

Native hCD138: (Uniprot id: P18827)

10	20	30	40	50	60	70	80	90	100
MRRALW	LW	CALALS	LQPA	LPQIVATNLP	PEDQDGS	GDD	SDNFGSGAG	ALQDITLSQ	Q
TPSTWKD	TQL	LTAIPTSP	EP	TGLEATAAST	STLPAGEGPK				
110	120	130	140	150	160	170	180	190	200
EGEAVVLP	EV	EPGLTAREQE	ATPRPRETTQ	LPTHLASTT	TATTAQEPAT	SHPRDMQPG	HHETSTPAGP	SQADLHTPHT	EDGGPSATER
AAEDGASSQL									
210	220	230	240	250	260	270	280	290	300
PAAEGSGEQD	FTFETSGENT	AVVAVEPDRR	NQSPVDQ	GAT	GASQGLLDRK	EVLG	GIAGG	LVGLIFAVCL	VGFM
310									
KPTKQEEFYA									

FIG. 1

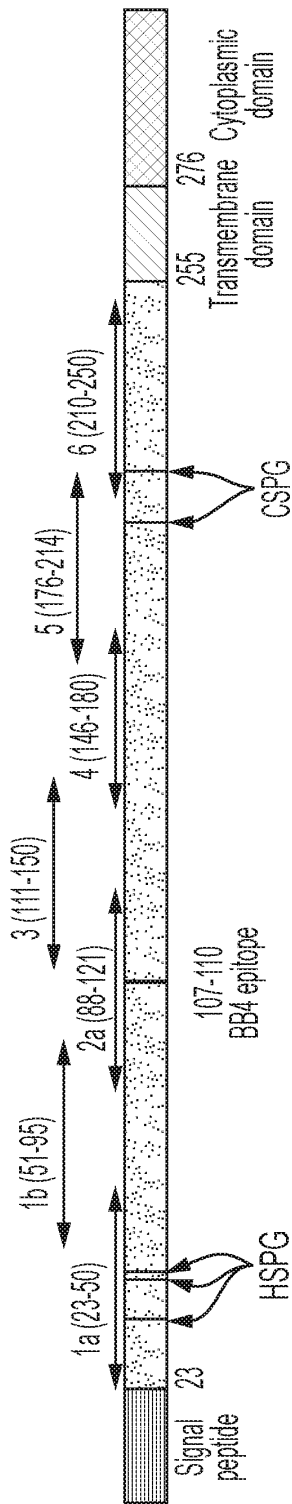


FIG. 2

3/25

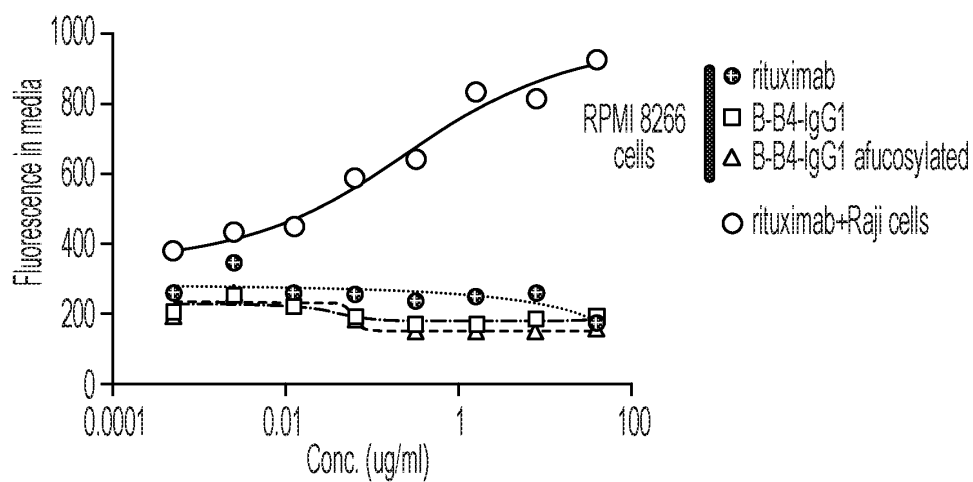


FIG. 3

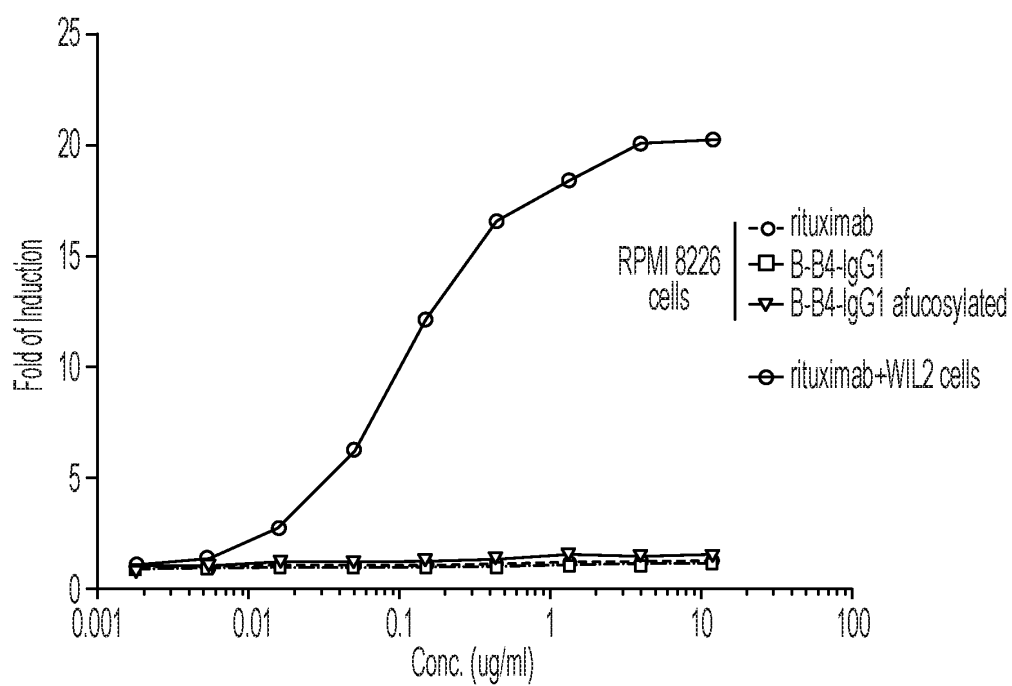


FIG. 4

4/25

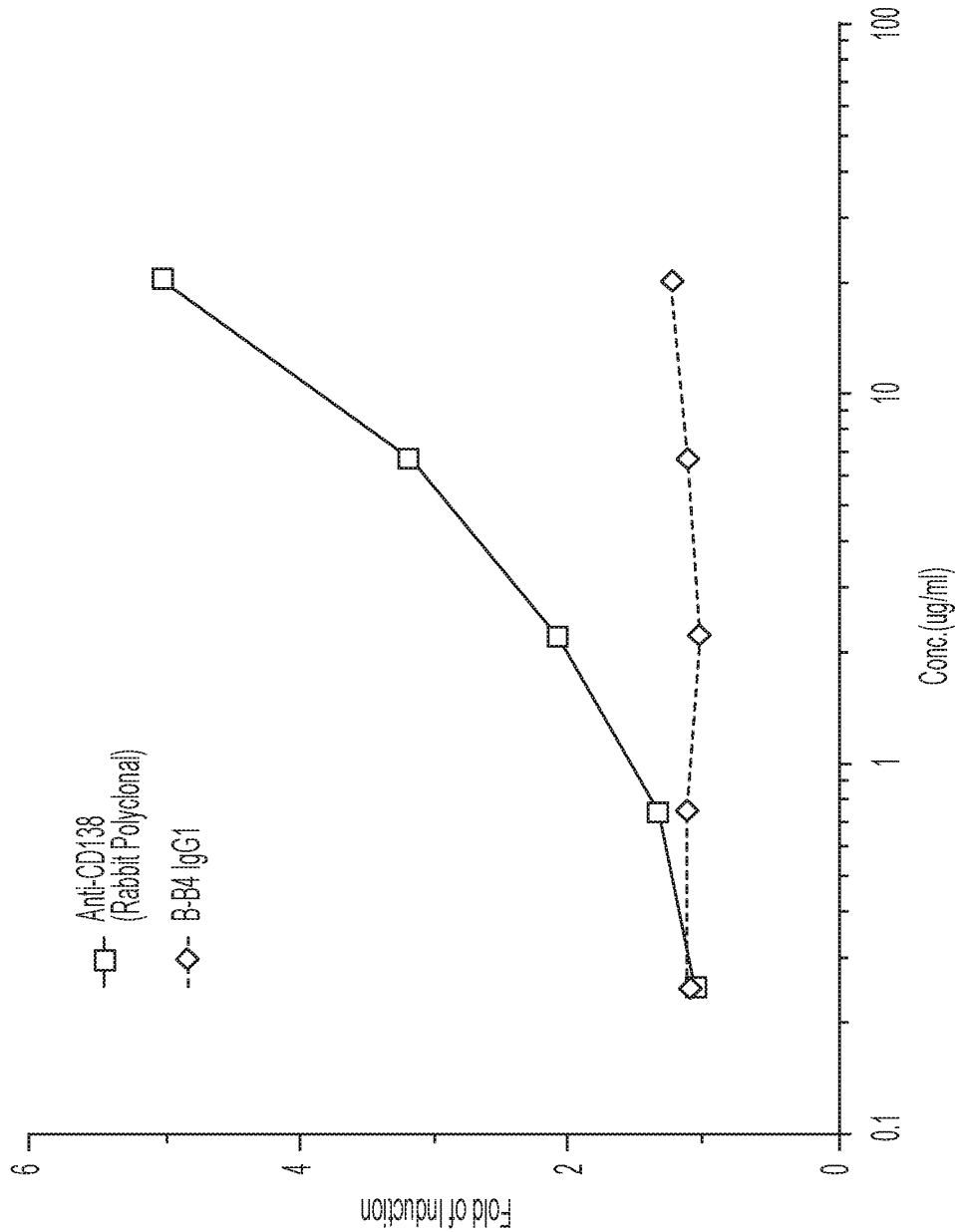


FIG. 5

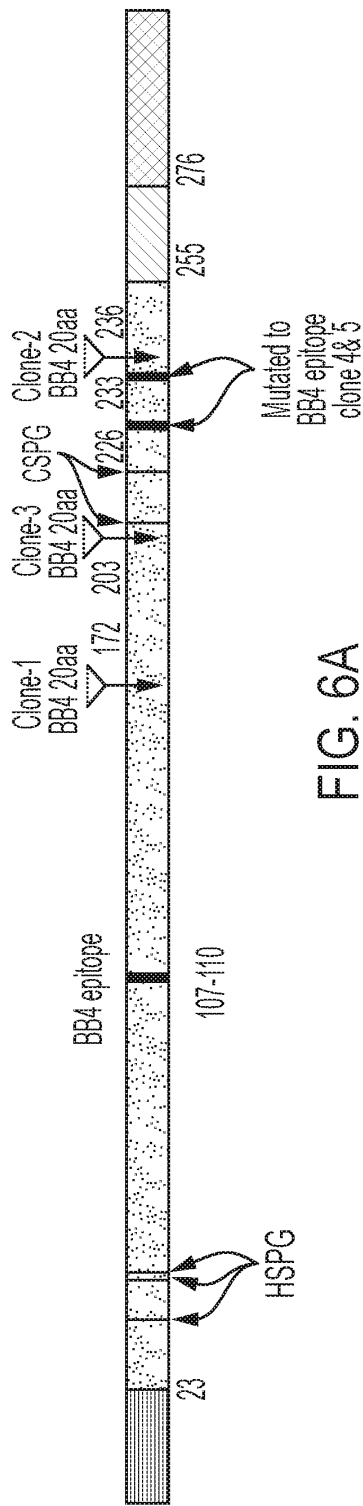


FIG. 6A

Clone 1: NativeCD138:BB4epitope between the GAGs
MRRALWNL CALALSQPA LPQIVATNLP PEDQDGSDD SNFSGSGAG ALQDITLSQ TPSTWKDTQL LTAIPTSEPP TGLEATAAST STLPAGEGPK
EGEAVVAAV EPGLTAREQE ATPRPRETQ LPTHLASTT TATTAQEPAT SHPRDMQPG HHETSTPACP SOEGEAVLPEV EPGLTAREQE ADLHTPHT
EDGGPSATER AAEDGASSQL PAAEGSGEQD FTFETSGENT AVVAPEPDRR NQSPVDQCAT GASQGLIDRK
EVLGGVIAGG LVGLIFAVCL VGFMLYRMKK KDEGSYSLEE PQANGGAYQ KPTKQEEFYA

Clone 2: NativeCD138:BB4epitope at JMD
MRRALWNL CALALSQPA LPQIVATNLP PEDQDGSDD SNFSGSGAG ALQDITLSQ TPSTWKDTQL LTAIPTSEPP TGLEATAAST STLPAGEGPK
EGEAVVAAV EPGLTAREQE ATPRPRETQ LPTHLASTT TATTAQEPAT SHPRDMQPG HHETSTPACP SQADLHTPHT EDGGPSATER AAEDGASSQL
PAAEGSGEQD FTFETSGENT AVVAPEPDRR NQSPVDEGEAVLPEV EPGLTAREQEQCAT GASQGLIDRK EVLGGVIAGG LVGLIFAVCL VGFMLYRMKK
KDEGSYSLEE PQANGGAYQ KPTKQEEFYA

Clone 3: NativeCD138:BB4epitope above and close to CS modification
MRRALWNL CALALSQPA LPQIVATNLP PEDQDGSDD SNFSGSGAG ALQDITLSQ TPSTWKDTQL LTAIPTSEPP TGLEATAAST STLPAGEGPK
EGEAVVAAV EPGLTAREQE ATPRPRETQ LPTHLASTT TATTAQEPAT SHPRDMQPG HHETSTPACP SQADLHTPHT EDGGPSATER AAEDGASSQL
PAAEGEAVLPEV EPGLTAREQ EGSQEQD FTFETSGENT AVVAPEPDRR NQSPVDQCAT GASQGLIDRK EVLGGVIAGG LVGLIFAVCL VGFMLYRMKK
KDEGSYSLEE PQANGGAYQ KPTKQEEFYA

FIG. 6B

Clone 4: NativeCD138:BB4epitope below the CS
MRRALNLWL CALALSLOPA LPQIVATNLIP PEDQDGSDD SDNFGSGAG ALQDITLSQQ TPSTWKDTQL LTAIPTSPPEP TGLEATAAST STLPAGEGPK
EGEAVVAAAV EPGLTAREQE ATPRPRETQ LPTHLASTT TATTAQEPAT SHPRDMQPG HHETSTPAGP SQADLHTPHT EDGGSATER AAEDGASSQL
PAAEGSGEQD FTFETSGENT AVAVLPEVE NQSPVDQGAT GASQGLLDK EVLGGVIAGG LVGLIFAVCL VGFMLYRMKK KDEGSYSLEE PKQANGGAYQ
KPTKQEEFYA

Clone 5: NativeCD138:BB4epitope below the CS
MRRALNLWL CALALSLOPA LPQIVATNLIP PEDQDGSDD SDNFGSGAG ALQDITLSQQ TPSTWKDTQL LTAIPTSPPEP TGLEATAAST STLPAGEGPK
EGEAVVAAAV EPGLTAREQE ATPRPRETQ LPTHLASTT TATTAQEPAT SHPRDMQPG HHETSTPAGP SQADLHTPHT EDGGSATER AAEDGASSQL
PAAEGSGEQD FTFETSGENT AVAVLPEDRR NOLPEVEGAT GASQGLLDK EVLGGVIAGG LVGLIFAVCL VGFMLYRMKK KDEGSYSLEE PKQANGGAYQ
KPTKQEEFYA

FIG. 6C

7/25

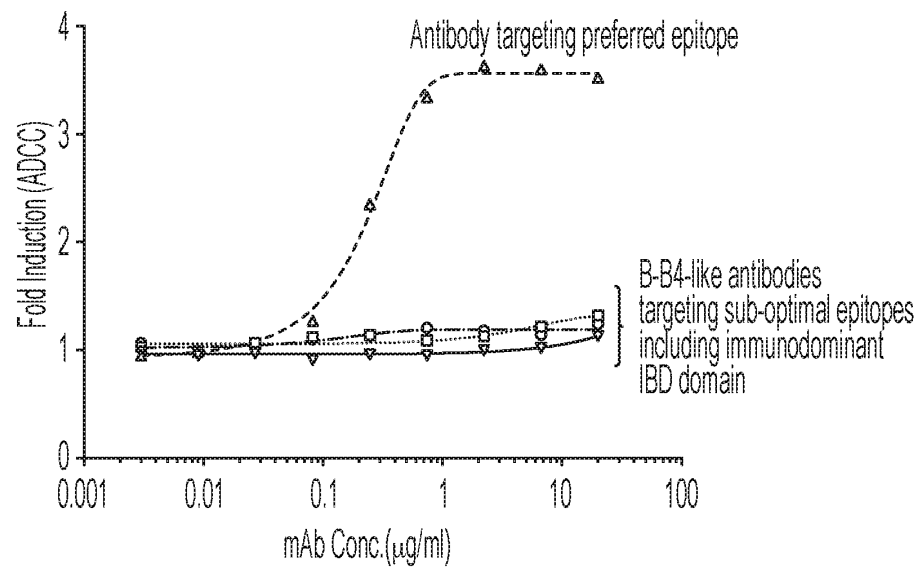


FIG. 7A

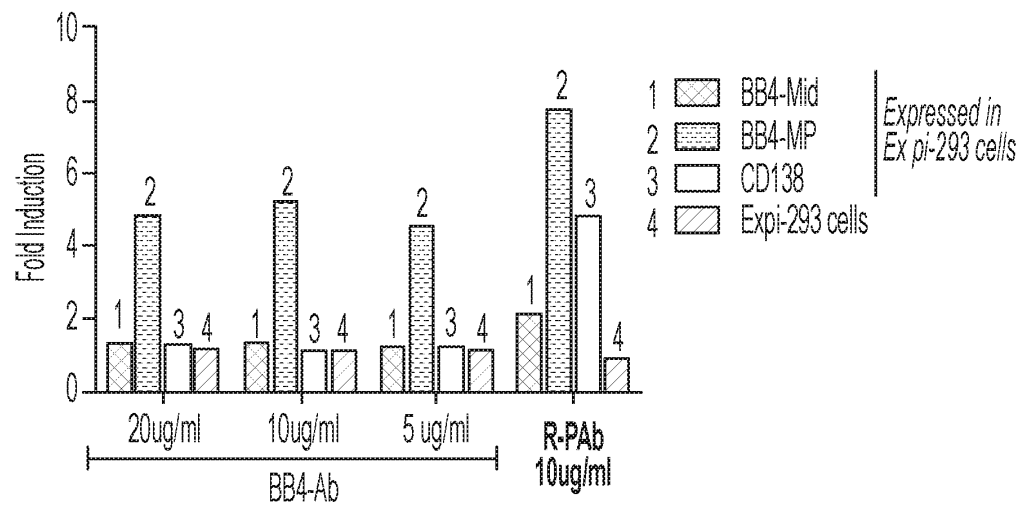


FIG. 7B

8/25

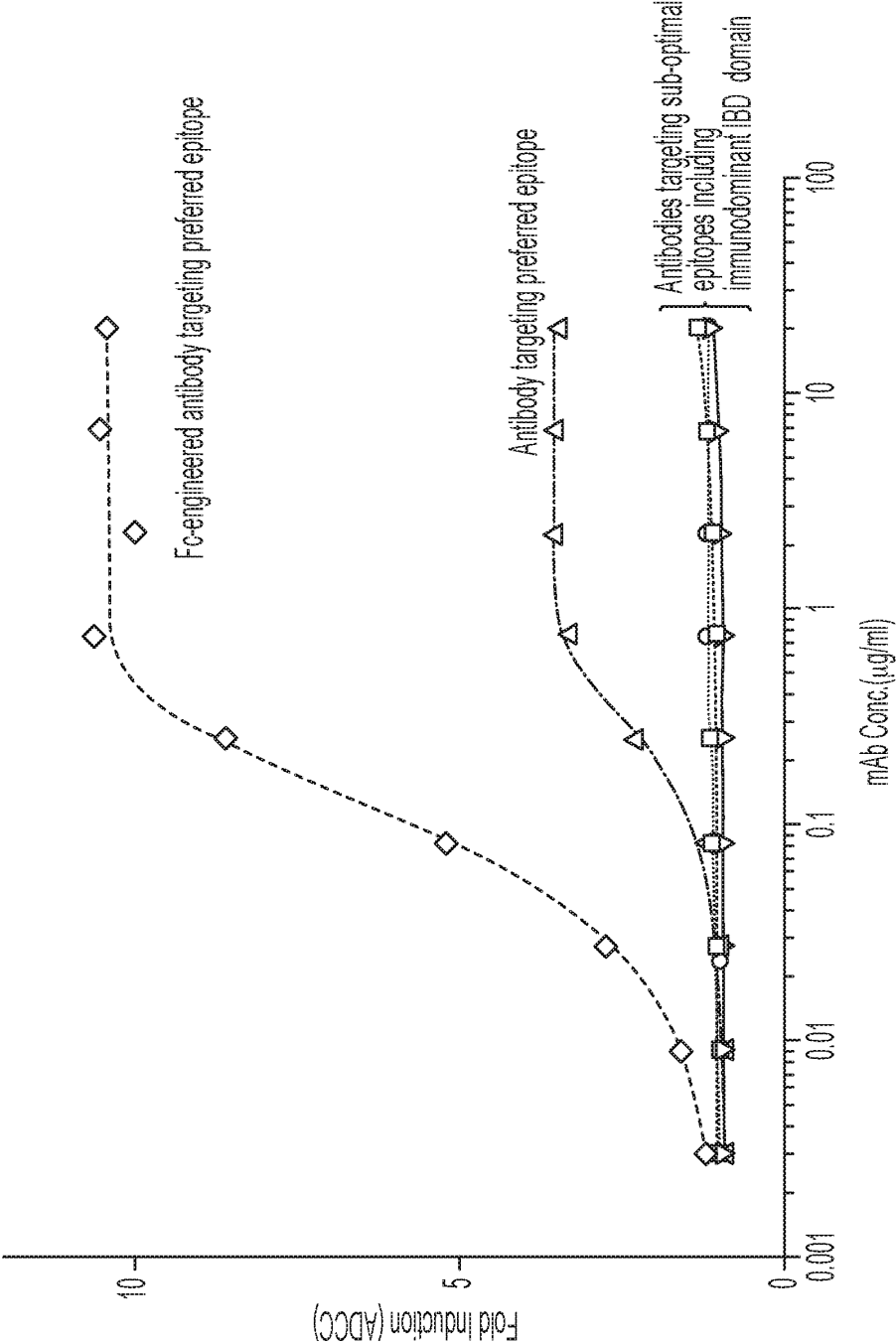


FIG. 7C

9/25

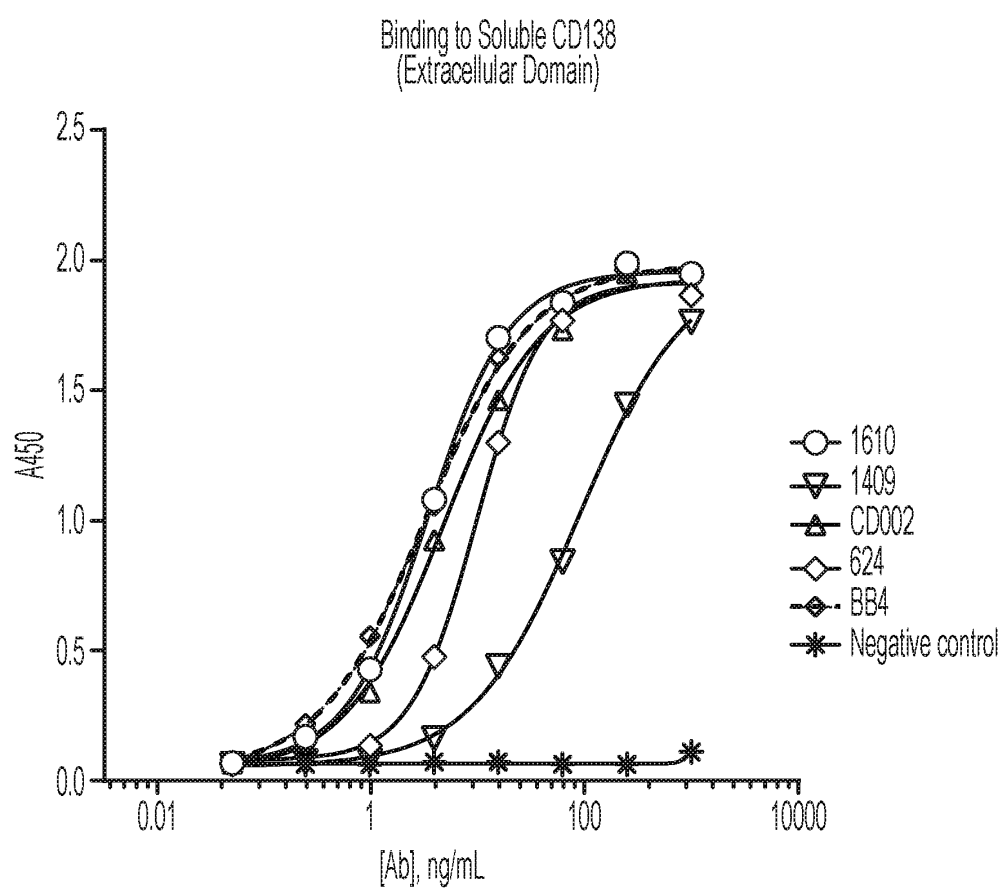


FIG. 8

10/25

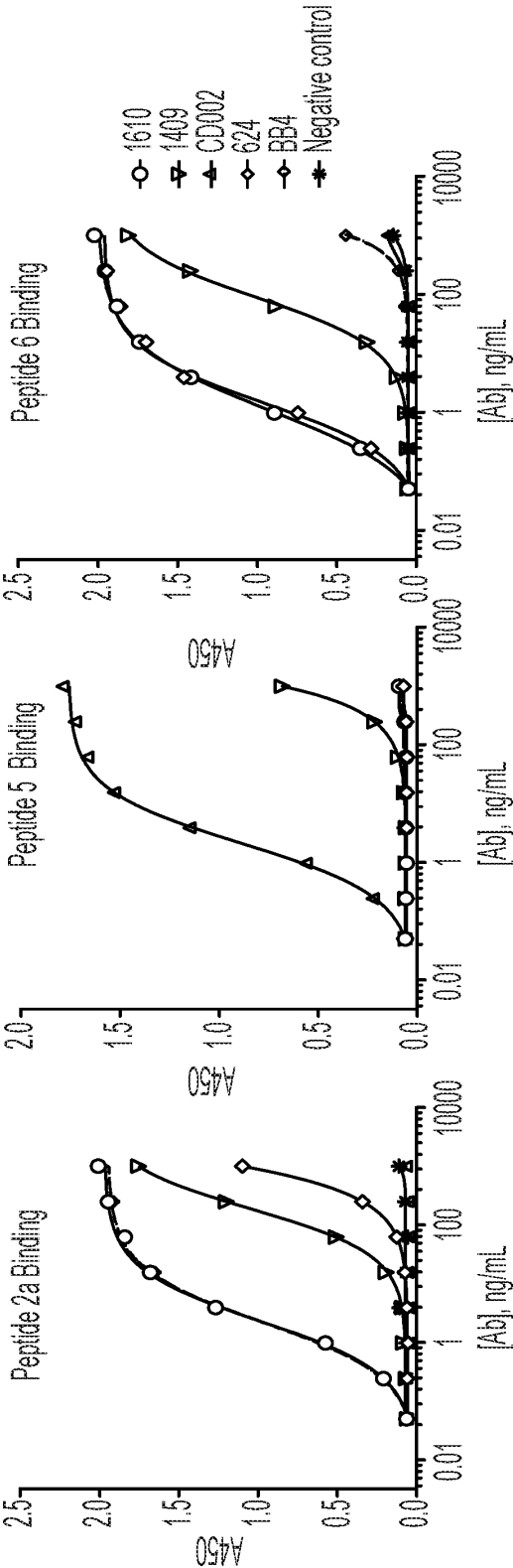


FIG. 9A

FIG. 9B

FIG. 9C

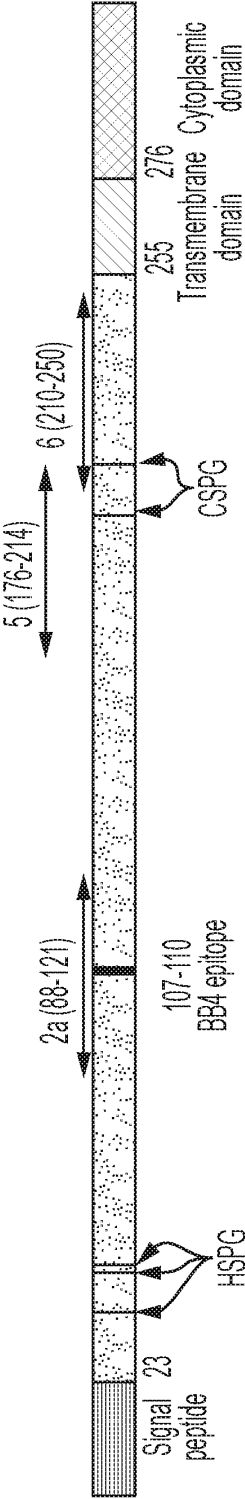


FIG. 9D

11/25

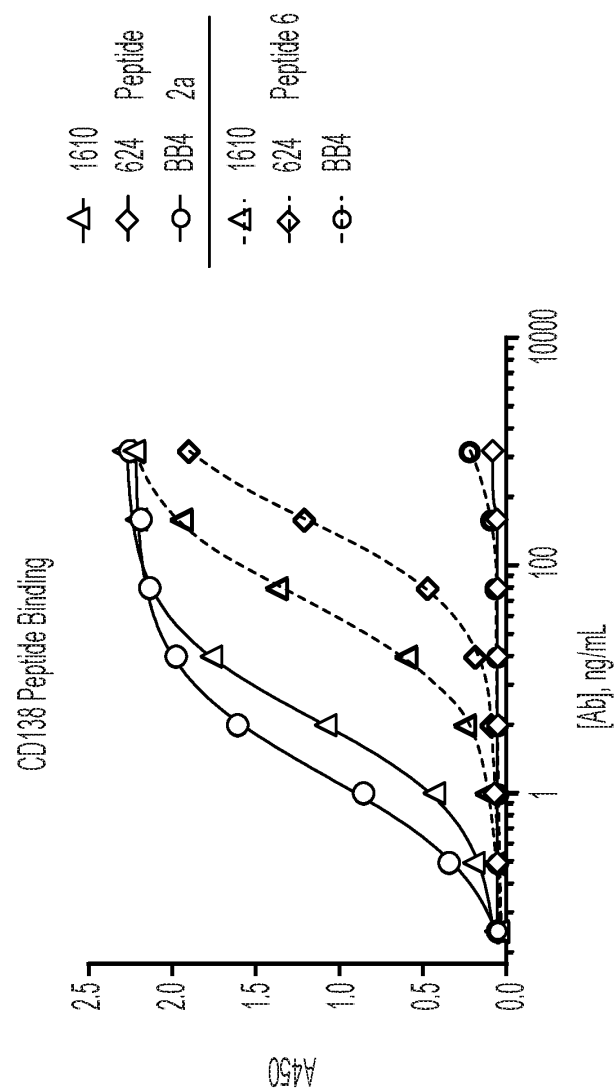


FIG. 10

12/25

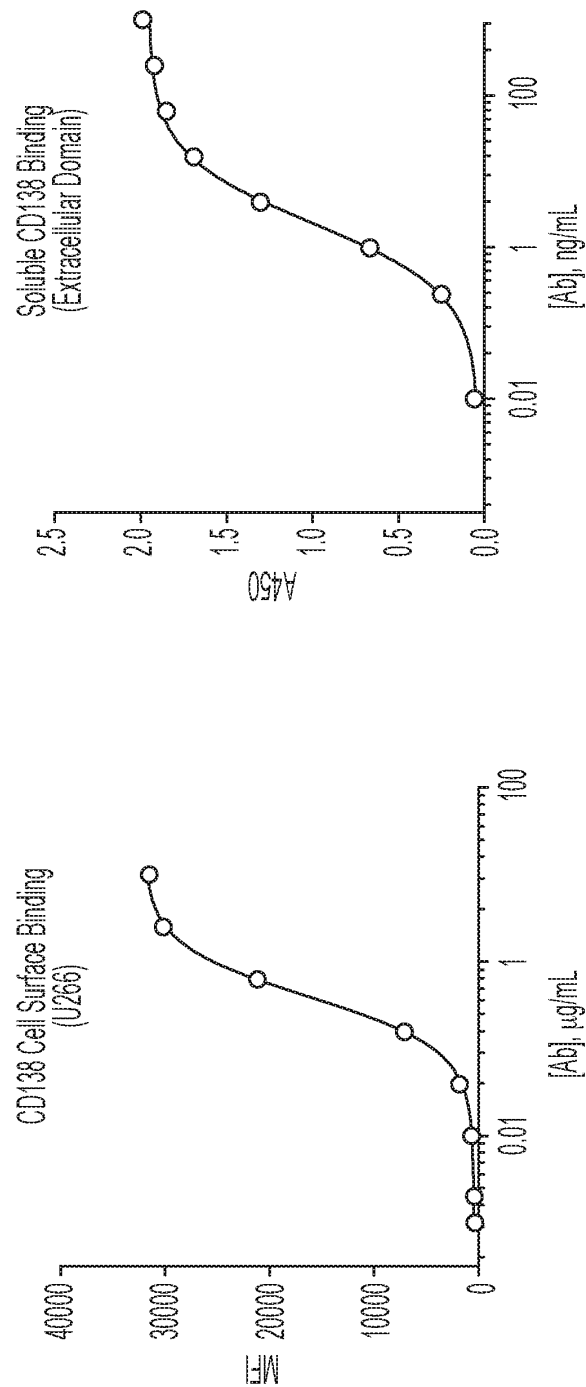


FIG. 11B

FIG. 11A

Soluble CD138 Binding EC50 (ng/mL)	Membrane CD138 Binding EC50 (ng/mL)
1.9	394

FIG. 11C

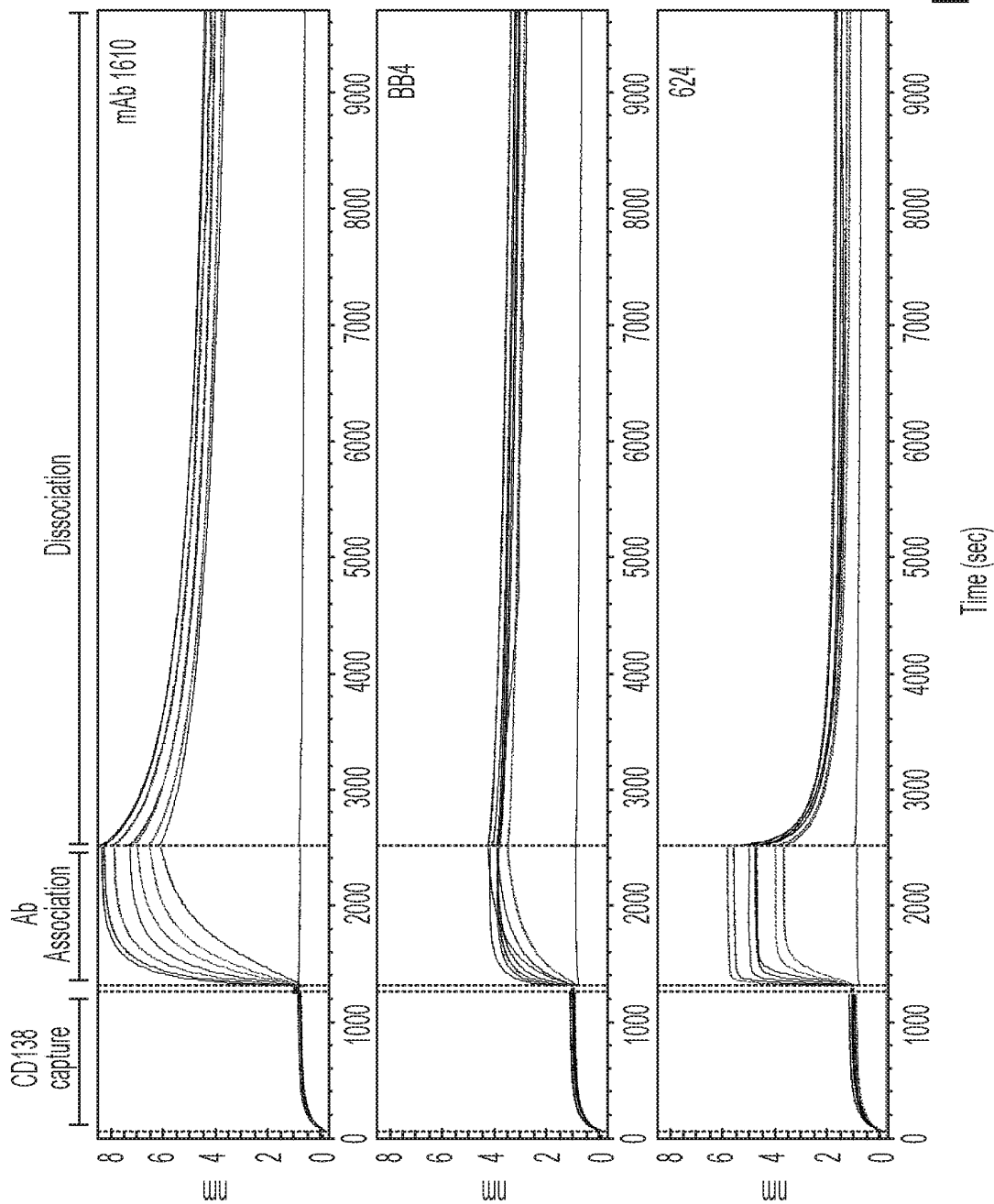


FIG. 12

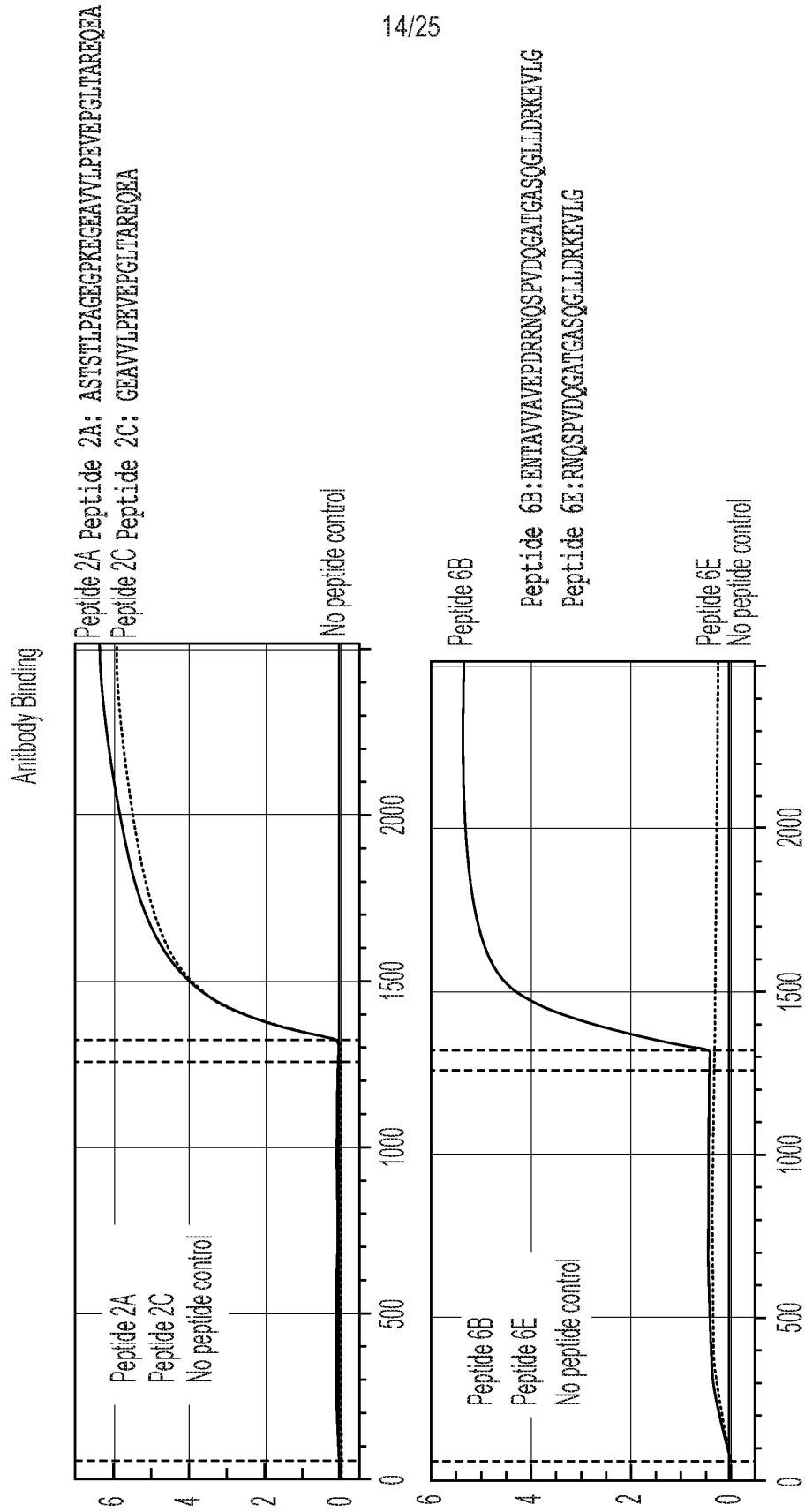


FIG. 13

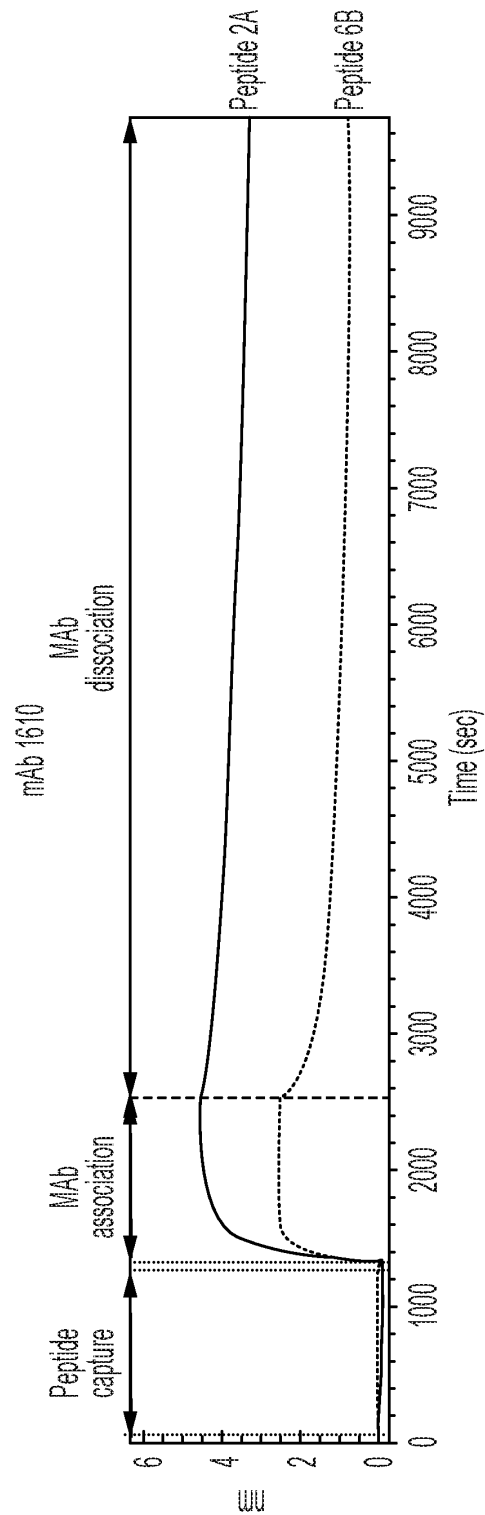


FIG. 14A

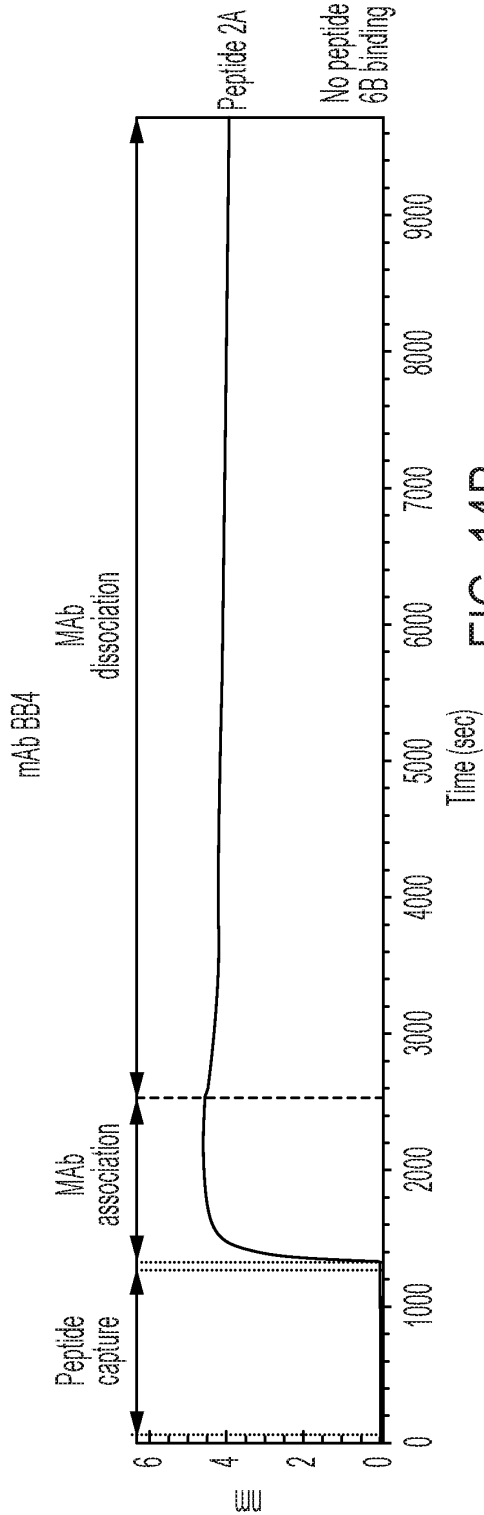


FIG. 14B

16/25

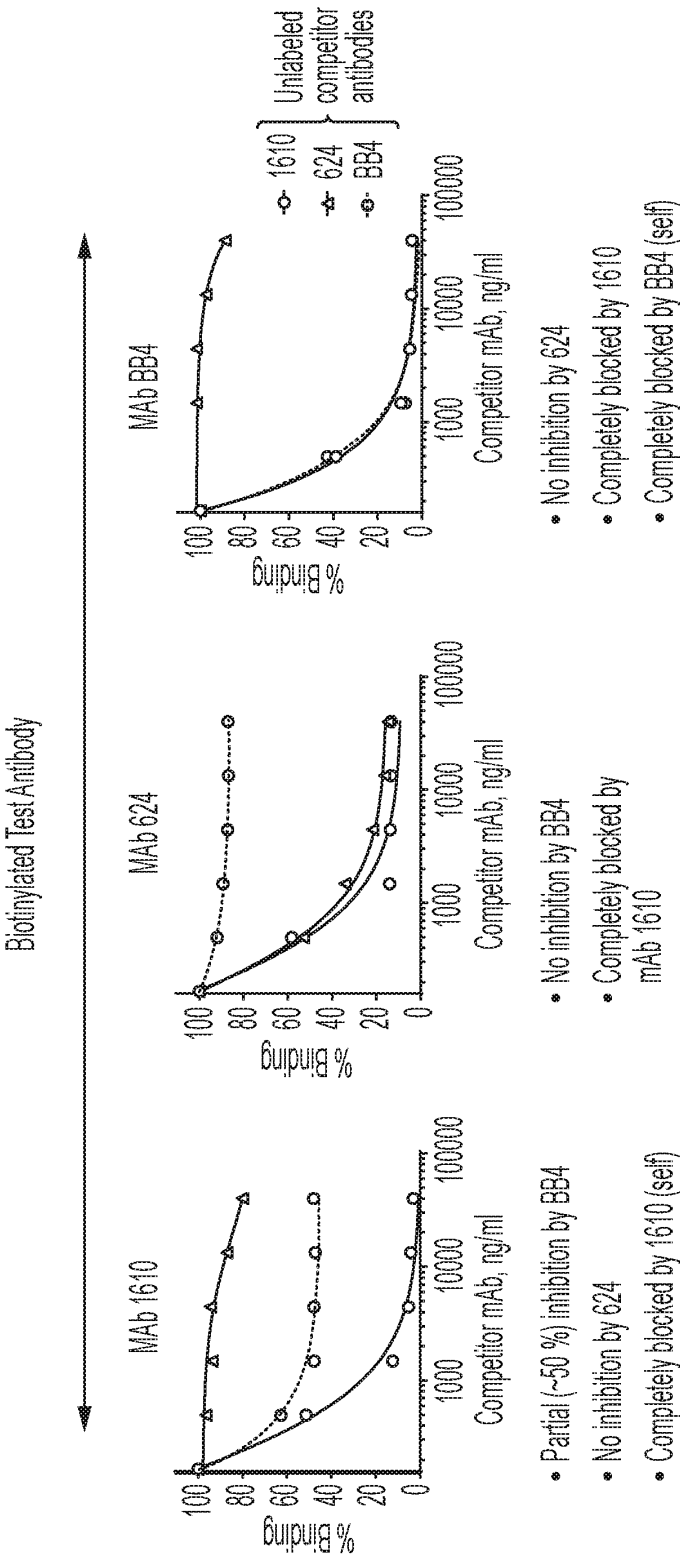


FIG. 15A

FIG. 15B

FIG. 15C

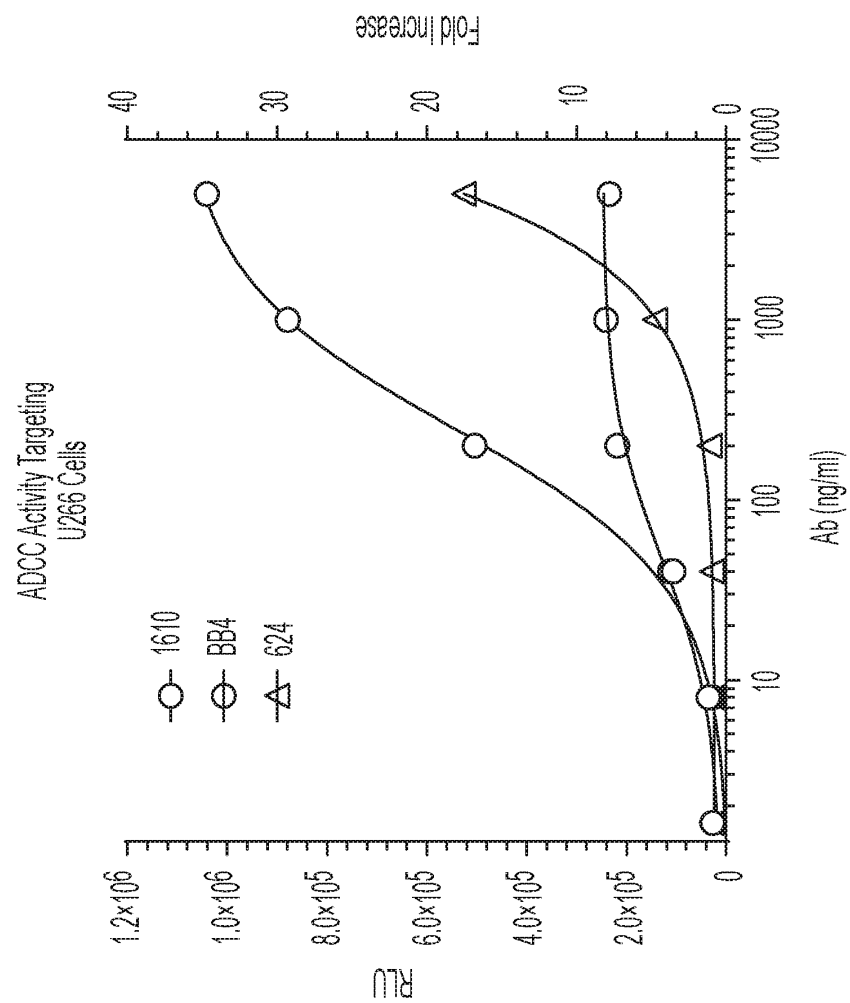


FIG. 16

Antibody ID	VH variant	Protein Titers
1610	wildtype	63.1
2510	C60Y	103.4
2610	N28S	13.7
2710	N28T	9.6
2810	N28S_C60Y	70.0
2910	N28T_C60Y	58.7

FIG. 17

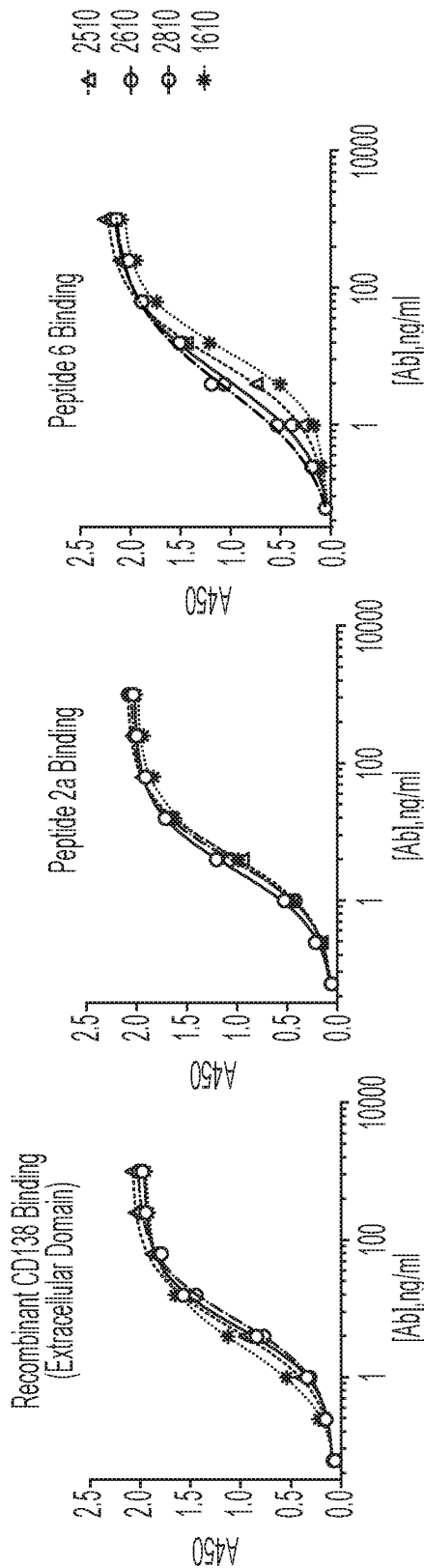


FIG. 18C

FIG. 18B

FIG. 18A

Methods: Binding measured by ELISA

Ab ID	Mutation	EC50 (ng/mL)	
		CD138	Peptide 2a
2510	C60Y	4.9	4.6
2610	N28S	7.0	3.8
2810	N28S/C60Y	5.3	2.8
1610	WT	2.7	3.9
			Peptide 6
			8.9
			4.9
			3.2
			12.3

FIG. 18D

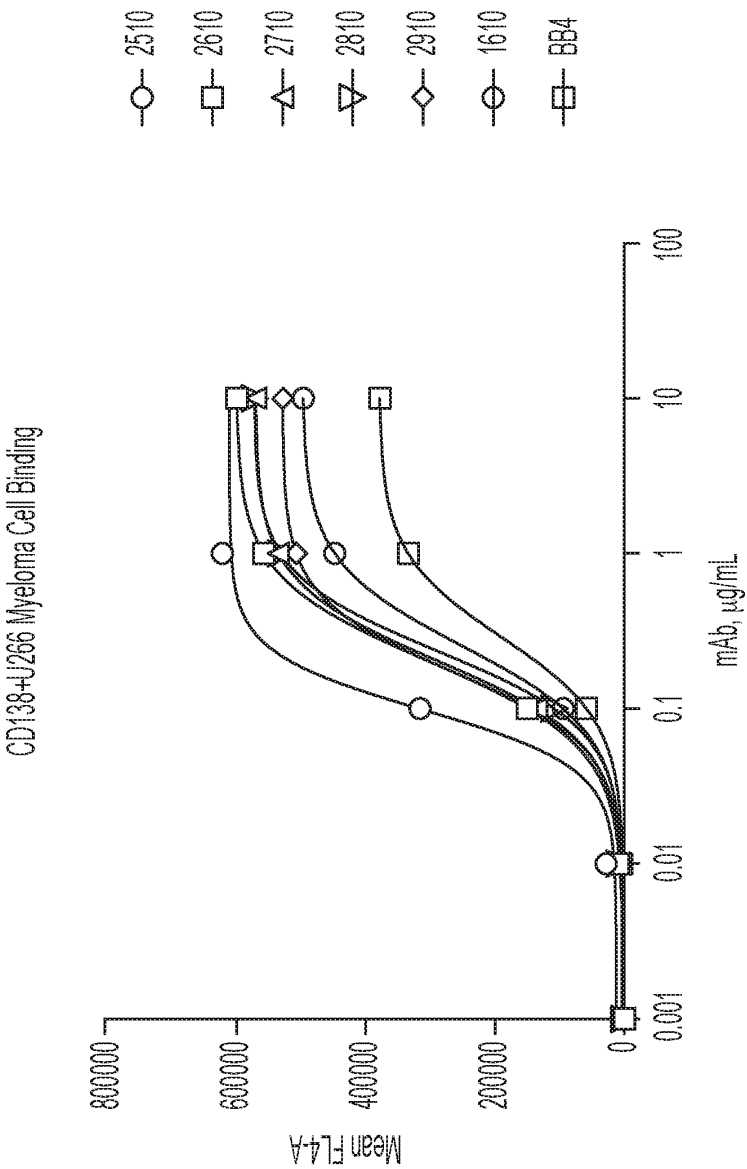


FIG. 19A

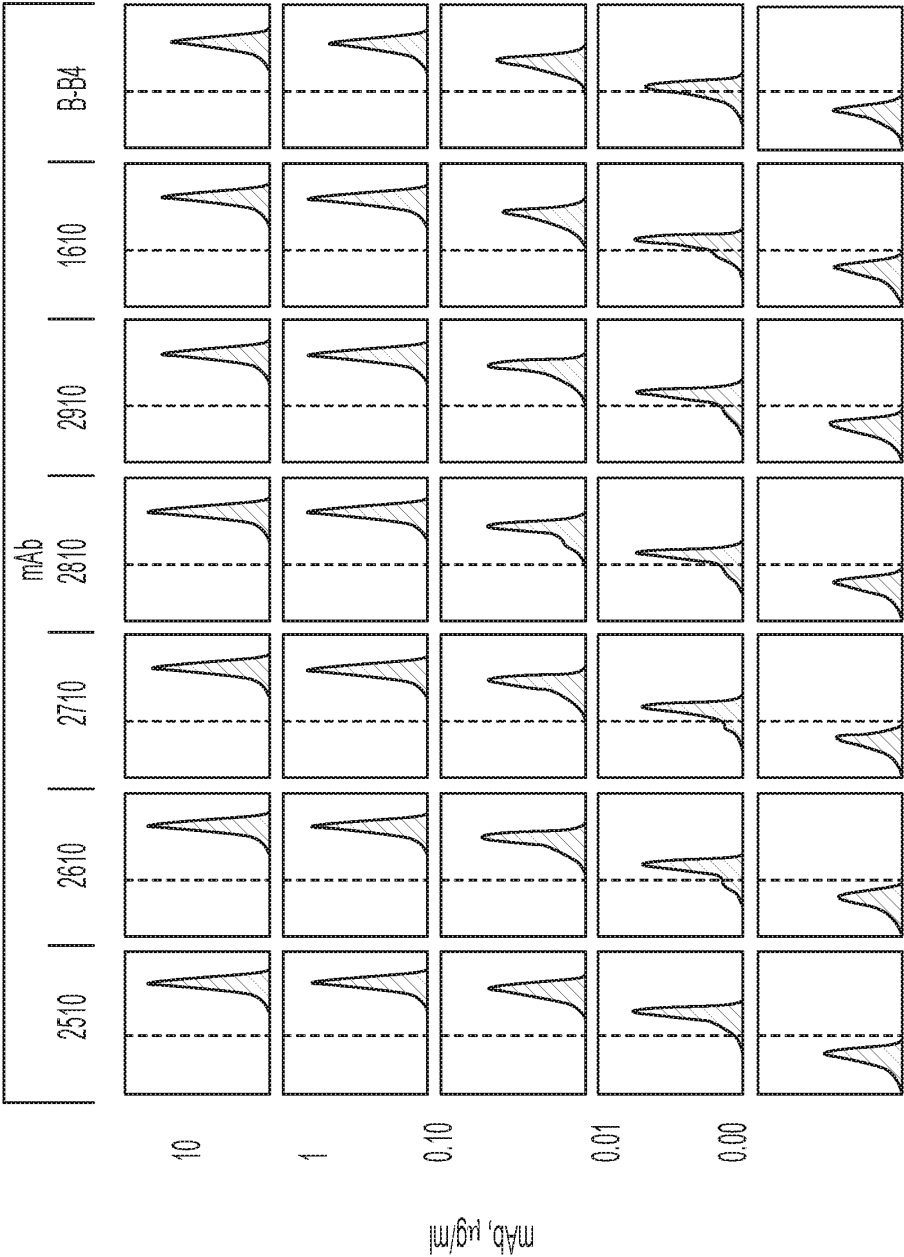


FIG. 19B

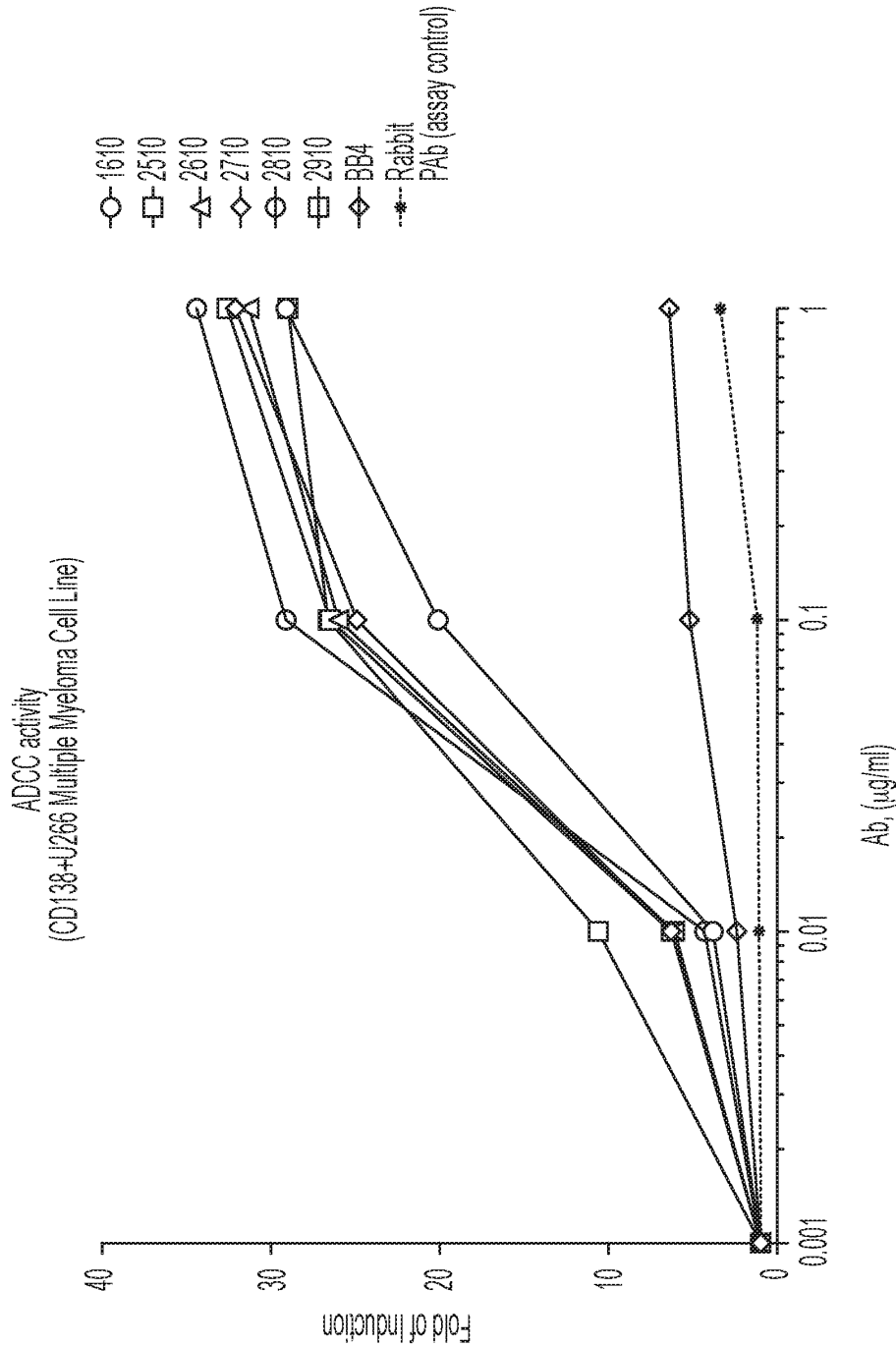


FIG. 20

Comparison of CD138 Derived Peptide Binding

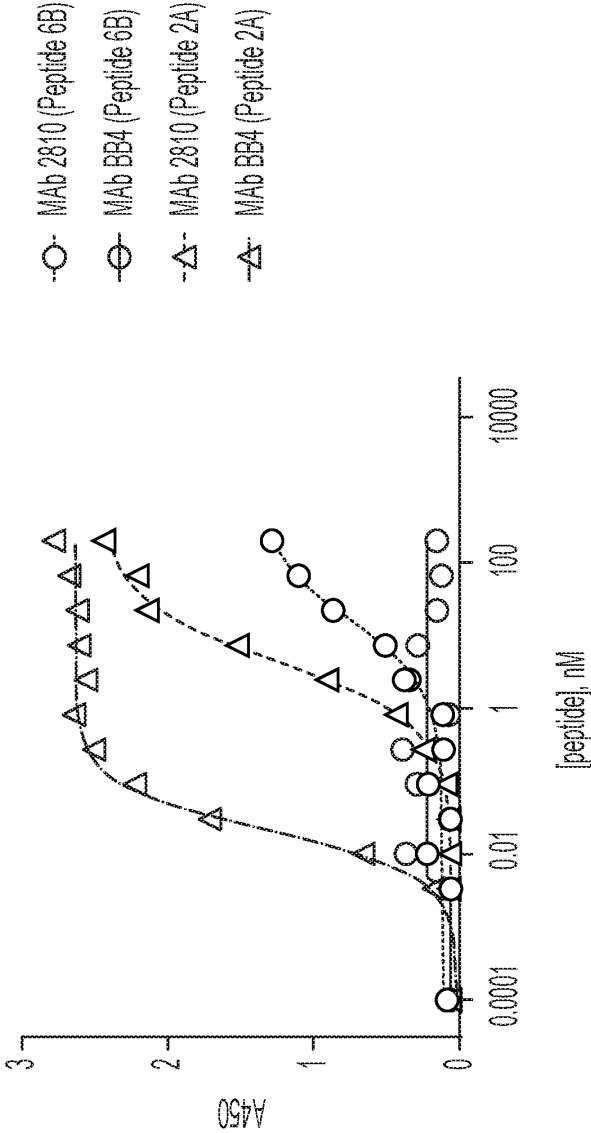
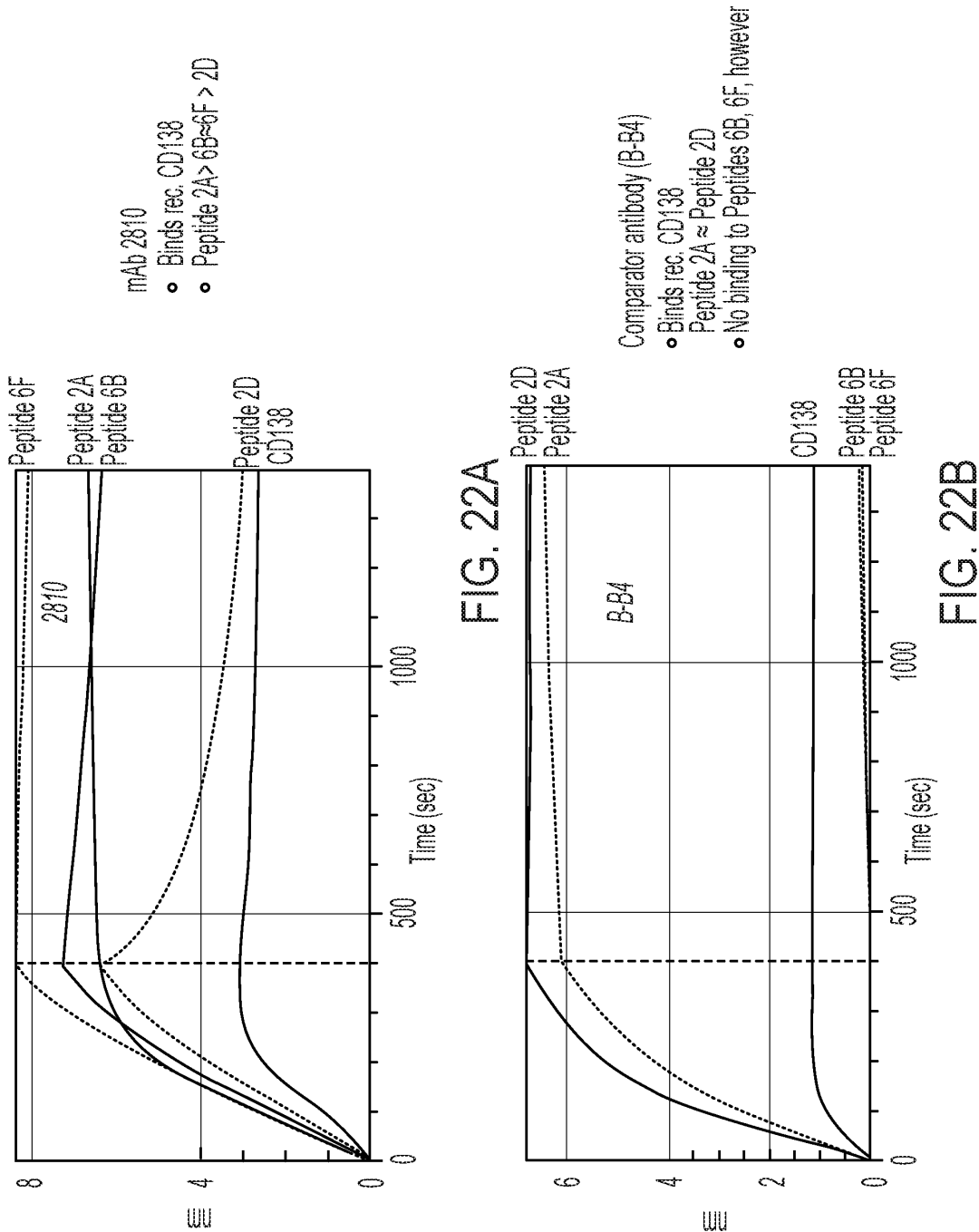


FIG. 21



(Mid region):	SPEPTGLEATAASTSTLPAGEGPKAGEAVLPEVEPGLTAREQEATPRPRRTTQ
Peptide 2A:	ASTSTLPAGEGPKAGEAVLPEVEPGLTAREQEA
Peptide 2C:	GEAVLPEVEPGLTAREQEA
Peptide 2D:	GEAWLPEVEPGLTA

(Membrane Proximal) :	GSGEQDFTFETSGENTAVVAVEPDRRNQSPVDQCATGASQGILLDRKEVLG
Peptide 6B:	ENTAVVAVEPDRRNQSPVDQCATGASQGILLDRKEVLG
Peptide 6E:	RNQSPVDQCATGASQGILLDRKEVLG
Peptide 6F:	ENTAVVAVEPDRRNQ

6F -ENTAVVAVEPDRRNQ----

2C GEAVLPEVEPGLTAREQEA

* .,: ***. :

15

20

FIG. 22C