

seq	10	20	30	40	50	
AbM	10	20	30	40	50	a
CBD1017vh	EVQLVQSGPELVKPGASVKISCKAS	RYTFTDYNLH	WVKLSHEKSLEWIG	FIYPYNGGCTG		
	* * * * *	*	*****	*		
1-46*01	QVQLVQSGAEVKKPGASVKVSKAS	GYTFTSYVMH	WVRQAPCQGLEWNG	IINPSGCGSTS		
h1017-H1	QVQLVQSGAEVKKPGASVKVSKAS	RYTFTDYNLH	WVRQAPCQGLEWNG	FIYPYNGGCTG		
h1017-H2	QVQLVQSGAEVKKPGASVKVSKAS	RYTFTDYNLH	WVRQAPCQGLEWNG	FIYPYNGGCTG		
h1017-H3	QVQLVQSGAEVKKPGASVKISCKAS	RYTFTDYNLH	WVRQAPCQGLEWIG	FIYPYNGGCTG		
h1017-H4	QVQLVQSGAEVKKPGASVKVSKAS	RYTFTDYNLH	WVRQAPCQGLEWNG	FIYPYNGGCTG		
h1017-H5	QVQLVQSGAEVKKPGASVKISCKAS	RYTFTDYNLH	WVRQAPCQGLEWIG	FIYPYNGGCTG		
E	V	#	L	Q		
seq	60	70	80	90	100	110
AbM	60	70	80	abc	100	110
CBD1017vh	YNQKFKNKAKLTVDYSSSTAYMELSLRSLTSVDAAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
	* *****	* * *	* * *	*		
1-46*01	YAQKFQGRVTMTREDTSTSTVYMELSLRSEDTAVYYCAR					
h1017-H1	YAQKFQGRVTMTREDTSTSTVYMELSLRSEDTAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
h1017-H2	YAQKFQGRVTMTVDYDSTSTAYMELSLRSEDTAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
h1017-H3	YAQKFQGRATLTVDYDSTSTAYMELSLRSEDTAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
h1017-H4	YAQKFQGRVTMTVDYDSTSTAYMELSLRSEDTAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
h1017-H5	YAQKFQGRATLTVDYDSTSTAYMELSLRSEDTAVYYCAR	DHRYNEGVSFDY	WGQCTTLTVSS			
	NQKFKN	#				

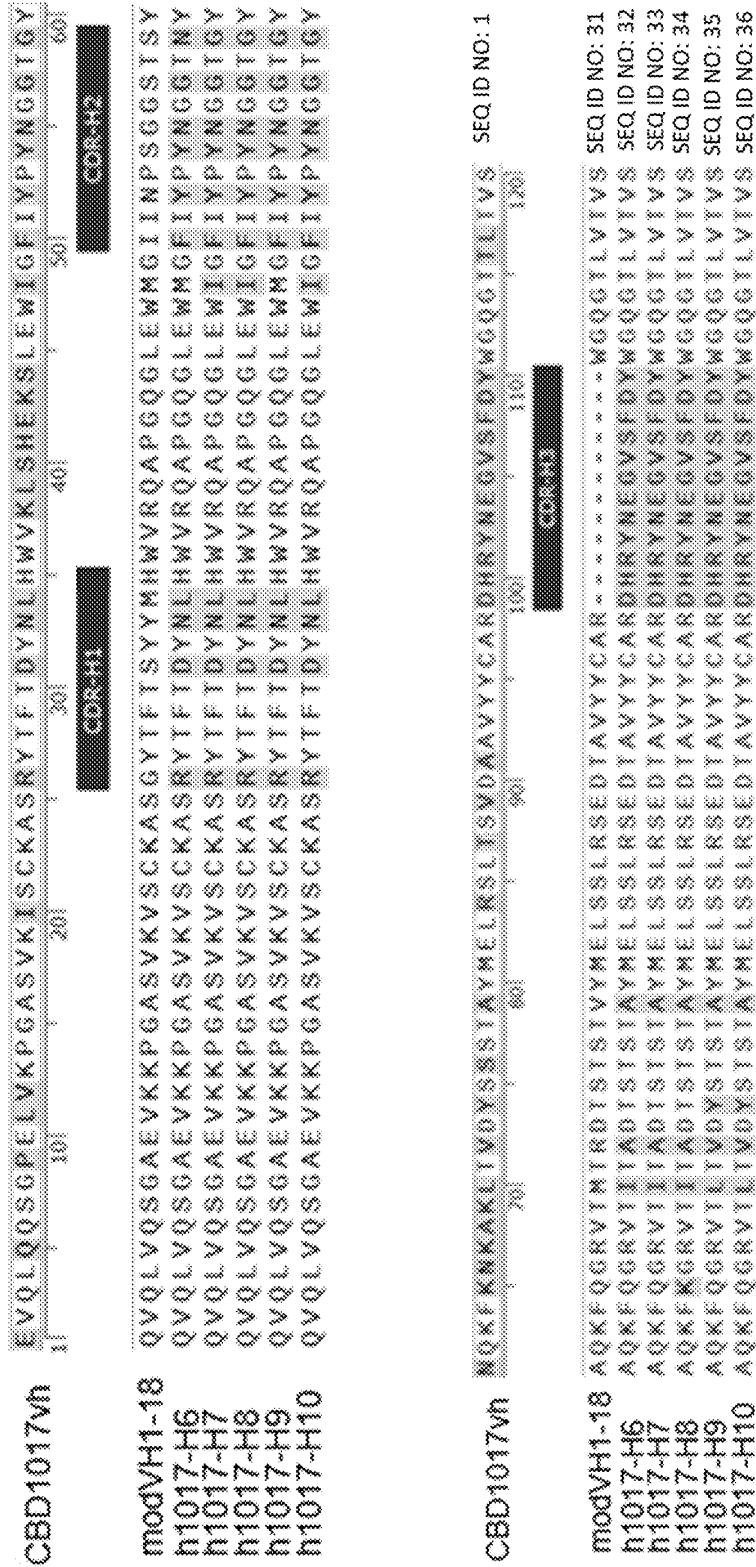
deamidation substitutions: Q/S/A
@ isoaspartate formation: S/Q/A

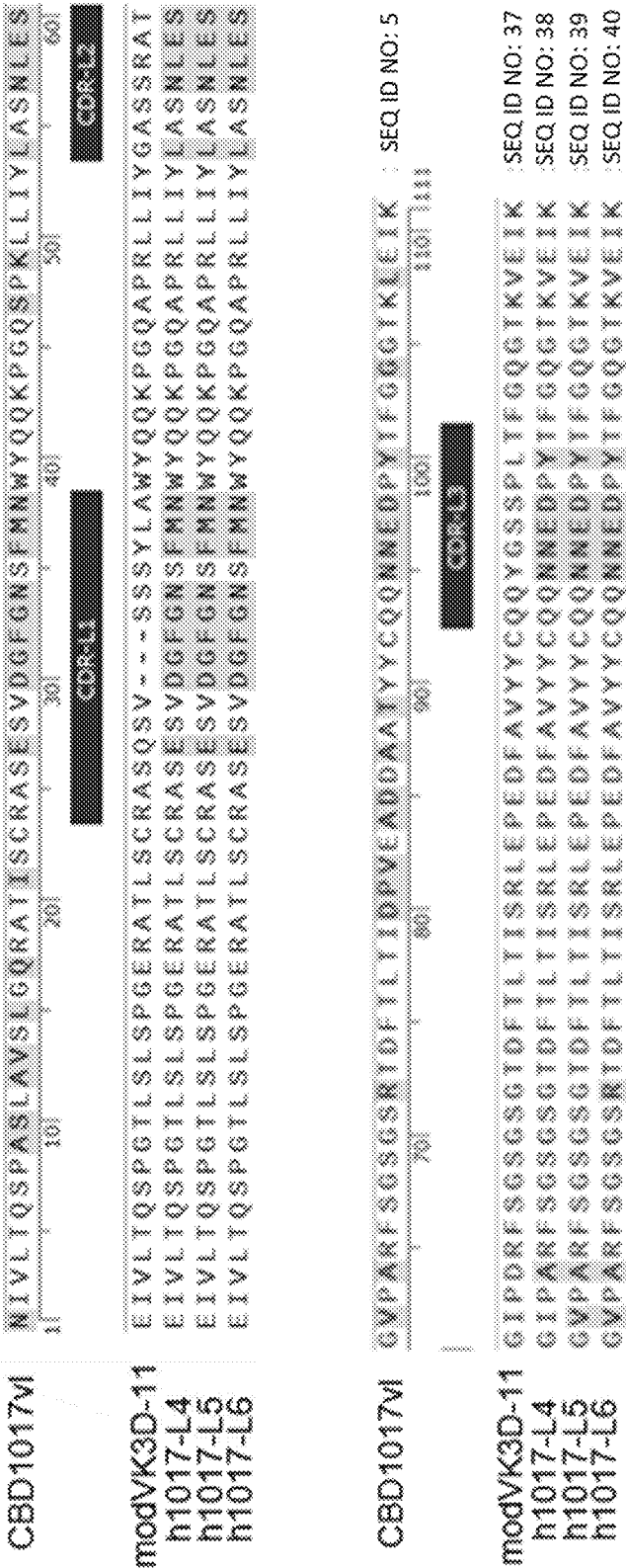
FIG. 1A

seq	10	20	30	40	50	60
AbM	10	20	30abcd	40	50	
CBD1017v1	NIVLTQSPASLASVSLQGRATISC	RASESVDFGFGNSFMN	WYQKPGQSPKLLIY	LASNLES		
	* **	* ** * * *		**		
1-39*01	DIQMTQSPSSLSASVCDRVITTC	RASQIS-----SYLN	WYQKPGCKAPKLLIY	AASSLOS		
h1017-L1	DIQMTQSPSSLSASVCDRVITTC	RASESVDFGFGNSFMN	WYQKPGCKAPKLLIY	LASNLES		
h1017-L2	DIQMTQSPSSLSASVCDRVITTC	RASESVDFGFGNSFMN	WYQKPGCKAPKLLIY	LASNLES		
h1017-L3	DIQMTQSPSSLSASVCDRVITTC	RASESVDFGFGNSFMN	WYQKPGCKAPKLLIY	LASNLES		
	V	@	#	S	#	
seq	70	80	90	100	110	
AbM	60	70	80	90	100	
CBD1017v1	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QNNEDPPT	FCGCTKLEIK	SEQ ID NO: 5		
	*	*****	*			
1-39*01	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QNNEDPPT	FCGCTKLEIK	SEQ ID NO: 15		
h1017-L1	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QNNEDPPT	FCGCTKLEIK	SEQ ID NO: 16		
h1017-L2	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QNNEDPPT	FCGCTKLEIK	SEQ ID NO: 17		
h1017-L3	GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	QNNEDPPT	FCGCTKLEIK	SEQ ID NO: 18		
	A	##	%			

deamidation substitutions: Q/S/A
@ isocaspate formation substitutions: E/S/
A% Asp-Pro fragmentation substitutions: E/S/A

FIG. 1B





F(ab) at 30°C

Binder	Name	K _D (nM)	k _{on} (1/Ms)	k _{off} (1/s)
CDB1017p	mouse CT8	1.19	6.51x10 ⁴	7.76x10 ⁻⁵
CBD1017ch	chimeric CT8	0.814	6.97x10 ⁴	5.67x10 ⁻⁵
CBD1032	h1017-H1/L1	1.84	5.15x10 ⁴	9.45x10 ⁻⁵
CBD1033	h1017-H2/L2	3.25	4.47x10 ⁴	1.45x10 ⁻⁴
CBD1034	h1017-H2/L3	9.90	2.09x10 ⁴	2.04x10 ⁻⁴
CBD1035	h1017-H3/L2	3.07	4.69x10 ⁴	1.44x10 ⁻⁴
CBD1036	h1017-H3/L3	6.16	3.37x10 ⁴	2.07x10 ⁻⁴
CBD1037	h1017-H4/L2	1.72	6.60x10 ⁴	1.14x10 ⁻⁴
CBD1038	h1017-H4/L3	2.31	6.33x10 ⁴	1.46x10 ⁻⁴
CBD1039	h1017-H5/L2	3.11	5.04x10 ⁴	1.57x10 ⁻⁴
CBD1040	h1017-H5/L3	6.07	2.80x10 ⁴	1.70x10 ⁻⁴

FIG. 2A

F(ab) at 37°C

Binder	Name	K _D (nM)	k _{on} (1/Ms)	k _{off} (1/s)
CBD1017ch	chimeric CT8	1.08	6.95x10 ⁴	7.53x10 ⁻⁵
CBD1032	h1017-H1/L1	1.59	3.37x10 ⁴	5.35x10 ⁻⁵
CBD1033	h1017-H2/L2	5.50	3.54x10 ⁴	1.94x10 ⁻⁴
CBD1034	h1017-H2/L3	1.82	1.03x10 ⁵	1.87x10 ⁻⁴
CBD1035	h1017-H3/L2	8.02	1.14x10 ⁴	9.12x10 ⁻⁵
CBD1036	h1017-H3/L3	1.68	1.17x10 ⁵	1.94x10 ⁻⁴
CBD1037	h1017-H4/L2	1.27	7.68x10 ⁴	9.71x10 ⁻⁵
CBD1038	h1017-H4/L3	7.42	1.89x10 ⁴	1.40x10 ⁻⁴
CBD1039	h1017-H5/L2	4.59	2.02x10 ⁴	9.27x10 ⁻⁵
CBD1040	h1017-H5/L3	7.39	1.40x10 ⁴	1.03x10 ⁻⁴

FIG. 2A (CONT'ED)

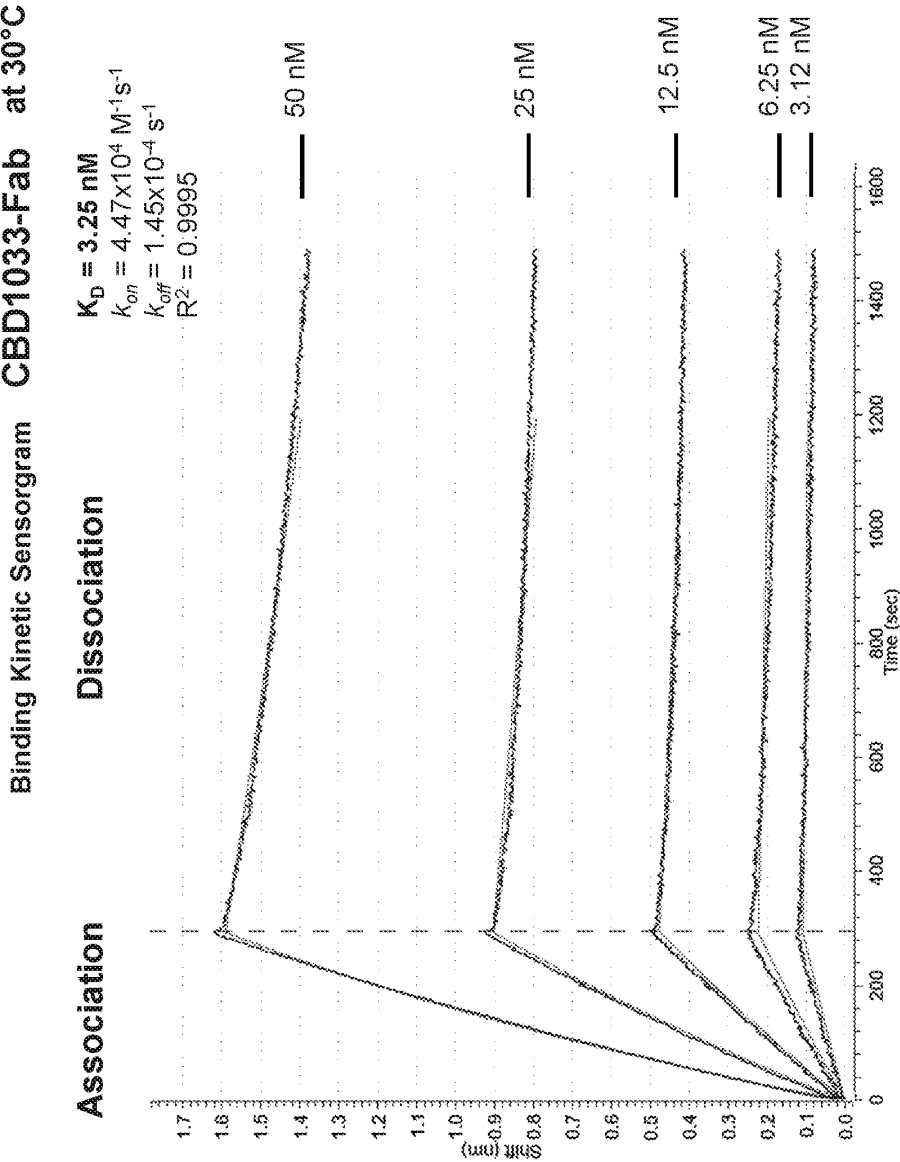


FIG. 2B

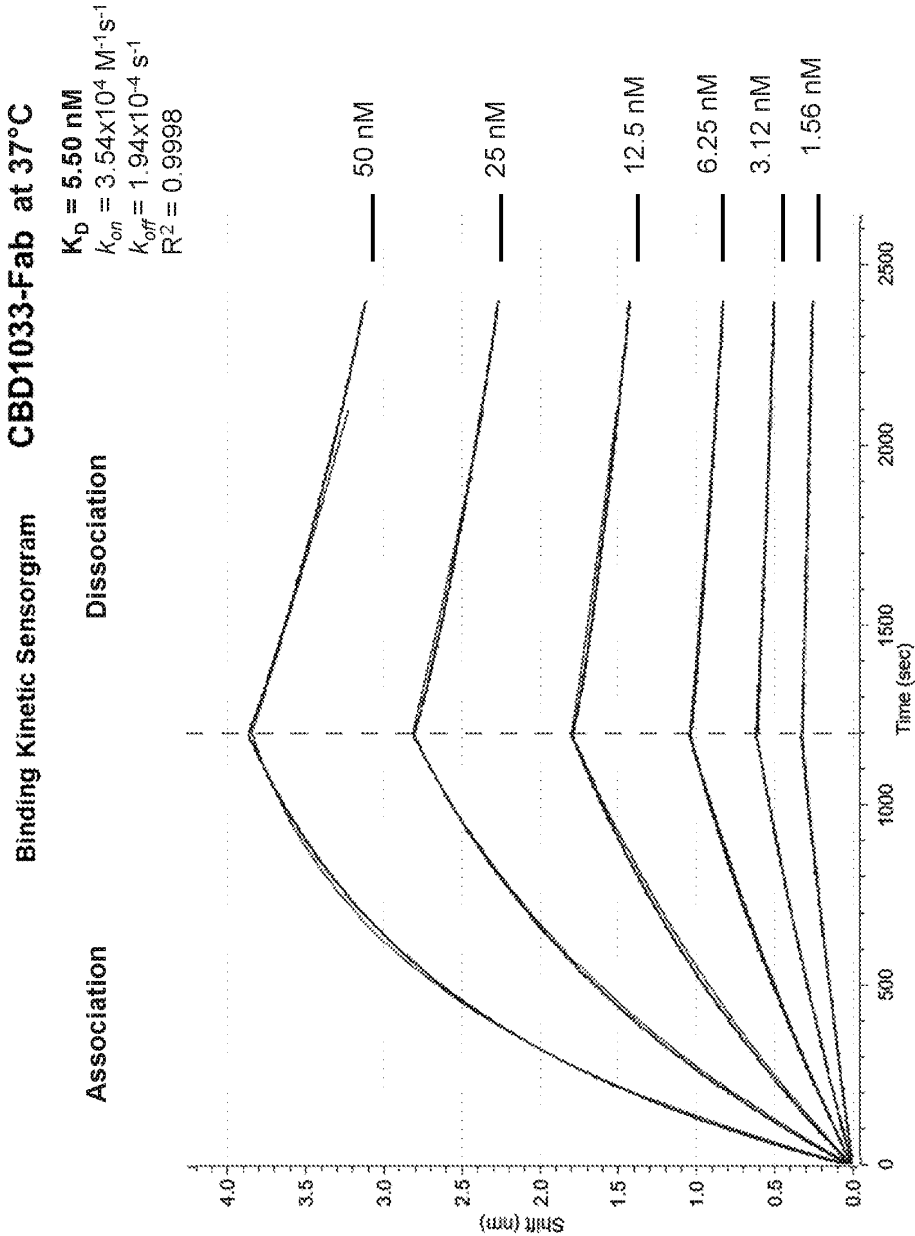


FIG. 2B (CONT'ED)

hIgG1-LALAPA at 30°C

Binder	Name	K _D (nM)
CDB1017ch	chimeric CT8	0.58
CBD1032	h1017-H1/L1	1.40
CBD1033	h1017-H2/L2	2.27
CBD1034	h1017-H2/L3	4.63
CBD1035	h1017-H3/L2	2.66
CBD1036	h1017-H3/L3	5.15
CBD1037	h1017-H4/L2	2.32
CBD1038	h1017-H4/L3	4.74
CBD1039	h1017-H5/L2	1.76
CBD1040	h1017-H5/L3	4.06

FIG. 2C

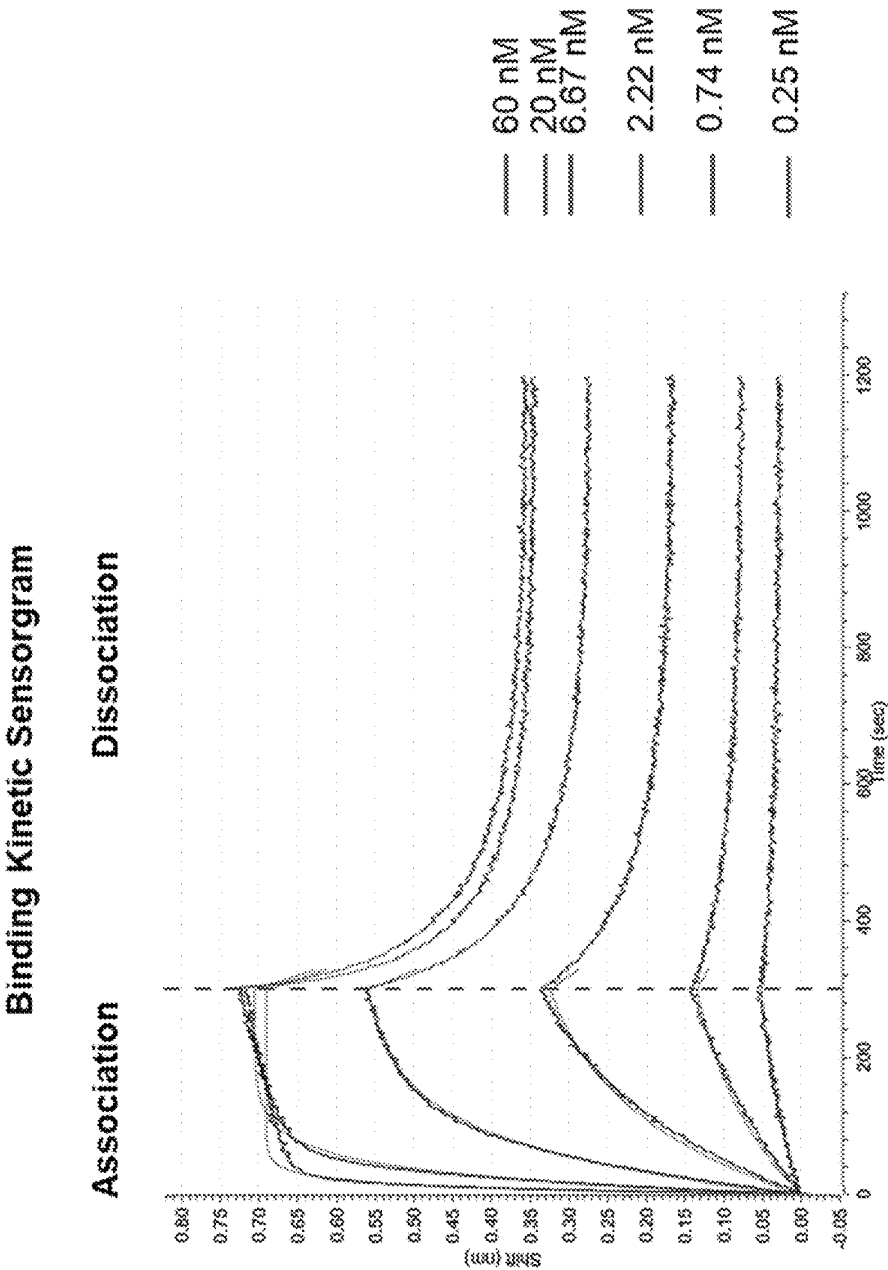


FIG. 2D

CBD1033-hlgG1-LALAPA

Steady State Analysis

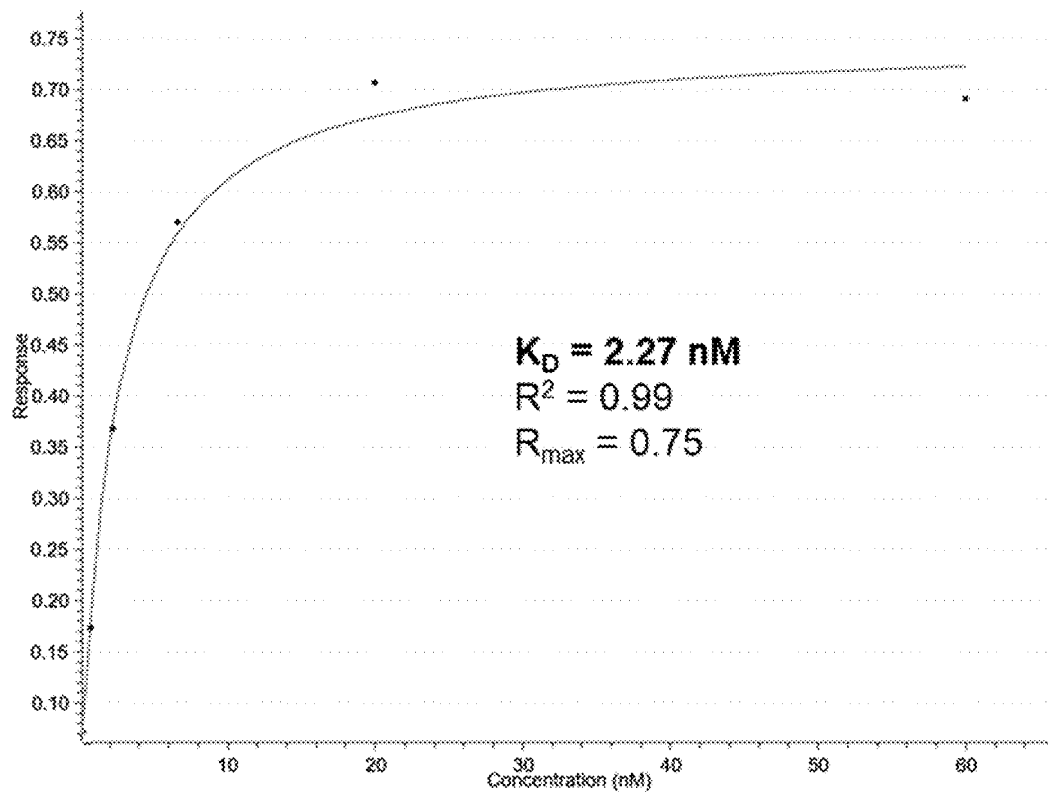


FIG. 2E

hIgG1-LALAPA at 30°C

Binder	Name	K _D (nM)
CDB1017ch	chimeric CT8	0.58
CBD1041	h1017-H6/L4	10.2
CBD1042	h1017-H7/L4	3.59
CBD1043	h1017-H7/L5	3.91
CBD1044	h1017-H7/L6	8.65
CBD1045	h1017-H8/L5	4.18
CBD1046	h1017-H8/L6	9.78
CBD1047	h1017-H9/L5	2.72
CBD1048	h1017-H9/L6	5.45
CBD1049	h1017-H10/L5	3.00
CBD1050	h1017-H10/L6	6.41

FIG. 2F

Binding Kinetic Sensorgram

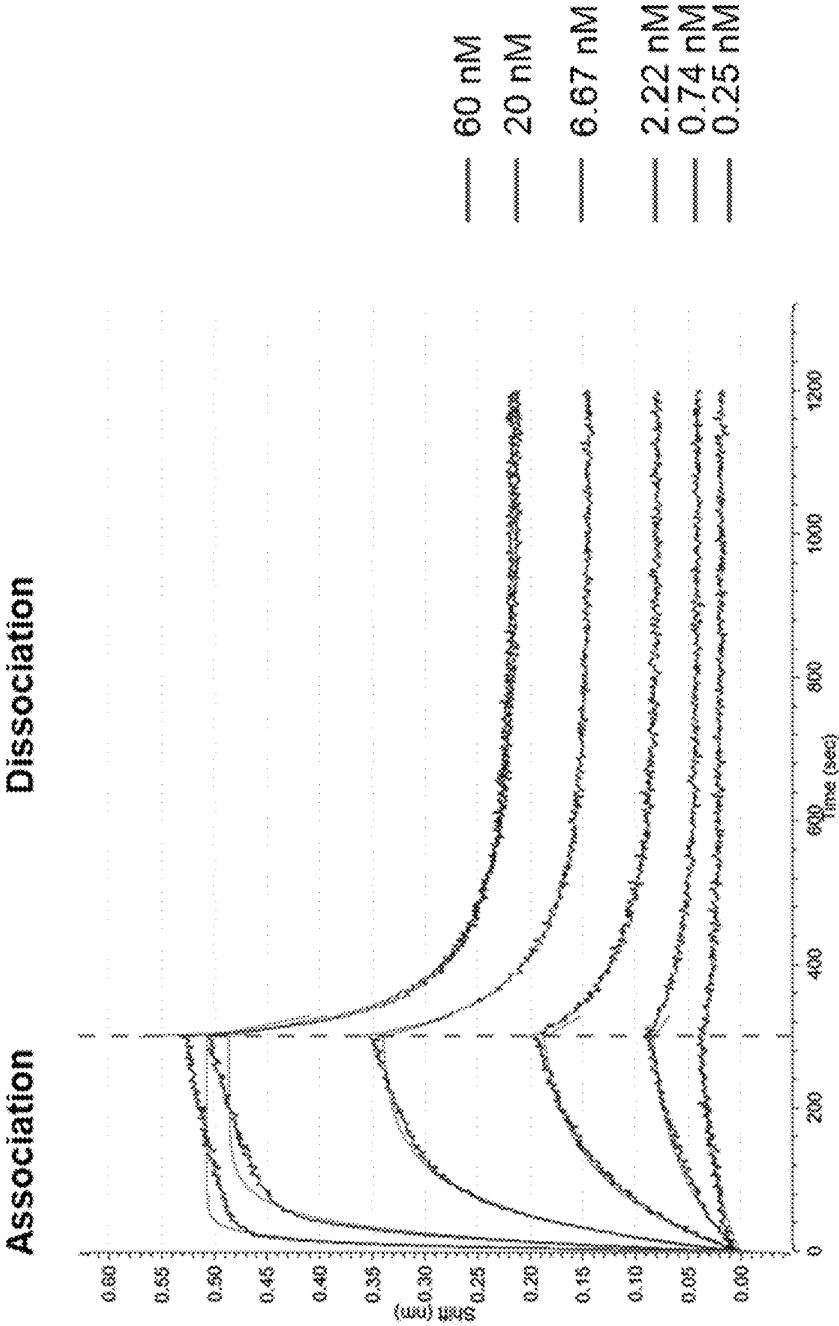


FIG. 2G

CBD1043- hIgG1LALAPA

Steady State Analysis

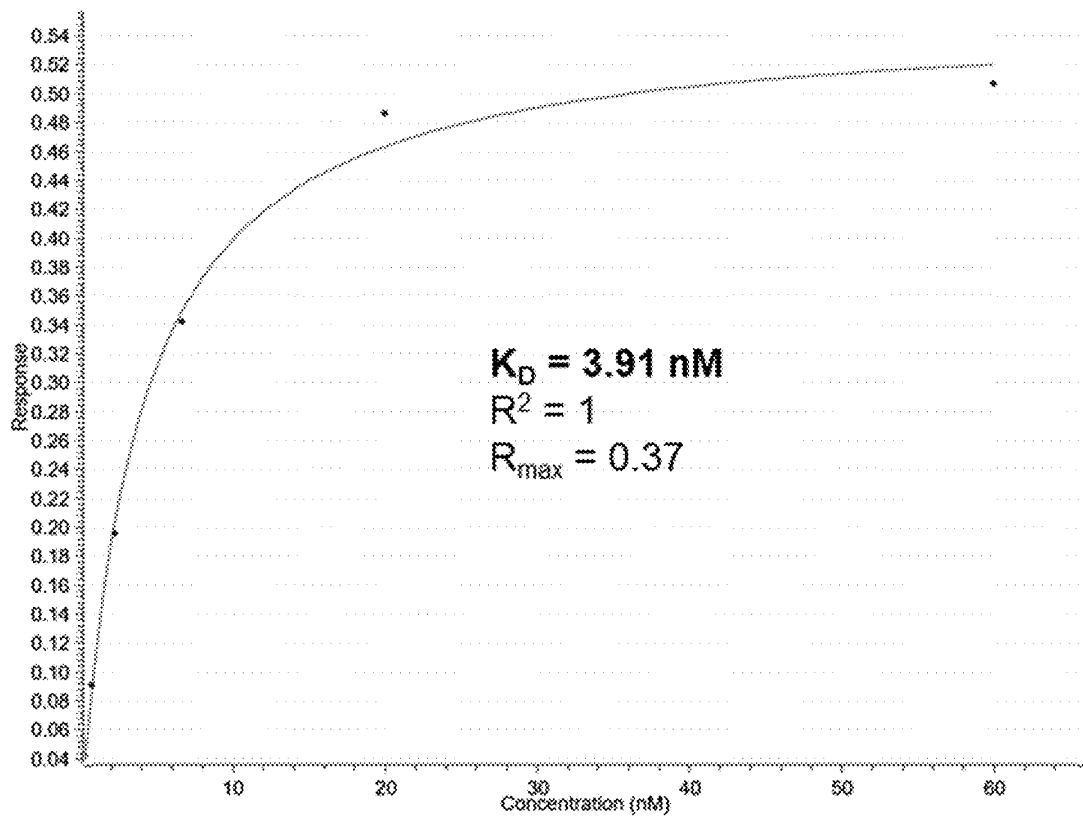


FIG. 2H

Binder	Antigen	K_D (nM)	k_{on} (1/Ms)	k_{off} (1/s)	Temp (°C)
CBD1017ch	Human CD8αα homodimer	1.08	6.95×10^4	7.53×10^{-5}	37
	Human CD8αβ heterodimer	5.75	3.12×10^4	1.79×10^{-4}	37
	Cynomolgus CD8αα homodimer	2.26	3.07×10^4	6.93×10^{-5}	37
	Cynomolgus CD8αβ heterodimer	24.8	2.03×10^4	5.03×10^{-4}	30
CBD1033	Human CD8αα homodimer	5.5	3.54×10^4	1.94×10^{-4}	37
	Human CD8αβ heterodimer	26.2	2.50×10^4	6.53×10^{-4}	37
	Cynomolgus CD8αα homodimer	10.4	2.54×10^4	2.64×10^{-4}	37
	Cynomolgus CD8αβ heterodimer	119	1.67×10^4	1.99×10^{-3}	30

FIG. 2I

Binding kinetic sensorgram against cynomolgus CD8αα homodimer

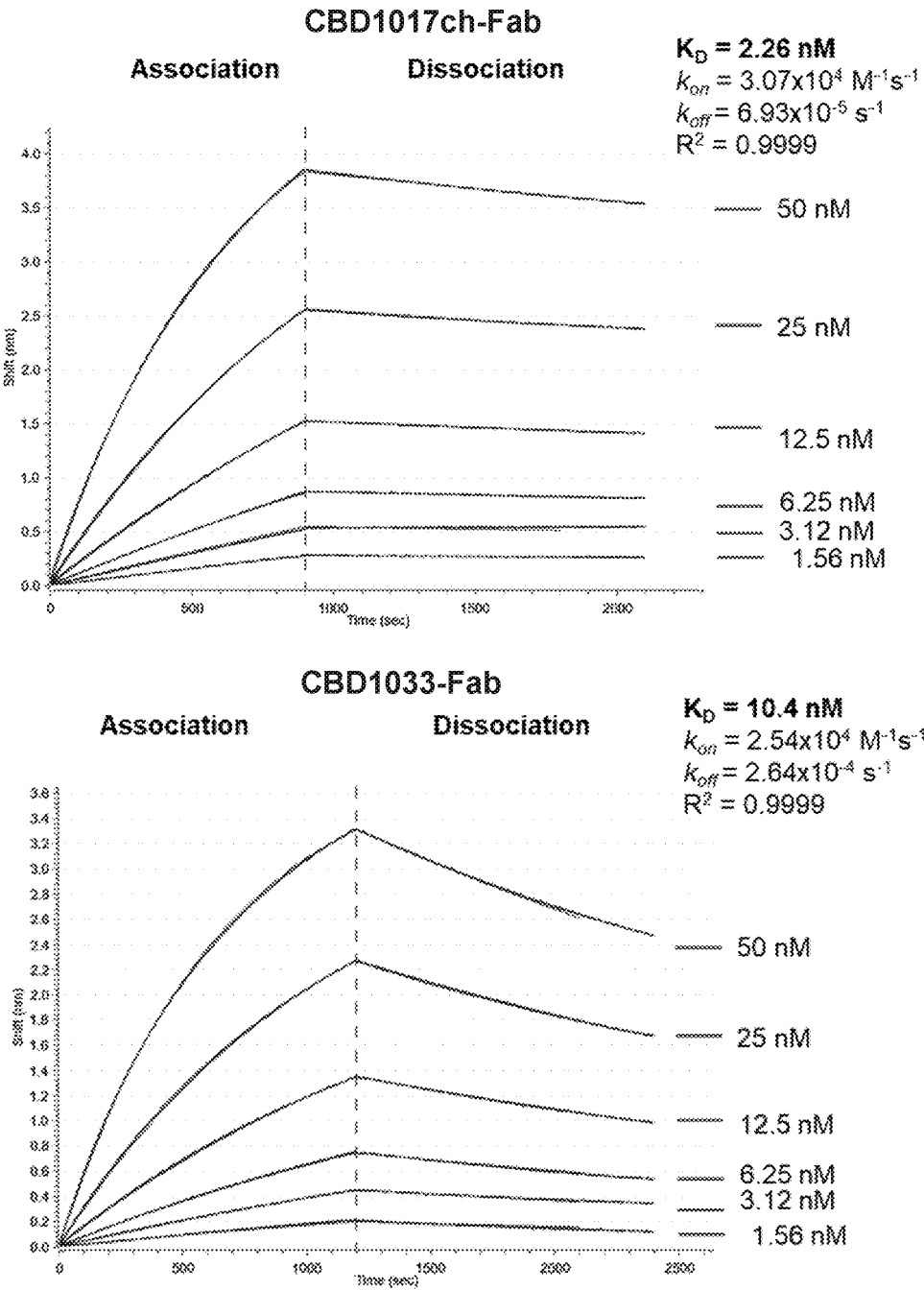


FIG. 2J

hIgG1-LALAPA

Binder	Antigen	K_D (nM)	k_{on} (1/Ms)	k_{off} (1/s)
CBD1033	Human CD8αα homodimer	2.46	1.17×10^5	2.89×10^{-4}
	Human CD8αβ heterodimer	8.99	1.24×10^5	1.11×10^{-3}
	Cynomolgus CD8αα homodimer	5.43	5.00×10^4	2.71×10^{-4}
	Cynomolgus CD8αβ heterodimer	31.0	3.68×10^4	1.14×10^{-3}

FIG. 2K

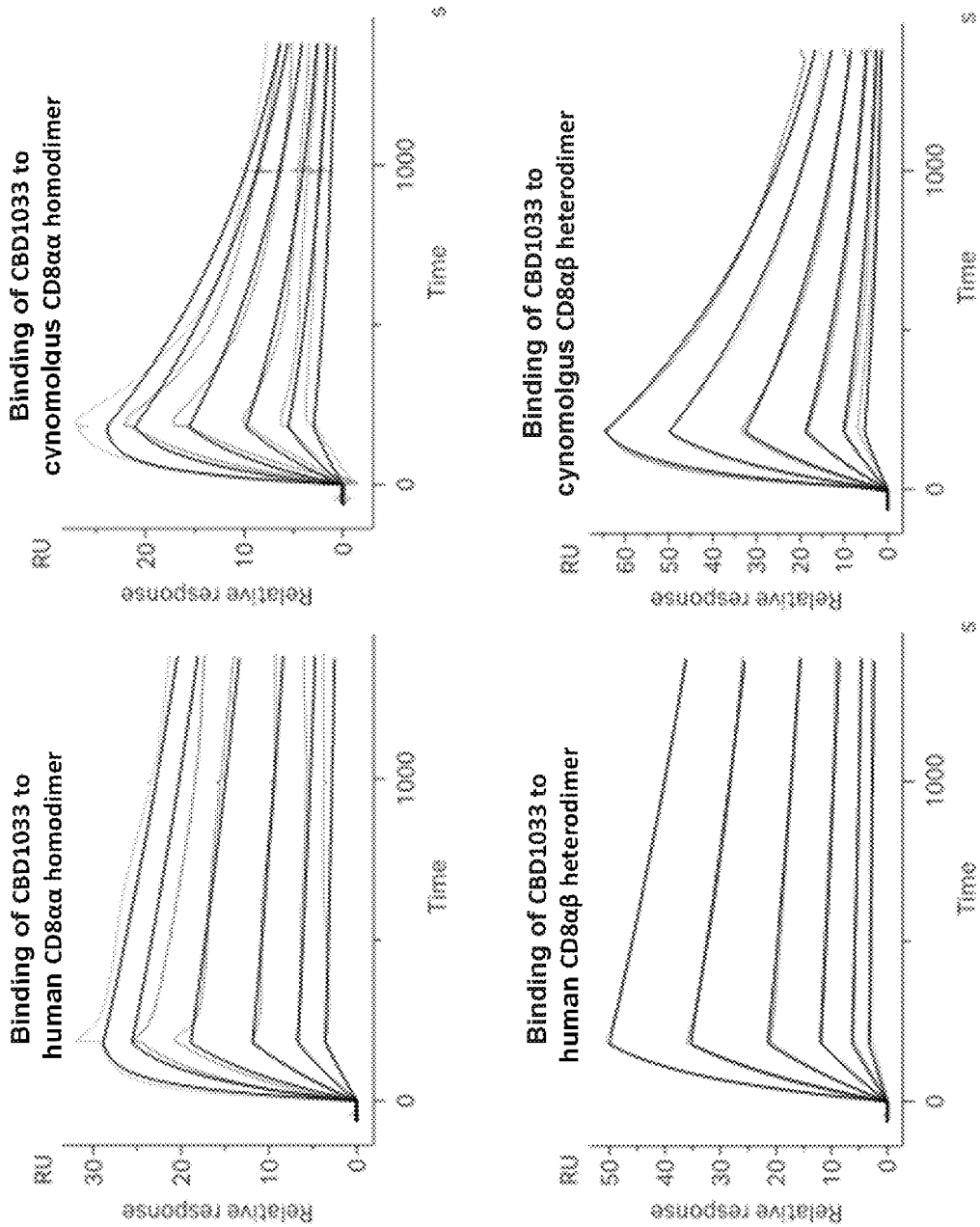


FIG. 2L

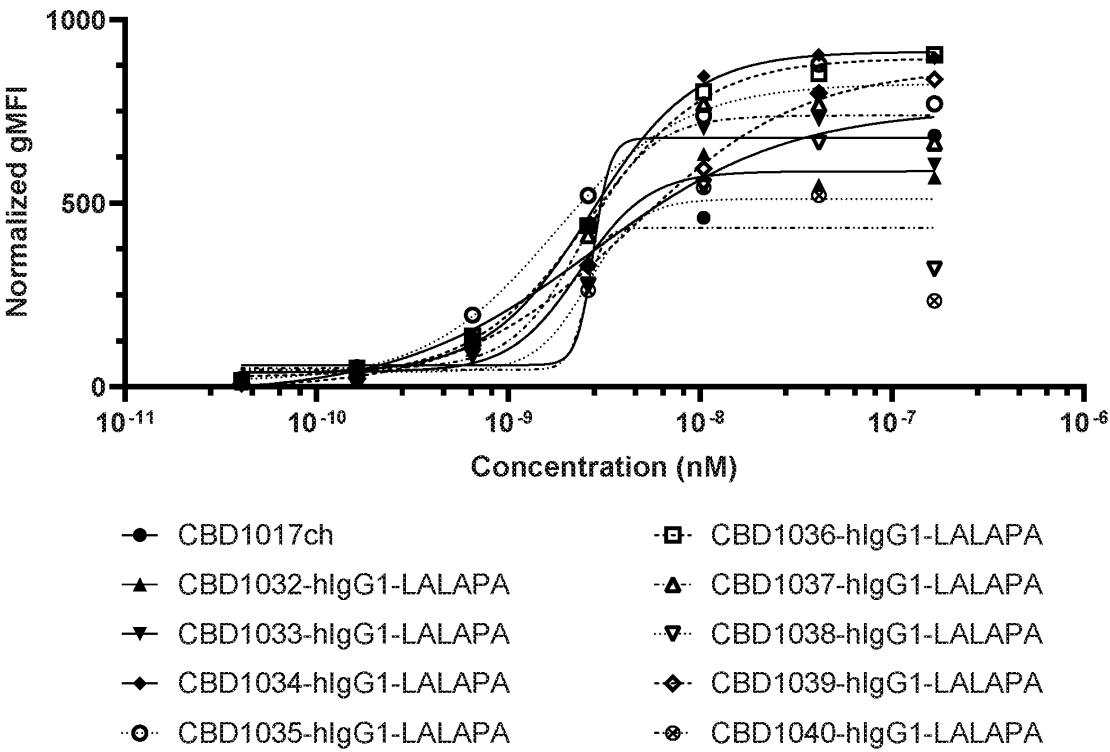


FIG. 3A

FIG. 3B

Binder	EC50 (nM)
CBD1017ch-LALAPA	2.75
CBD1032	2.35
CBD1033	2.78
CBD1034	2.71
CBD1035	1.75
CBD1036	2.69
CBD1037	2.42
CBD1038	2.57
CBD1039	4.39
CBD1040	2.54

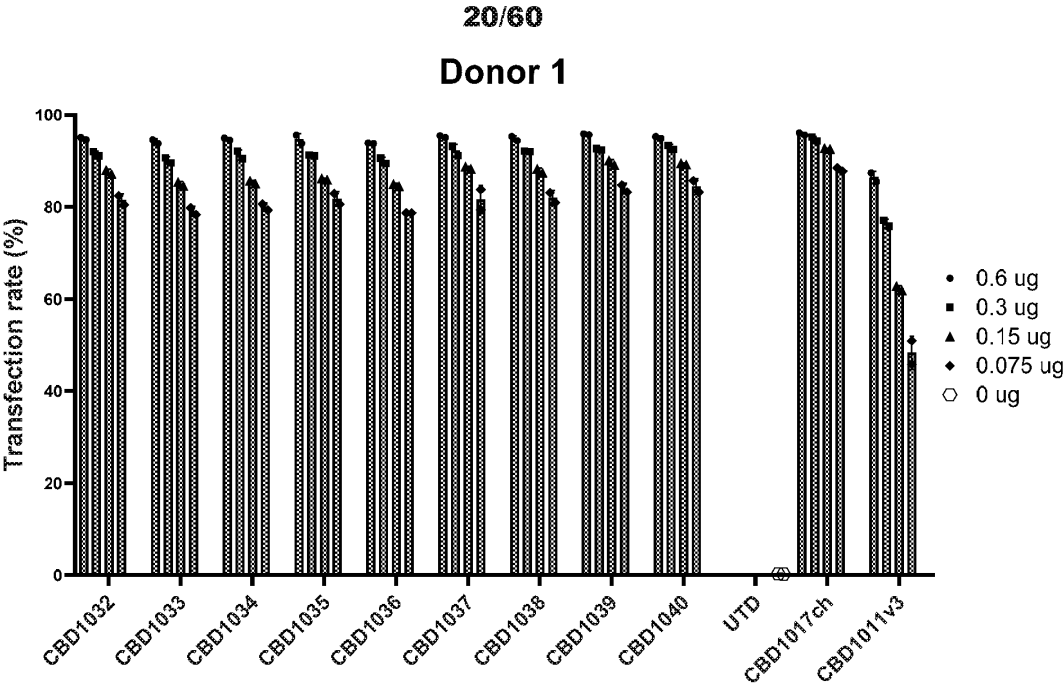


FIG. 4A

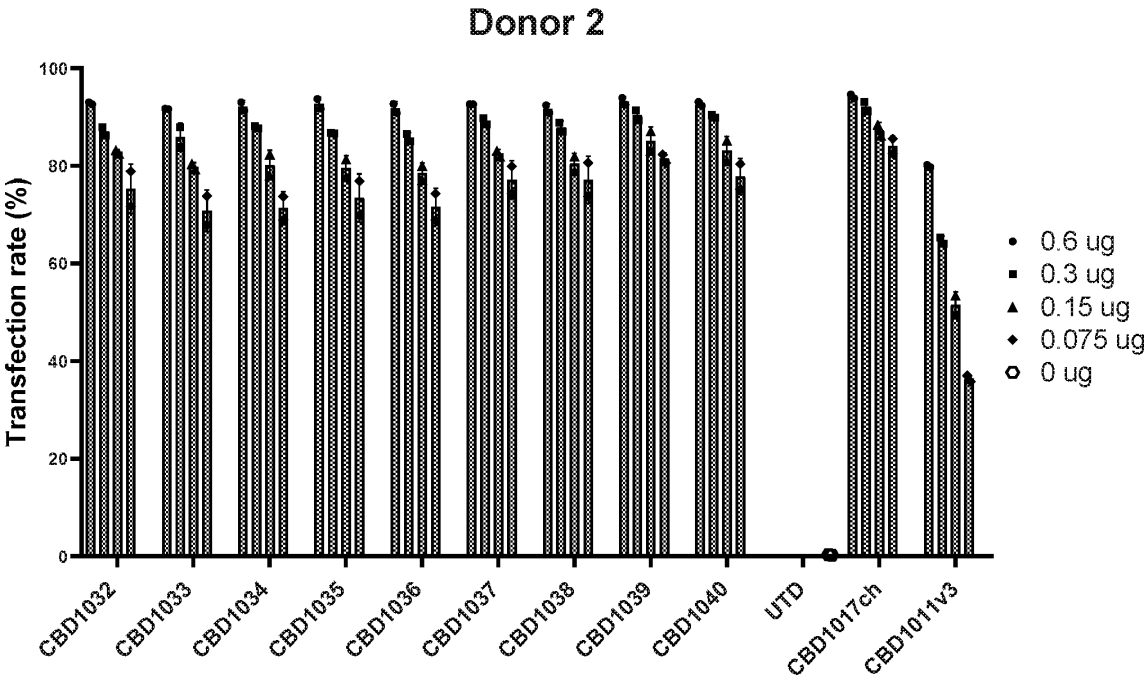


FIG. 4B

21/60
Donor 1

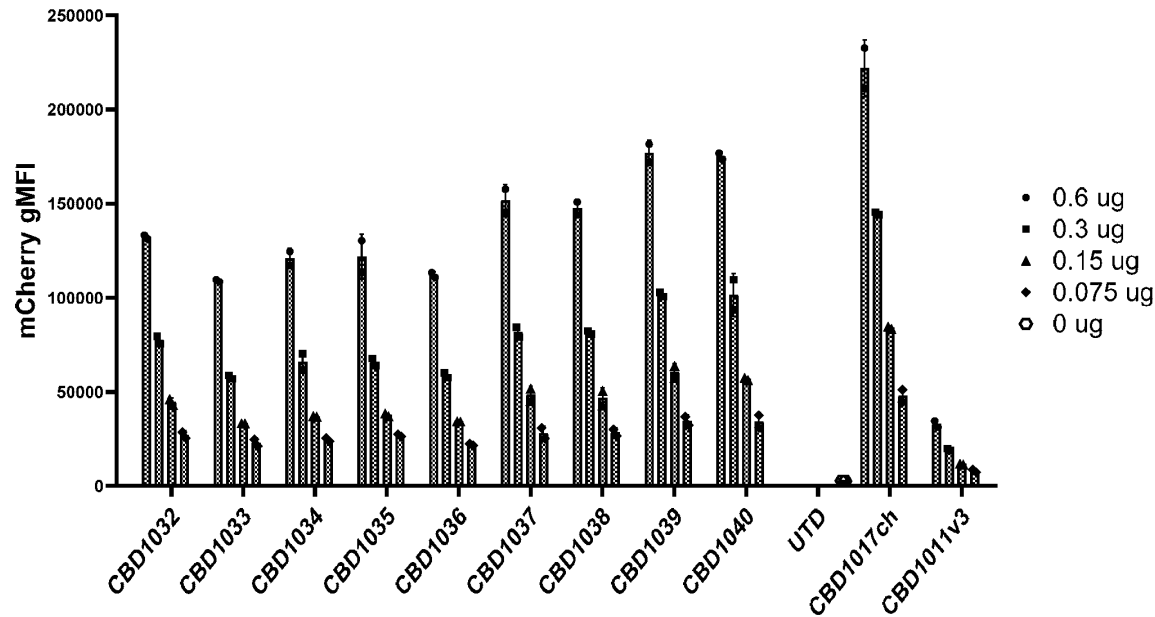


FIG. 4C

Donor 2

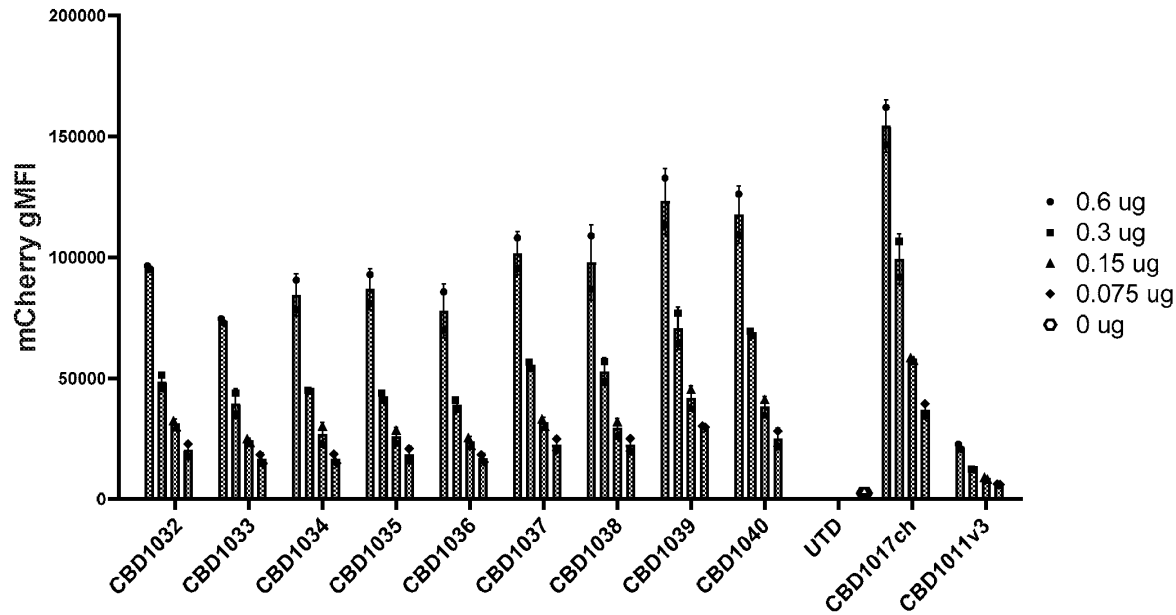


FIG. 4D

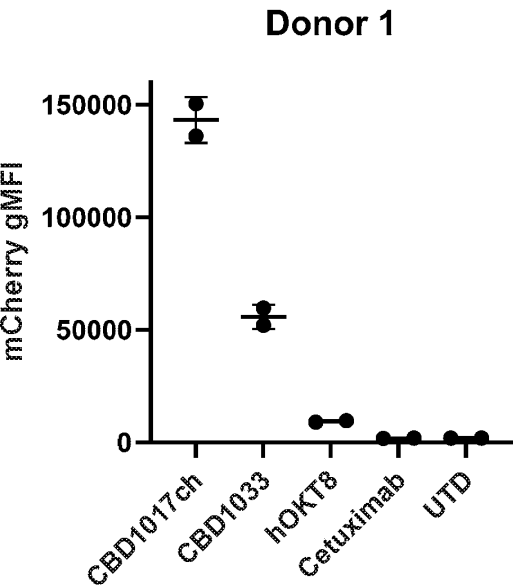


FIG. 5A

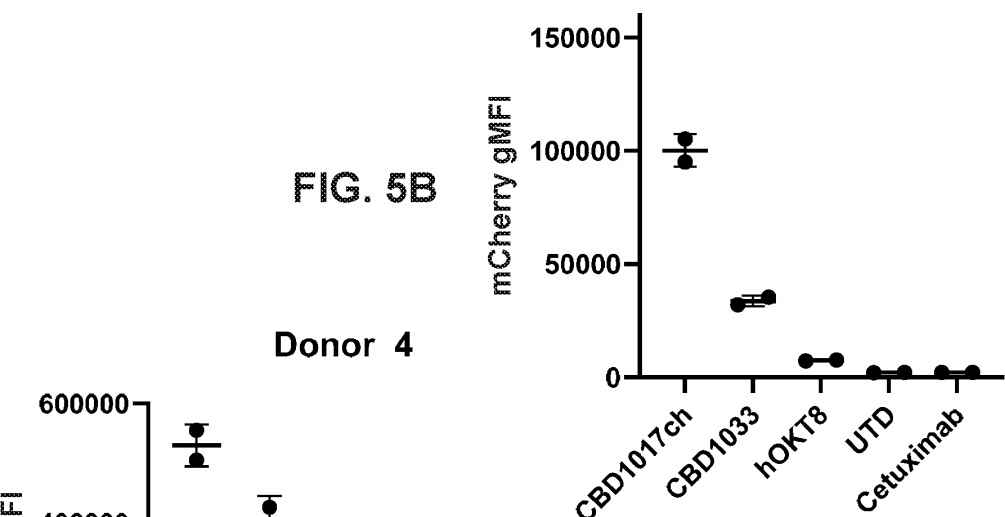


FIG. 5B

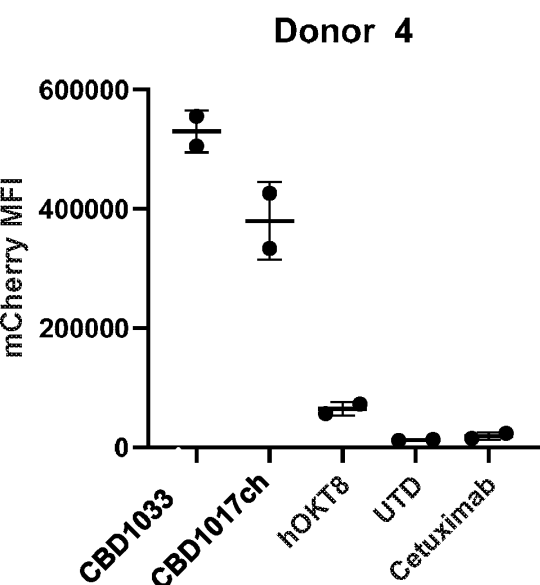


FIG. 5C

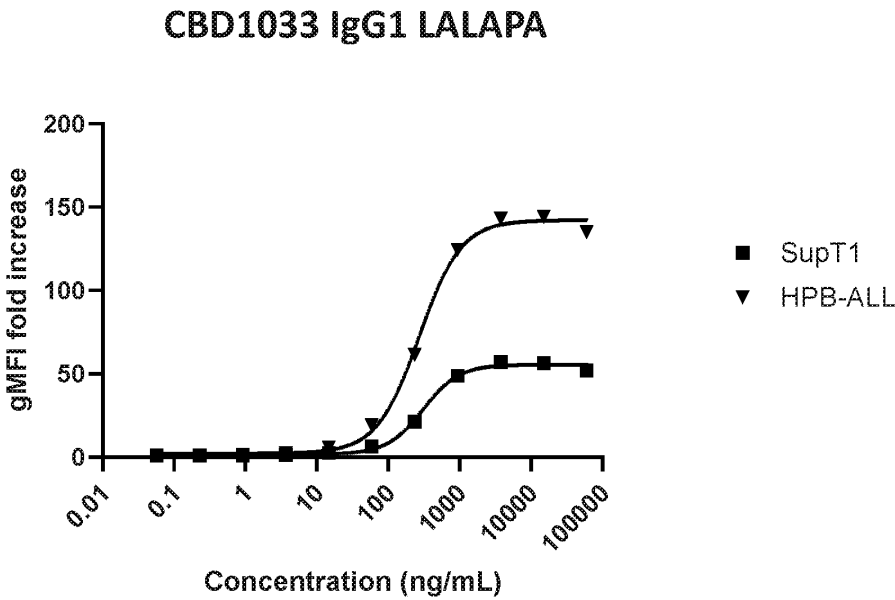


FIG. 6

24/60

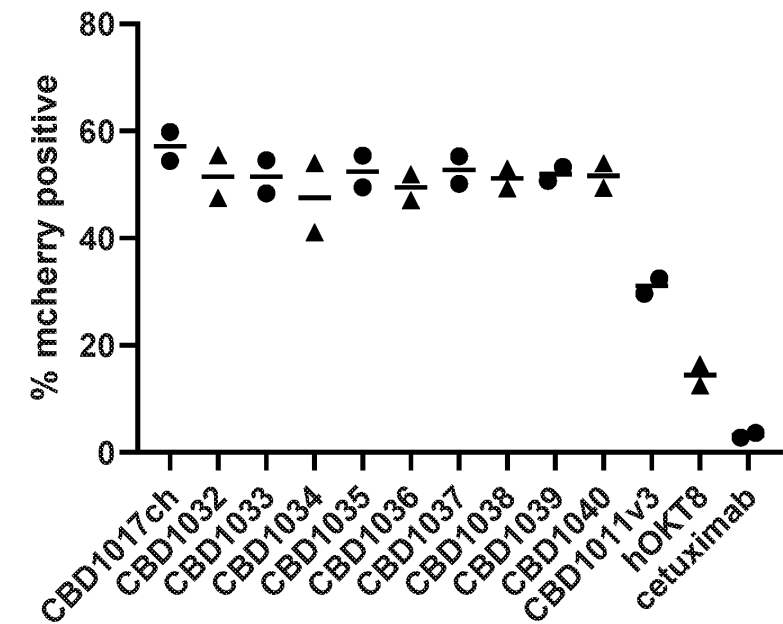


FIG. 7A

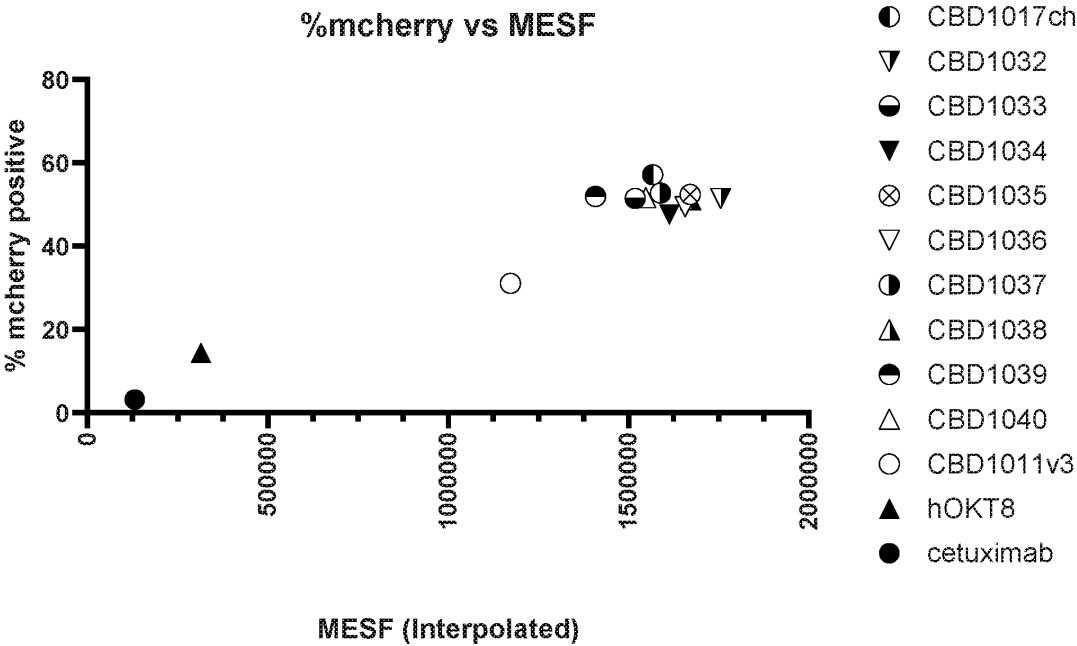


FIG. 7B

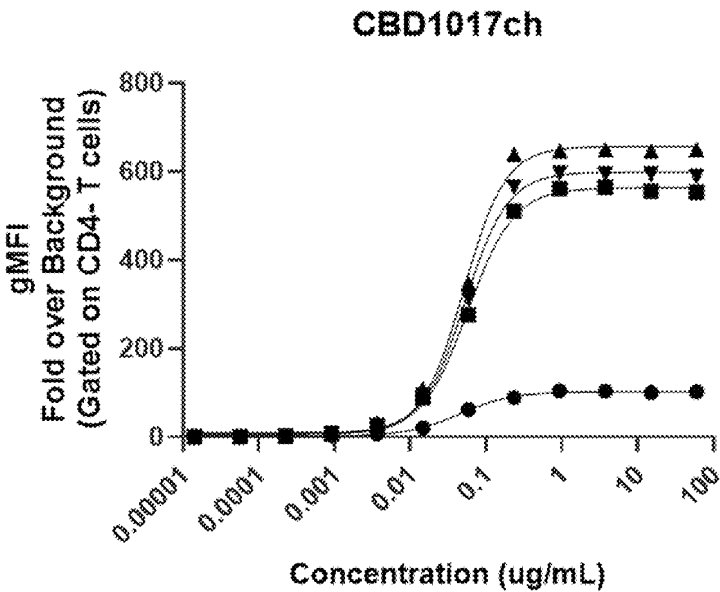
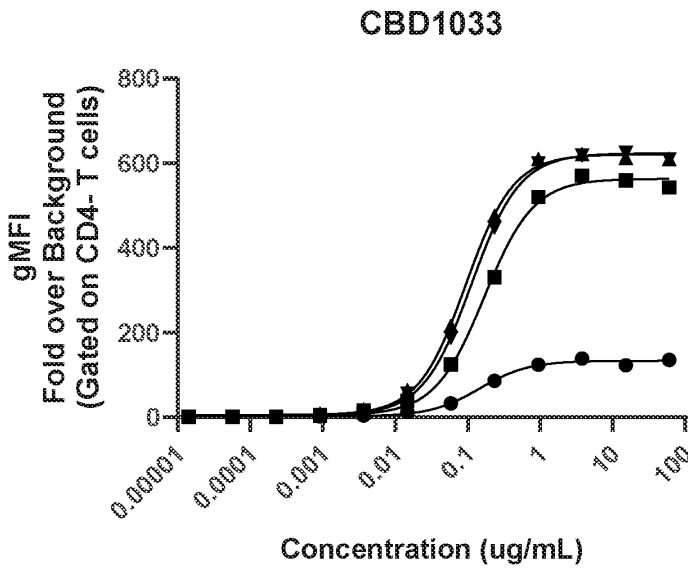


FIG. 8A



- Rhesus Expanded T cells Donor 8
- Cyno Expanded T cells Donor 9
- ▲ Human Expanded T cells Donor 5
- ▼ Human Expanded T cells Donor 6

FIG. 8B

EC50 in $\mu\text{g/mL}$

Name	CBD#	Rhesus Expanded T cells Donor 8	Cyno Expanded T cells Donor 10	Human Expanded T cells Donor 5	Human Expanded T cells Donor 8	Rhesus Expanded T cells Donor 9	Cyno Expanded T cells Donor 9	Human Expanded T cells Donor 5	Human Expanded T cells Donor 8
		Gated on live CD8 T cells (via CD3+CD4-)				Gated on live CD4 T cells (via CD3+CD4+)			
h1017-H2/L2	CBD1033	0.145	0.169	0.094	0.112	Insufficient binding to determine			
Chimeric CT8	CBD1017ch	0.045	0.057	0.051	0.052	Insufficient binding to determine			
Anti-CD5	CBD1011v3	0.105	0.132	0.155	0.190	0.180	0.158	0.185	0.179

FIG. 9A

EC50 in nM

Name	CBD#	Rhesus Expanded T cells Donor 8	Cyno Expanded T cells Donor 10	Human Expanded T cells Donor 5	Human Expanded T cells Donor 8	Rhesus Expanded T cells Donor 9	Cyno Expanded T cells Donor 9	Human Expanded T cells Donor 5	Human Expanded T cells Donor 8
		Gated on live CD8 T cells (via CD3+CD4-)				Gated on live CD4 T cells (via CD3+CD4+)			
h1017-H2/L2	CBD1033	0.993	1.158	0.844	0.767	Insufficient binding to determine			
Chimeric CT8	CBD1017ch	0.308	0.390	0.349	0.356	Insufficient binding to determine			
Anti-CD5	CBD1011v3	0.719	0.904	1.062	1.301	1.096	1.089	1.130	1.226

FIG. 9B

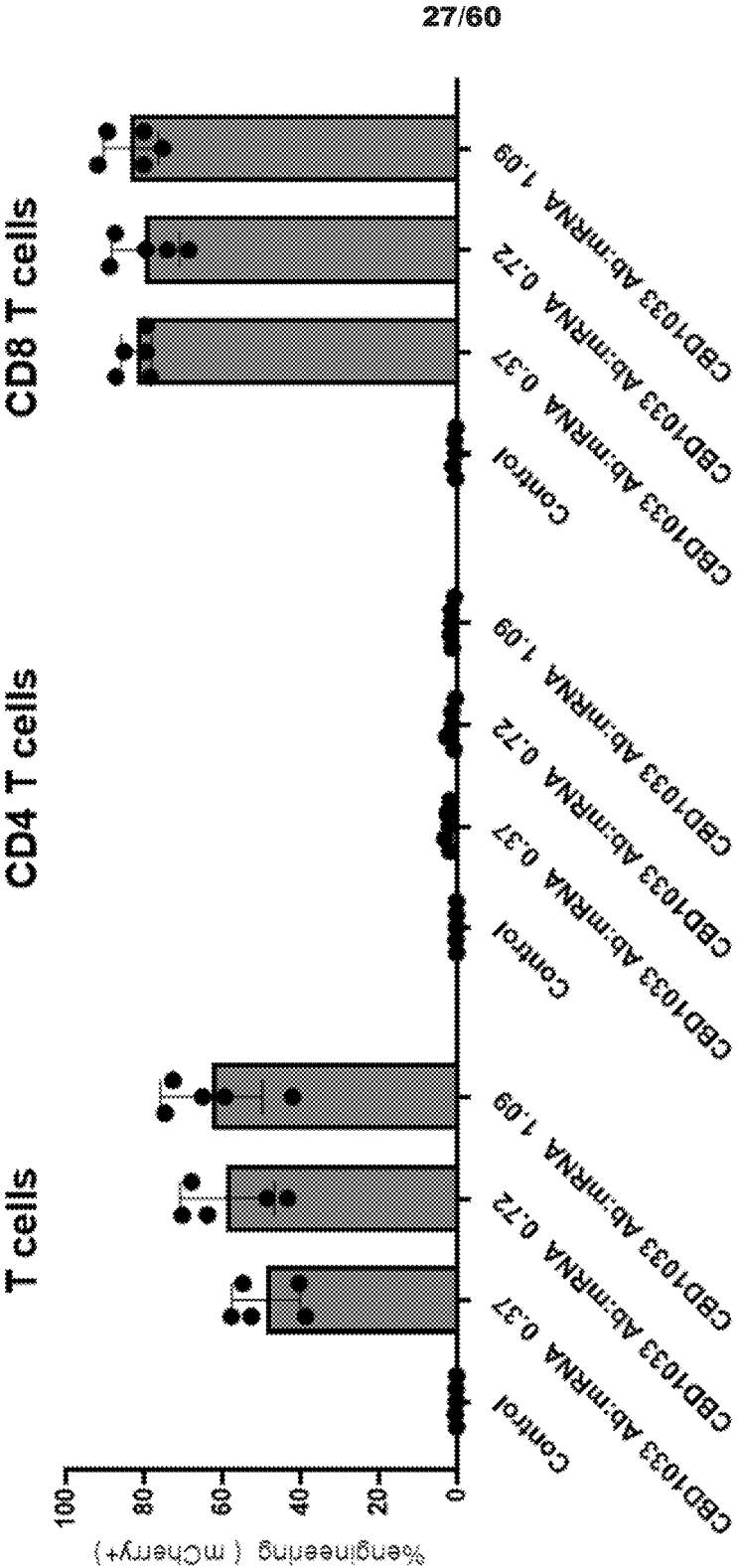


FIG. 10

AC-SINS scores summary table

Antibody ID	Mean $\Delta\lambda_{\text{max}}$ (nm)	Standard deviation (nm)
Alirocumab	1	0.77
Bococizumab	19	1.66
Bococizumab NEI	1	0.01
CBD1032-hIgG1-LALAPA	0	0.32
CBD1033-hIgG1-LALAPA	-1	1.04
CBD1034-hIgG1-LALAPA	-2	0.23
CBD1035-hIgG1-LALAPA	-2	1.14
CBD1039-hIgG1-LALAPA	-1	0.94
CBD1040-hIgG1-LALAPA	1	0.18

FIG. 11A

Graphical representation of the AC-SINS scores $\pm$ 1SD.

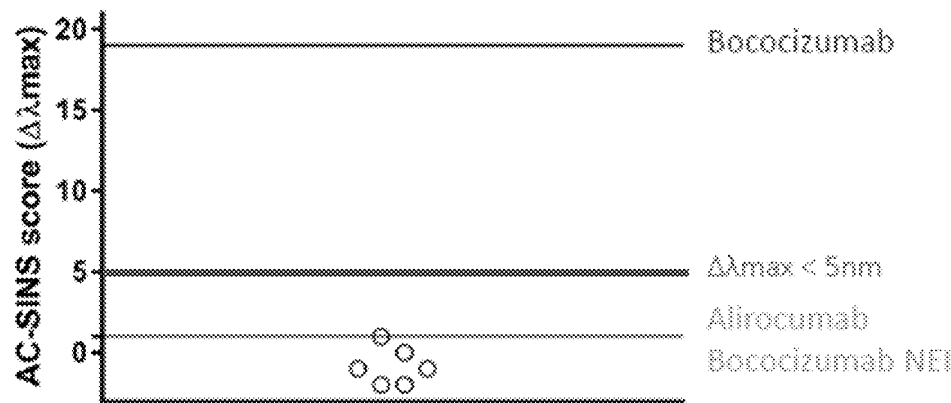


FIG. 11B

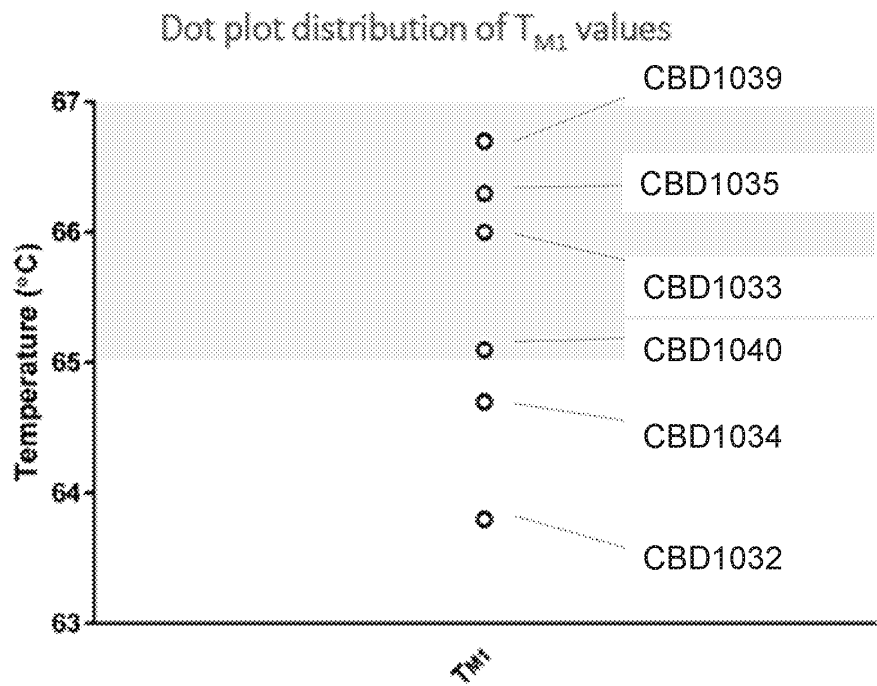


FIG. 12A

Binder	Thermostability		
	DSF		SLS
	T_{M1} (°C)	T_{M2} (°C)	T_{agg} (°C)
CBD1032	63.80	-	59.0
CBD1033	66.00	76.90	61.0
CBD1034	64.70	-	60.8
CBD1035	66.30	-	63.2
CBD1039	66.70	-	63.6
CBD1040	65.10	-	62.4

FIG. 12B

Dot plot distribution of the Polyreactive ELISA scores

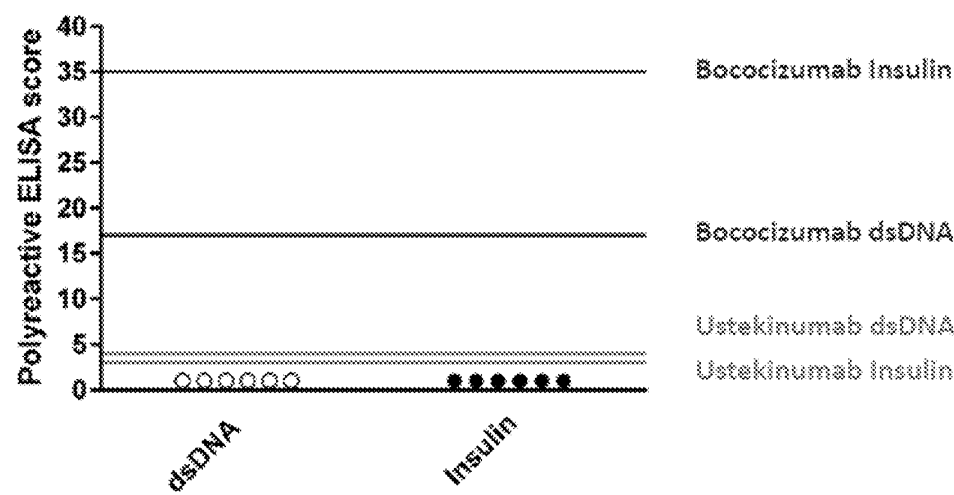


FIG. 13A

Sample ID	Unspecific binding	
	Polyreactive ELISA	
	DNA score	Insulin score
CBD1032	1	1
CBD1033	1	1
CBD1034	1	1
CBD1035	1	1
CBD1039	1	1
CBD1040	1	1

FIG. 13B

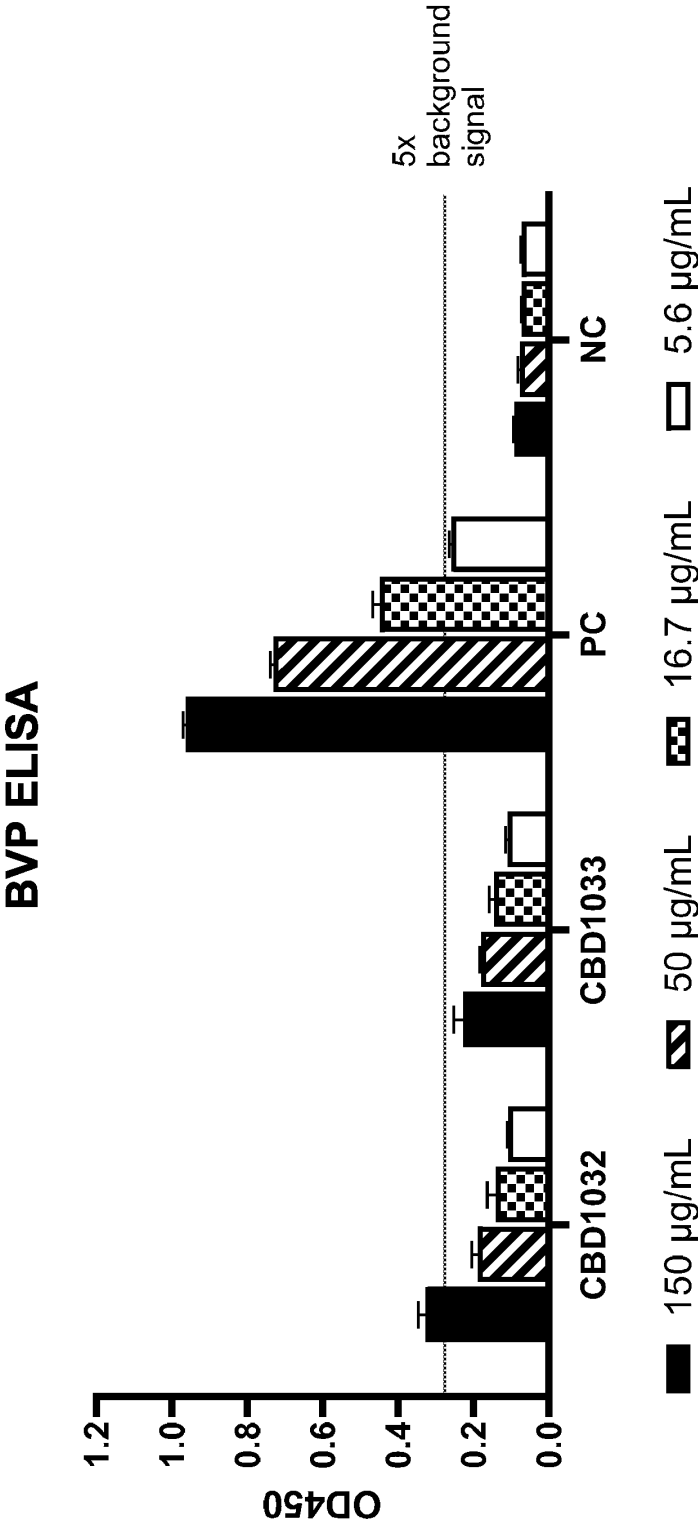


FIG. 14

CBD#	Gene ID	Library screen Pool of 4 test antibodies (fixed cells)		Confirmation screen (fixed cells)		Protein expressed by the gene ID
		Rep 1	Rep 2	Rep 1	Rep 2	
CBD1017ch	CD8A	1	1	2	2	235aa, isoform 1, single-pass type I membrane protein
	CD8A	6	6	4	5	198aa, isoform 2, secreted
	CD8A	6	6	5	6	198 aa, isoform 2, secreted
	CD8A+	1	1	1	2	235aa, isoform 1, single-pass type I membrane protein +
	CD8B					210 aa, isoform 1, single-pass type I membrane protein
CBD1033	CD8A	6	6	3	3	198aa, isoform 2, secreted
	CD8A	6	6	3	4	198aa, isoform 2, tethered
	CD8A	6	6	3	3	198aa, isoform 2, secreted
CBD1035	CD8A	6	6	4	4	198aa, isoform 2, tethered
	CD8A	6	6	3	3	198aa, isoform 2, secreted
CBD1039	CD8A	6	6	5	5	198aa, isoform 2, tethered

CD8A: T-cell surfaces glycoprotein CD8 alpha chain (UniProt ID: P01732-1)

CD8B: T-cell surfaces glycoprotein CD8 beta chain (UniProt ID: P10966-1)

1 - very weak

4 - medium

2 - weak

5 - medium/strong

3 - weak/medium

6 - strong

FIG. 15

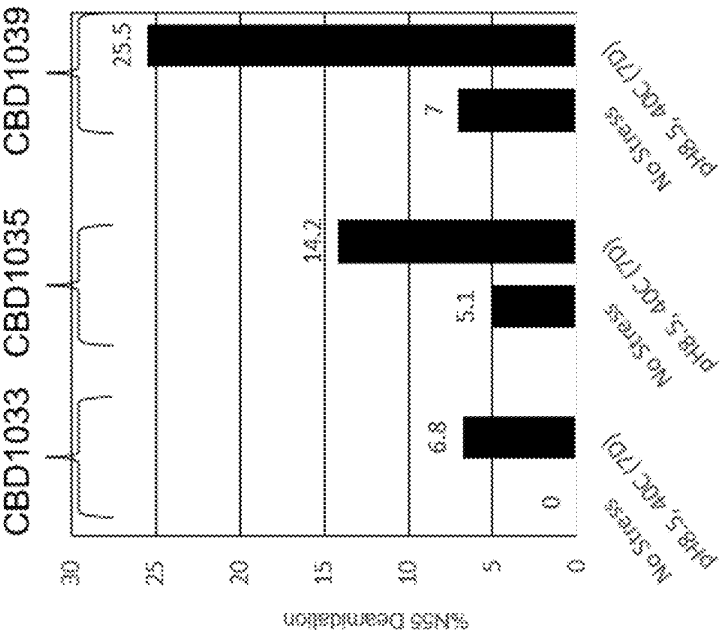


FIG. 16B

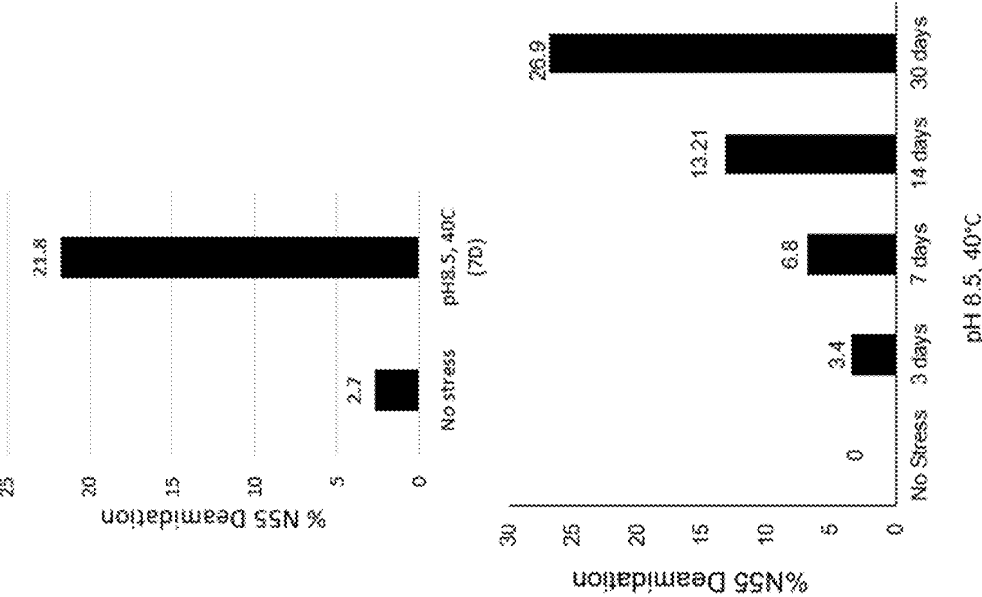


FIG. 16A

FIG. 16C

Sample	Stress Condition	Binding Kinetic Analysis			Steady State Analysis
		k_{on} (1/Ms)	k_{off} (1/s)	K_D (nM)	
CBD1017ch	pH 7.2, 4C (unstressed)	1.53×10^6	6.55×10^{-4}	0.43	0.36
	pH 8.5, 40°C, 7 days	1.45×10^6	7.95×10^{-4}	0.55	0.53
CBD1033	pH 7.2, 4C (unstressed)	1.85×10^6	3.08×10^{-3}	1.66	1.45
	pH 8.5, 40°C, 3 days	1.57×10^6	3.14×10^{-3}	2.00	1.71
	pH 8.5, 40°C, 7 days	1.41×10^6	3.09×10^{-3}	2.19	2.12

FIG. 16D

BLI data									
CBD#	Description	Purity (%) – SEC	Concentration (mg/mL)	Volume (mL)	Yield (mg)	K-on (1/Ms)	K-off (1/s)	Steady State Dissociation Constant KD (x10 ⁻⁹ M)	R ²
CBD1380	hRPA-T8_H2L2_N55S-LALAPA	-	5.68	3	17.0	1.86x10E6	1.92x10E-3	0.76	1
CBD1381	hRPA-T8_H2L2_N55Q-LALAPA	-	5.57	3.1	17.3	1.91x 10E6	7.95x10E-4	0.50	0.98
CBD1382	hRPA-T8_H2L2_N55A-LALAPA	99.7	7.4	2.2	16.3	1.63x10E6	1.95x10E-3	0.88	0.99
CBD1383	hRPA-T8_H2L2_N55D-LALAPA (mimic of 100% deamidation)	99.8	6.1	3.6	22.0	1.1x10E6	3.03x10E-3	7.94	0.99
CBD1033	hRPA-T8_H2L2-LALAPA	-	7.94	-	-	1.85x10 ⁶	3.07x10 ⁻³	1.43	0.99

FIG. 16E

CBD#	Description	Dissociation Constant K_D (nM)	K_{on} (1/Ms)	K_{off} (1/s)
CBD1033	hRPA-T8_H2L2	5.50	3.54×10^4	1.95×10^{-4}
CBD1380	hRPA-T8_H2L2_ N55S_HC	1.93	5.99×10^4	1.16×10^{-4}
CBD1381	hRPA-T8_H2L2_ N55Q_HC	1.22	7.86×10^4	9.59×10^{-5}
CBD1382	hRPA-T8_H2L2_ N55A_HC	0.86	8.03×10^4	6.91×10^{-5}
CBD1443	hRPA-T8_H2L2_ D30E_LC	10.0	2.84×10^4	2.84×10^{-4}
CBD1444	hRPA-T8_H2L2_ D30S_LC	7.69	2.55×10^4	1.96×10^{-4}
CBD1445	hRPA-T8_H2L2_ D30A_LC	15.6	3.07×10^4	4.80×10^{-4}
CBD1622	hRPA-T8_H2L2_ D30S_LC_HC_N55Q	2.91	3.43×10^4	9.97×10^{-5}
CBD1623	hRPA-T8_H2L2_ D30S_LC_HC_N55A	0.617	1.14×10^5	7.02×10^{-5}

FIG. 16F

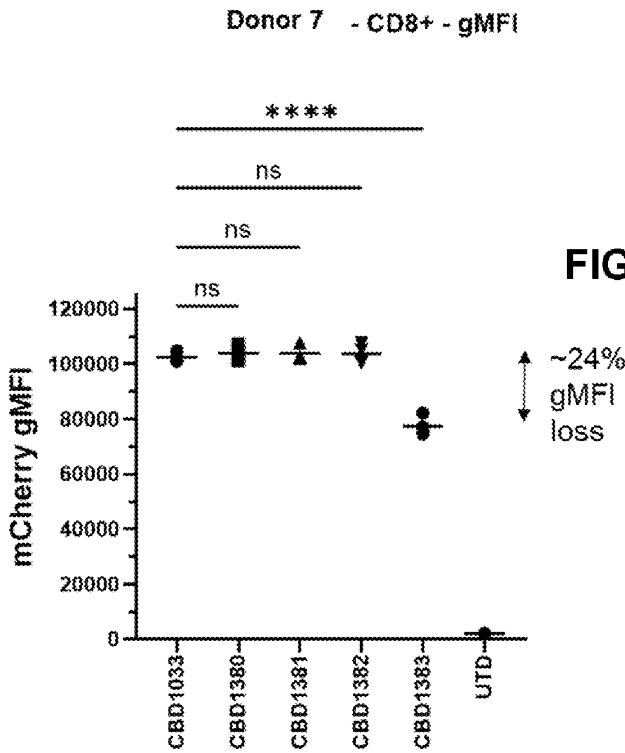


FIG. 17A

Binder	VH N55 Mutation
CBD1033	none
CBD1380	N55S
CBD13801	N55Q
CBD1382	N55A
CBD1383	N55D

FIG. 17C

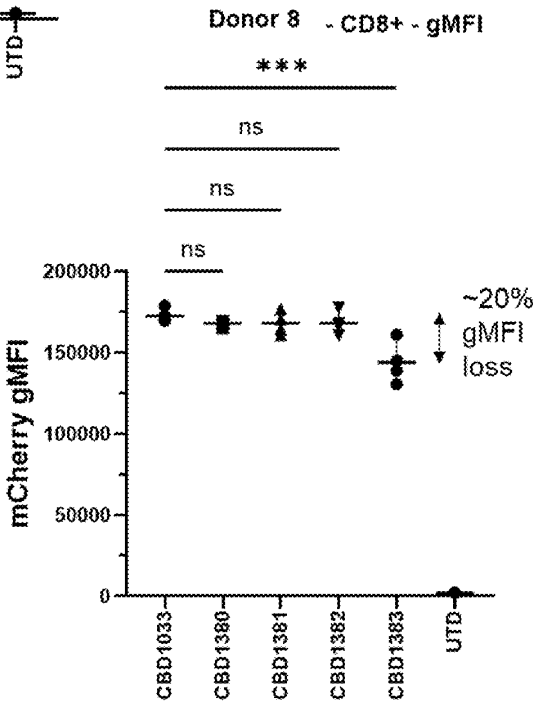


FIG. 17B

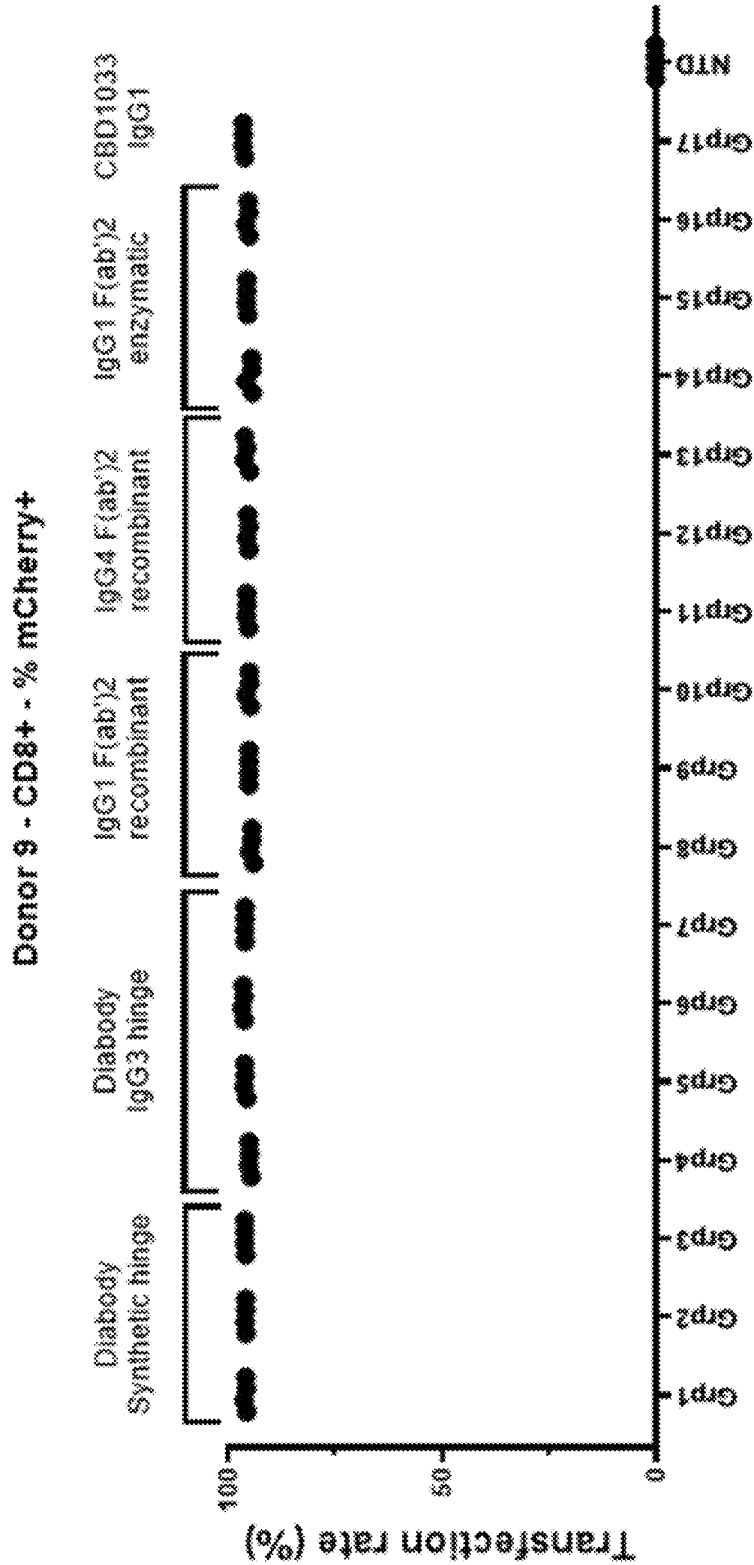


FIG. 18A

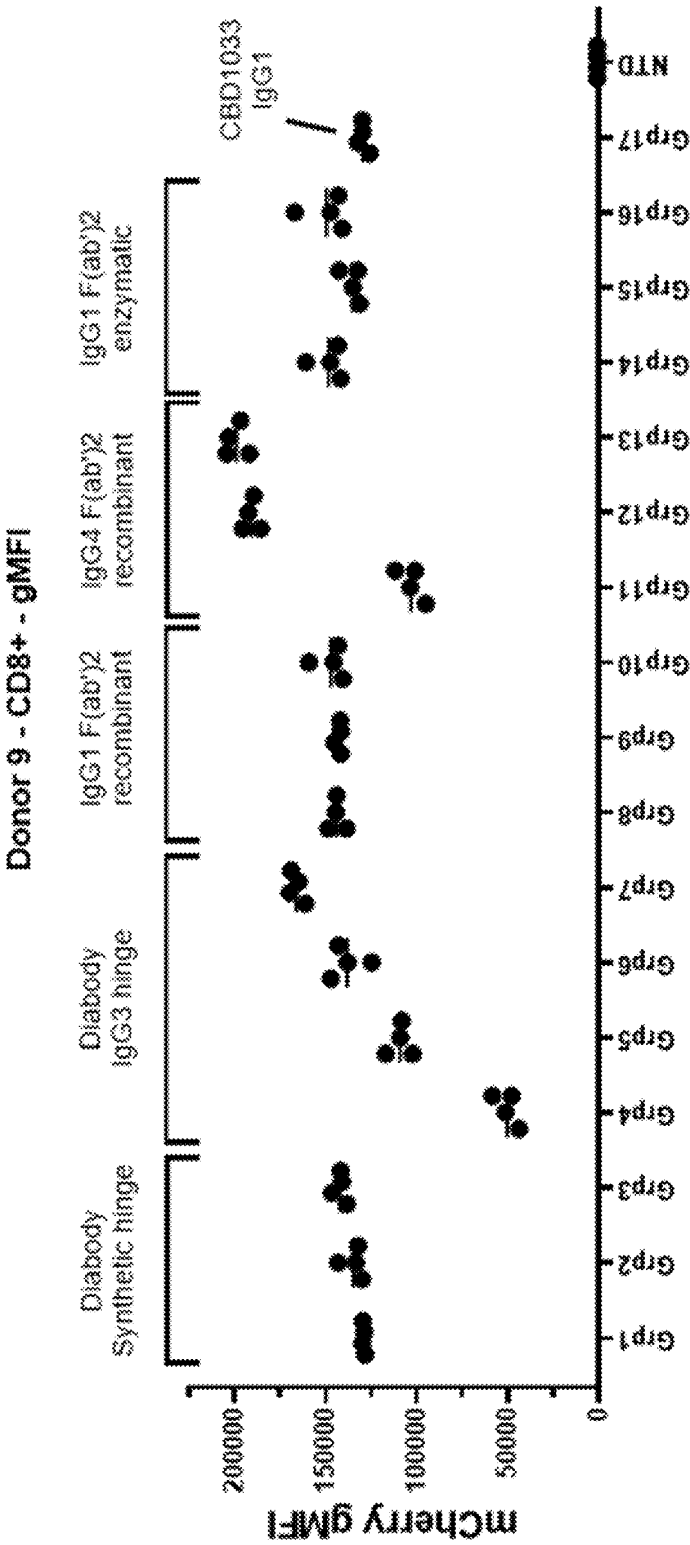
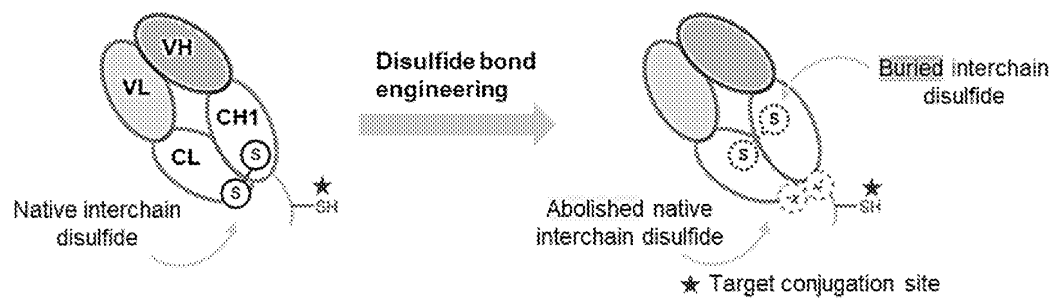
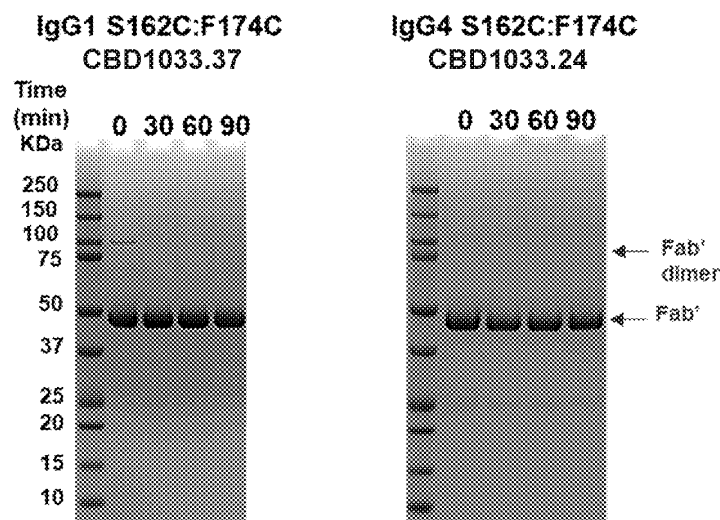


FIG. 18B

40/60

**FIG. 19A**

**Fab binders with the engineered disulfide bond
show resistance to mild reduction condition**



Reduction condition: 5 mM 2-MEA, rt; Sample load: 4ug

FIG. 19B

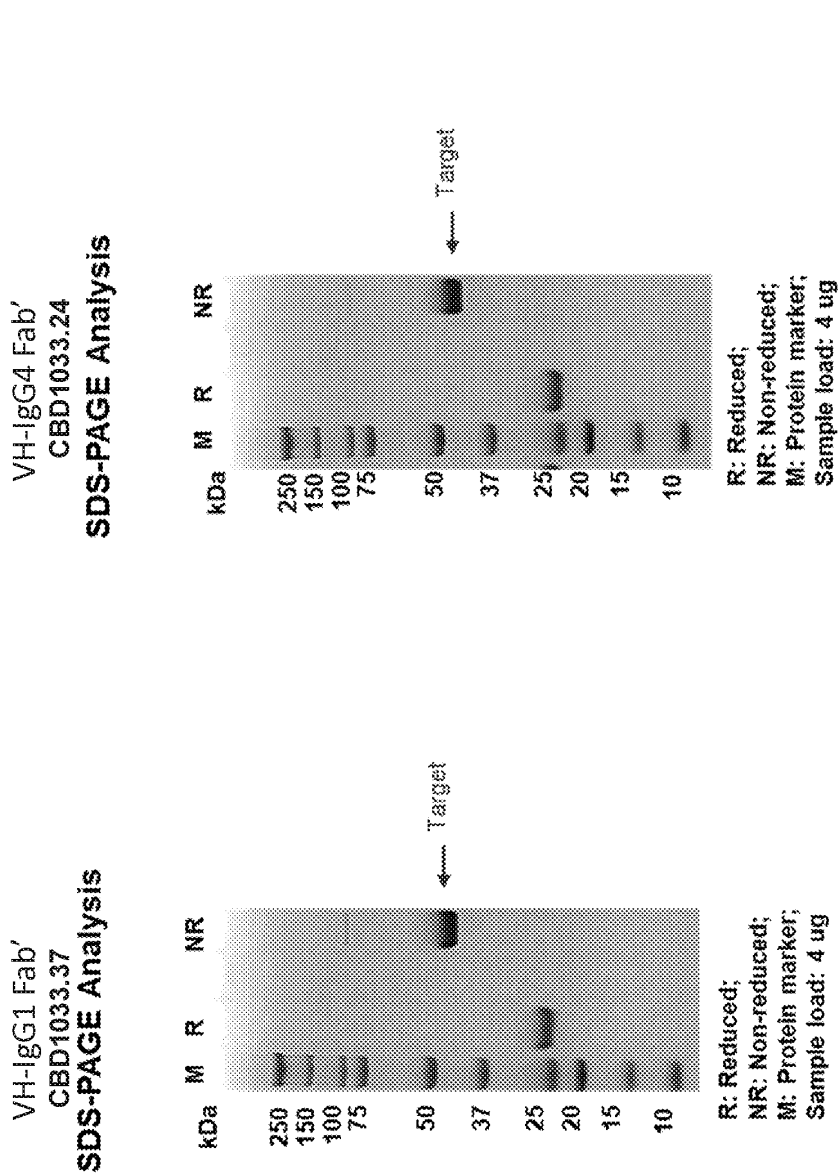
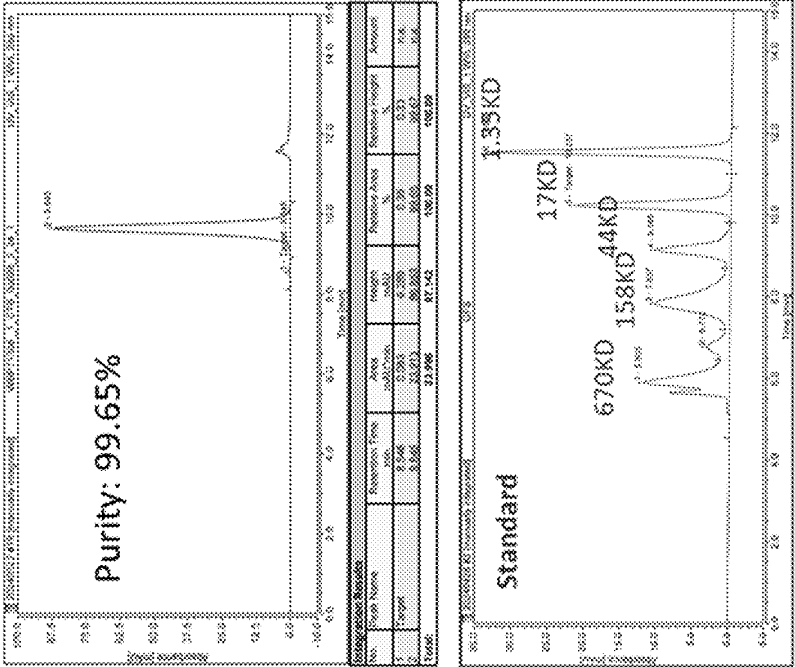


FIG. 20A

VH-IgG4 Fab'
CBD1033.24
SEC-HPLC Analysis



VH-IgG1 Fab'
CBD1033.37
SEC-HPLC Analysis

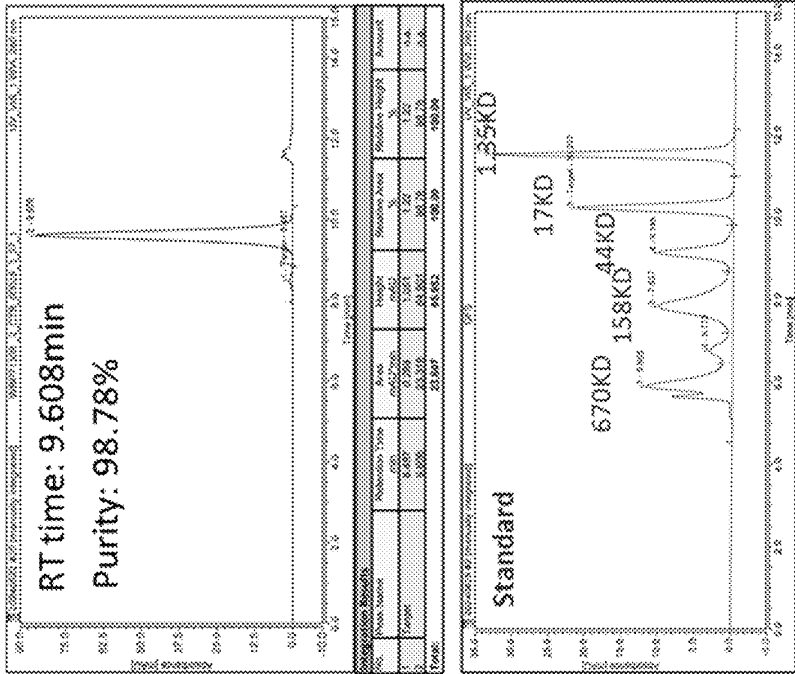


FIG. 20B

VH-IgG1 Fab'
CBD1033.37

Non-reducing LC-MS Analysis						
Species	Modification	Theoretical Mass (Da)	Observed Mass (Da)	Mass Intensity	Mass Error %	Abundance %
HC1[Q1-C230]+LC1	pE(Q)	48443.8	48445.2	28.5	2599.5	1.9
HC1[Q1-A231]+LC1	pE(Q)	48514.9	48516.1	24.7	4207.9	3.1
Fab (HC1+LC1)	pE(Q)	48587.0	48587.4	9.0	123393.7	90.9
	pE(Q),Glycation	48749.1	48749.5	8.1	3567.2	2.6
Fab' dimer {HC1*2+LC1*2}	pE(Q)*2	97173.9	97173.3	-6.4	1987.6	1.5

VH-IgG4 Fab'
CBD1033.24

Non-reducing LC-MS Analysis						
Species	Modification	Theoretical Mass (Da)	Observed Mass (Da)	Mass Intensity	Mass Error %	Abundance %
HC1[Q1-C227]+LC1	pE(Q)	48238.6	48239.9	27.8	4180.3	2.1
HC1[Q1-A228]+LC1	pE(Q)	48309.6	48311.1	30.2	3425.1	1.7
Fab (HC1+LC1)	pE(Q)	48381.7	48382.2	10.2	187548.3	93.3
	pE(Q),Glycation	48543.8	48544.2	7.3	4270.4	2.1
Fab' dimer {HC1*2+LC1*2}	pE(Q)*2	96763.4	96763.5	0.9	1630.3	0.8

FIG. 20C

Fab fragment	K _D (nM)	k _{on} (1/Ms)	k _{off} (1/s)	R ²
CBD1033.37	4.01	1.56x10 ⁴	6.28x10 ⁻⁵	0.9997
CBD1033.42	5.09	1.26x10 ⁴	6.41x10 ⁻⁵	0.9998
CBD1033.44	7.23	1.23x10 ⁴	8.88x10 ⁻⁵	0.9997
CBD1033.45	9.03	1.30x10 ⁴	1.17x10 ⁻⁴	0.9997

FIG. 21A

BLI measurement shows retained binding affinity
in a disulfide-engineered Fab'

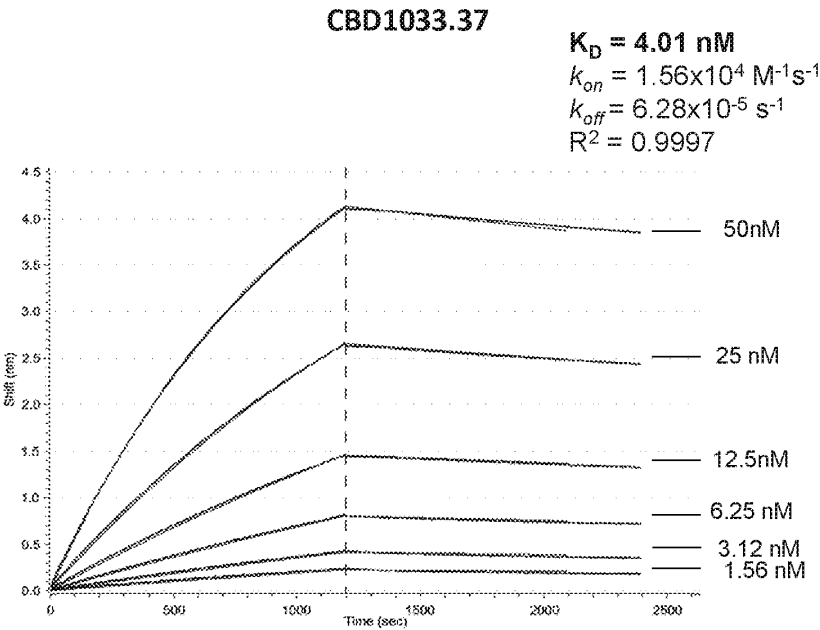


FIG. 21B

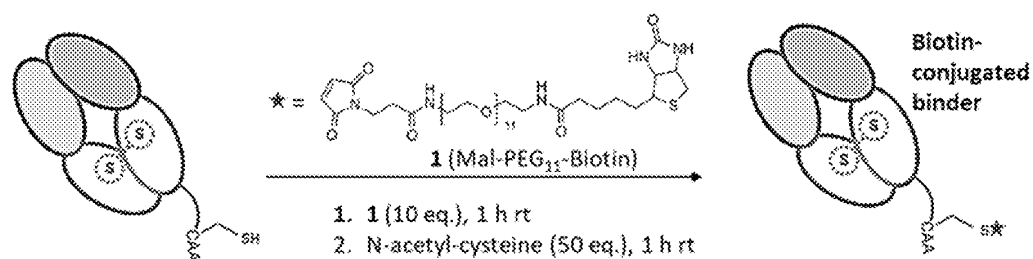


FIG. 22A

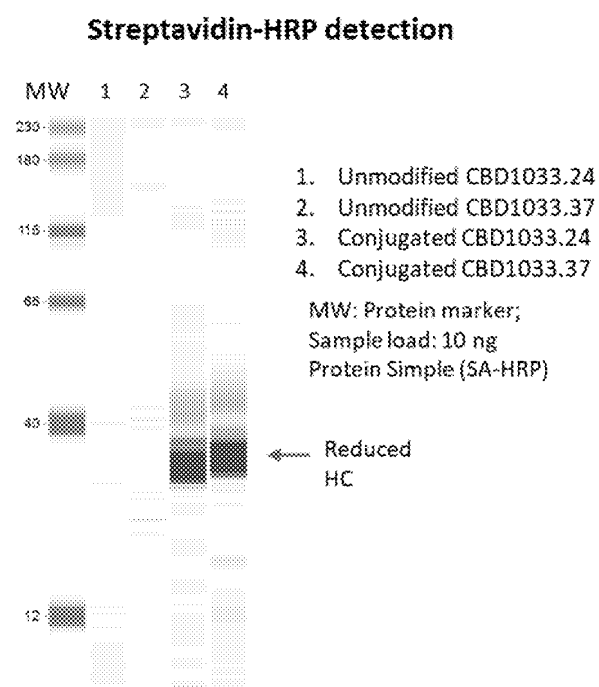


FIG. 22B

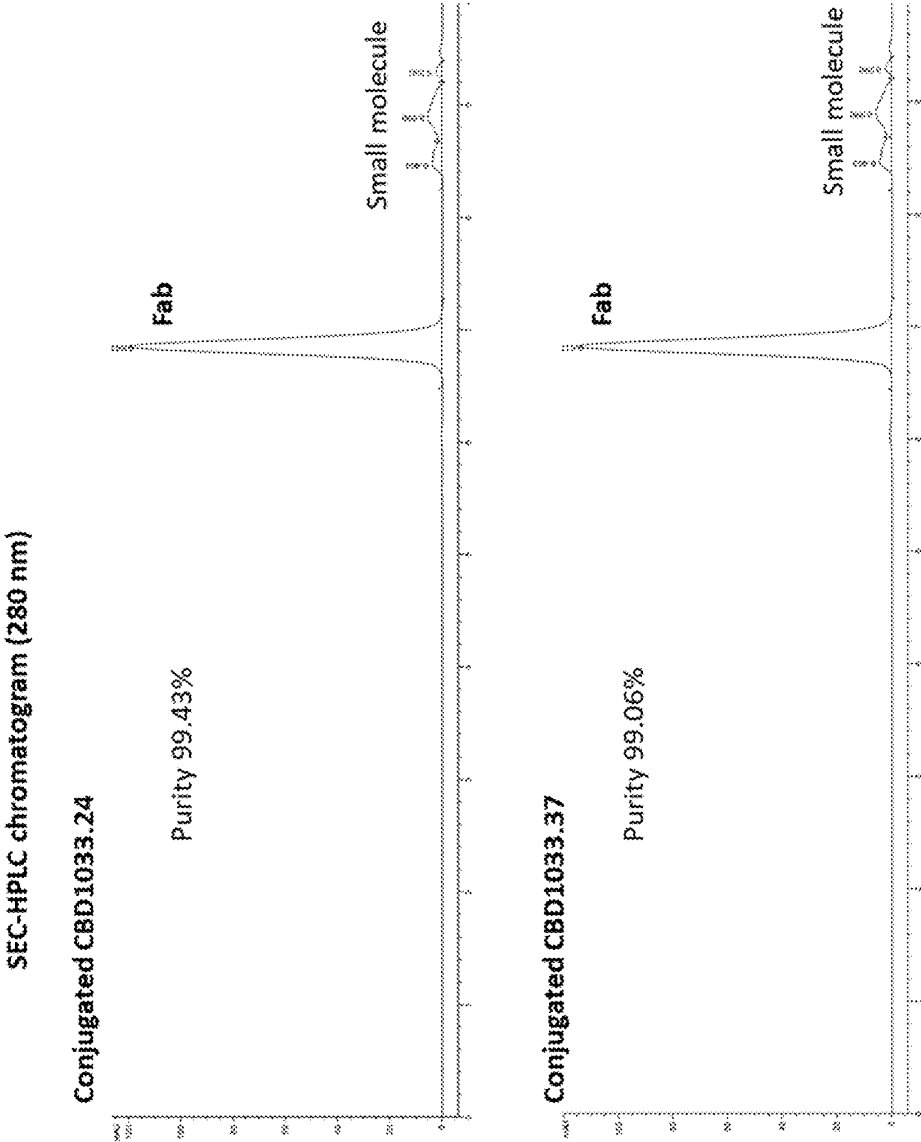


FIG. 22C

CBD1033.24

Non-reducing Denatured Mass					
Species	Theoretical Mass (Da)	Observed Mass (Da)	Mass Intensity	Mass Error %	Abundance %
HC1+LC1[P99-S218,D98/P99] + 1*MPB	38754.2	38755.0	5.80E+07	-	2.20%
Fab' (HC1+LC1) +1*MPB	49302.7	49303.0	2.57E+09	0.001	97.80%

CBD1033.37

Non-reducing Denatured Mass					
Species	Theoretical Mass (Da)	Observed Mass (Da)	Mass Intensity	Mass Error %	Abundance %
HC1+LC1[P99-S218,D98/P99] + 1*MPB	38959.4	38960.0	4.98E+07	-	1.98%
Fab' (HC1+LC1) +1*MPB	49508.0	49508.0	2.46E+09	0.000	98.02%

FIG. 22D

CBD1033.24

Peptide Mapping		
Protein*	Modification	Abundance
LC	~D30+H2O loss	1.58%
LC	M37+Oxidation	1.54%
HC	Q1+NH3 loss	100.00%
HC	~M48+Oxidation	2.14%
HC	~N55+NH3 loss	1.95%
HC	C227+Maleimide PEG11 Biotin	95.47%

CBD1033.37

Peptide Mapping		
Protein*	Modification	Abundance
LC	~D30+H2O loss	1.54%
HC	Q1+NH3 loss	100.00%
HC	~M48+Oxidation	1.77%
HC	~N55+NH3 loss	1.63%
HC	C230+Maleimide PEG11 Biotin	100.00%

FIG. 22E

Antigen	F(ab') fragment	K_D (nM)	k_{on} (1/Ms)	k_{off} (1/s)
HuCD8a mouse Fc fusion	CBD1033.24	4.01	3.24×10^4	1.30×10^{-4}
	CBD1033.37	6.85	2.09×10^4	1.44×10^{-4}

FIG. 23A

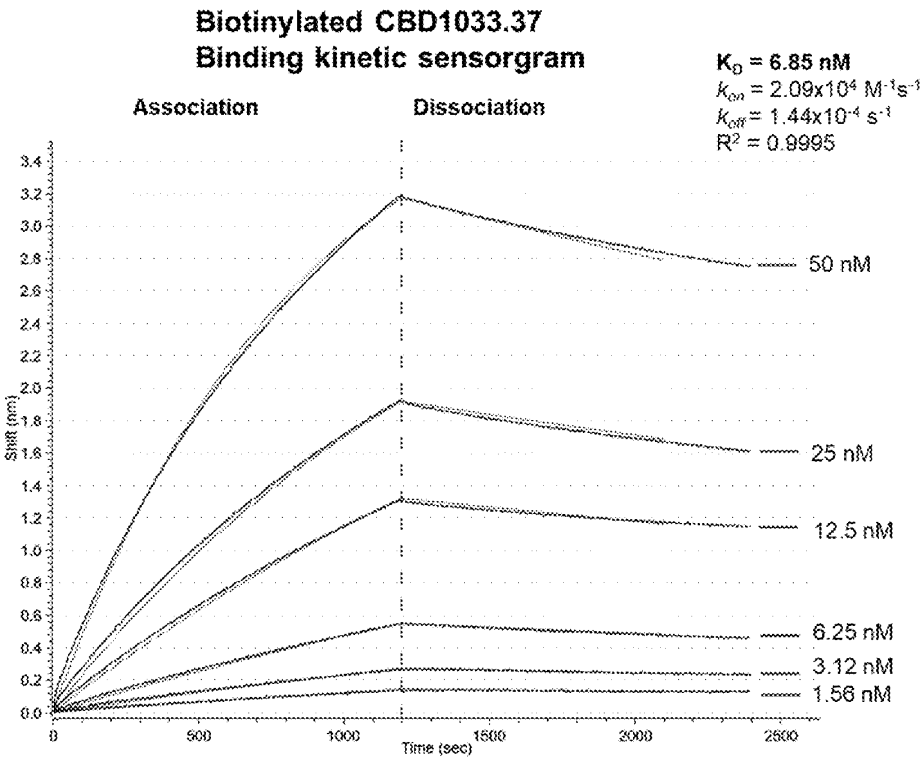


FIG. 23B

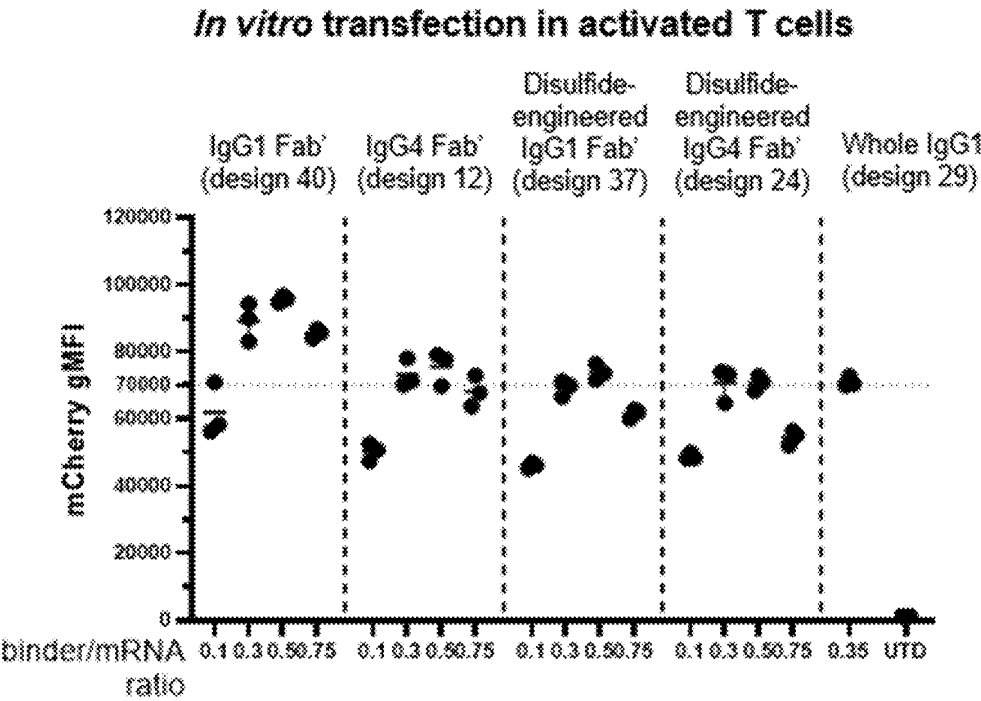


FIG. 24A

In vivo delivery of mCherry-encoding tLNP in NSG-PBMC mice

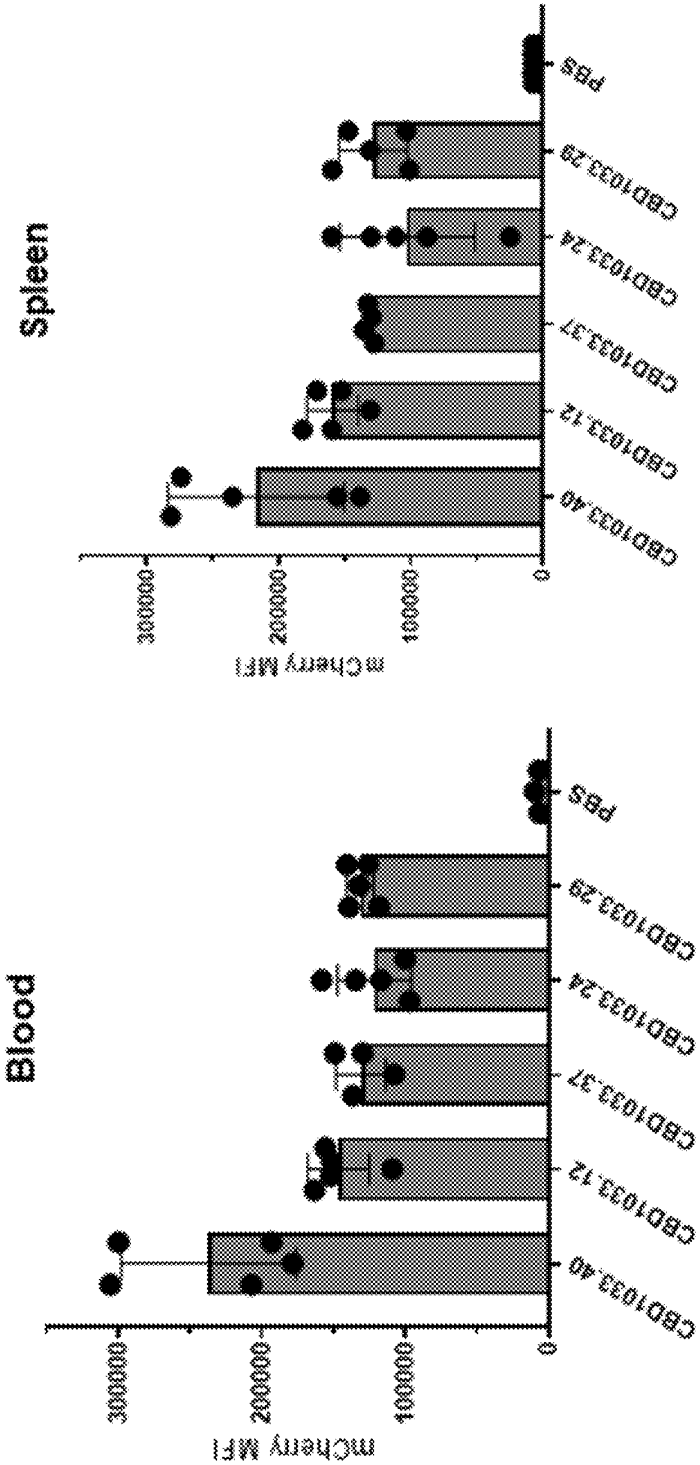


FIG. 24B

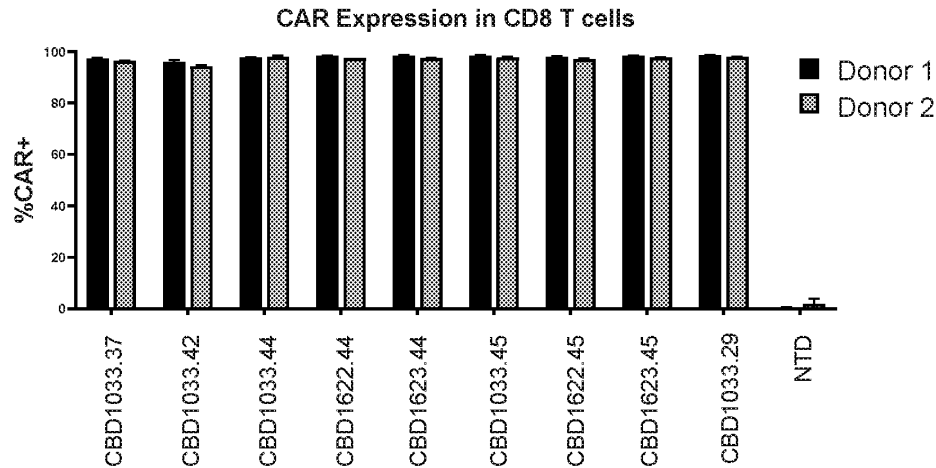


FIG. 25A

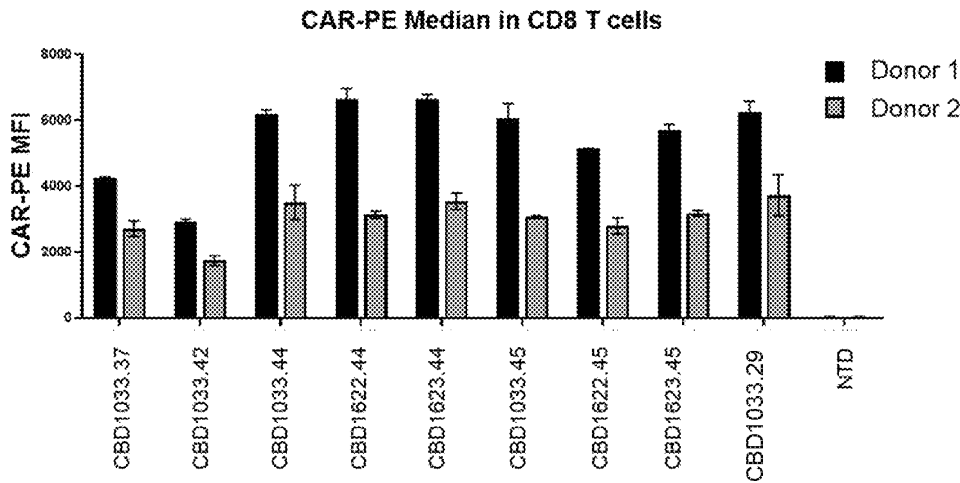
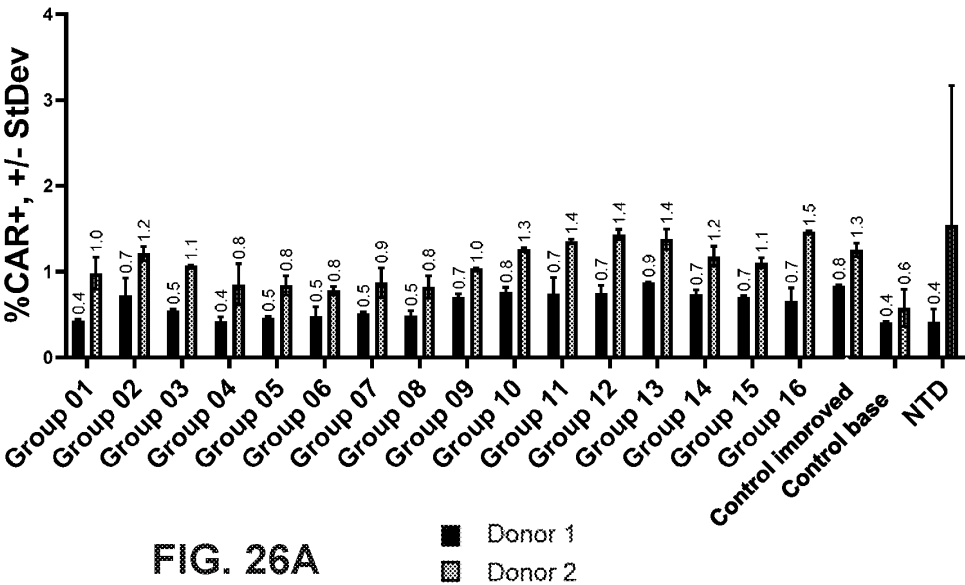
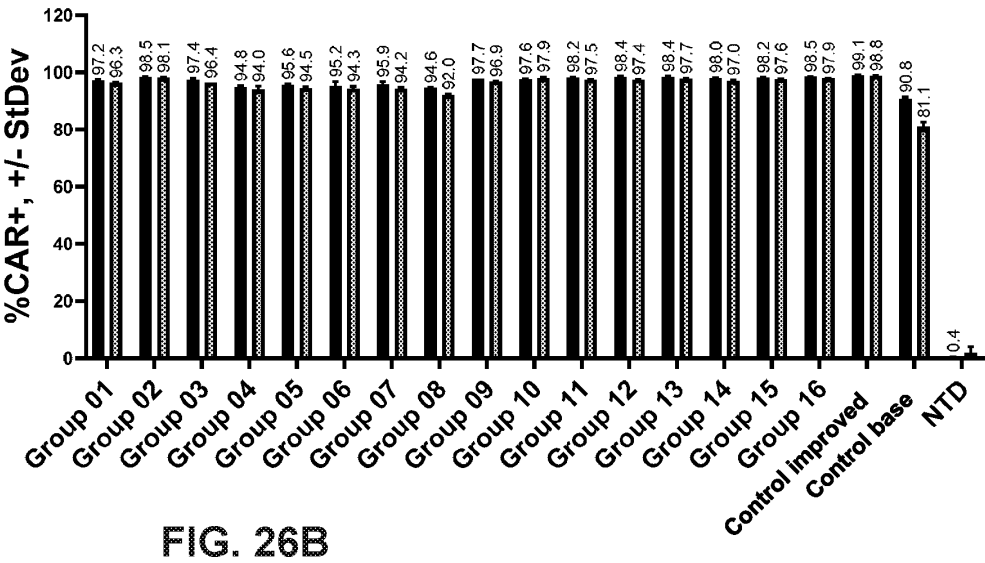


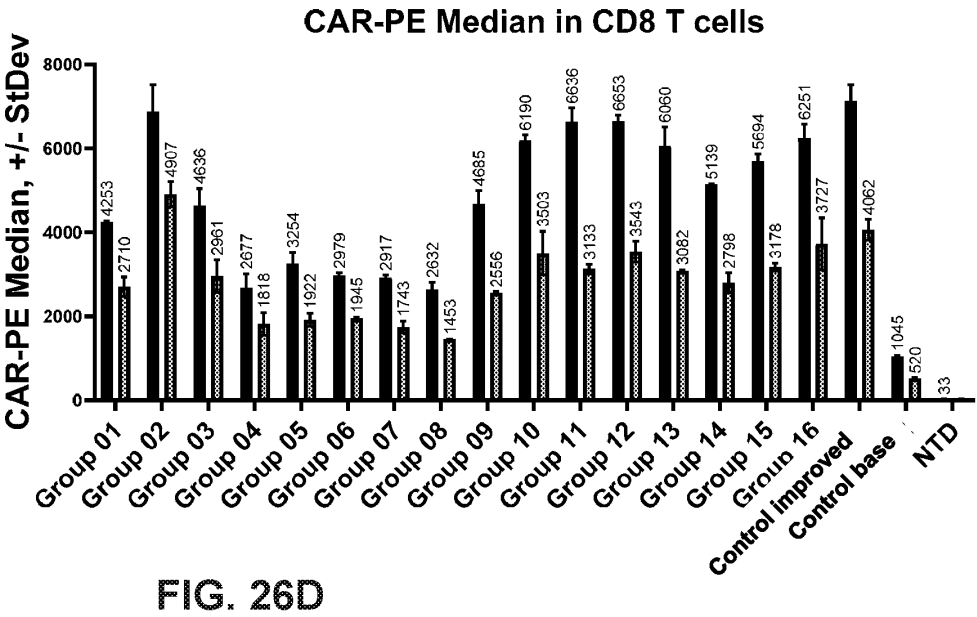
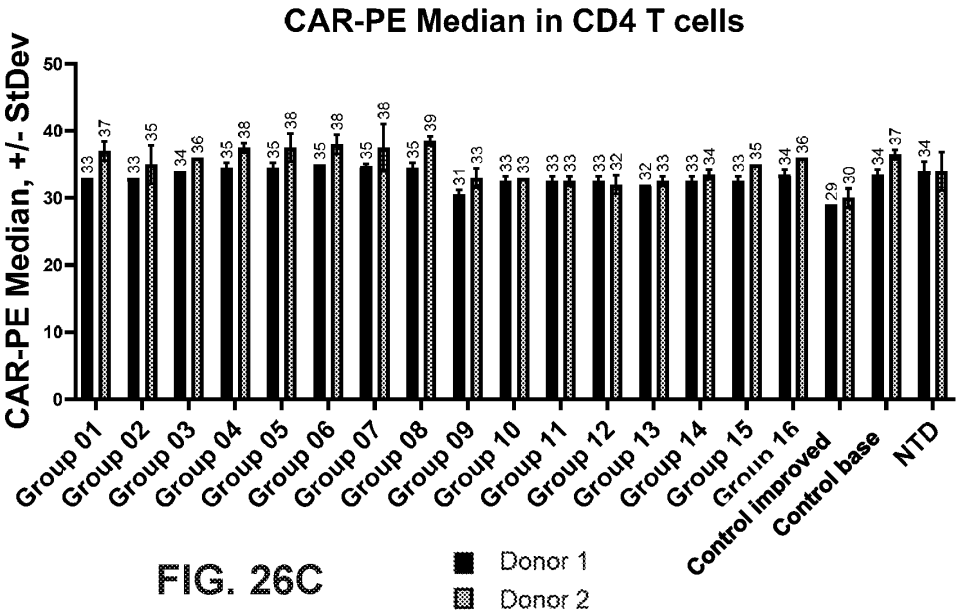
FIG. 25B

CAR Expression in CD4 T cells



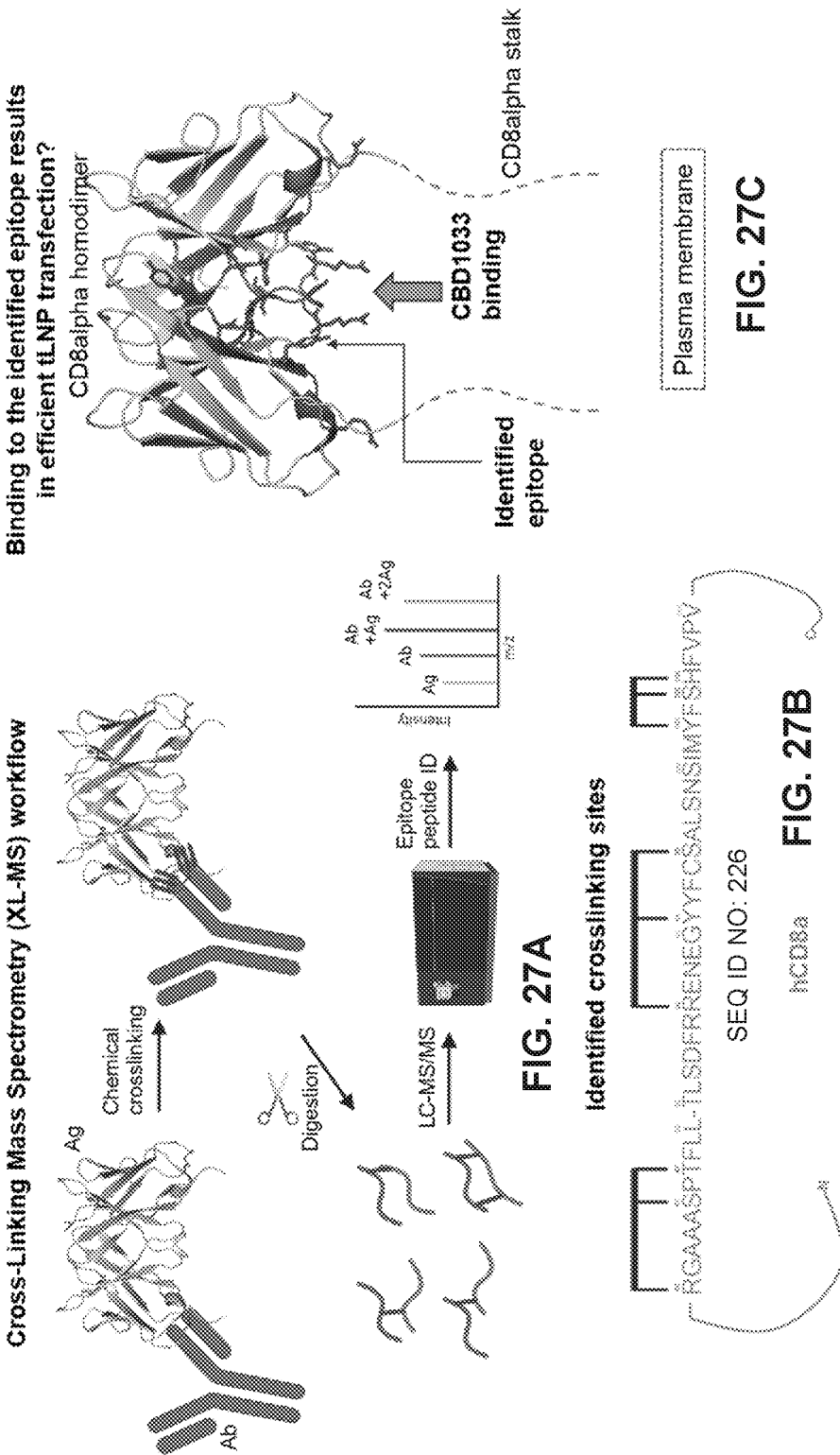
CAR Expression in CD8 T cells





Group	Format design	CBD number	Liability-engineered mutation
1	37	CBD1033.37	None
2		CBD1381.37	HC_N55Q
3		CBD1382.37	HC_N55A
4		CBD1444.37	LC_D30S
5		CBD1622.37	LC_D30S/HC_N55Q
6		CBD1623.37	LC_D30S/HC_N55A
7	42	CBD1033.42	None
8		CBD1622.42	LC_D30S/HC_N55Q
9		CBD1623.42	LC_D30S/HC_N55A
10	44	CBD1033.44	None
11		CBD1622.44	LC_D30S/HC_N55Q
12		CBD1623.44	LC_D30S/HC_N55A
13	45	CBD1033.45	None
14		CBD1622.45	LC_D30S/HC_N55Q
15		CBD1623.45	LC_D30S/HC_N55A
16	IgG (LALAPA) (AJICAP)	CBD1033.29	None

FIG. 26E



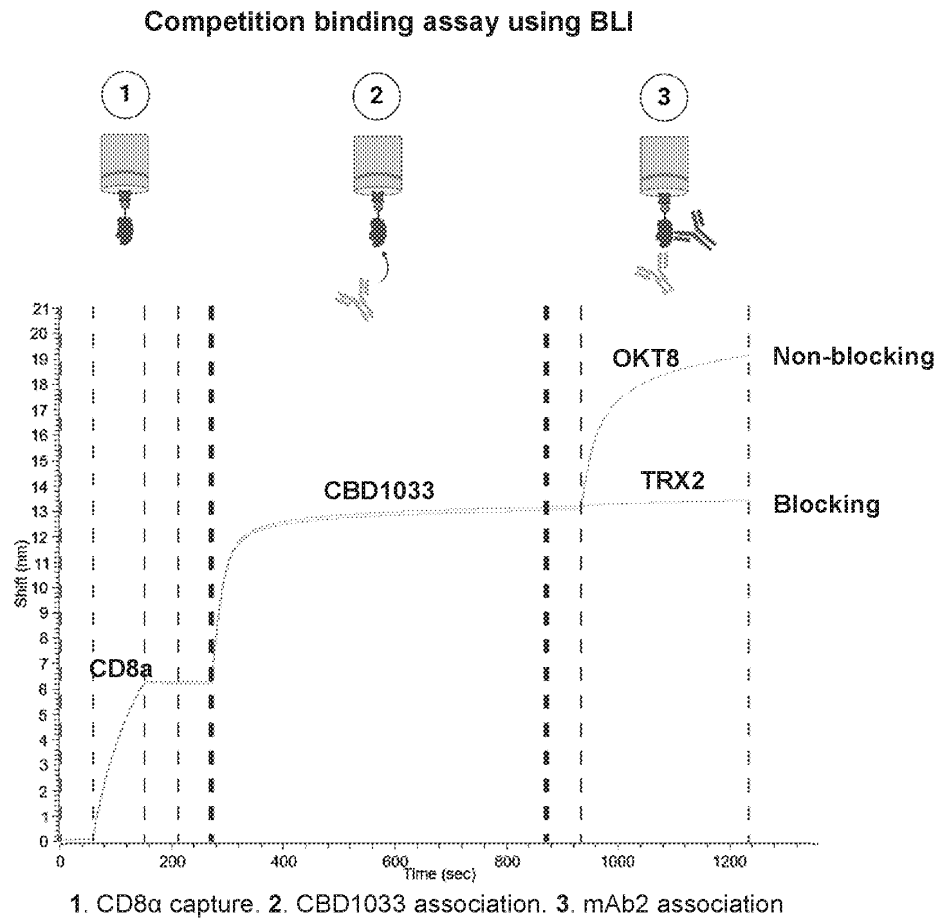


FIG. 28A

Cross-competition of known anti-CD8 antibodies

Sample	CBD1033	TRX2	YTC182.20	OKT8	SK1	HIT8a
CBD1033	0.001	-0.005	-0.01	1.691	1.991	1.826
TRX2	0.069	0.005	-0.006	1.946	0.153	2.251
YTC182.20	0.061	-0.005	0.003	1.941	0.244	2.073
OKT8	2.882	3.052	3.196	0.048	2.024	0.338
SK1	3.314	2.415	2.206	2.822	0.069	0.151
HIT8a	2.472	2.661	2.52	1.206	0.057	0.056

FIG. 28B

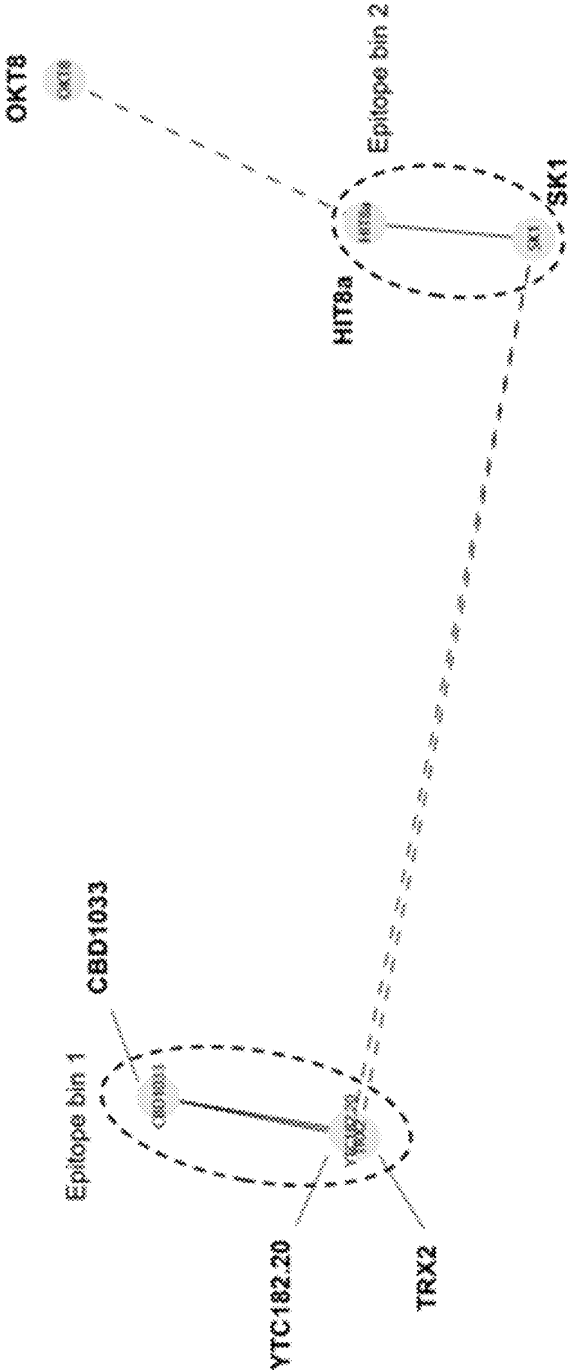


FIG. 28C

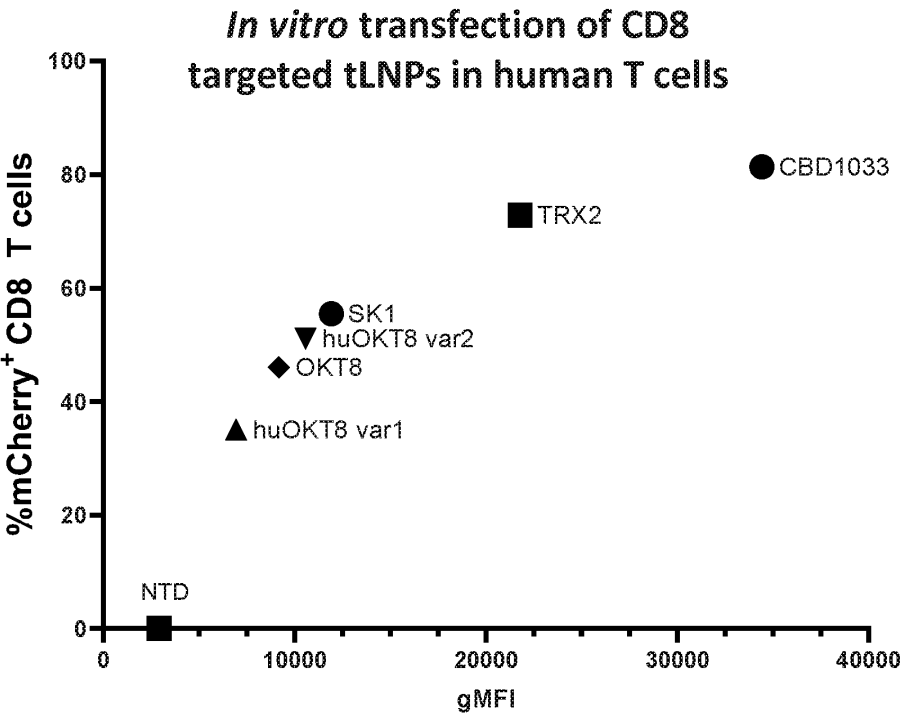


FIG. 29A

Transfection of CD8 targeting tLNPs in NSG-PBMC

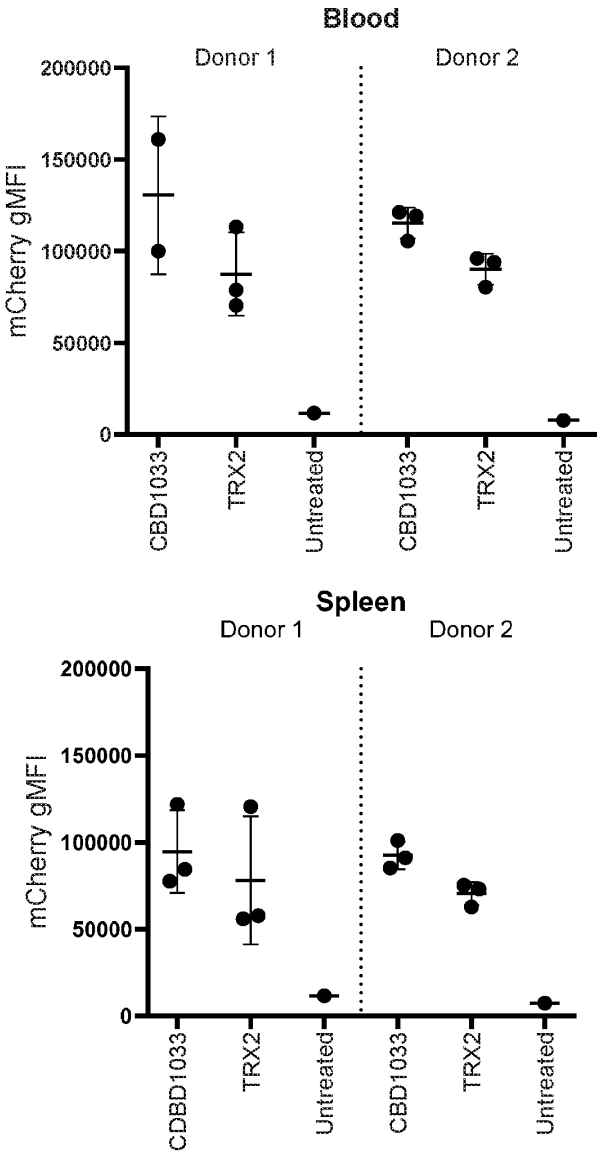


FIG. 29B