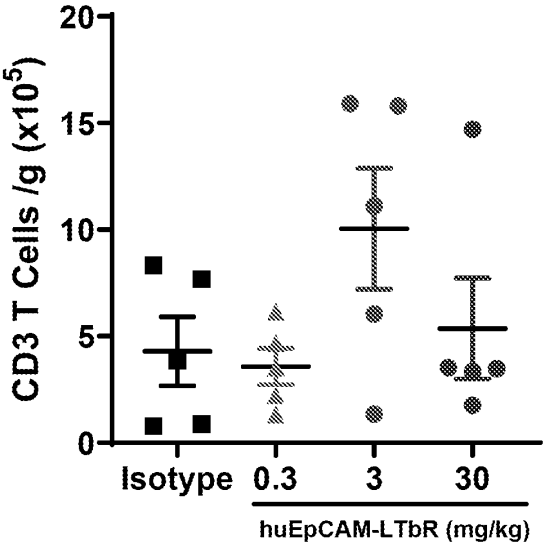

CD3 T Cells /g (x10^5)
20
15
10
5
0
Isotype
0.3
3
30
huEpCAM-LTbR (mg/kg)

FIG. 1A

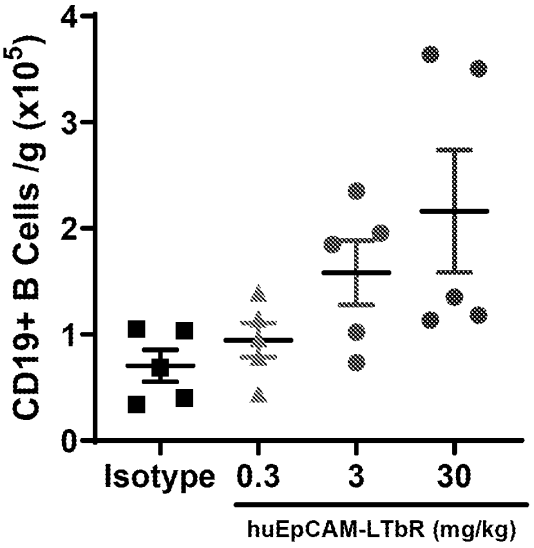

CD19+ B Cells /g (x10^5)
4
3
2
1
0
Isotype
0.3
3
30
huEpCAM-LTbR (mg/kg)

FIG. 1B

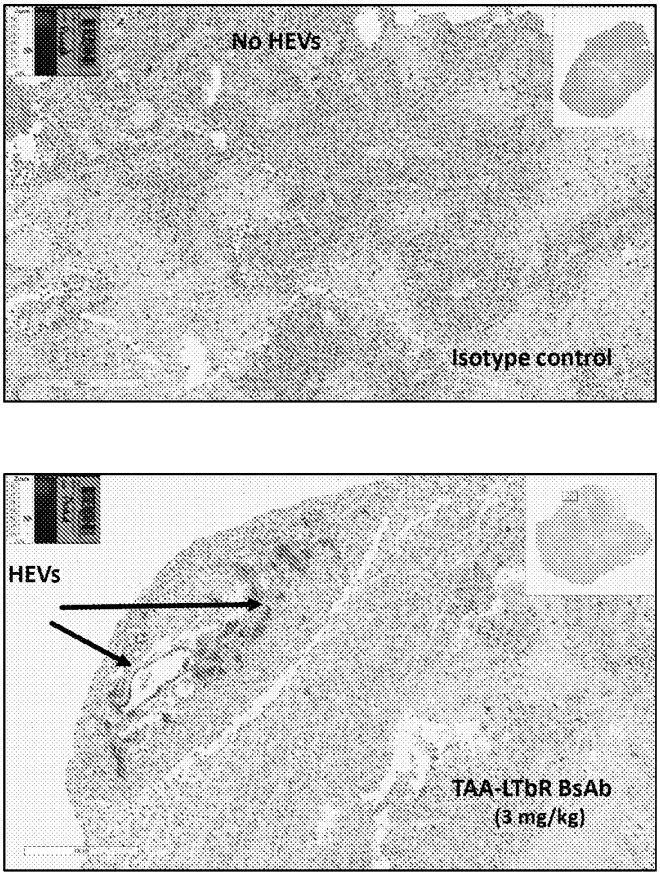


FIG. 2

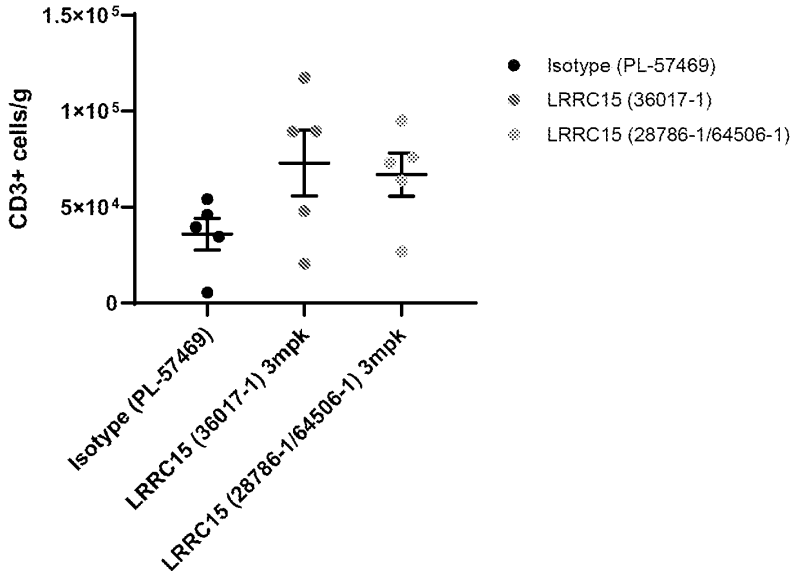

1.5×10^5
1×10^5
5×10^4
0
CD3+ cells/g
Isotype (PL-57469)
LRRC15 (36017-1)
LRRC15 (28786-1/64506-1)
Isotype (PL-57469)
LRRC15 (36017-1) 3mpk
LRRC15 (28786-1/64506-1) 3mpk

FIG. 3

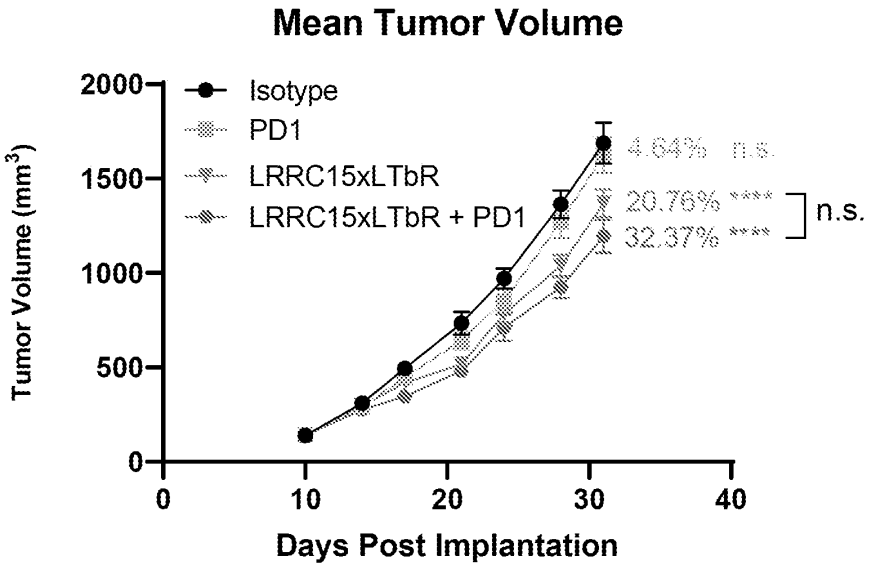

Mean Tumor Volume
Isotype
PD1
LRRC15xLTbR
LRRC15xLTbR + PD1
4.64% n.s.
20.76% ****
32.37% ****
n.s.
Tumor Volume (mm^3)
2000
1500
1000
500
0
0
10
20
30
40
Days Post Implantation

FIG. 4

TABLE A. LTβR Antibody Characteristics

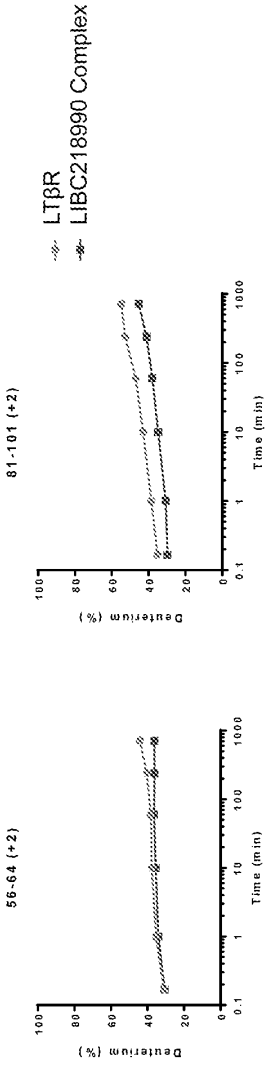
Antibody LIBC No.	Antibody ID	Harvest		Functional Potency		Ligands inhibition		Geomean shift in 293 transient transfected cells (Fold over mock transfected cells)				
			Bin	Transit EC50 (nM)	Max Activity	LIGHT % inhibition	LTa1b2 % inhibition	TNFR1	TNFR2	Cyno Major	Cyno Minor	Mouse
218966	16G1	1.2	A	0.29	6.9	100%	108%	1.0	1.1	169.4	26.2	1.7
218973	21A5	1.2	A	0.38	7.3	84%	93%	0.9	1.0	170.3	21.1	1.3
218985	26H4	3.4	A	0.36	7.4	99%	106%	0.9	0.9	272.4	29.0	17.9
219028	33E8	4.3	A.1	0.67	7.6	100%	108%	1.0	1.1	49.9	18.7	15.9
219049	35E4	4.4	A.1	0.70	7.9	100%	104%	0.9	0.9	250.0	20.6	4.5
219053	35C8	4.4	A.1	0.27	8.1	103%	110%	0.9	1.0	298.1	29.7	28.1
219062	36C9	4.4	A.1	0.30	7.4	100%	107%	0.9	0.9	75.1	24.2	17.7
219076	39B5	4.4	A.1	0.39	7.5	97%	105%	1.0	1.0	180.5	25.1	1.7
218989	29G8	3.4	B	0.17	7.6	80%	103%	1.0	1.0	511.9	27.4	1.0
218990	30H1	3.4	B	0.14	7.5	23%	43%	1.1	1.0	200.9	22.1	1.2
218994	31A3	3.4	B	0.06	7.3	10%	73%	0.9	1.1	143.2	20.3	1.0
219037	34D1	4.4	B	0.08	7.7	32%	104%	1.0	1.0	83.4	26.6	1.1
219044	34F10	4.4	B	0.21	7.3	86%	99%	0.8	0.9	283.6	28.3	0.9
219051	35F5	4.4	C	2.50	5.8	-13%	15%	0.8	0.9	147.7	0.9	1.5
219058	36G2	4.4	C	0.10	7.4	40%	-43%	0.9	1.0	191.3	26.9	1.0
219098	44B1	5.2	C	0.30	6.9	59%	51%	0.9	1.0	129.9	21.0	1.0
218979	23E9	2.3	D	1.36	6.1	29%	30%	0.9	1.0	129.8	24.1	1.0
219081	41B2	5.2	D	1.12	7.3	33%	43%	0.9	0.9	174.8	22.0	1.0
218992	31D1	3.4	E	0.47	7.6	96%	105%	0.9	0.9	218.7	24.4	1.0
219093	43H3	5.2	E	0.32	7.6	101%	108%	0.9	0.7	290.7	20.5	0.9
219097	43D9	5.2	F	0.42	6.9	87%	90%	1.0	1.1	42.7	1.1	1.1
219070	38G3	4.4	A.1	0.63	7.3	98%	109%	1.0	1.0	148.6	26.7	4.6
218967	17F5	1.2	B	0.21	6.8	47%	94%	0.9	0.9	134.1	1.6	1.1
218981	25C9	3.3	B	0.20	7.1	58%	103%	0.8	0.8	98.6	12.5	1.0
218995	31C9	3.4	B	0.12	7.3	53%	99%	0.9	0.9	330.6	21.8	0.9
218996	31B10	3.4	B	0.11	7.5	35%	82%	0.9	0.9	135.9	23.7	1.0
218998	32A2	3.4	B	0.09	7.5	41%	100%	1.1	1.1	90.2	3.8	1.0
219083	41H7	5.2	B	0.09	7.1	77%	104%	0.8	0.9	210.7	4.8	1.0
219092	43C1	5.2	B	0.16	6.9	45%	91%	1.1	1.0	74.4	21.0	0.8
219023	33G6	4.3	C	0.75	6.3	0%	14%	1.0	1.1	105.3	1.2	1.1
219095	43G5	5.2	D	1.24	6.7	52%	57%	1.0	1.0	5.6	2.4	1.2
218997	31E12	3.4	A	0.83	7.0	89%	97%	0.9	1.0	176.1	26.3	1.0
219102	44G11	6.3	B	0.06	7.2	78%	102%	1.0	0.9	20.7	2.8	1.1

FIG. 5

TABLE B. LTβR Antibody Characteristics

Antibody LIBC No.	Antibody ID	Harvest	Biacore Affinity Measurement human			Biacore Affinity Measurement Cyno			Human/Cyno Affnity Gap
			ka (1/Ms)	kd (1/s)	KD (nM)	ka (1/Ms)	kd (1/s)	KD (nM)	<10 fold
218966	16G1	1.2	3.07E+05	2.26E-03	7.36	7.57E+05	2.91E-03	3.85	Y
218973	21A5	1.2	2.13E+05	9.14E-04	4.29	3.08E+05	6.27E-03	20.34	Y
218985	26H4	3.4	4.30E+05	<1.76e-04	<0.41	4.30E+05	4.06E-04	0.94	Y
219028	33E8	4.3	3.69E+05	1.04E-03	2.82	3.68E+05	4.92E-03	13.40	Y
219049	35E4	4.4	1.79E+05	2.41E-04	1.34	1.42E+05	4.04E-04	2.85	Y
219053	35C8	4.4	2.49E+05	1.93E-04	0.77	2.45E+05	3.29E-04	1.34	Y
219062	36C9	4.4	1.93E+05	8.68E-04	4.50	2.05E+05	8.90E-04	4.35	Y
219076	39B5	4.4	4.84E+05	1.30E-03	2.68	3.99E+05	9.37E-04	2.34	Y
218989	29G8	3.4	1.61E+06	<1.76e-04	<0.11	2.32E+06	2.38E-04	0.10	Y
218990	30H1	3.4	5.42E+05	<1.76e-04	<0.33	6.63E+05	1.70E-03	2.56	Y
218994	31A3	3.4	1.57E+06	2.62E-04	0.17	1.76E+07	2.49E-02	1.41	Y
219037	34D1	4.4	3.22E+06	<1.76E-4	<0.055	1.40E+07	2.82E-03	0.20	Y
219044	34F10	4.4	4.68E+05	<1.76E-4	<0.38	4.56E+05	<1.76E-4	<0.39	Y
219051	35F5	4.4	2.16E+05	2.65E-04	1.23	2.12E+05	3.19E-04	1.50	Y
219058	36G2	4.4	1.35E+06	<1.76E-04	<0.13	1.67E+06	1.76E-04	0.11	Y
219098	44B1	5.2	1.11E+06	<1.76e-04	<0.16	1.13E+06	1.76E-04	0.16	Y
218979	23E9	2.3	1.40E+05	2.34E-03	16.71	2.40E+05	7.73E-03	32.24	Y
219081	41B2	5.2	2.06E+05	<1.76e-04	<0.85	1.78E+05	<1.76E-4	<0.99	Y
218992	31D1	3.4	1.76E+05	<1.76e-04	<1.0	1.90E+05	<1.76E-4	<0.93	Y
219093	43H3	5.2	1.52E+05	<1.76e-04	<1.16	1.43E+05	1.76E-04	1.23	Y
219097	43D9	5.2	1.59E+05	2.14E-04	1.35	3.32E+05	5.17E-04	1.56	Y
219070	38G3	4.4	1.58E+05	4.33E-04	2.74	weak/poor binding			N
218967	17F5	1.2	9.13E+05	<1.76e-04	<0.19	weak/poor binding			N
218981	25C9	3.3	1.96E+06	1.87E-04	0.10	binding too weak to fit			N
218995	31C9	3.4	1.10E+06	<1.76e-04	<0.16	binding too weak to fit			N
218996	31B10	3.4	1.11E+06	<1.76e-04	<0.16	binding too weak to fit			N
218998	32A2	3.4	9.87E+05	3.51E-04	0.36	binding too weak to fit			N
219083	41H7	5.2	2.09E+06	2.87E-04	0.14	binding too weak to fit			N
219092	43C1	5.2	9.65E+05	5.02E-04	0.52	fits not good but very fast on/off.			N
219023	33G6	4.3	1.72E+05	<1.76e-04	<1.02	binding too weak to fit			N
219095	43G5	5.2	1.73E+05	<1.76e-04	<1.02	weak/poor binding			N
218997	31E12	3.4	5.06E+05	2.52E-04	0.50	binding too weak to fit			N
219102	44G11	6.3	6.57E+05	3.96E-04	0.60	weak/poor binding			N

FIG. 5 (Cont.)

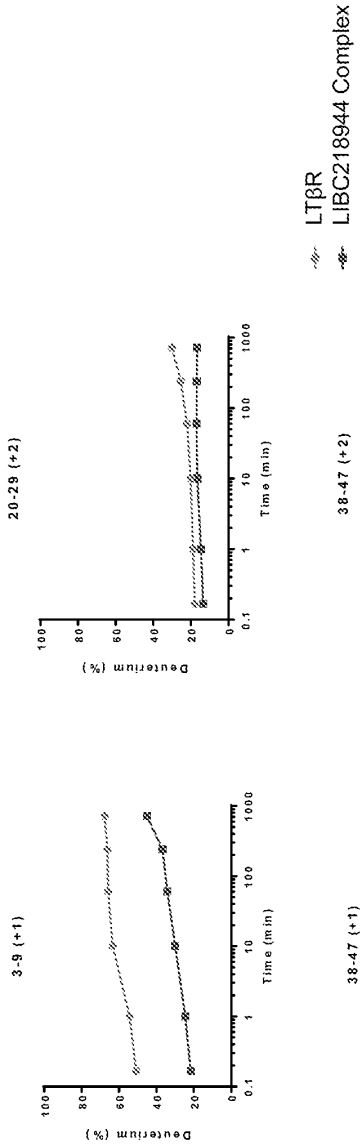


QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 6

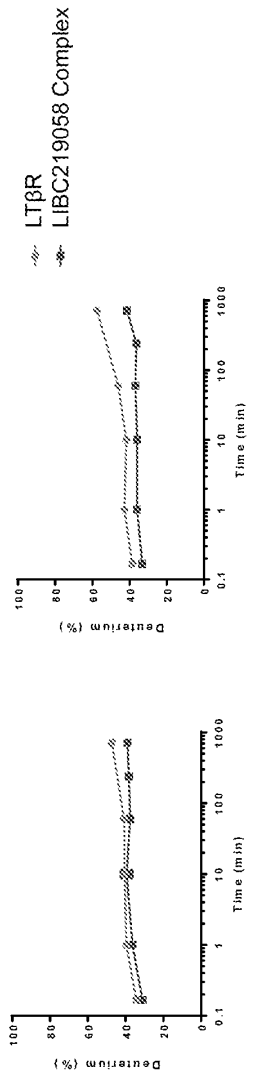


QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 7

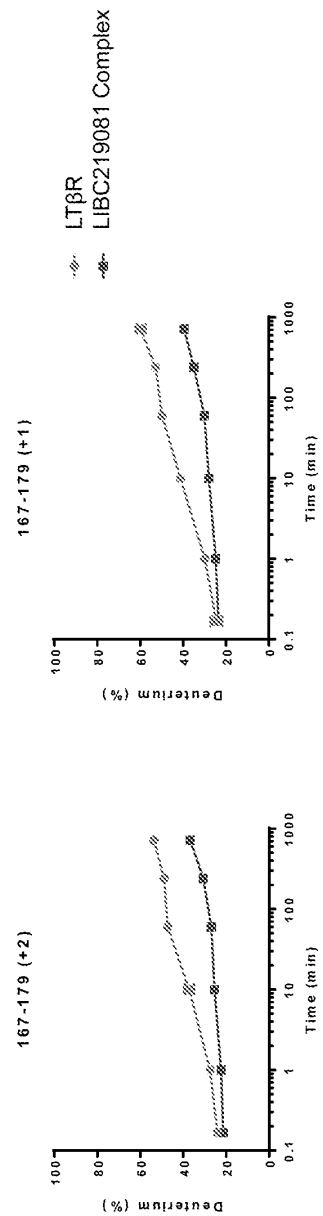


QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 8

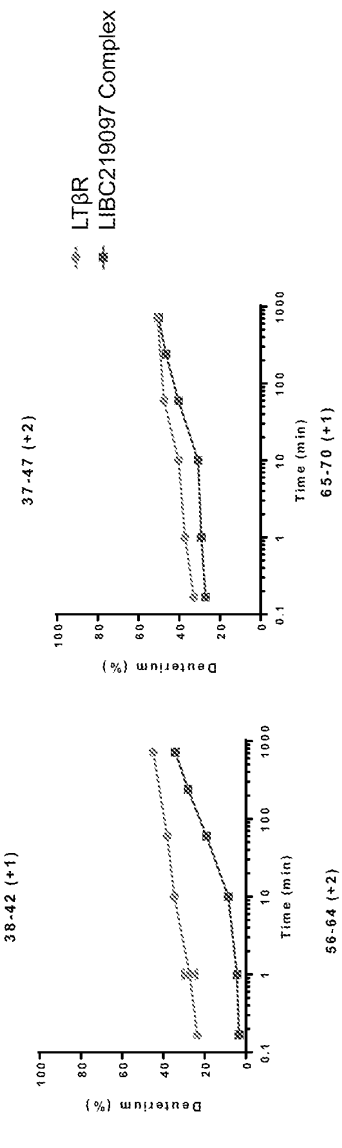


QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 9



QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 10

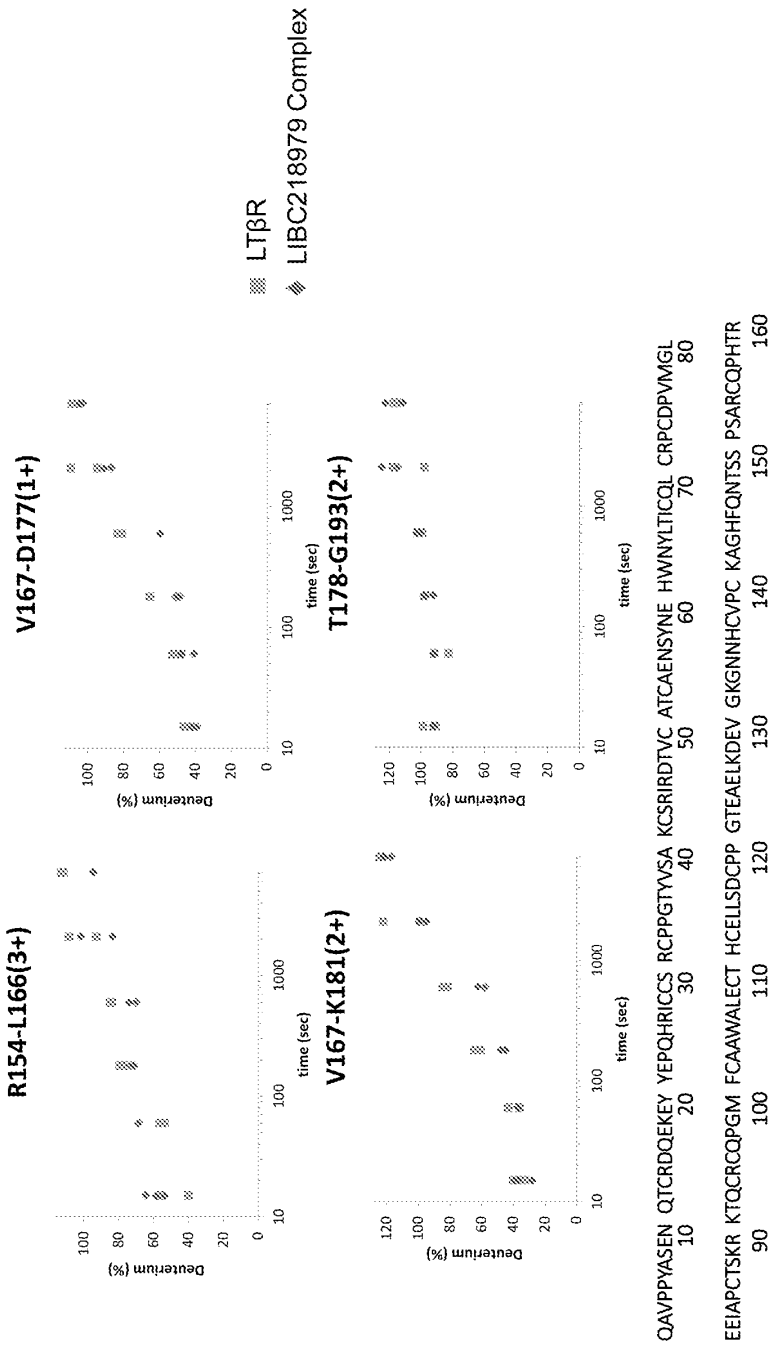
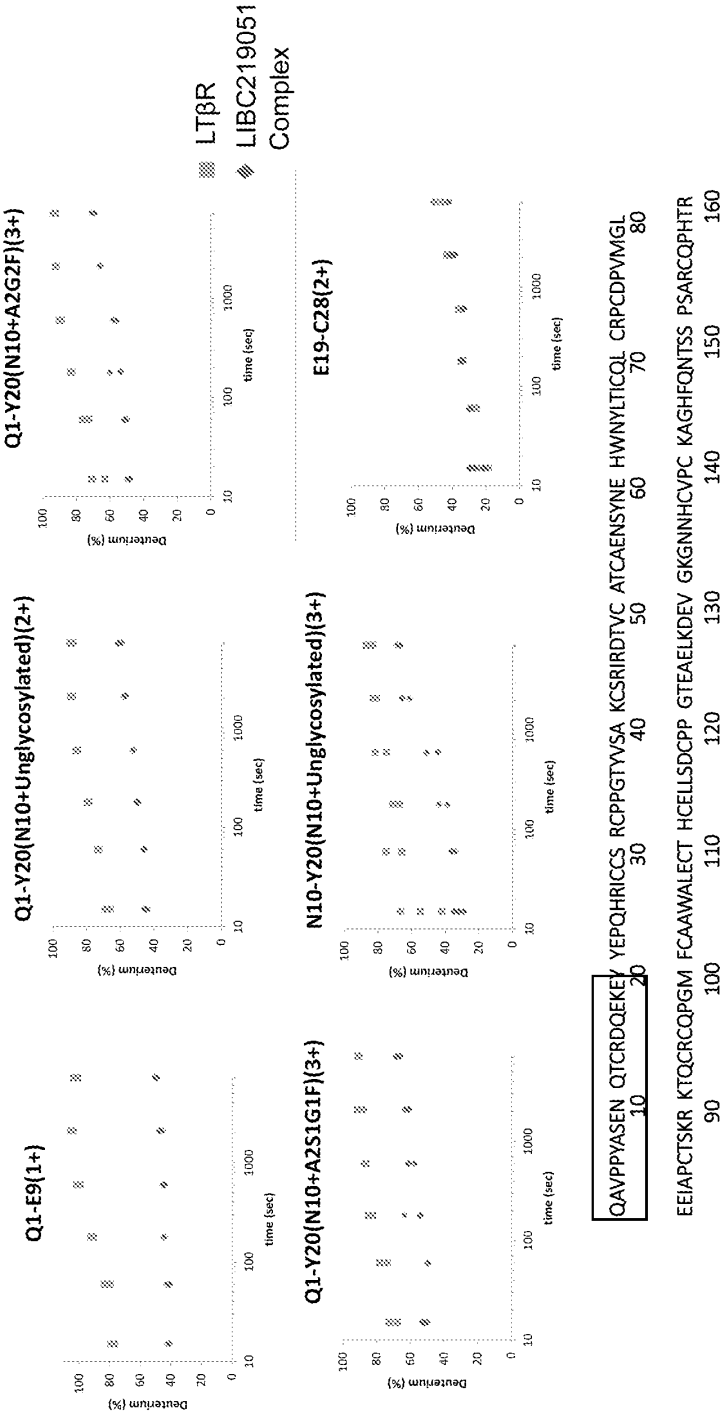

LTβR
LIBC218979 Complex
R154-L166(3+)
V167-D177(1+)
V167-K181(2+)
T178-G193(2+)
Deuterium (%)
time (sec)
QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80
EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160
CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 11

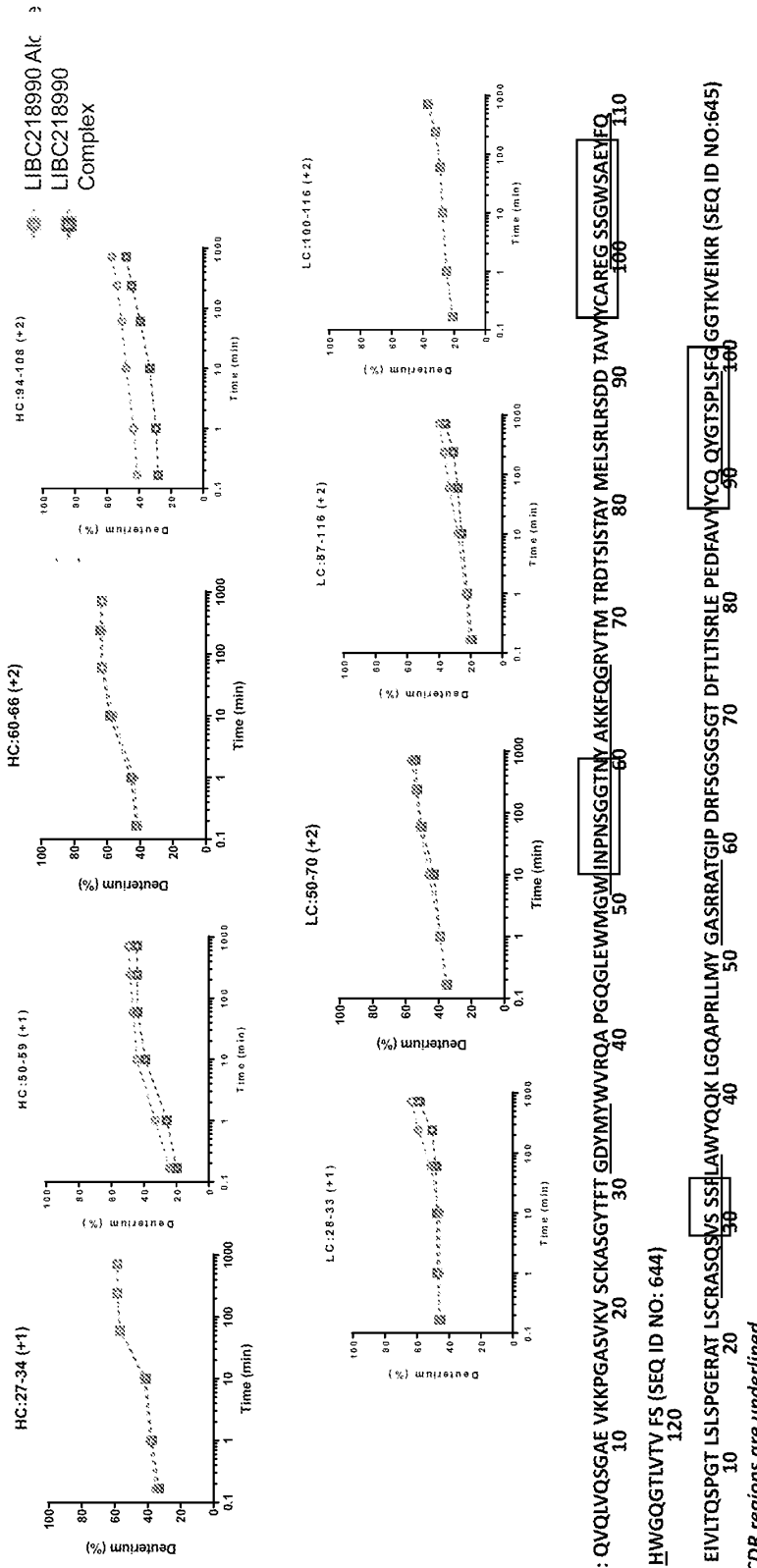


QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC ATCAENSYNE HWNYLTICQL CRPCDPVMGL
10 20 30 40 50 60 70 80

EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV GKGNNHCVPC KAGHFQNTSS PSARCQPHTR
90 100 110 120 130 140 150 160

CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSGTMLM (SEQ ID NO: 4)
170 180 190

FIG. 12



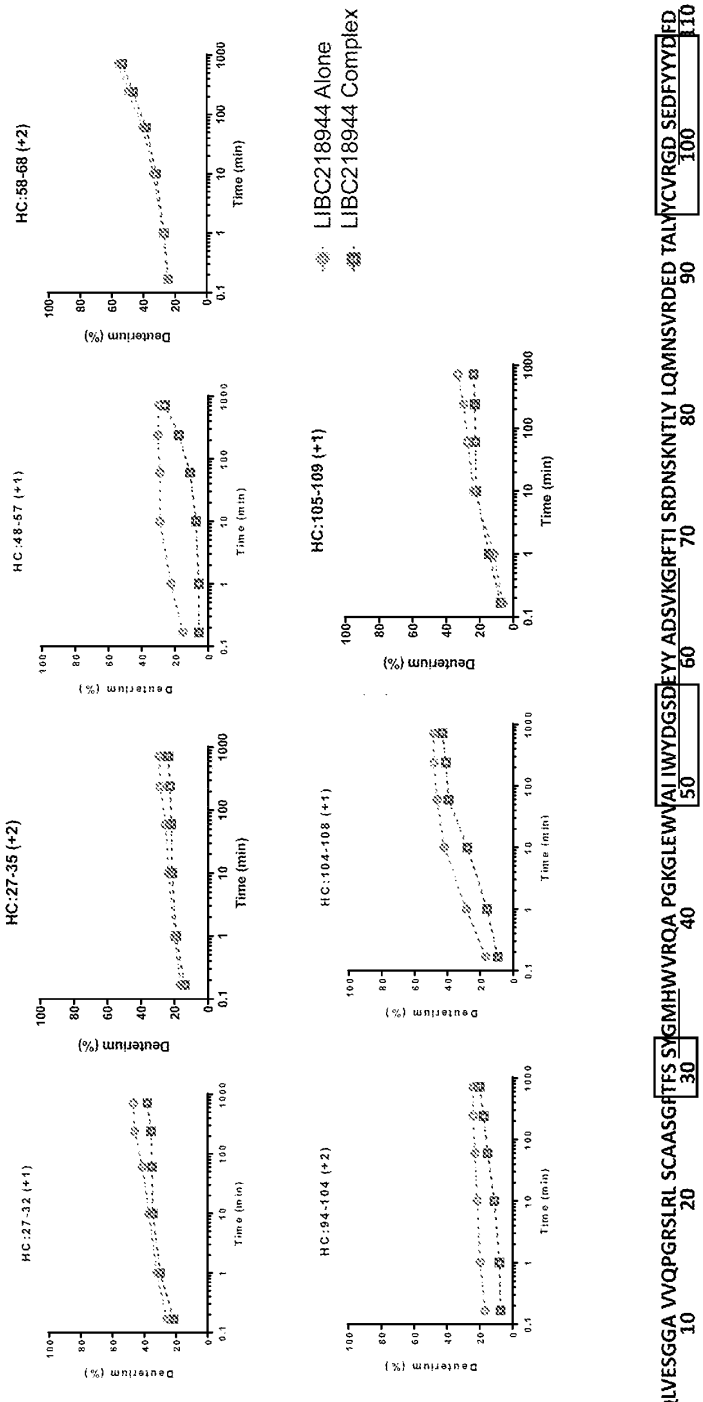
VH: QVQLVQSGAE VKKPGASVKV SCKASGYTFT GDYMYWVRQA PGQGLEWMGW INPNSGGTNY AKKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCAREG SSGWSAEYFQ
10 20 30 40 50 60 70 80 90 100 110

HWGQGTLVTV FS (SEQ ID NO: 644)
120

VL: EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSFLAWYQQK LGQAPRLLMY GASRRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGTSPLSFG GGTKVEIKR (SEQ ID NO:645)
10 20 30 40 50 60 70 80 90 100

***CDR regions are underlined.*

FIG. 13



VH: QVQLVESGGA VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAL IWYDGSDEYY ADSVKGRFTI SRDNSKNTLY LQMNSVRDED TALYYCVRGD SEDFYYDFD
10 20 30 40 50 60 70 80 90 100 110

VWGQGTTVTV SS (SEQ ID NO: 646)
120

FIG. 14A

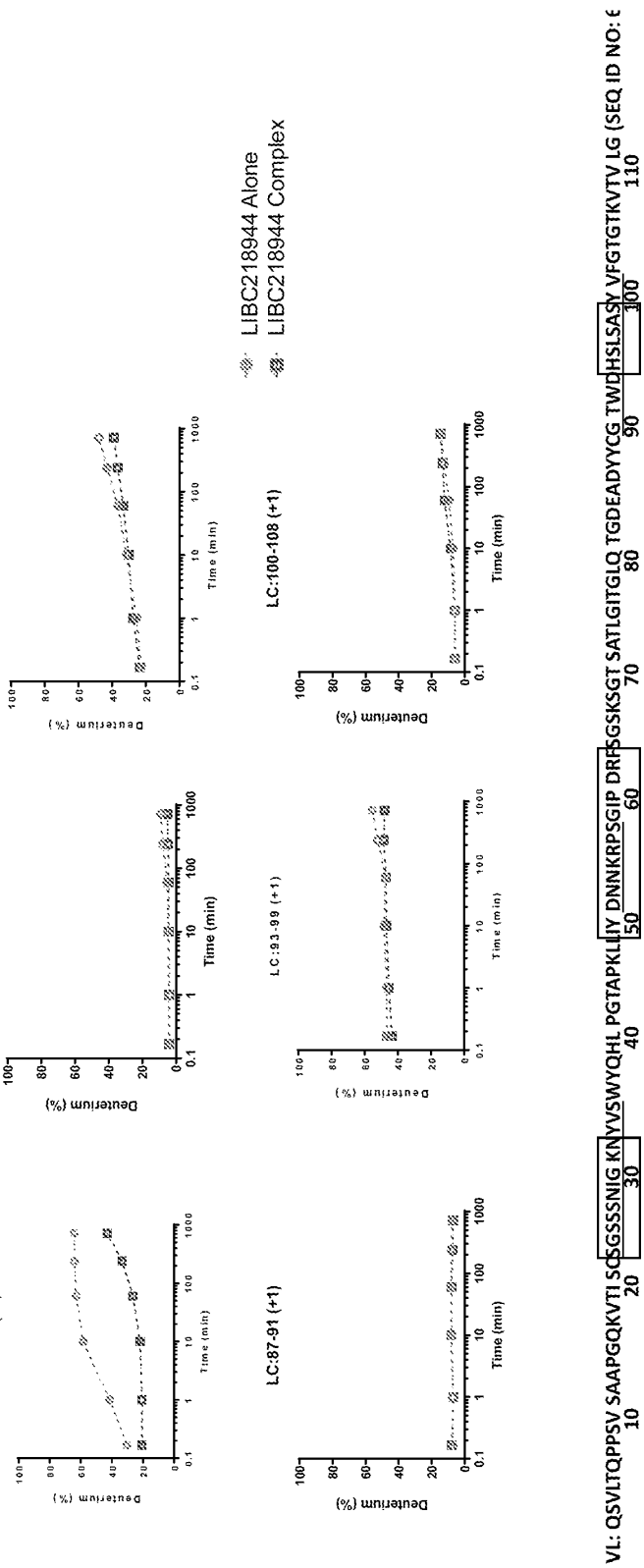
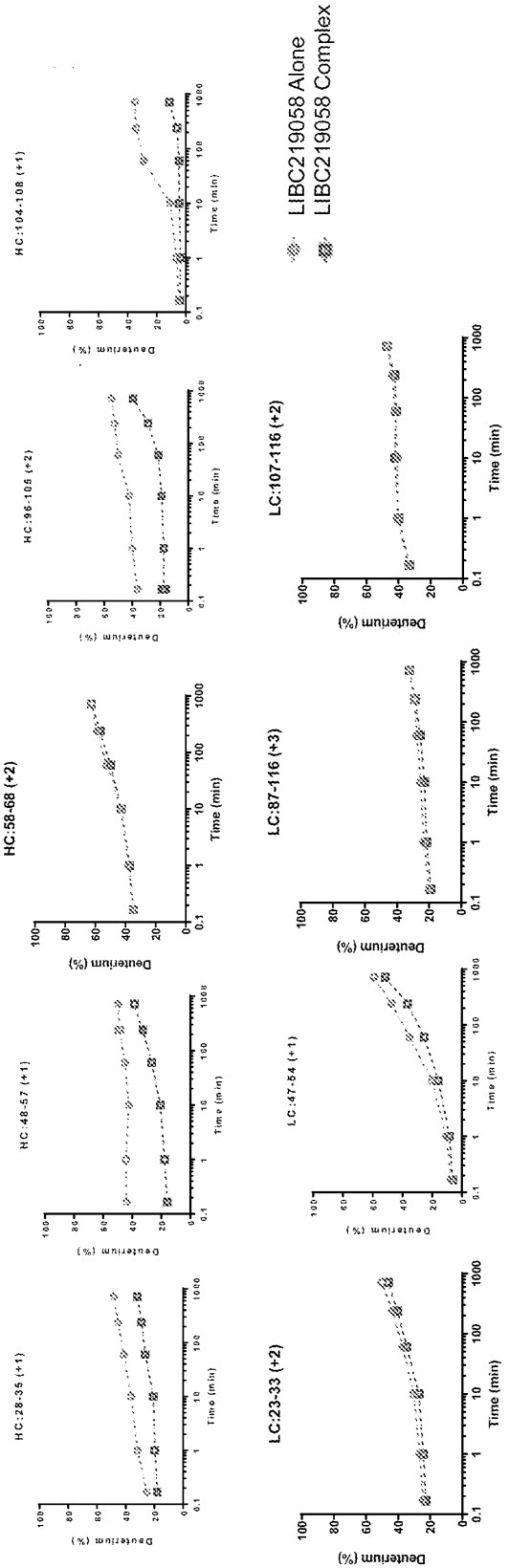

LIBC218944 Alone
LIBC218944 Complex
LC:22-32 (+1)
LC:33-36 (+1)
LC:48-63 (+3)
LC:87-91 (+1)
LC:93-99 (+1)
LC:100-108 (+1)
Deuterium (%)
Time (min)
VL: QSVLTQPPSV SAAPGQKVTI SCSGSSNIG KNYVSWYQHL PGTAPKLLIY DNNKRPSGIP DRFSGSKSGT SATLGITGLQ TGDEADYYCG TWDHSLSASV VFGTGTKVTV LG (SEQ ID NO: 6

FIG. 14B



VH: EVQLVESGGG LVKPGGSLRL SCAASGFTFS TSGMNWVRQA PGKGLEWVSS VSSSGSIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAGAR YNWHFDASDI WGQGTVVTVS S (SEQ ID NO: 648)

VL: DIQMTQSPSS LSASVGDRVT ITCRASQSIS SDLNWYQQKP GKAPNLLIYA ASSLHSGVPS RFSGSGSGTD FTLTISSLLP EDFATYYCQQ SYNTPLTFGG GTKVEIKR (SEQ ID NO: 649)

FIG. 15

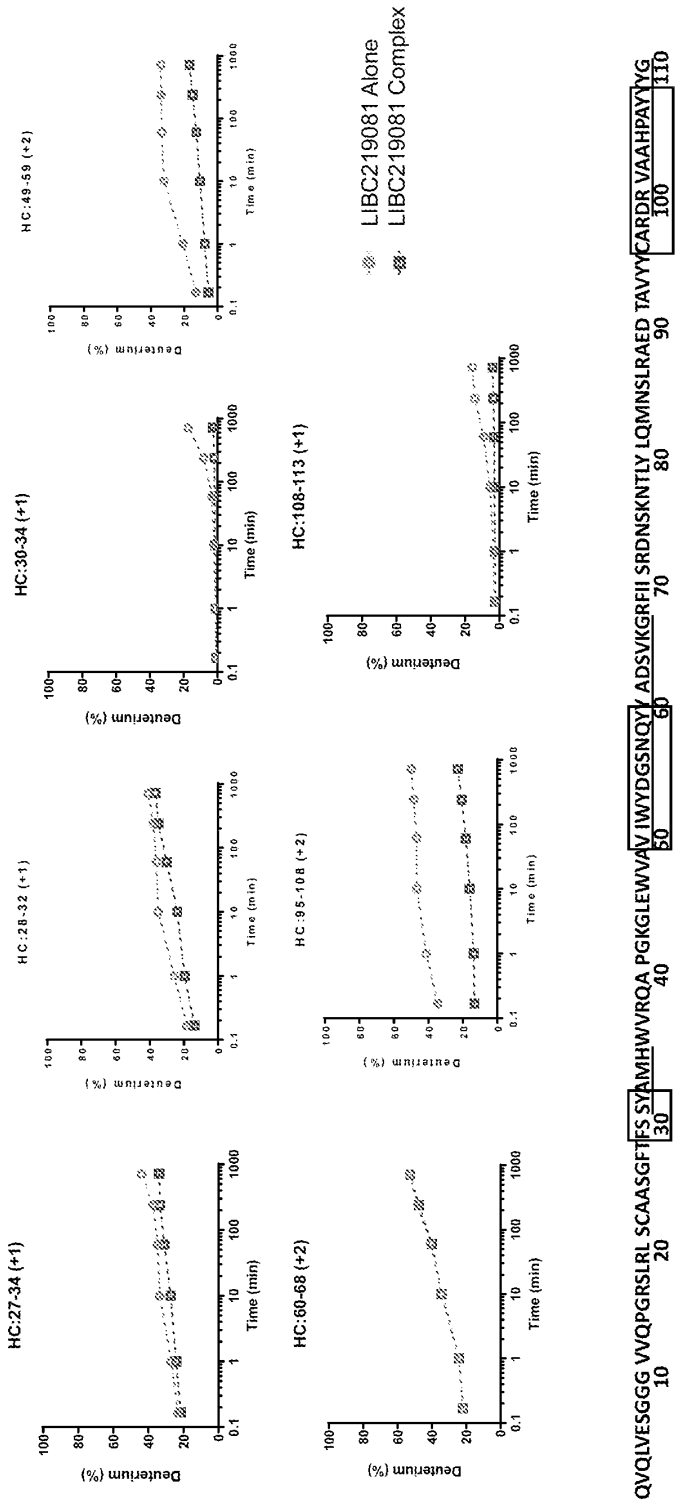

HC:27-34 (+1)
HC:28-32 (+1)
HC:30-34 (+1)
HC:49-59 (+2)
HC:60-68 (+2)
HC:95-108 (+2)
HC:108-113 (+1)
Deuterium (%)
Time (min)
LIBC219081 Alone
LIBC219081 Complex
VH: QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV IWYDGSNQYY ADSVKGRFII SRDNSKNTLY LQMNSLRAED TAVYYCARDR VAAHPAYYYG
10 20 30 40 50 60 70 80 90 100 110
LDVWGQGTV VTVSS (SEQ ID NO: 121)
120

FIG. 16A

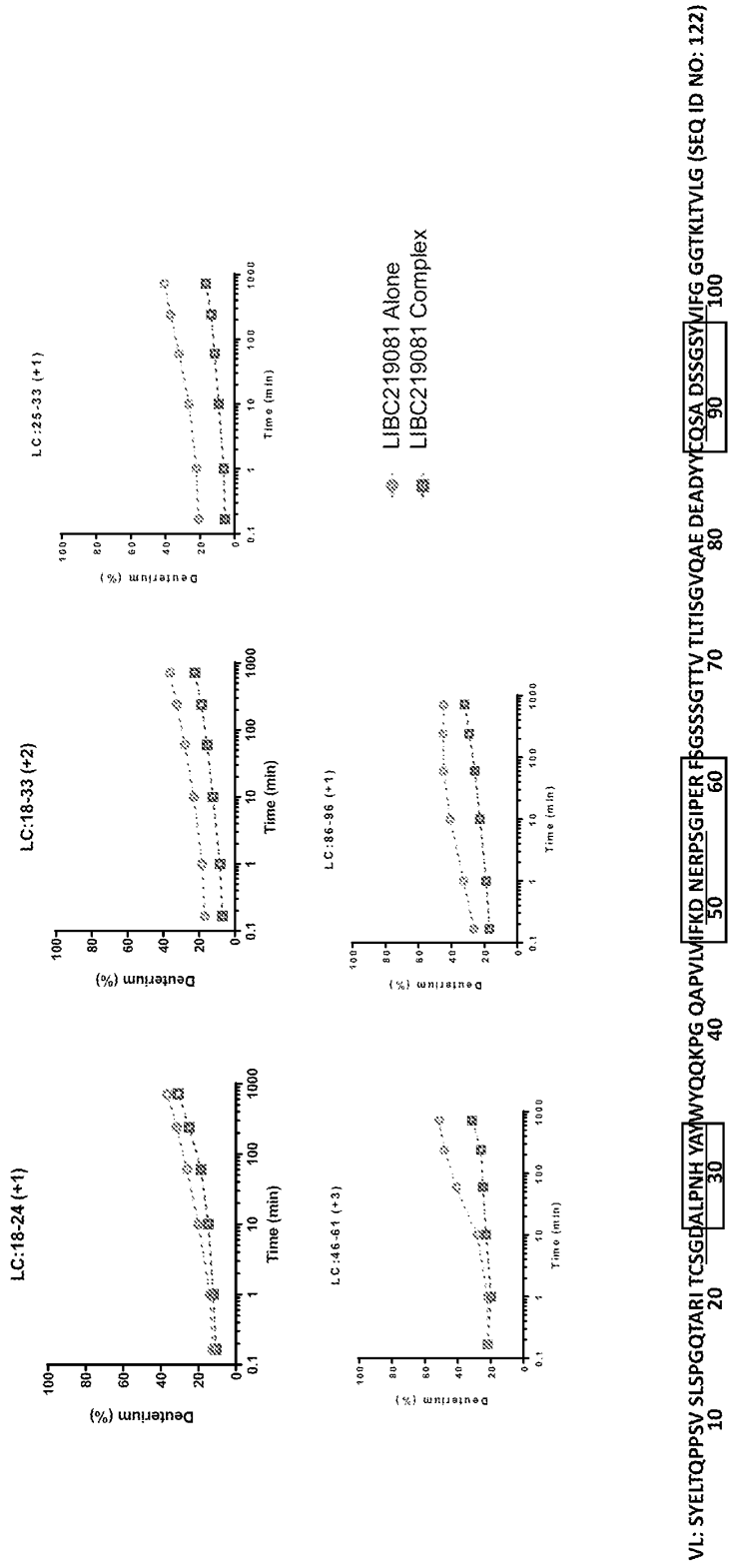
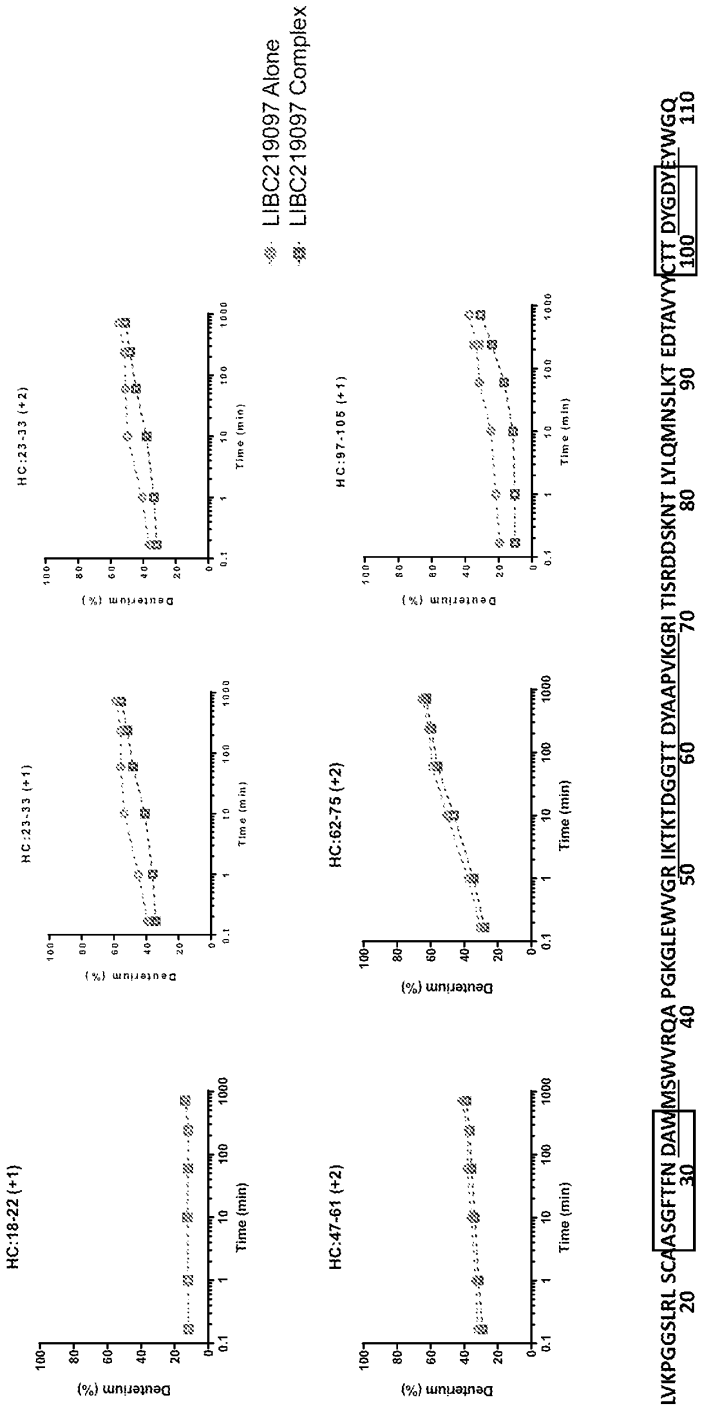

LC:18-24 (+1)
LC:18-33 (+2)
LC:25-33 (+1)
LC:46-61 (+3)
LC:86-96 (+1)
Deuterium (%)
Time (min)
LIBC219081 Alone
LIBC219081 Complex
VL: SYELTQPPSV SLSPGQTARI TCSGDALPNH YAYWYQQKPG QAPVLVIFKD NERPSGIPER FSGSSSGTTV TLTISGVQAE DEADYYCQSA DSSGSYVIFG GGTKLTVLG (SEQ ID NO: 122)
10 20 30 40 50 60 70 80 90 100

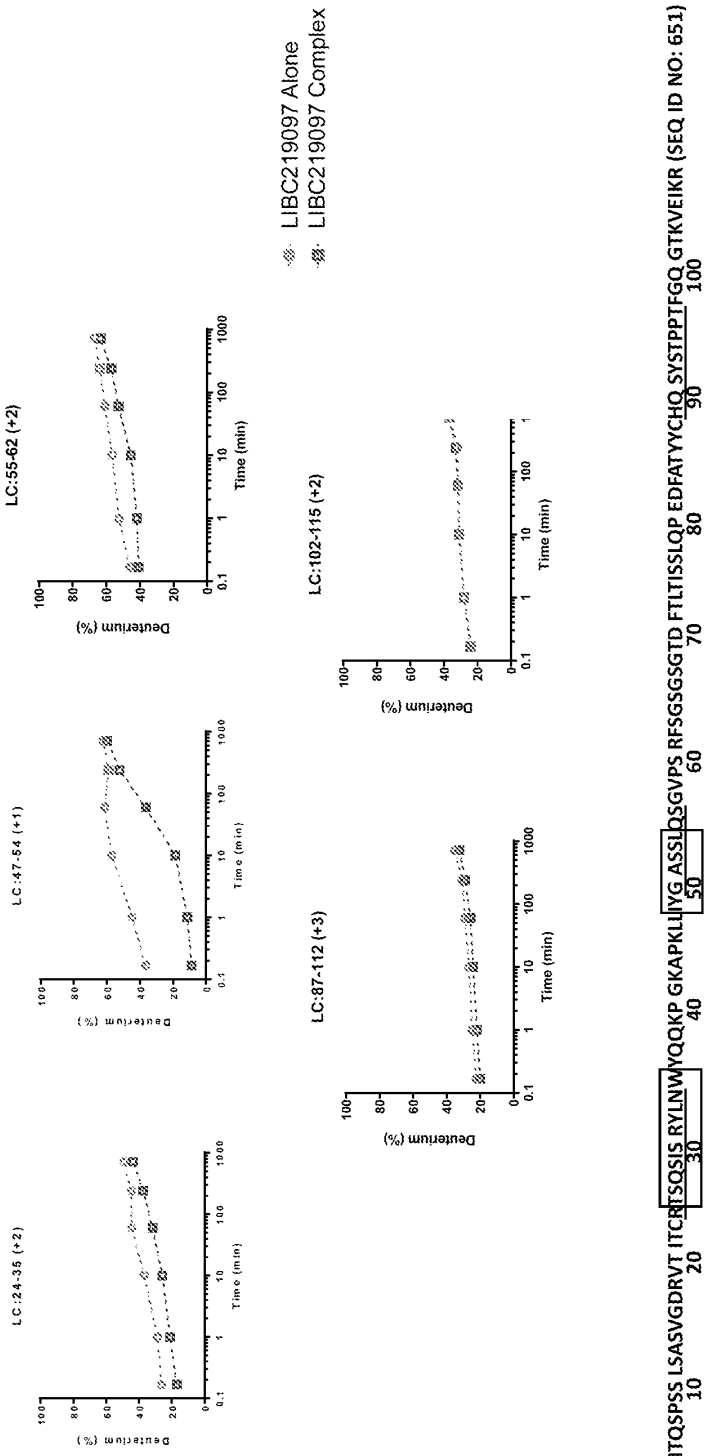
FIG. 16B



VH: EVQLVESGGG LVKPGGSLRL SCAASGFTFN DAWMSWVRQA PGKGLEWVGR IKTKTDGGTT DYAAPVKGRI TISRDDSKNT LYLQMNSLKT EDTAVYYCTT DYGDYEYWGQ
10 20 30 40 50 60 70 80 90 100 110

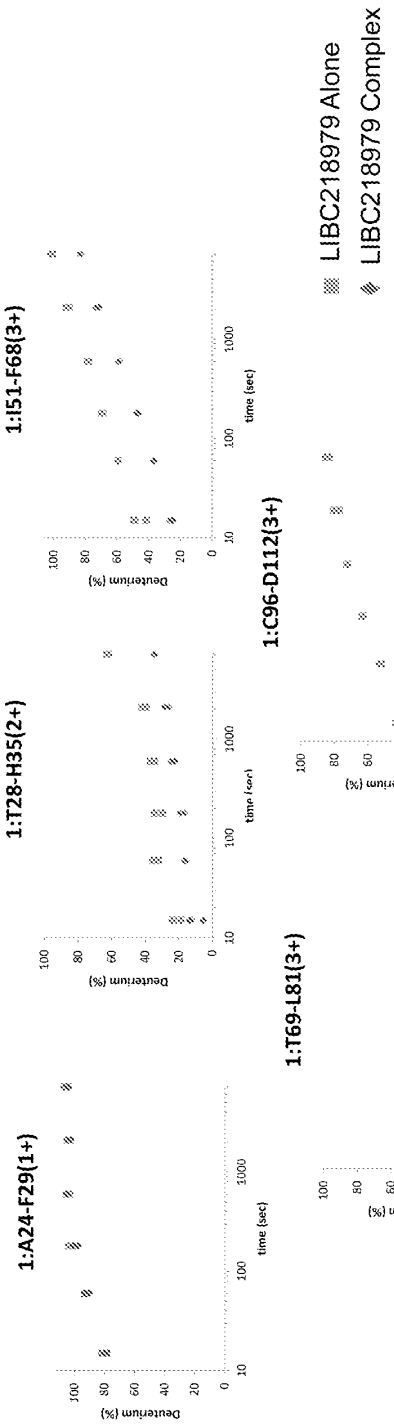
GTLVTVSS (SEQ ID NO: 650)

FIG. 17A



VL: DIQMTQSPSS LSASVGDRVT ITCRTSQSIS RYLNWYQQKP GKAPKLLIYG ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ SYSTPPTFGQ GTKVEIKR (SEQ ID NO: 651)

FIG. 17B



VH: QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMH WVRQA PGKGLEWVAV IWYDGSNKYY ADSVKGRFTI SRDNSKNTLS LQMNSLRAED
10 20 30 40 50 60 70 80 90
TAVYYCARER IAAAPYYYYG MDV WGQGTTV TVSS0 (SEQ ID NO: 123)
100 110 120

FIG. 18A

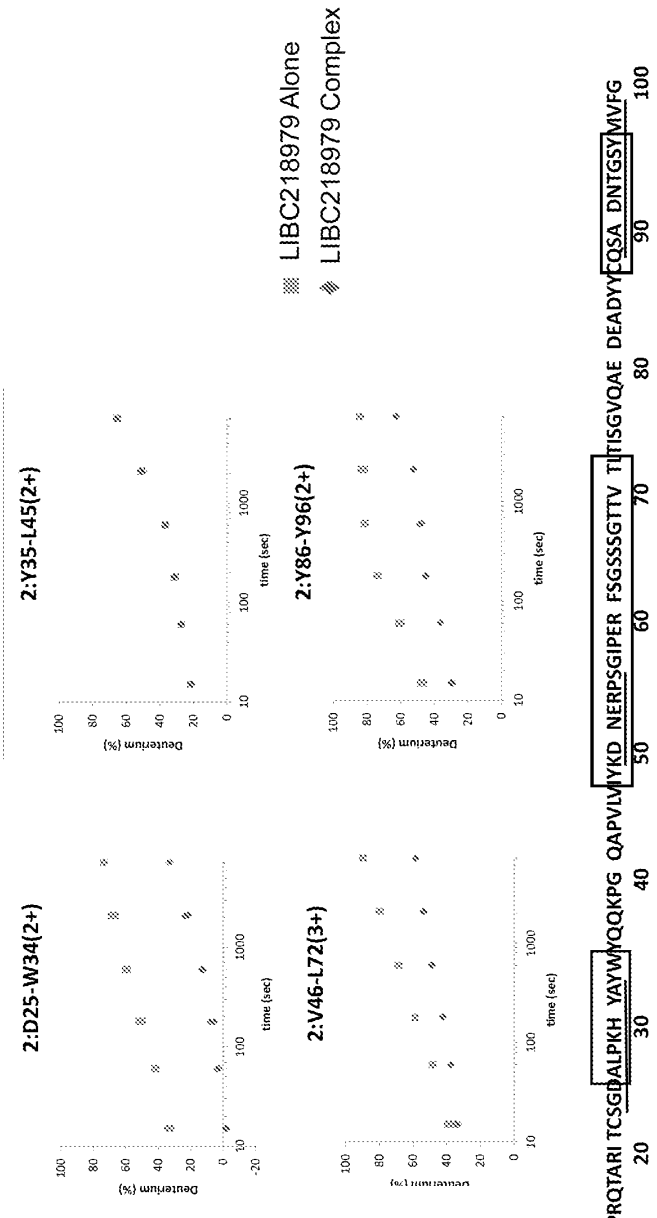
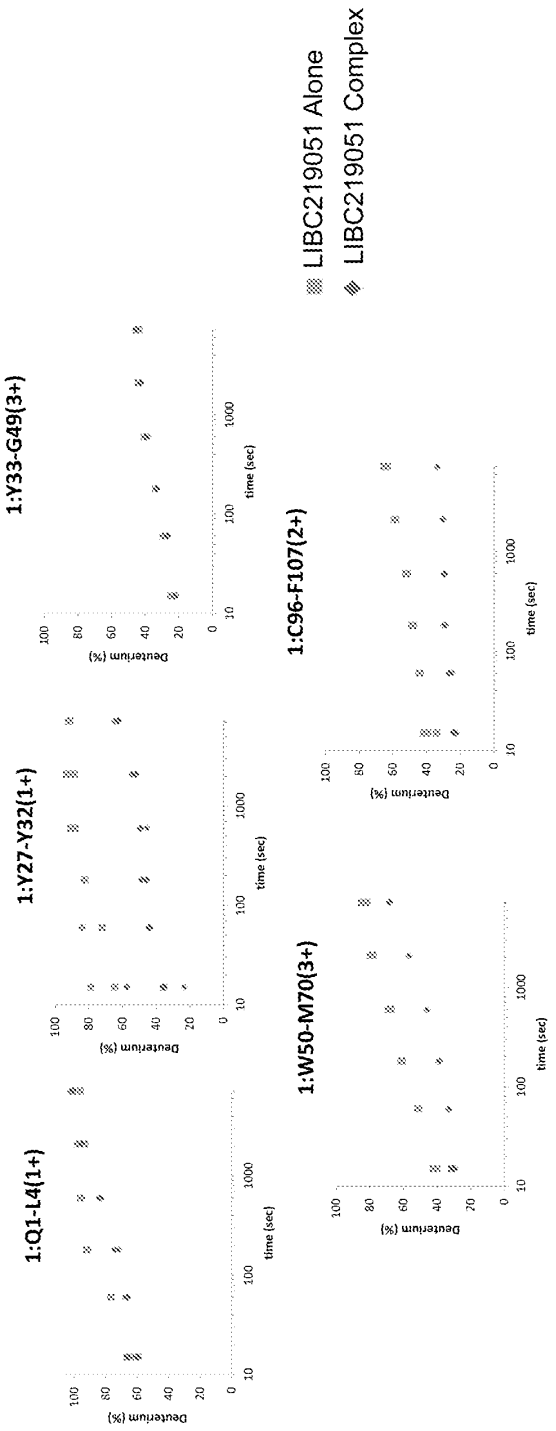

LIBC218979 Alone
LIBC218979 Complex
2:Y35-L45(2+)
2:Y86-Y96(2+)
2:D25-W34(2+)
2:V46-L72(3+)
Deuterium (%)
time (sec)
VL: SYELTQPPSV SVSPRQTARI TCSGDALPKH YAYWYQQKPG QAPVLVIYKD NERPSGIPER FSGSSSGTTV TLTISGVQAE DEADYYCQSA DNTGSYMVFG
10 20 30 40 50 60 70 80 90 100
GGTKLTVLG (SEQ ID NO: 124)

FIG. 18B


LIBC219051 Alone
LIBC219051 Complex
1:Q1-L4(1+)
1:Y27-Y32(1+)
1:Y33-G49(3+)
1:W50-M70(3+)
1:C96-F107(2+)
Deuterium (%)
time (sec)

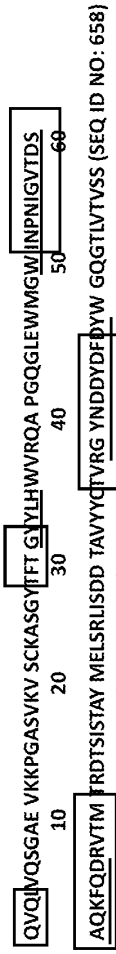

VH: QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYLHWVRQA PGQGLEWMGW INPNIGVTDS
10 20 30 40 50 60
AQKFQDRVTM TRDTSISTAY MELSRLISDD TAVYYCTVRG YNDDYDFDYW GQGTLVTVSS (SEQ ID NO: 658)
70 80 90 100 110 120

FIG. 19A

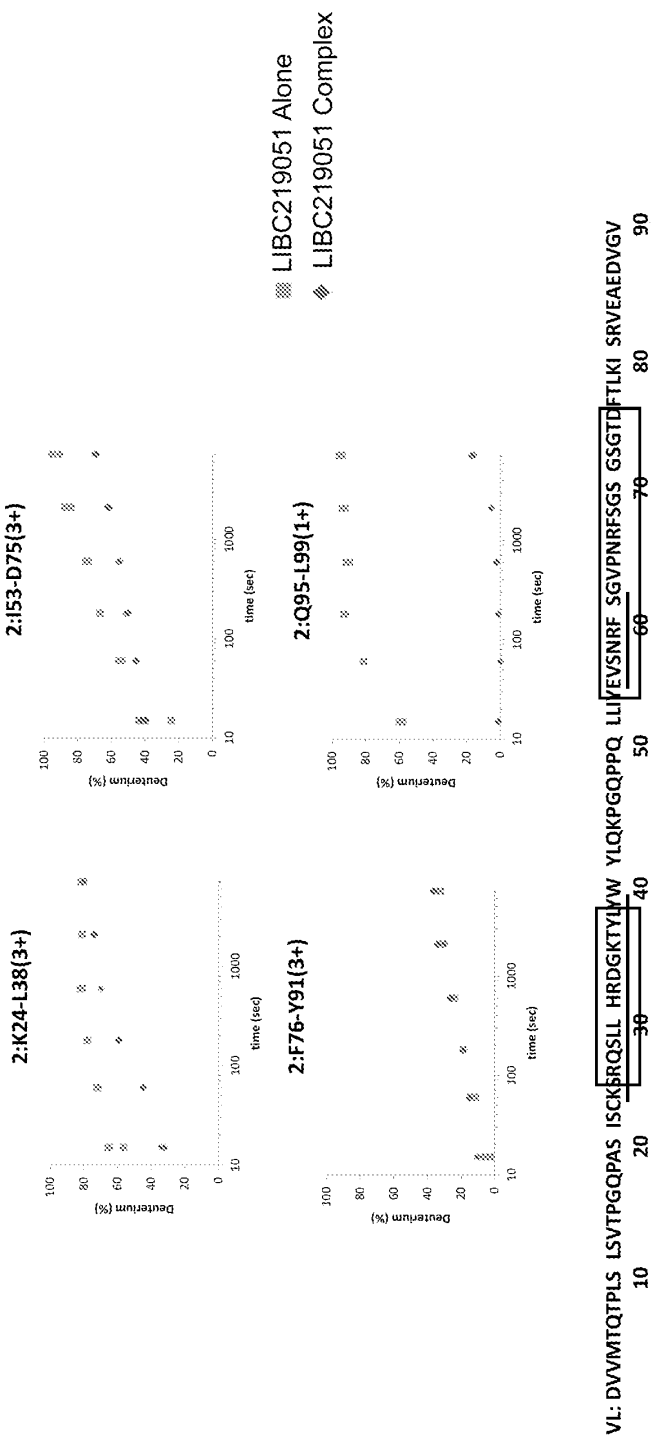

LIBC219051 Alone
LIBC219051 Complex
2:I53-D75(3+)
2:Q95-L99(1+)
2:K24-L38(3+)
2:F76-Y91(3+)
Deuterium (%)
time (sec)
VL: DVVMTQTPLS LSVTPGQPAS ISCKSRQSLL HRDGKTYLYW YLQKPGQPPQ LLIYEVSNRF SGVPNRFSGS GSGTDFTLKI SRVEAEDVGV
YYCMQSIQLP LIFGGGTRVD IKR (SEQ ID NO: 659)

FIG. 19B

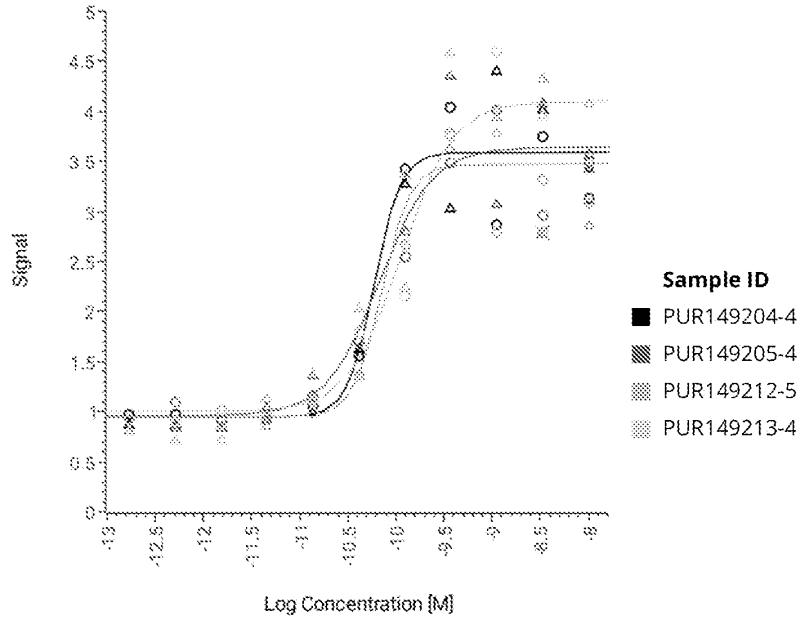

Signal
Log Concentration [M]
Sample ID
PUR149204-4
PUR149205-4
PUR149212-5
PUR149213-4

FIG. 20

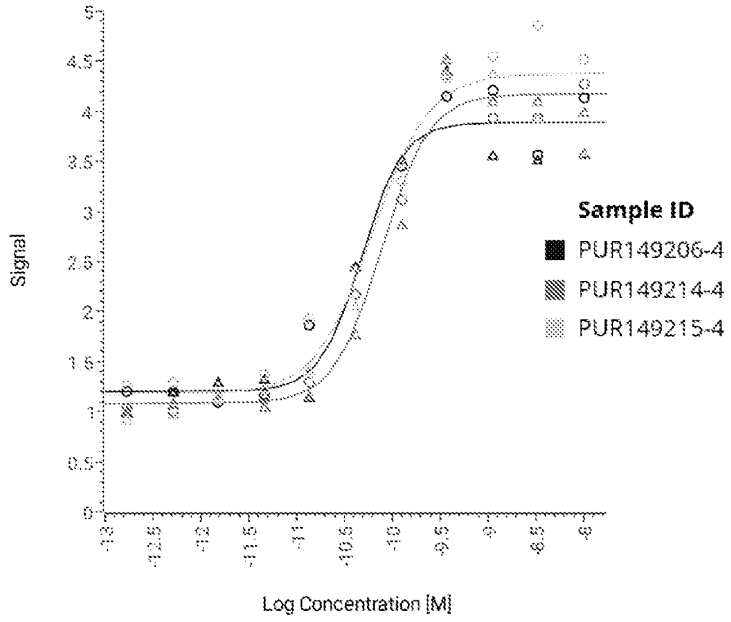

Signal
Log Concentration [M]
Sample ID
PUR149206-4
PUR149214-4
PUR149215-4

FIG. 21

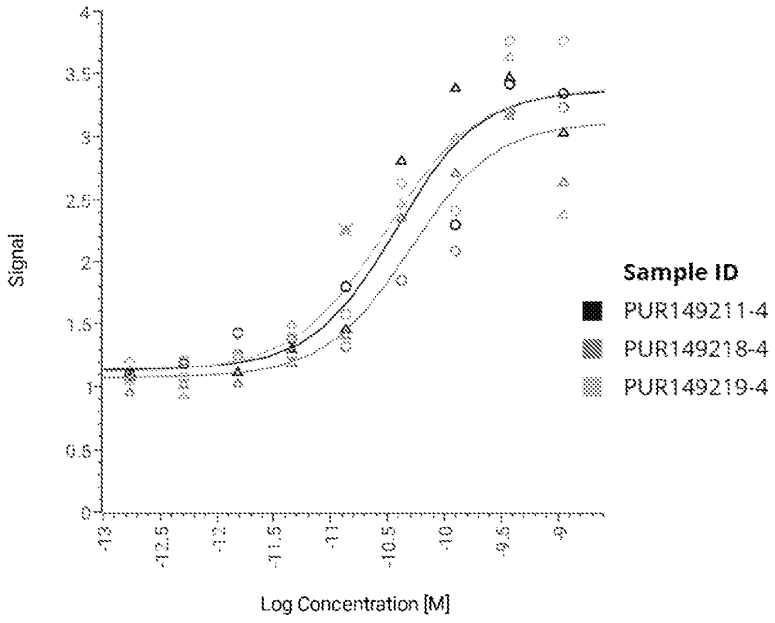

Signal
Log Concentration [M]
Sample ID
PUR149211-4
PUR149218-4
PUR149219-4

FIG. 22

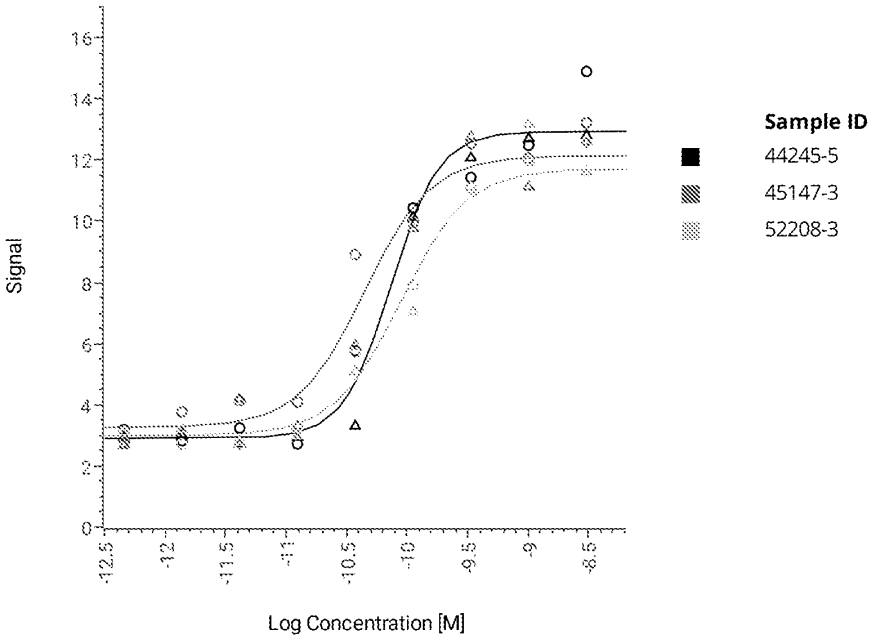


FIG. 23

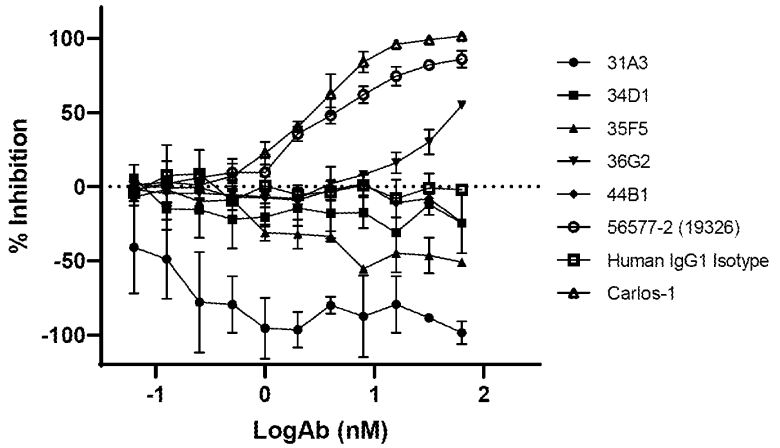


FIG. 24A

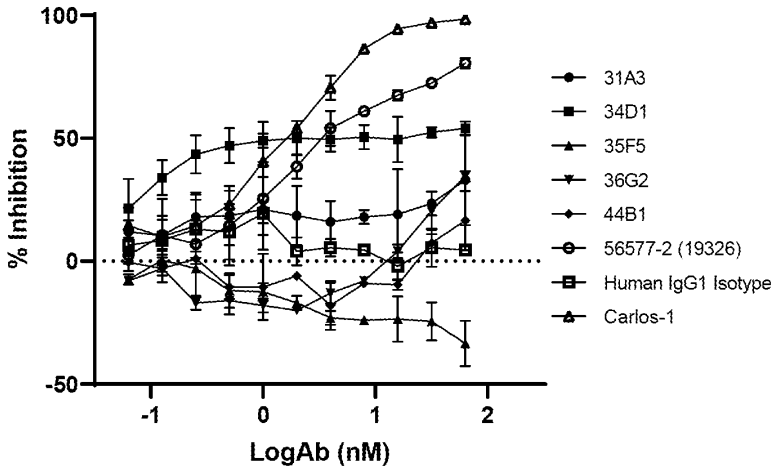


FIG. 24B

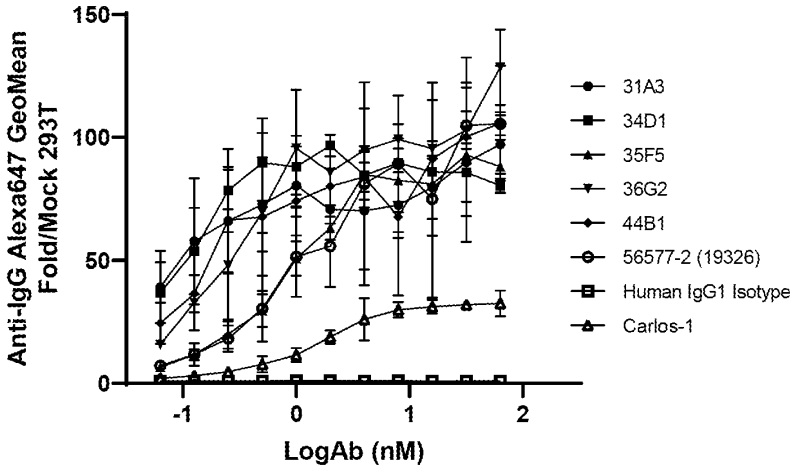


FIG. 24C

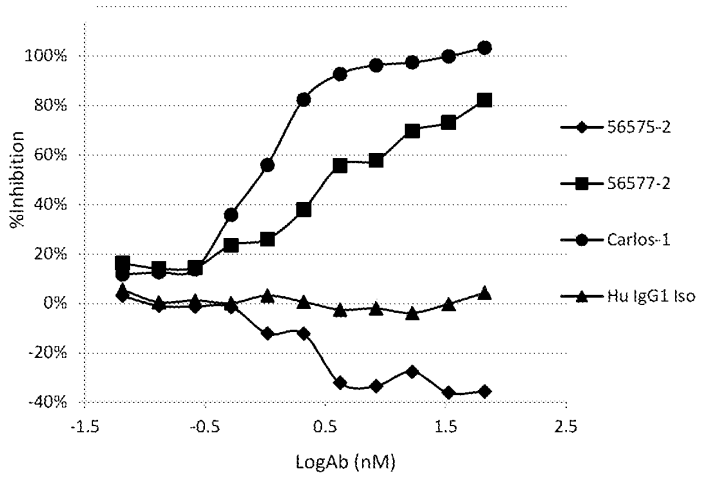


FIG. 25A

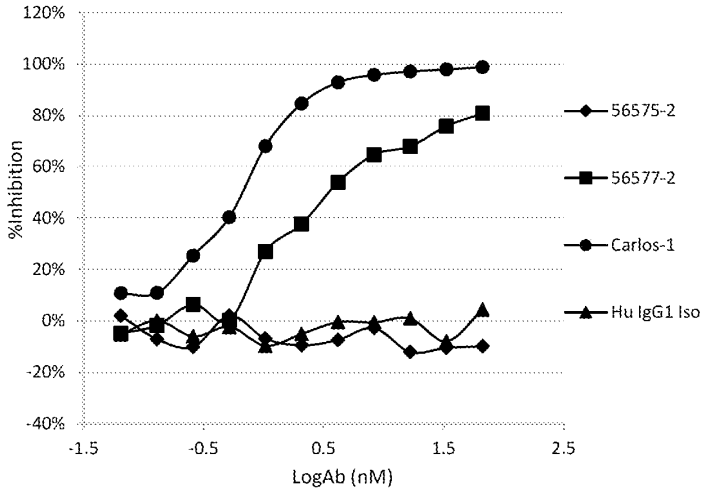


FIG. 25B

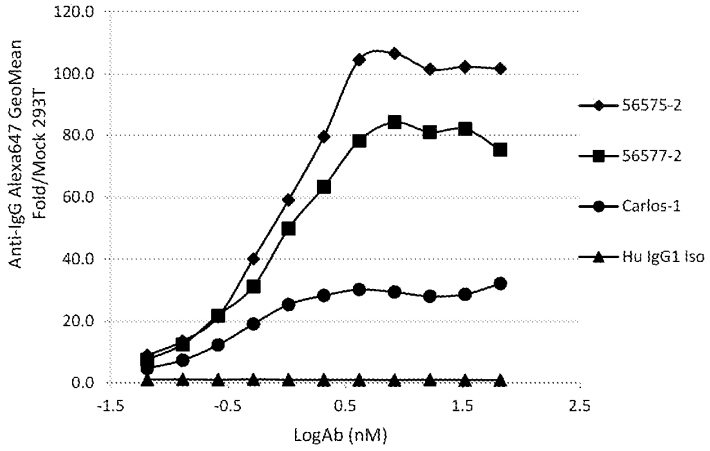


FIG. 25C

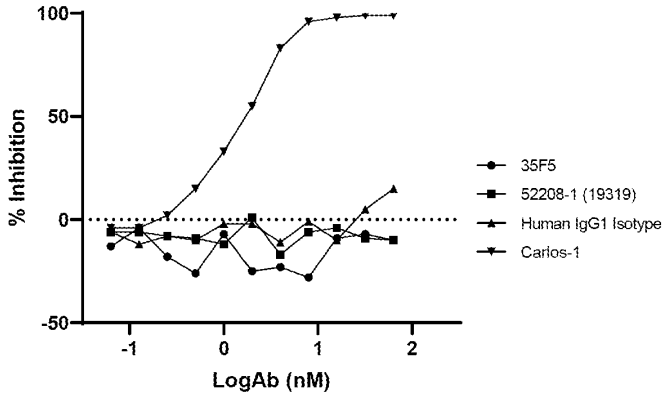


FIG. 26A

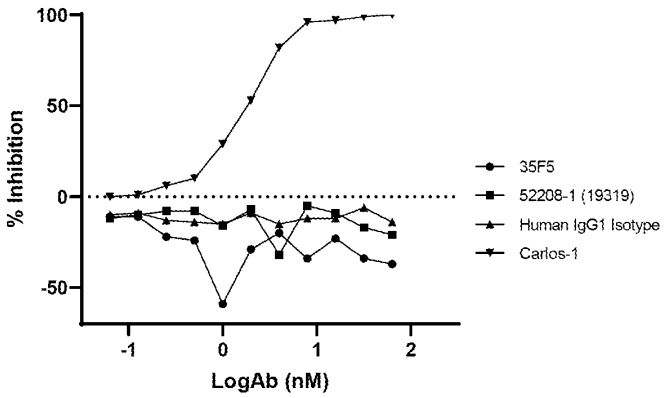


FIG. 26B

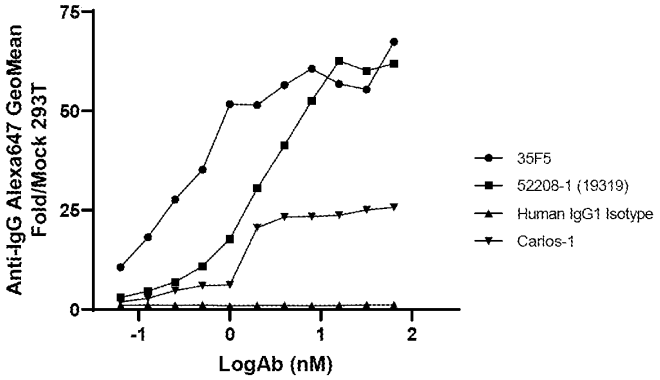


FIG. 26C

LTβR Antibody Ligand Blocking Activity and Affinity Data

LIBC	Cell Based R-L Binding Assay		Cell Based R-L Binding Assay		Carterra R-L Binding	Human LTbR Affinity K_D (M)	Cyno LTbR Affinity K_D (M)	affinity gap Cy/Hu KD
	LIGHT % Inhibition	LTa1b2 % Inhibition	LIGHT % Inhibition	LTa1b2 % Inhibition				
LIBC1314899	-42%	-26%	-20%	-41%	non-blocker	N/A	8.11E-11	NA
LIBC1314198	-41%	-21%	-41%	-29%	non-blocker	7.47E-10	2.13E-10	0.28
LIBC1314607	-38%	-19%	-43%	-30%	non-blocker	N/A	1.51E-09	NA
LIBC1303255	-45%	-6%	-34%	12%	NA	6.77E-08	6.15E-09	0.09
LIBC1303446	-44%	-16%	-33%	4%	NA	7.19E-09	3.03E-08	4.21
LIBC1303507	-37%	-1%	-31%	1%	NA	6.54E-08	1.23E-08	0.19
LIBC1303574	-36%	-21%	-33%	15%	NA	1.69E-08	7.97E-09	0.47
LIBC1303613	-34%	-15%	-36%	7%	NA	3.67E-08	1.24E-08	0.34
LIBC1303716	-40%	-7%	-47%	-6%	NA	3.59E-09	7.34E-09	2.04
LIBC1306053	-51%	-38%	-60%	-38%	non-blocker	1.09E-09	4.95E-10	0.45
LIBC1306153	-48%	-45%	-59%	-29%	non-blocker	1.31E-09	6.76E-10	0.52
LIBC1306164	-25%	-42%	-53%	-22%	NA	2.11E-08	5.08E-09	0.24
LIBC1306251	-35%	-39%	-52%	-26%	non-blocker	1.25E-09	5.53E-10	0.44
LIBC1306253	-24%	-44%	-46%	-29%	NA	2.46E-08	5.80E-09	0.24
LIBC1306294	-36%	-27%	-56%	-20%	non-blocker	2.18E-09	1.70E-09	0.78
LIBC1306424	-39%	-50%	-49%	-22%	NA	2.44E-09	1.22E-10	0.05
LIBC1306622	-43%	-57%	-46%	-34%	non-blocker	2.20E-09	1.52E-10	0.07
LIBC1306674	-45%	-33%	-46%	-22%	non-blocker	1.21E-09	9.15E-09	7.54
LIBC1306800	-34%	-42%	-50%	-30%	non-blocker	1.29E-09	3.49E-10	0.27
LIBC1306965	-42%	-25%	-43%	-10%	non-blocker	2.94E-09	1.20E-09	0.41
LIBC1307105	-24%	-1%	-42%	-3%	non-blocker	7.56E-10	3.93E-10	0.52
LIBC1307329	-21%	-25%	-55%	-30%	non-blocker	1.08E-09	8.44E-10	0.78
LIBC1307739	-35%	-32%	-45%	-18%	non-blocker	2.82E-09	5.85E-10	0.21
LIBC1308006	-16%	-18%	-38%	-15%	non-blocker	1.50E-09	1.32E-09	0.87

FIG. 27

LIBC	Cell Based R-L Binding Assay		Cell Based R-L Binding Assay		Carterra R-L Binding	Human LTbR Affinity K_D (M)	Cyno LTbR Affinity K_D (M)	affinity gap Cy/Hu KD
	LIGHT % Inhibition	LTa1b2 % Inhibition	LIGHT % Inhibition	LTa1b2 % Inhibition				
LIBC1308236	-26%	-27%	-42%	-14%	non-blocker	1.74E-09	2.78E-10	0.16
LIBC1308563	-15%	-24%	-34%	-3%	non-blocker	2.19E-09	9.87E-11	0.05
LIBC1308591	-8%	-1%	-35%	18%	NA	5.54E-09	8.50E-09	1.53
LIBC1308640	-2%	-9%	-32%	8%	NA	1.47E-09	2.62E-10	0.18
LIBC1308929	-38%	-37%	-55%	-31%	non-blocker	1.47E-09	7.91E-10	0.54
LIBC1308943	-18%	-22%	-40%	-5%	non-blocker	2.32E-09	3.06E-09	1.31
LIBC1309633	-16%	-24%	-59%	-25%	non-blocker	6.26E-09	6.25E-09	1.00
LIBC1309682	-21%	-7%	-40%	-24%	non-blocker	8.08E-09	9.31E-10	0.12
LIBC1310489	-20%	-45%	-37%	-19%	non-blocker	2.25E-09	2.84E-10	0.13
LIBC1318188	-35%	-16%	-34%	-32%	non-blocker	3.34E-09	5.15E-09	1.54
LIBC1318198	-29%	-10%	-45%	-23%	non-blocker	4.77E-10	4.83E-10	1.01
LIBC1318209	-25%	-19%	-42%	-19%	non-blocker	2.08E-10	6.60E-10	3.17
LIBC1318253	-34%	-25%	-54%	-33%	non-blocker	N/A	1.52E-09	NA
LIBC1318301	-14%	-6%	-29%	-24%	non-blocker	2.07E-09	2.25E-09	1.09
LIBC1318341	-11%	-2%	-43%	-29%	non-blocker	9.36E-10	9.41E-10	1.01
LIBC1318394	-27%	-2%	-44%	-17%	non-blocker	5.66E-10	5.06E-10	0.90
LIBC1318409	-34%	-19%	-47%	-29%	non-blocker	8.61E-10	1.41E-09	1.64
LIBC1318412	-22%	-22%	-40%	-22%	non-blocker	4.94E-10	5.79E-10	1.17
LIBC1318496	-30%	-11%	-31%	-30%	non-blocker	1.09E-09	1.91E-09	1.76
LIBC1318693	-38%	-15%	-43%	-16%	non-blocker	8.48E-10	5.81E-10	0.69
LIBC1318738	-42%	-21%	-36%	-39%	non-blocker	1.42E-09	2.15E-09	1.51
LIBC1318991	-53%	-22%	-30%	-19%	non-blocker	8.57E-10	6.32E-10	0.74
LIBC1319003	-30%	-10%	-46%	-18%	non-blocker	4.44E-09	5.62E-09	1.27
LIBC1319078	-40%	-11%	-54%	-17%	non-blocker	8.52E-10	2.15E-10	0.25
LIBC1319182	-42%	-7%	-38%	-18%	non-blocker	5.61E-10	1.43E-09	2.54
LIBC1319275	-45%	-3%	-49%	-21%	non-blocker	1.77E-09	3.61E-09	2.04

FIG. 27 (Cont.)

LIBC	Cell Based R-L Binding Assay		Cell Based R-L Binding Assay		Carterra R-L Binding	Human LTbR Affinity K_D (M)	Cyno LTbR Affinity K_D (M)	affinity gap Cy/Hu KD
	LIGHT % Inhibition	LTa1b2 % Inhibition	LIGHT % Inhibition	LTa1b2 % Inhibition				
LIBC1319279	-34%	-8%	-27%	-16%	non-blocker	2.40E-09	2.44E-09	1.02
LIBC1319390	-46%	-7%	-49%	-25%	non-blocker	1.86E-09	4.64E-09	2.49
LIBC1319499	-36%	-6%	-41%	-26%	non-blocker	9.72E-09	9.34E-09	0.96
LIBC1319569	-44%	-8%	-48%	-32%	NA	8.45E-09	6.16E-10	0.07
LIBC1319908	-29%	0%	-48%	-25%	non-blocker	2.80E-10	4.56E-10	1.63
LIBC1320038	-33%	-5%	-39%	-19%	non-blocker	7.94E-10	1.82E-09	2.29

FIG. 27 (Cont.)