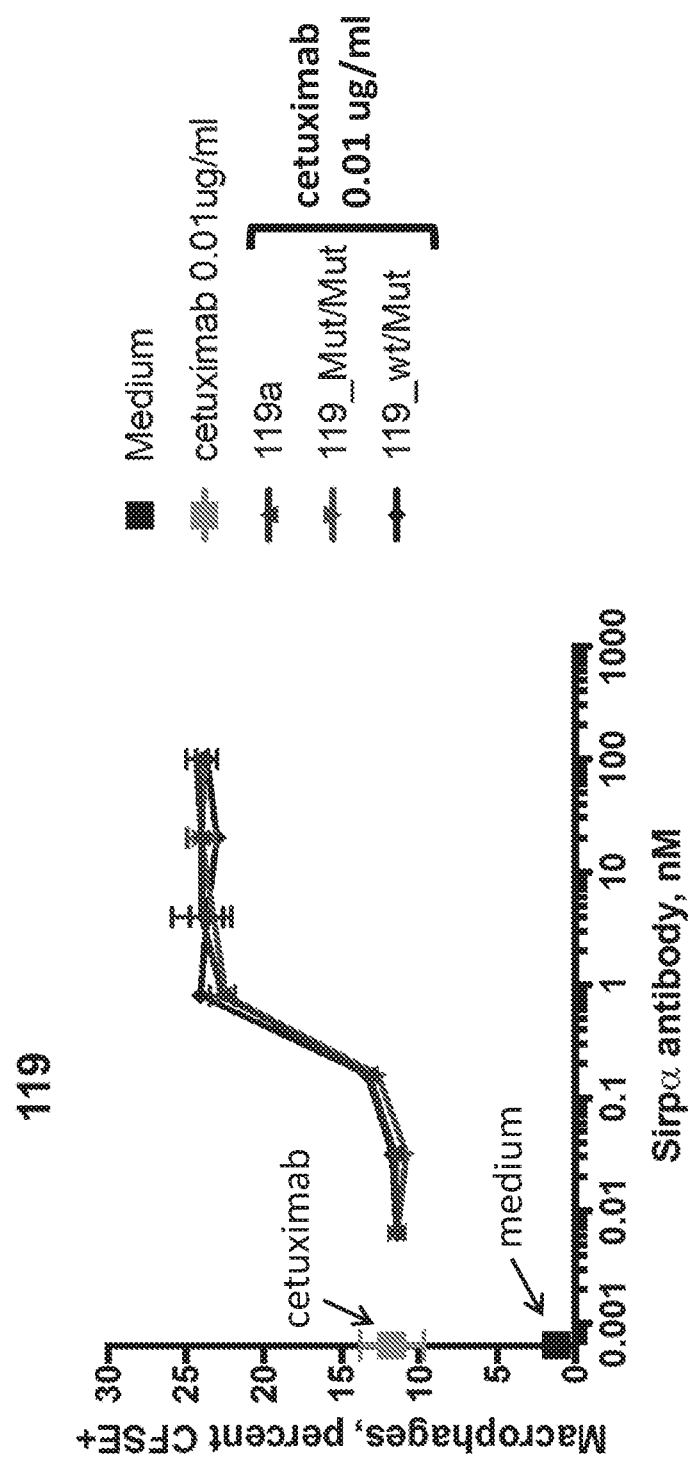


FIG. 35

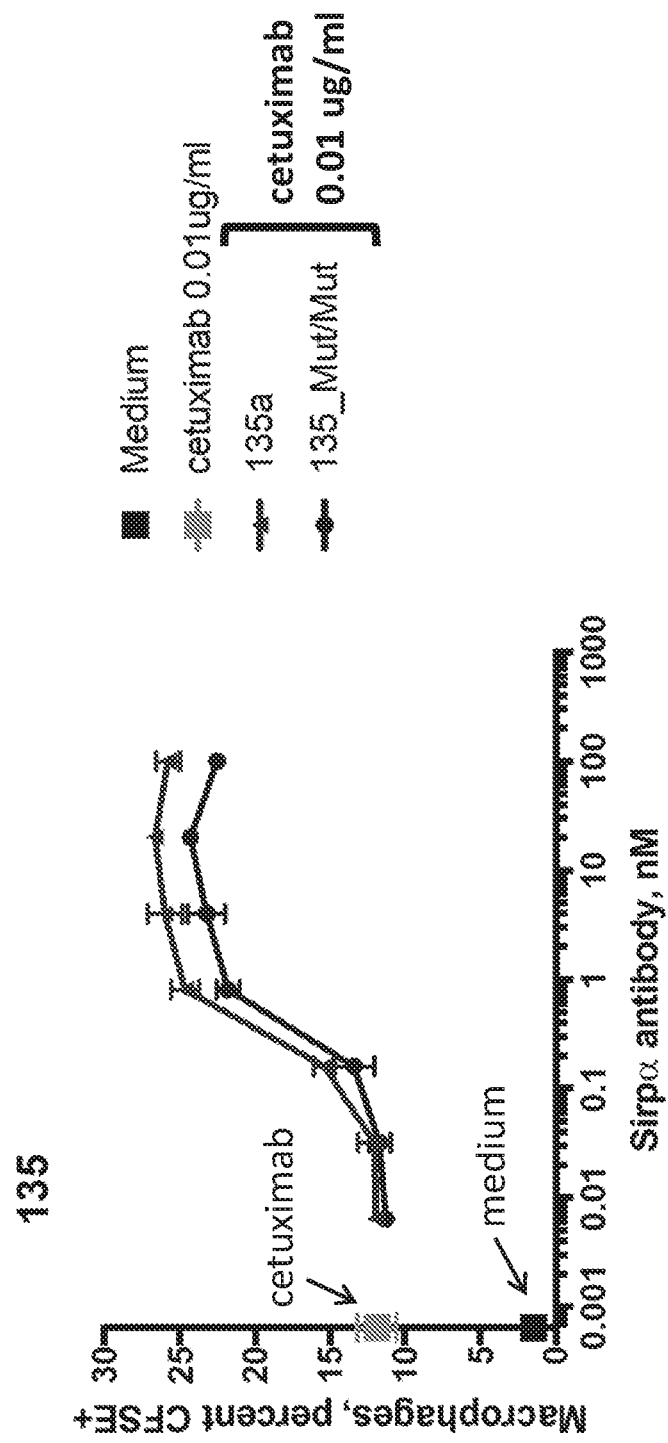


FIG. 36

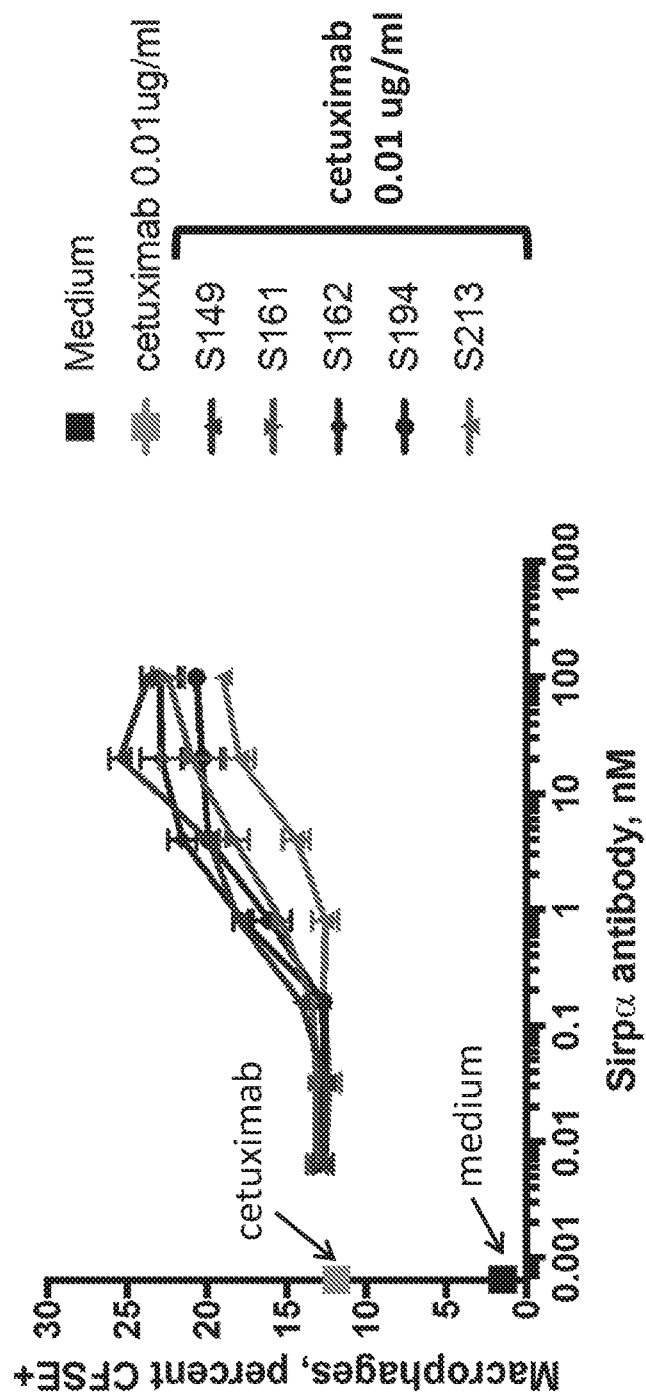


FIG. 37

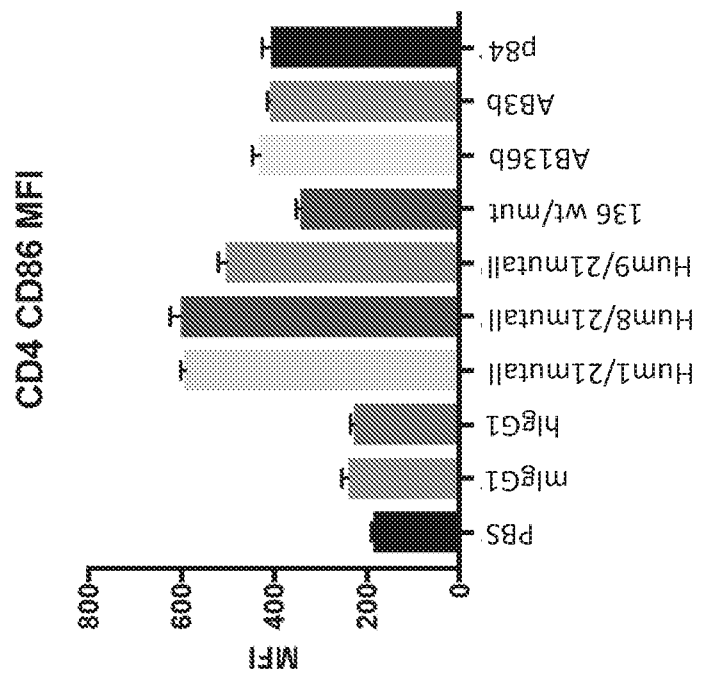


FIG. 38A

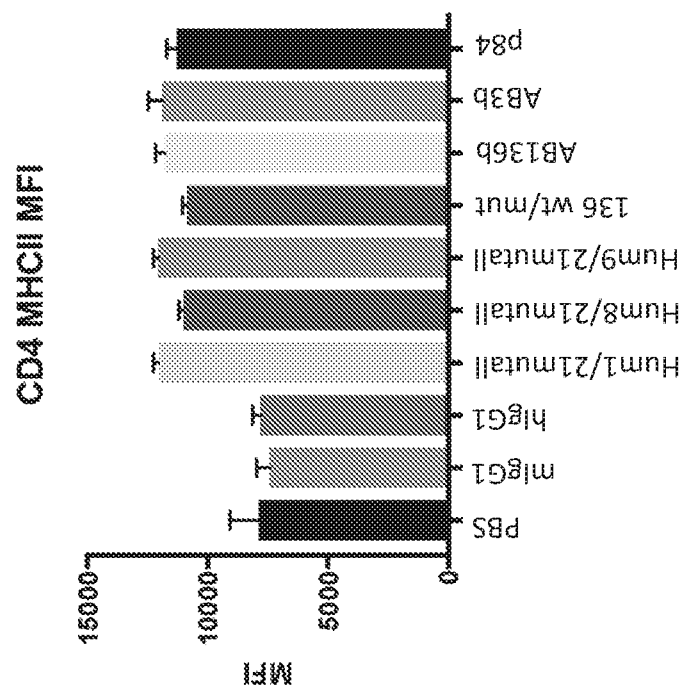


FIG. 38B

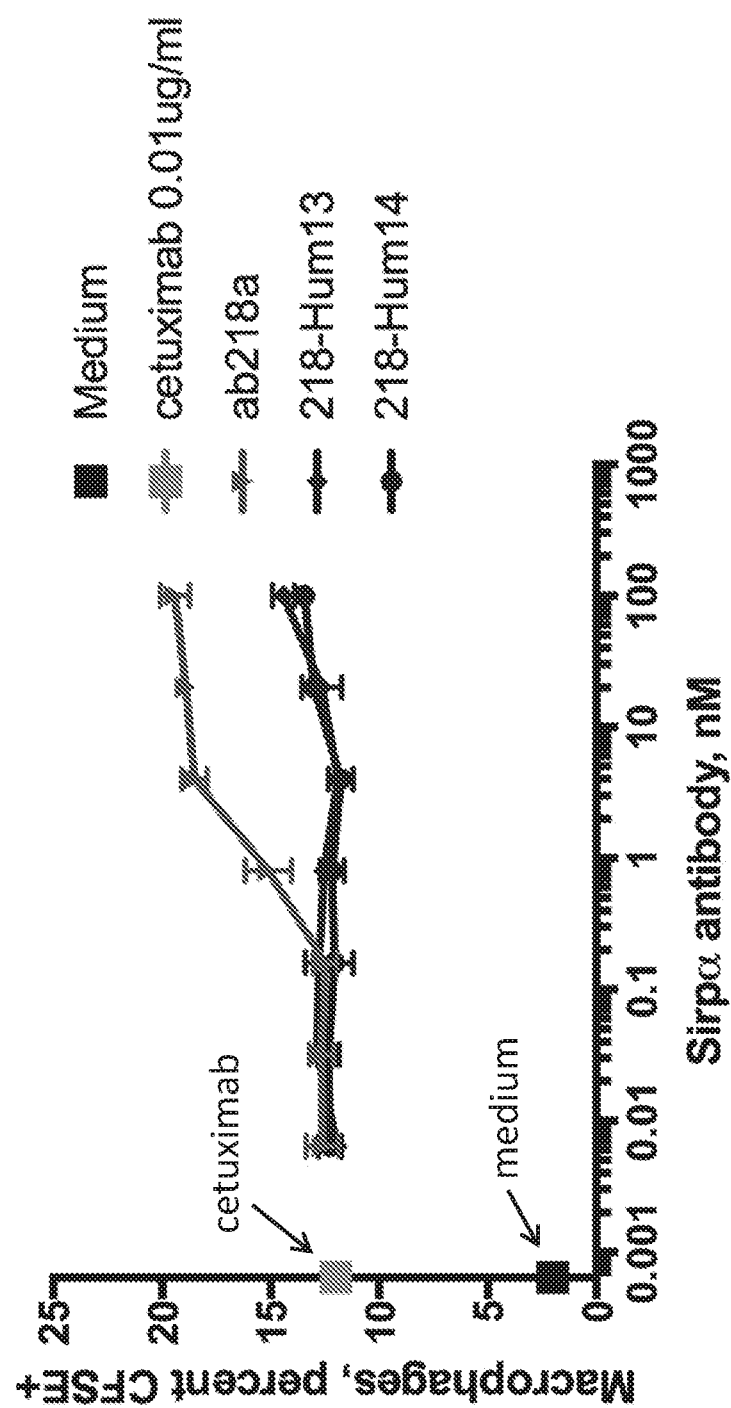


FIG. 39A

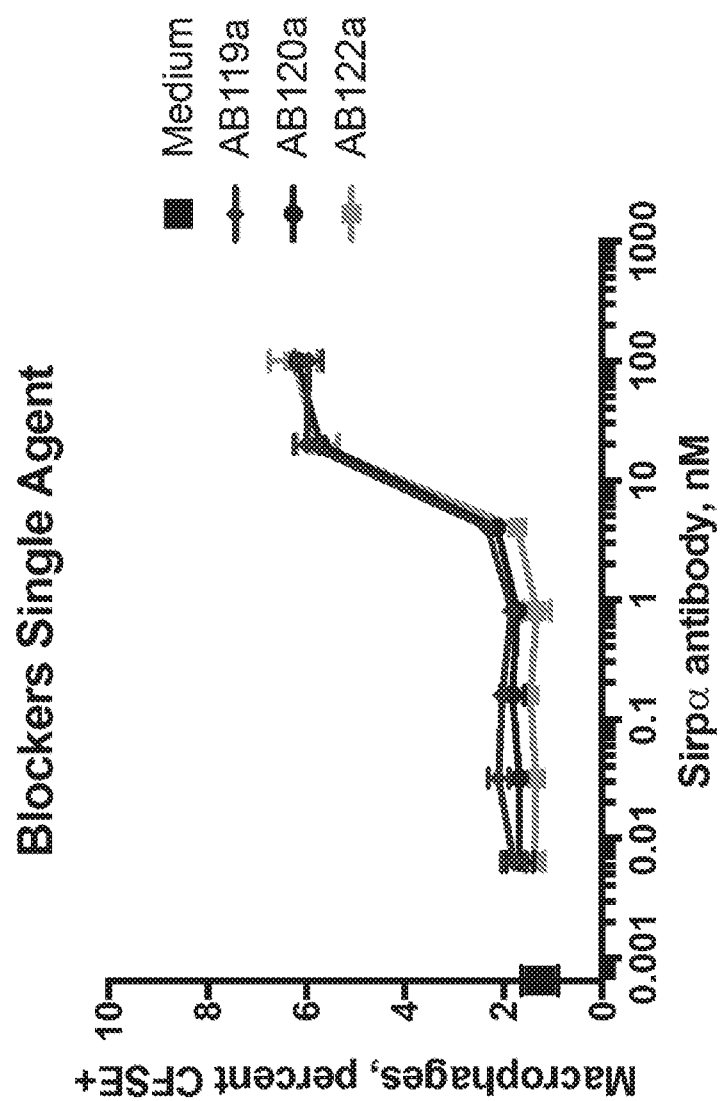


FIG. 39B

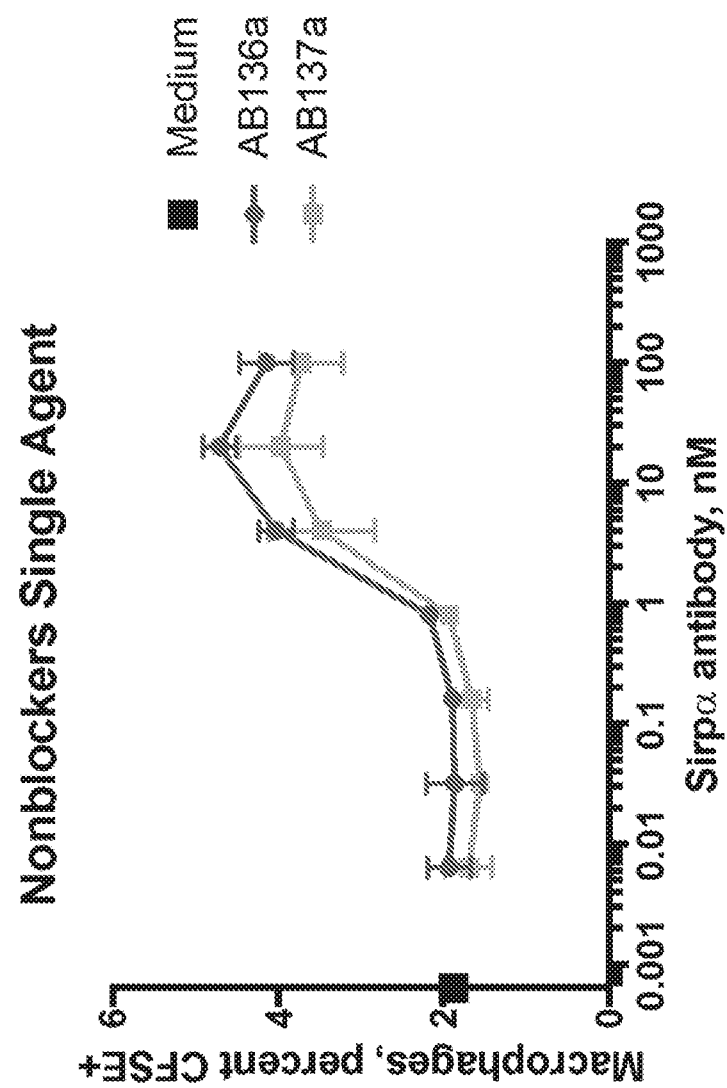


FIG. 39C

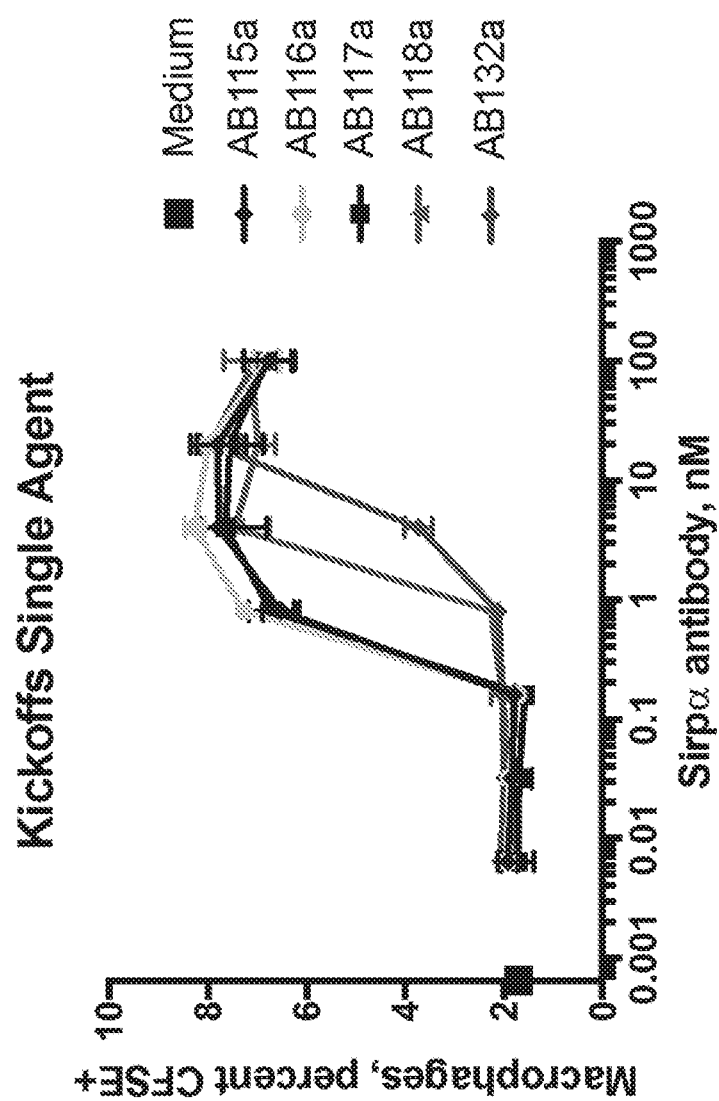
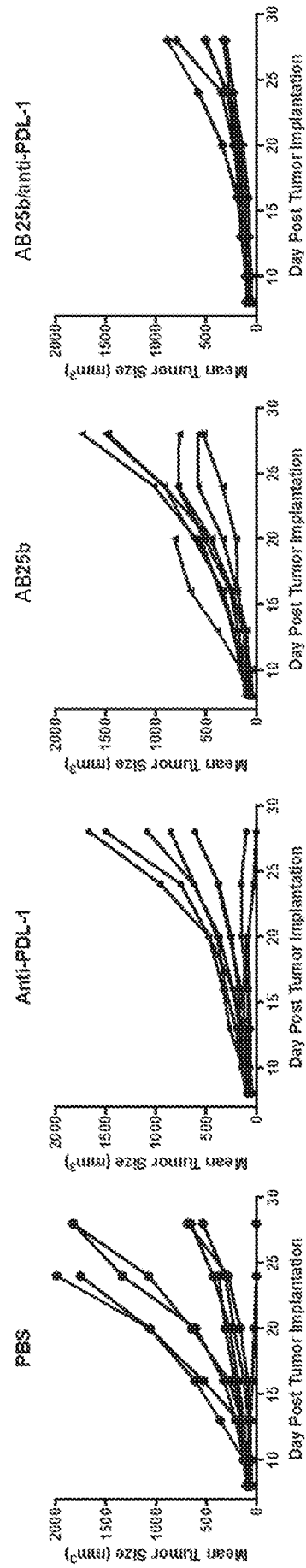
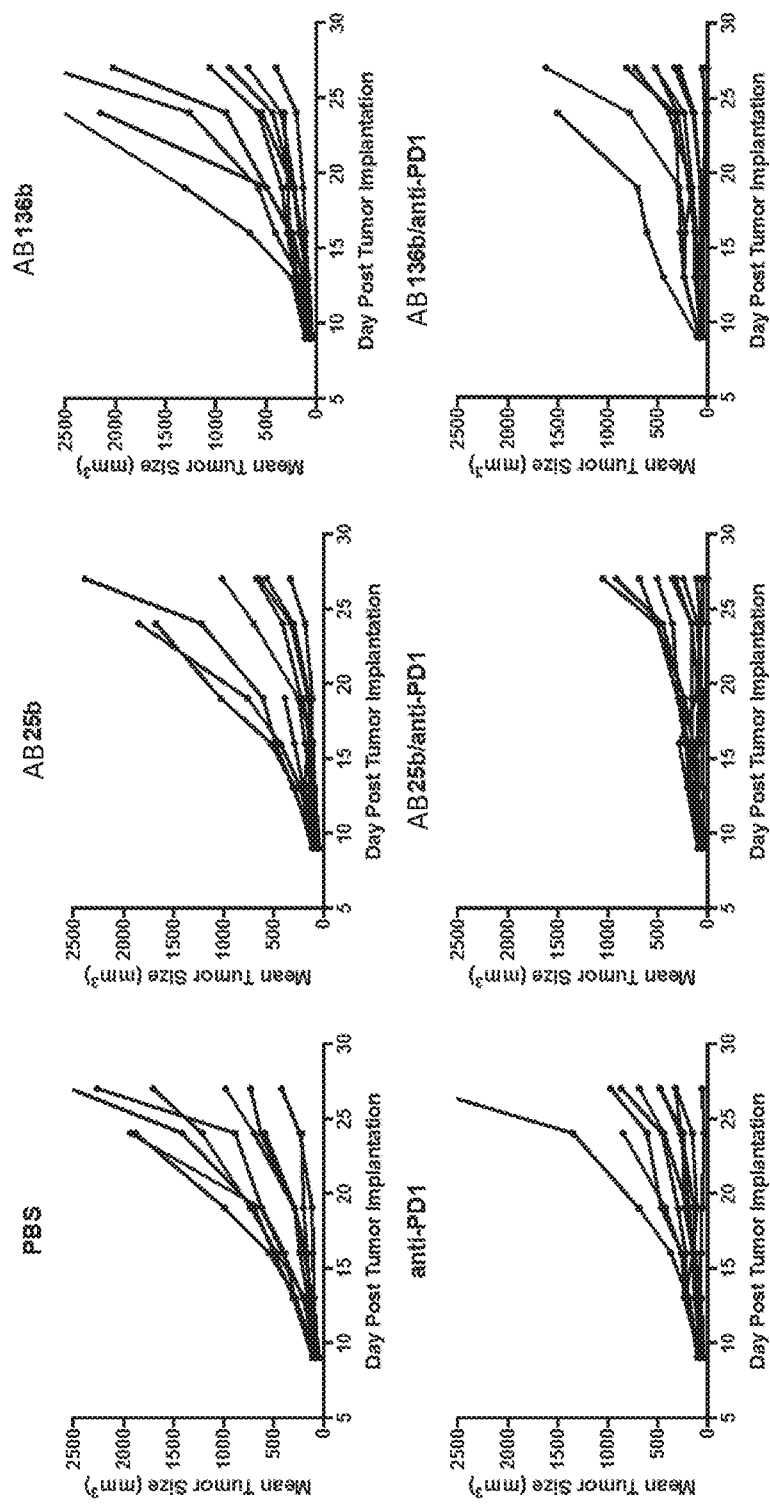


FIG. 39D



	PBS	Anti-PDL1	AB25b	AB25b/anti-PDL1
Mice with tumor volume <600 mm ³	2	2	2	6

FIG. 40



	PBS	Anti-PD1	AB25b	AB25b/anti-PD1	AB136b	AB136b/anti-PD1
Mice with tumor volume <600 mm ³	1	5	2	7	1	6

FIG. 41