

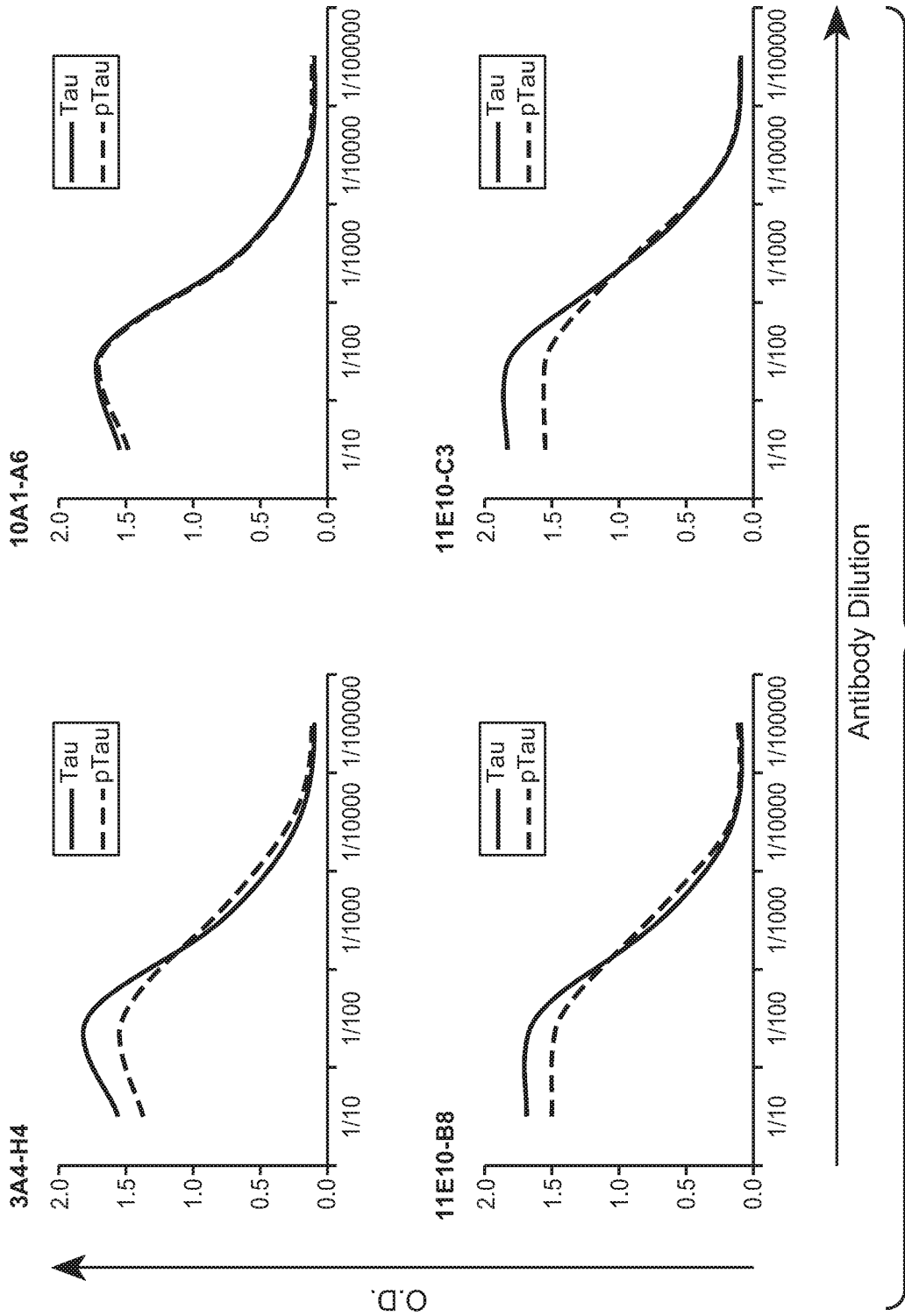


FIG. 1A

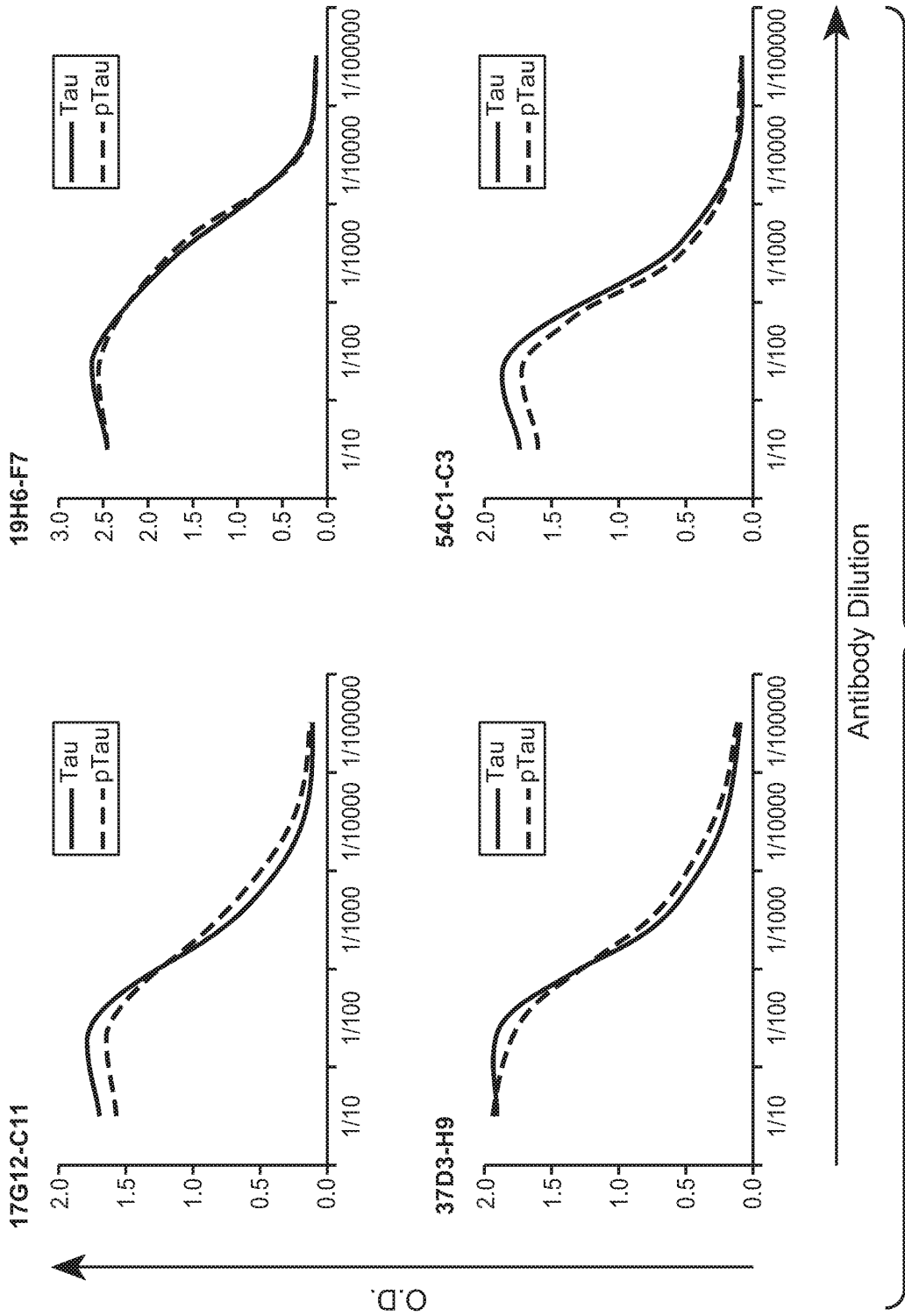


FIG. 1B

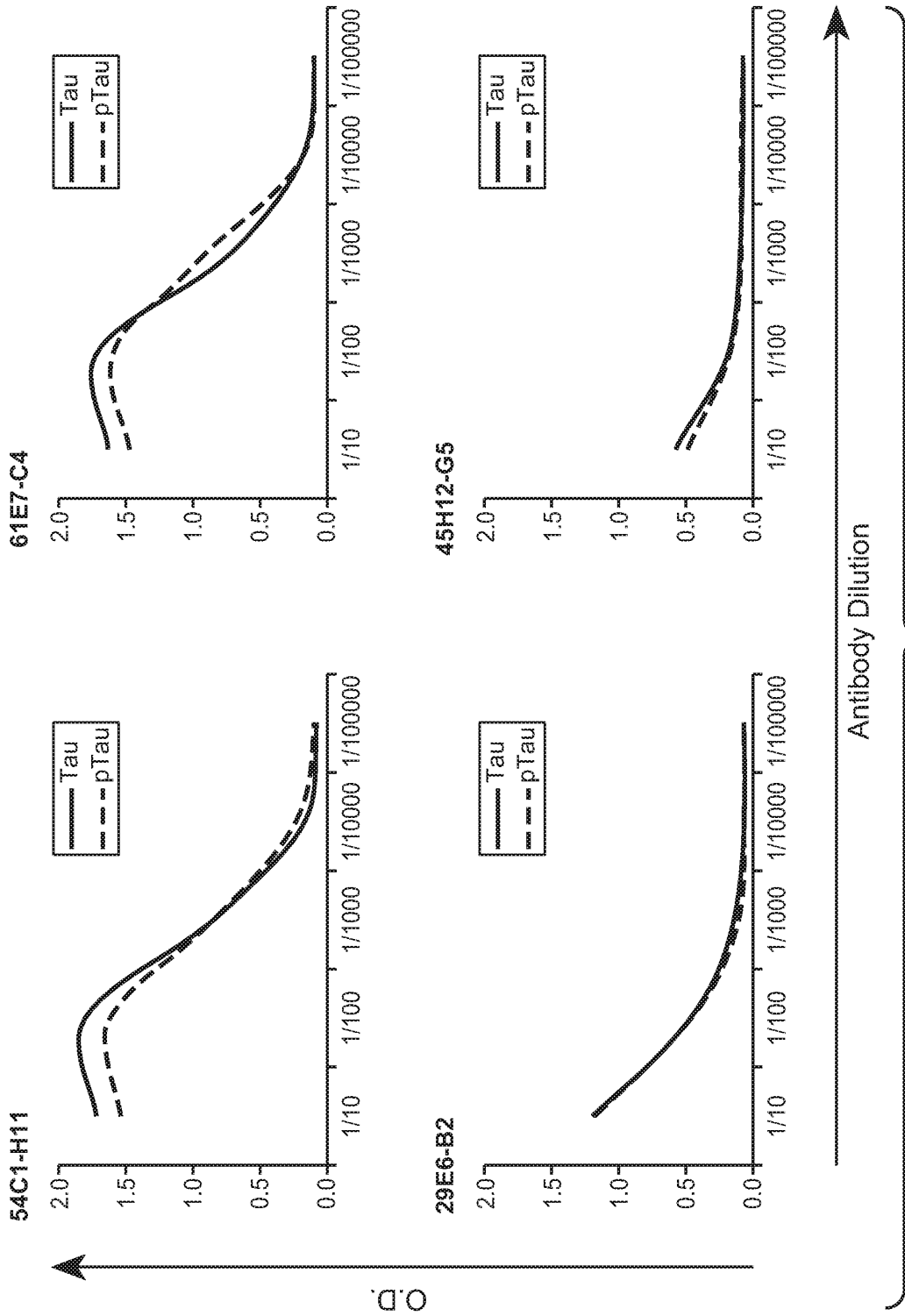


FIG. 1C

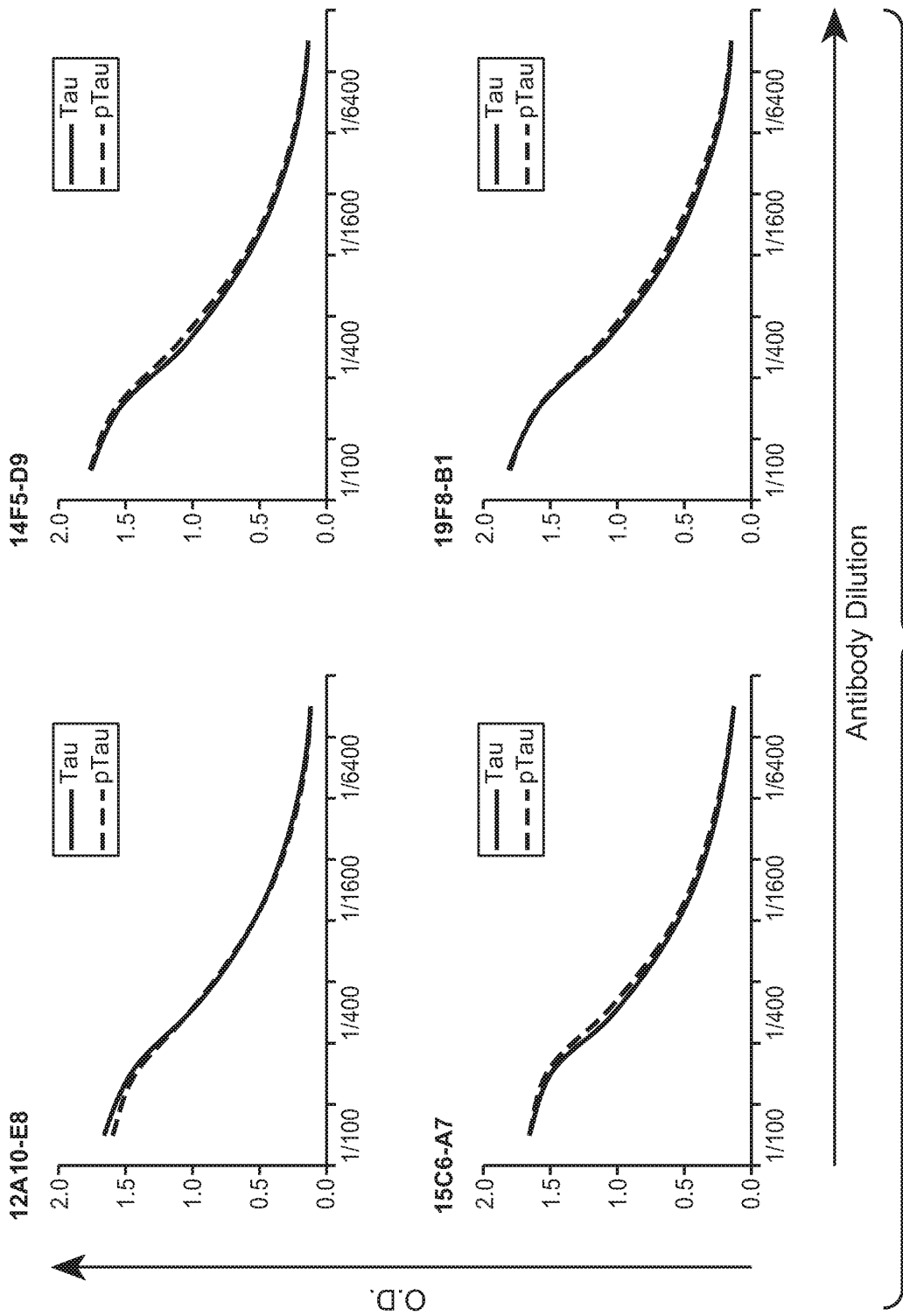


FIG. 1D

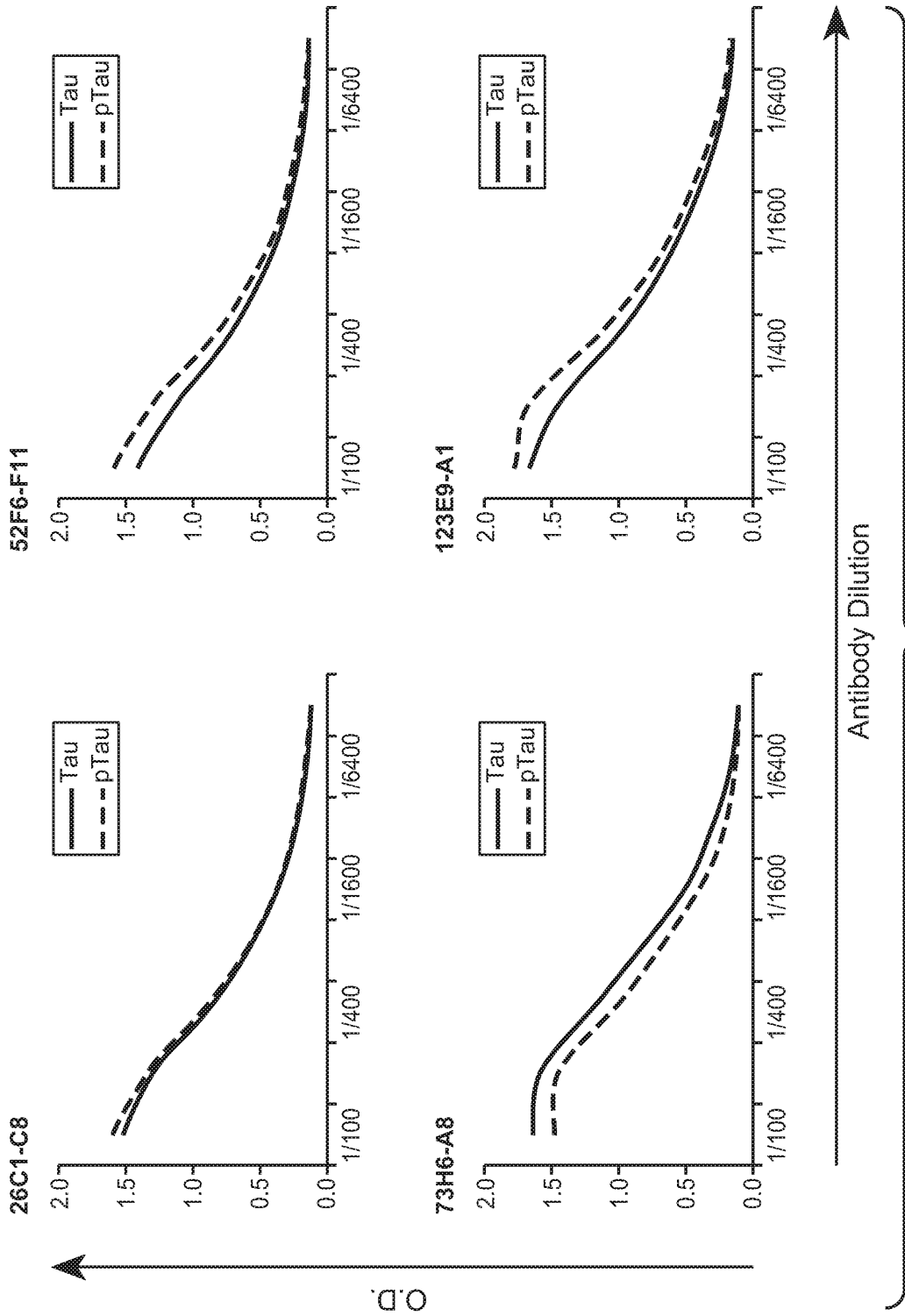
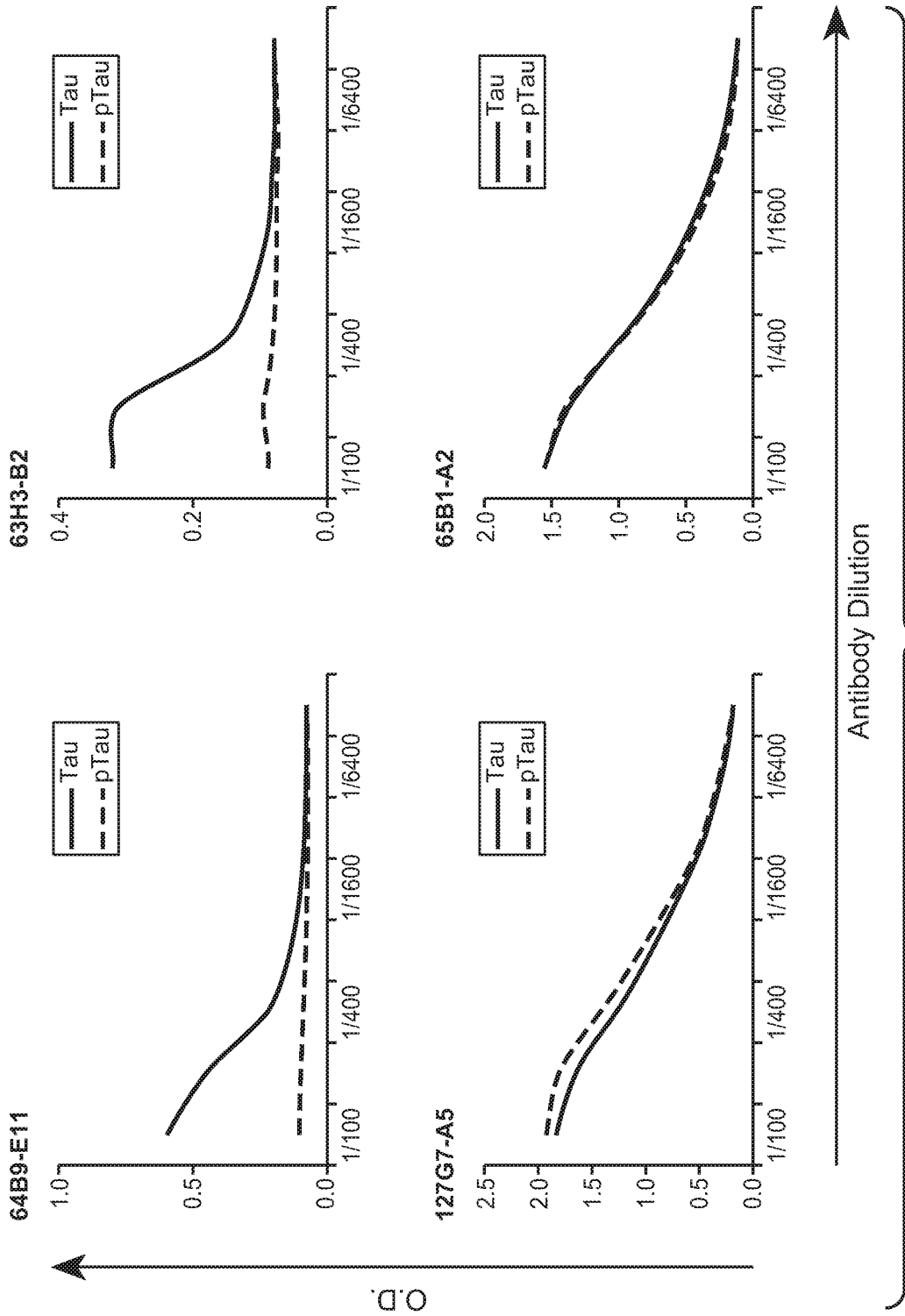


FIG. 1E



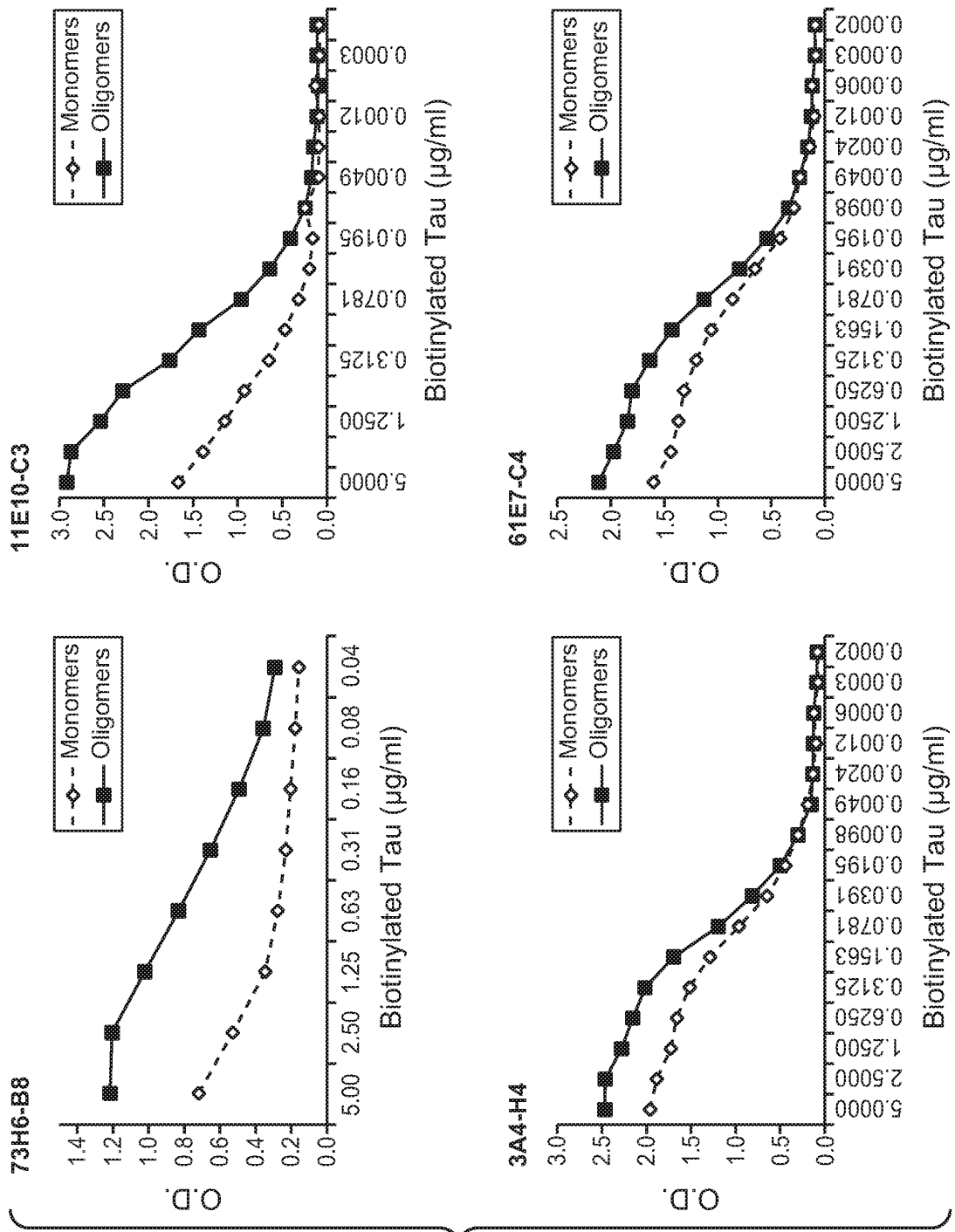


FIG. 2A

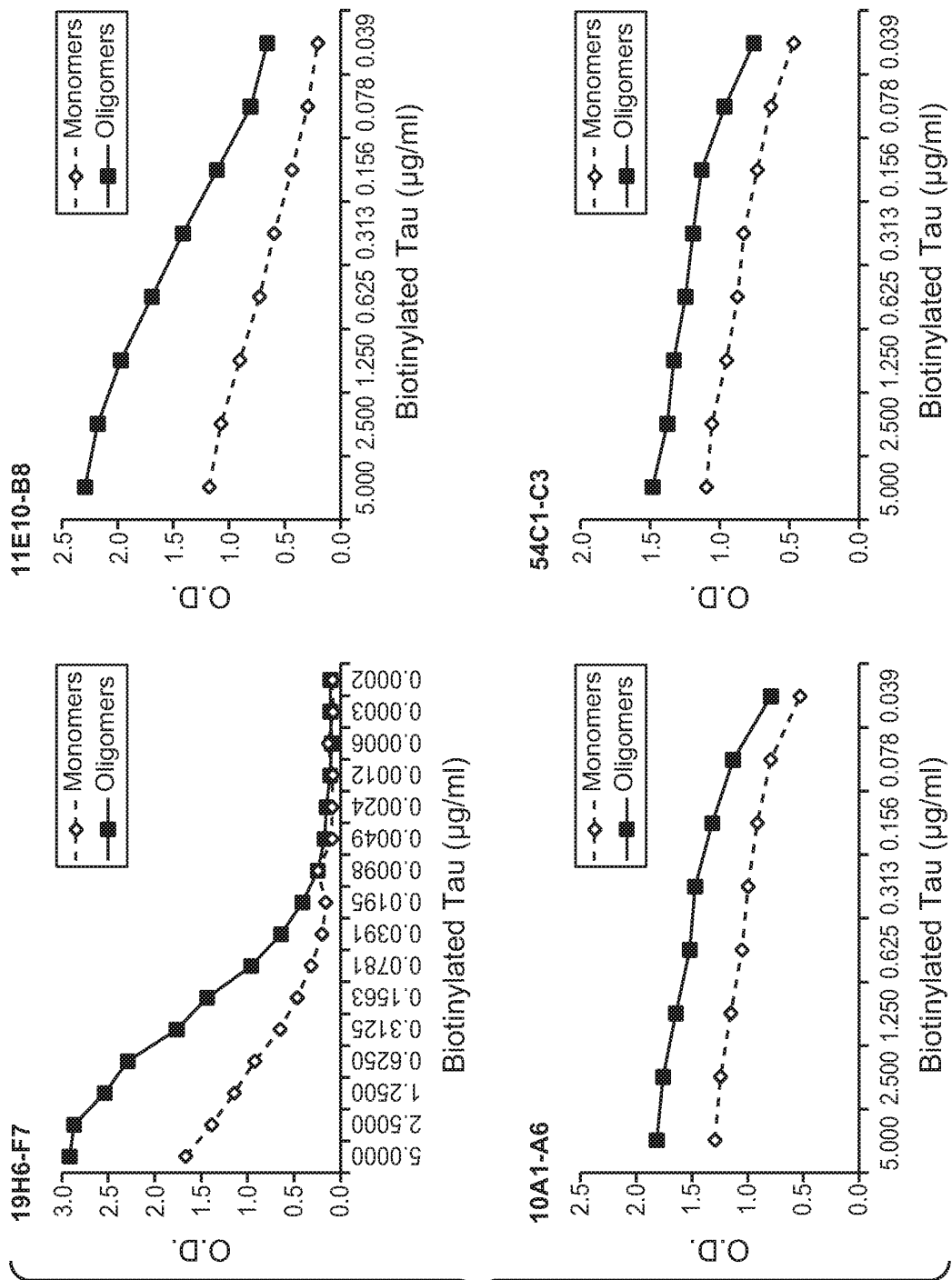


FIG. 2B

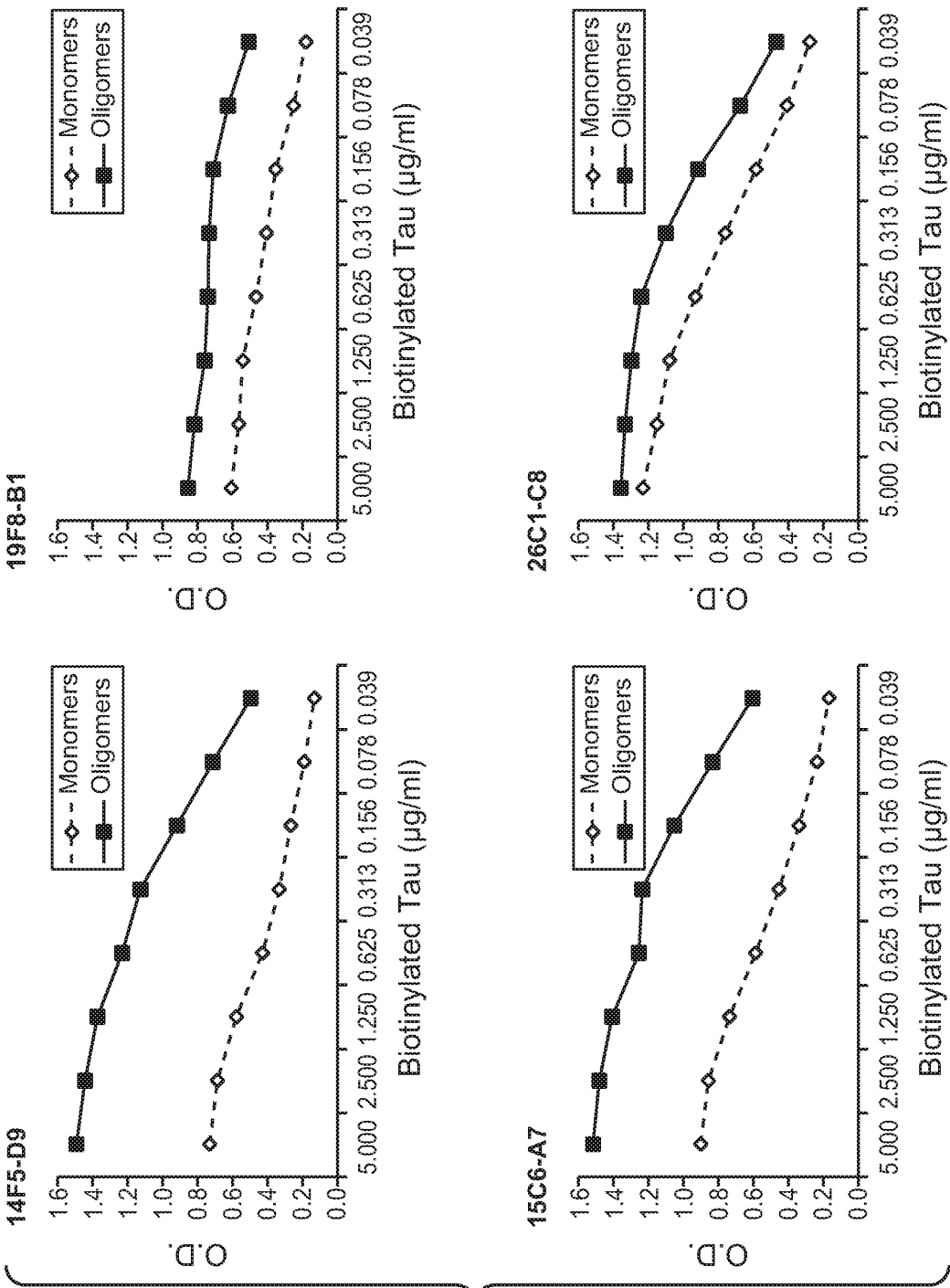
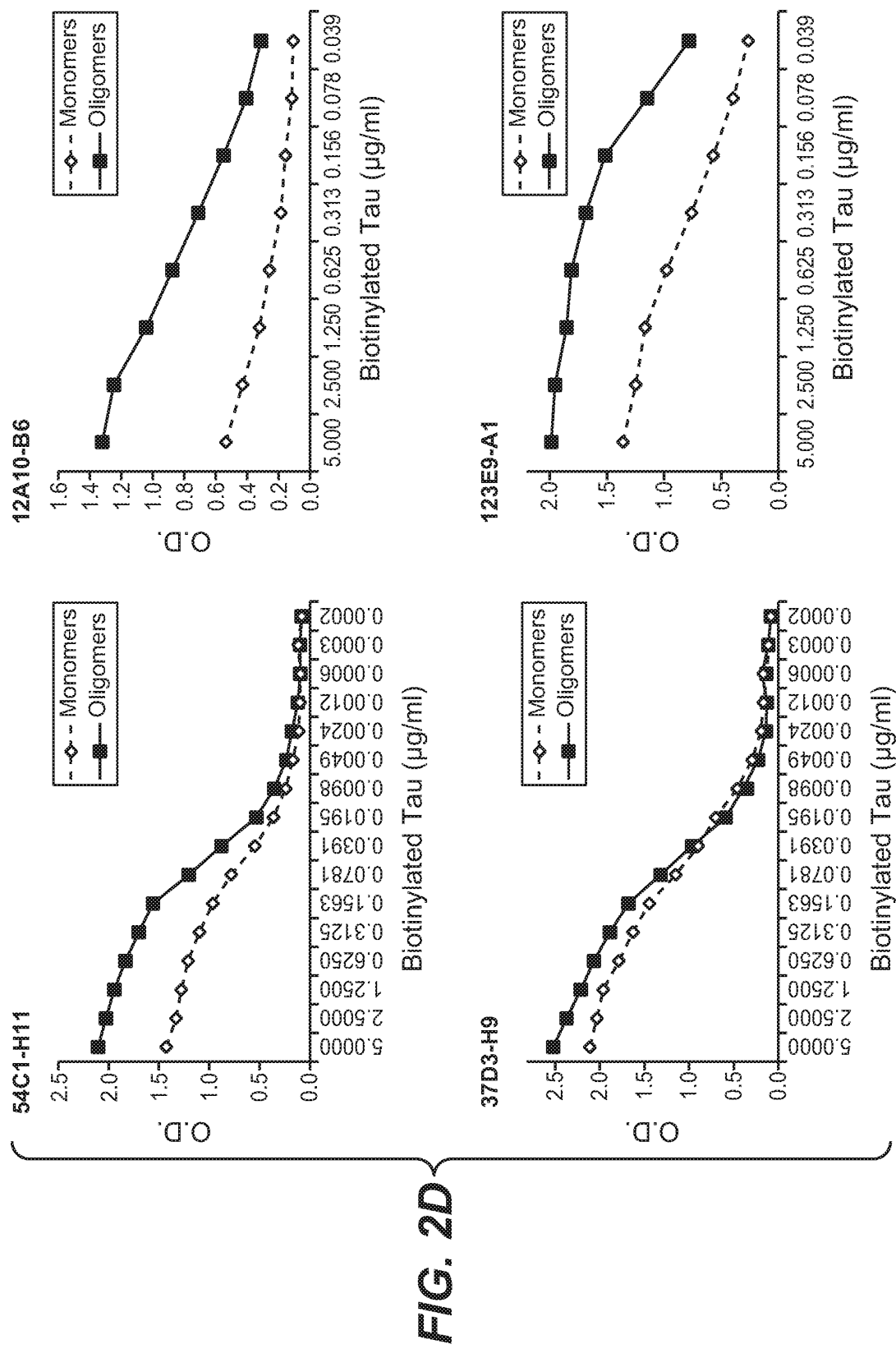


FIG. 2C



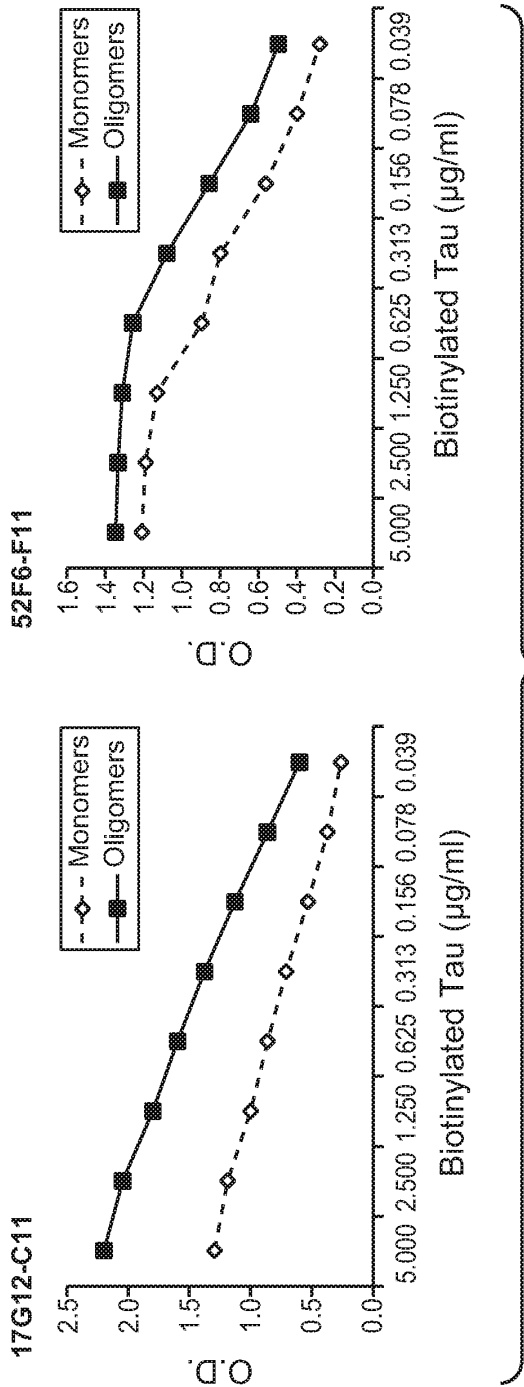
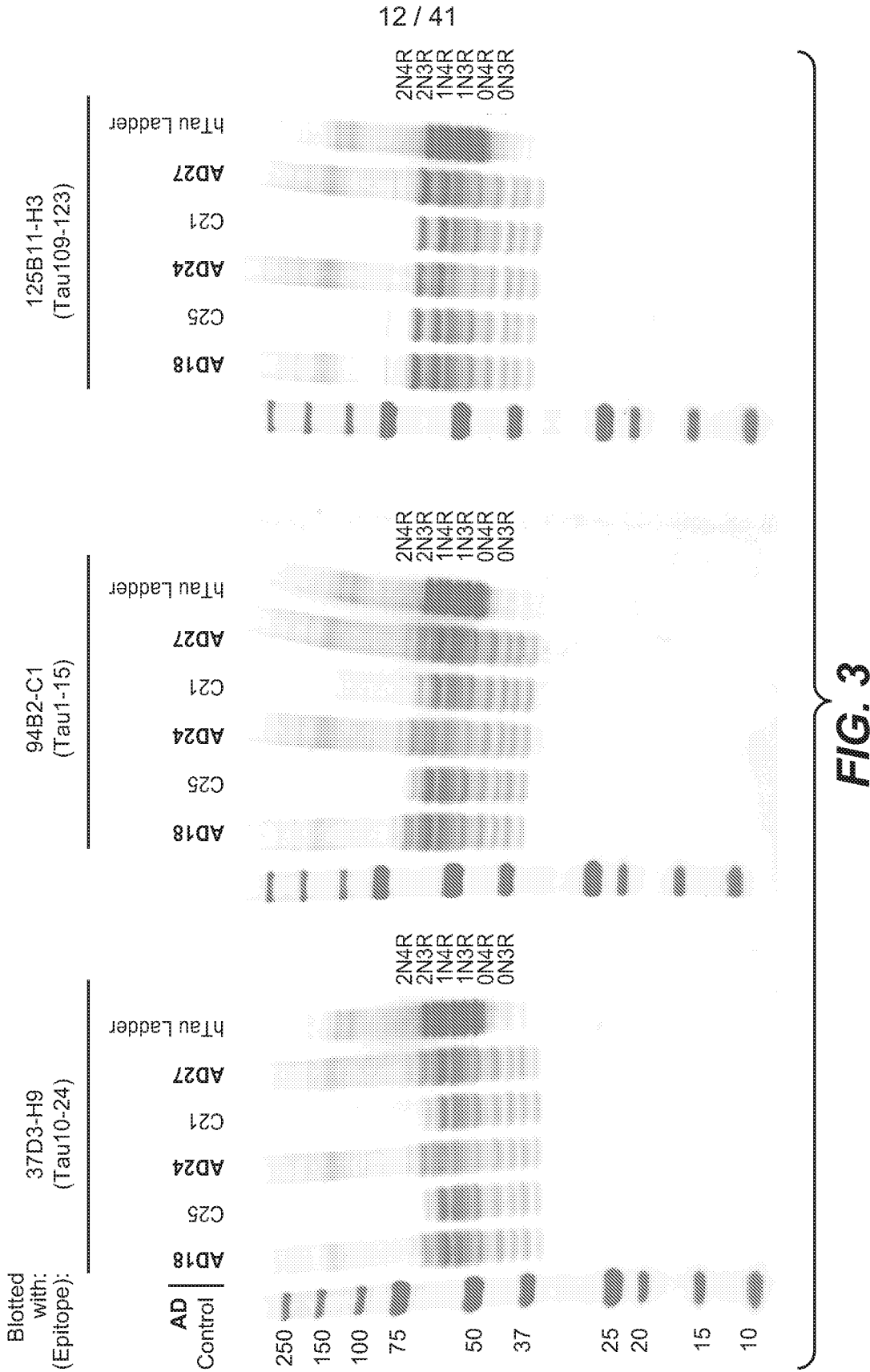


FIG. 2E



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FIG. 4A

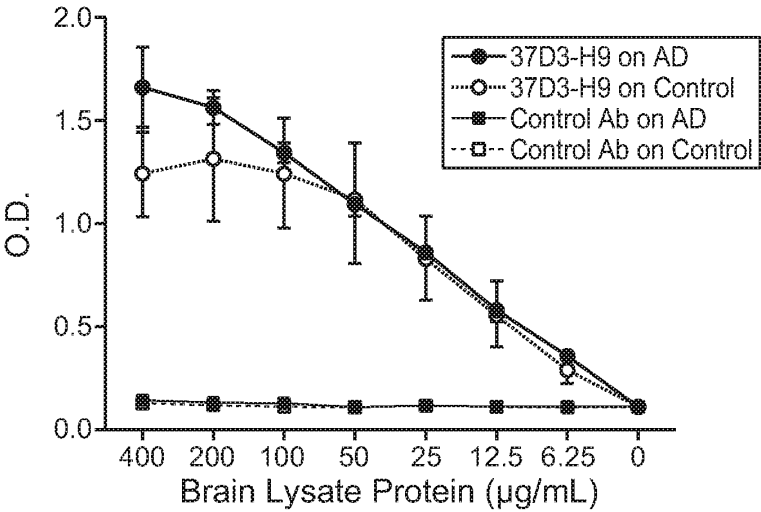


FIG. 4B

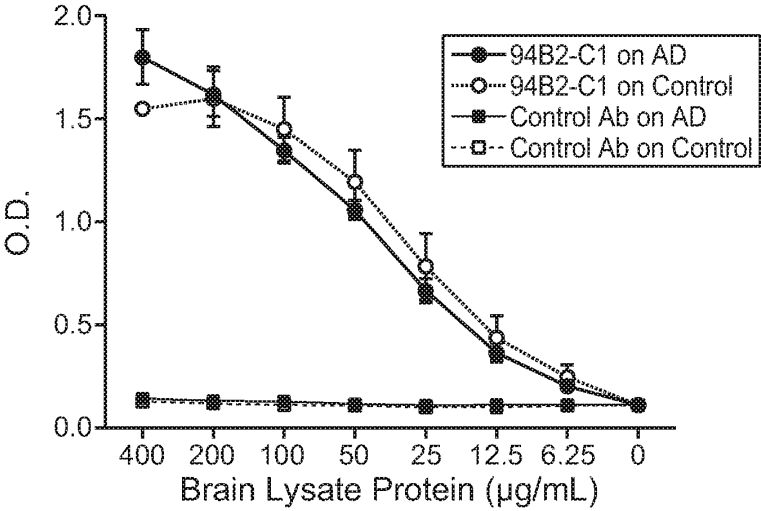
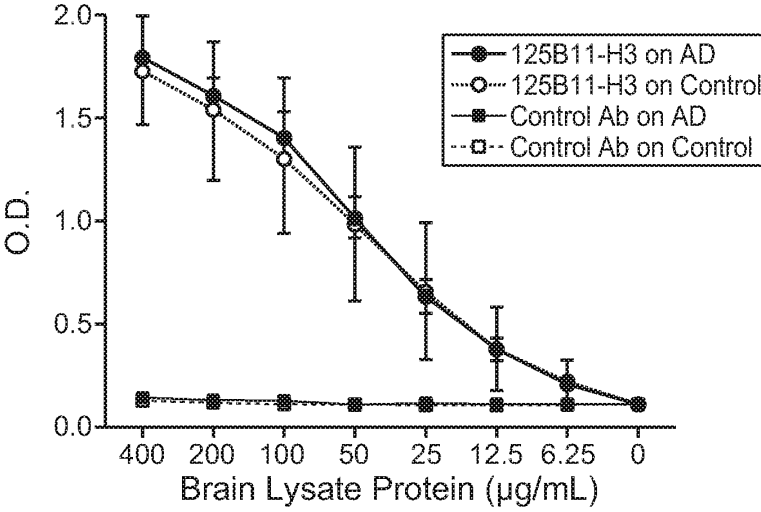


FIG. 4C



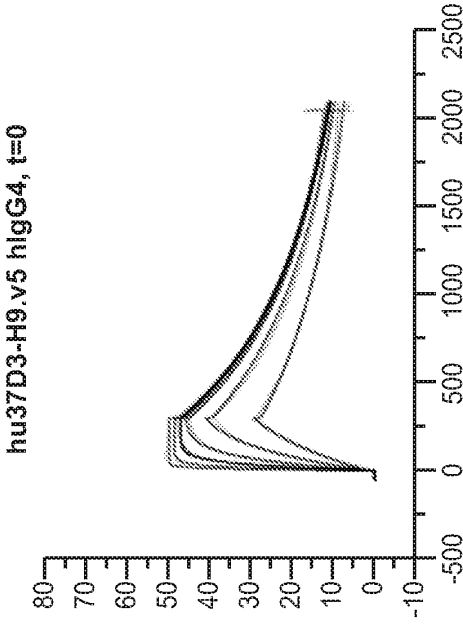
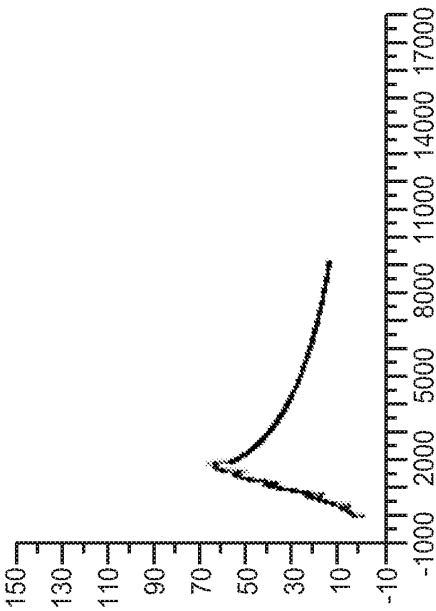
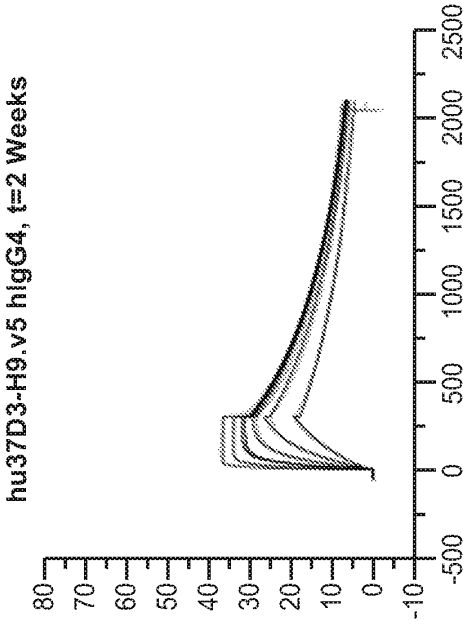
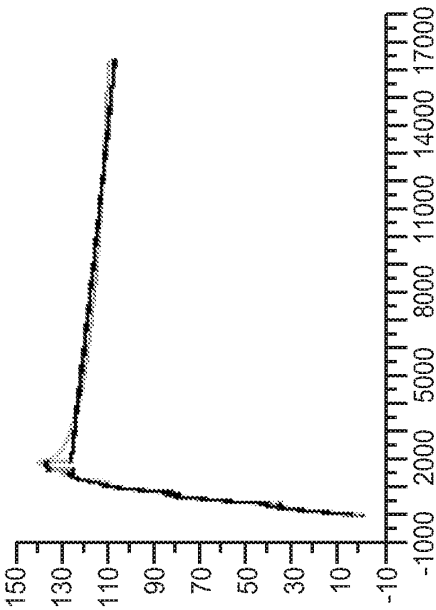


FIG. 5

FIG. 6

FIG. 7

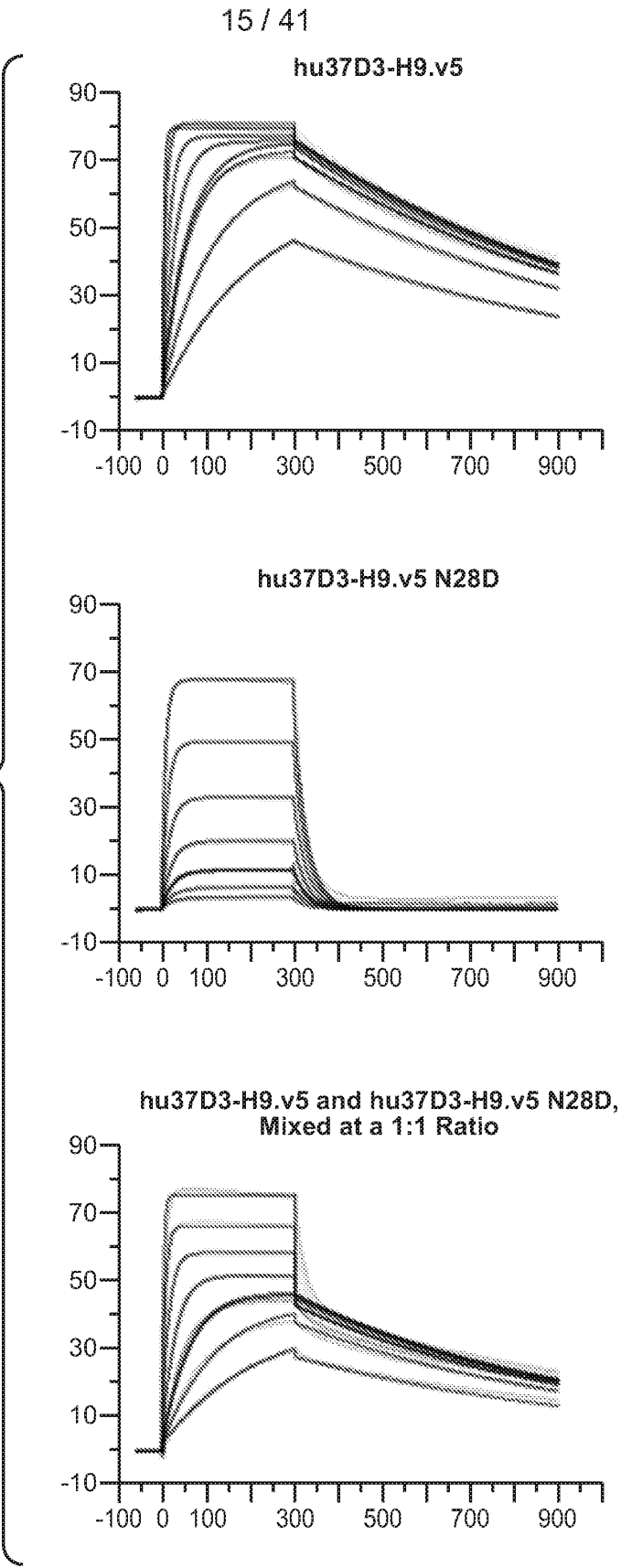


FIG. 8

FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D

FIG. 8A

Antibody	KD (nM)	Stability Index	Chi2 < 10% Rmax and Normalized Rmax (Pre-stress) > 0.1?	VL Residues at Selected Locations (Kabat Numbering)												SEQ ID:	
				1	2	4	27D	27E	28	29	30	31	32	33	93		
Unstressed Control (mean, n=9)	1.0	106%	Yes	E	D	L	H	S	N	G	N	T	Y	F	L	350	
hu37D3-H9.v5	0.9	73%	Yes	E	D	L	H	S	N	G	N	T	Y	F	L	351	
hu37D3-H9.v5.1	4.0	72%	Yes	E	D	L	H	S	N	A	N	T	Y	F	L	352	
hu37D3-H9.v5.2	10.9	97%	Yes	E	D	L	H	S	S	G	N	T	Y	F	L	353	
hu37D3-H9.v5.3	73.2	70%	Yes	E	D	L	H	S	S	D	N	T	Y	F	L	354	
hu37D3-H9.v5.4	36.1	78%	-	E	D	L	H	S	S	Q	N	T	Y	F	L	355	
hu37D3-H9.v5.5	64.5	75%	-	E	D	L	H	S	S	E	N	T	Y	F	L	356	
hu37D3-H9.v5.6	36.6	67%	-	E	D	L	H	S	S	A	N	T	Y	F	L	357	
hu37D3-H9.v5.7	13.0	67%	Yes	E	D	L	H	S	S	N	G	D	T	Y	F	L	358
hu37D3-H9.v5.8	2.2	90%	Yes	E	D	L	H	S	S	N	G	Q	T	Y	F	L	359
hu37D3-H9.v5.9	5.3	95%	Yes	E	D	L	H	S	S	N	G	E	T	Y	F	L	360
hu37D3-H9.v5.10	4.7	78%	Yes	E	D	L	H	S	S	N	G	A	T	Y	F	L	361
hu37D3-H9.v5.11	97.7	71%	Yes	E	D	L	H	S	S	N	G	S	T	Y	F	L	362
hu37D3.v28	0.9	78%	Yes	D	D	L	H	S	N	G	N	T	Y	F	L	363	
hu37D3.v28.A2	32.6	72%	Yes	D	D	L	H	S	N	G	N	T	Y	F	H	364	
hu37D3.v28.A4	1.2	96%	Yes	D	D	L	H	S	N	G	N	T	Y	L	L	365	
hu37D3.v28.A6	38.3	82%	Yes	D	D	L	H	S	N	G	N	T	Y	L	H	366	
hu37D3.v28.A8	1.8	57%	Yes	D	D	M	H	S	N	G	N	T	Y	F	L	367	

hu37D3.v28.A10	41.8	37%	Yes	D	D	M	H	S	N	G	N	T	Y	F	H	368
	1.8	88%	Yes	D	D	M	H	S	N	G	N	T	Y	L	L	369
hu37D3.v28.A12	51.4	70%	Yes	D	D	M	H	S	N	G	N	T	Y	L	H	370
hu37D3.v28.A14	3.9	89%	Yes	D	V	L	H	S	N	G	N	T	Y	F	L	371
hu37D3.v28.A16	17.3	83%	Yes	D	V	L	H	S	N	G	N	T	Y	F	H	372
hu37D3.v28.A18	7.1	93%	Yes	D	V	L	H	S	N	G	N	T	Y	L	L	373
hu37D3.v28.A20	27.8	70%	Yes	D	V	L	H	S	N	G	N	T	Y	L	H	374
hu37D3.v28.A22	4.7	95%	Yes	D	V	M	H	S	N	G	N	T	Y	F	L	375
hu37D3.v28.A24	22.5	78%	Yes	D	V	M	H	S	N	G	N	T	Y	F	H	376
hu37D3.v28.A26	11.4	89%	Yes	D	V	M	H	S	N	G	N	T	Y	L	L	377
hu37D3.v28.A28	34.4	77%	-	D	V	M	H	S	N	G	N	T	Y	L	H	378
hu37D3.v28.A30	24.3	101%	Yes	D	D	L	H	S	N	G	N	T	F	F	L	379
hu37D3.v28.B1	31.8	83%	Yes	D	D	L	H	S	N	G	N	T	F	F	L	380
hu37D3.v28.B3	0.4	208%	-	D	D	L	H	S	N	G	N	T	W	F	L	381
hu37D3.v28.B4	10.5	288%	-	D	D	L	H	S	N	G	N	T	H	F	L	382
hu37D3.v28.B6	85.6	46%	Yes	D	D	L	H	S	N	G	N	T	R	F	L	383
hu37D3.v28.B7	4.1	607%	-	D	D	L	H	S	N	G	N	T	K	F	L	384
hu37D3.v28.B8	1.8	456%	-	D	D	L	H	S	N	G	N	T	R	F	L	385
hu37D3.v28.C1	1.4	77%	Yes	D	D	L	H	S	N	N	D	T	Y	F	L	386
hu37D3.v28.C2	9.6	75%	Yes	D	D	L	H	S	N	N	D	T	Y	F	L	387
hu37D3.v28.D1	5.7	73%	Yes	D	D	L	H	S	N	G	N	T	Y	F	L	388

FIG. 8B

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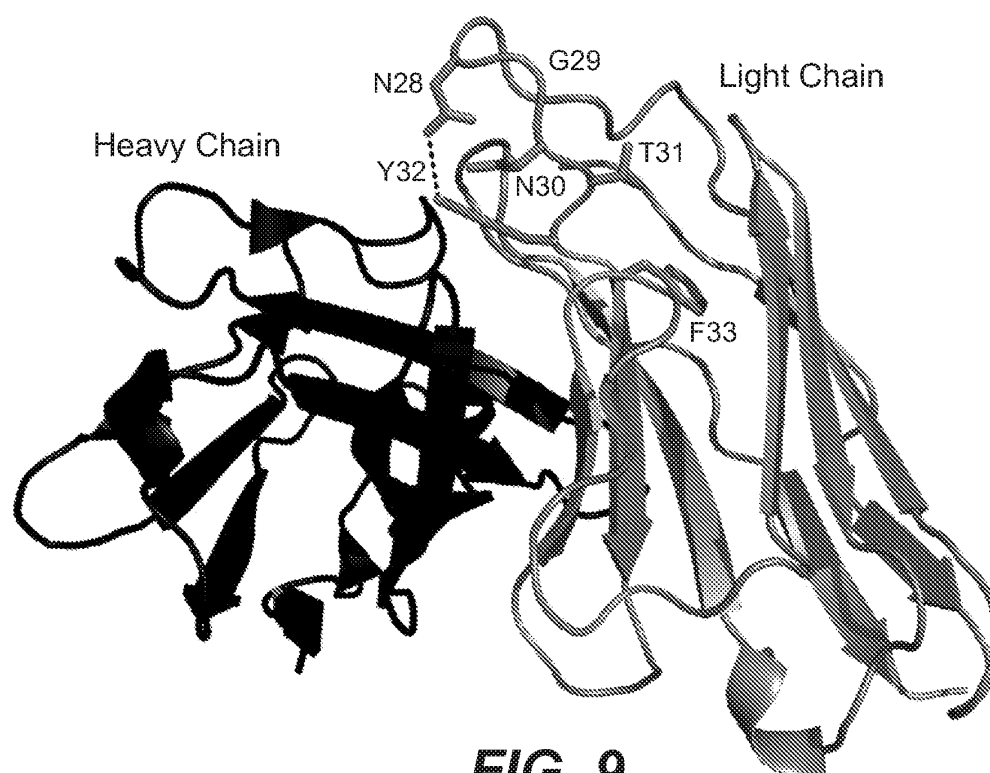
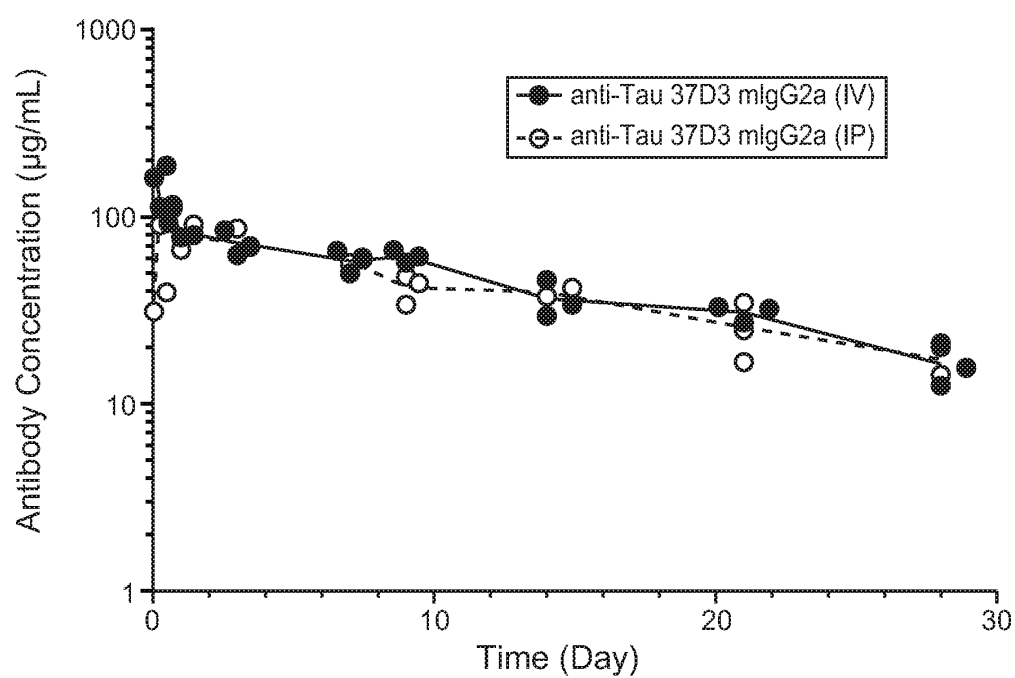
Antibody	KD (nM)	Stability Index	Chi2 < 10% Rmax and Normalized Rmax (Pre-stress) > 0.1?	VL Residues at Selected Locations (Kabat Numbering)														SEQ ID:	
				1	2	4	27D	27E	28	29	30	31	32	33	93				
Unstressed Control (mean, n=9)				1.0	106%	Yes	E	D	L	H	S	N	G	N	T	Y	F	L	
hu37D3.v28.E1	20.1	46%	Yes		D	D	L	N	S	N	G	N	T	Y	F	L		389	
hu37D3.v28.E2	22.5	28%	Yes		D	D	L	Q	S	N	G	N	T	Y	F	L		390	
hu37D3.v28.E3	1.1	364%	-		D	D	L	D	S	D	G	N	T	Y	F	L		391	
hu37D3.v28.F1	2.1	81%	Yes		D	D	L	H	S	N	T	N	T	Y	F	L		392	
hu37D3.v28.F2	1.9	51%	Yes		D	D	L	H	T	N	G	N	T	Y	F	L		393	
hu37D3.v28.F3	9.5	70%	Yes		D	D	L	H	T	N	A	N	T	Y	F	L		394	
hu37D3.v28.51	35.6	74%	-		E	D	L	H	S	H	G	N	T	Y	F	L		395	
hu37D3.v28.52	17.6	80%	Yes		E	D	L	H	S	K	G	N	T	Y	F	L		396	
hu37D3.v28.53	22.9	76%	Yes		E	D	L	H	S	R	G	N	T	Y	F	L		397	
hu37D3.v28.54	24.8	82%	Yes		E	D	L	H	S	L	G	N	T	Y	F	L		398	
hu37D3.v28.55	2.6	82%	Yes		D	D	L	H	S	N	Q	N	T	Y	F	L		399	
hu37D3.v28.56	5.4	76%	Yes		D	D	L	H	S	N	Y	N	T	Y	F	L		400	
hu37D3.v28.57	4.4	88%	Yes		D	D	L	H	S	N	F	N	T	Y	F	L		401	
hu37D3.v29.1	13.5	70%	Yes		E	D	L	H	S	N	G	N	T	Y	F	L		402	
hu37D3.v29.2	2.6	88%	Yes		E	D	L	H	S	N	G	D	T	Y	F	L		403	
hu37D3.v29.3	5.6	93%	Yes		E	D	L	H	S	N	G	Q	T	Y	F	L		404	
hu37D3.v29.4	4.9	76%	Yes		E	D	L	H	S	N	G	E	T	Y	F	L		405	
hu37D3.v29.5	1.4	64%	Yes		E	D	L	H	S	N	G	A	T	Y	F	L		406	
hu37D3.v29.6	1.4	62%	Yes		E	D	L	H	S	N	G	H	T	Y	F	L		407	
hu37D3.v29.7	4.6	90%	Yes		E	D	L	H	S	N	G	K	T	Y	F	L		408	
hu37D3.v29.8	40.9	77%	-		E	D	L	H	S	N	N	L	T	Y	F	L		409	
hu37D3.v29.9	7.3	86%	Yes		E	D	L	H	S	N	A	D	T	Y	F	L		410	
hu37D3.v29.10	17.4	100%	Yes		E	D	L	H	S	N	A	Q	T	Y	F	L		411	
					E	D	L	H	S	N	A	E	T	Y	F	L		412	

FIG. 8C

hu37D3.v29.11	27.9	67%	Yes	E	D	L	H	S	N	A	A	T	Y	F	L	SEQ ID: 413
hu37D3.v29.12	7.0	50%	Yes	E	D	L	H	S	N	A	H	T	Y	F	L	414
hu37D3.v29.13	6.7	79%	Yes	E	D	L	H	S	N	A	K	T	Y	F	L	415
hu37D3.v29.14	22.0	92%	Yes	E	D	L	H	S	N	A	L	T	Y	F	L	416
hu37D3-H9.v30.1	23.5	87%	Yes	D	D	L	H	S	G	N	N	T	Y	F	L	417
hu37D3-H9.v30.2	4.2	96%	Yes	D	D	L	H	S	T	G	N	T	Y	F	L	418
hu37D3-H9.v30.3	38.1	83%	Yes	D	D	L	H	S	V	G	N	T	Y	F	L	419
hu37D3-H9.v30.4	22.0	87%	Yes	D	D	L	H	S	L	G	N	T	Y	F	L	420
hu37D3-H9.v30.5	29.1	80%	Yes	D	D	L	H	S	I	G	N	T	Y	F	L	421
hu37D3-H9.v30.6	19.1	270%	-	D	D	L	H	S	P	G	N	T	Y	F	L	422
hu37D3-H9.v30.7	34.9	93%	-	D	D	L	H	S	F	G	N	T	Y	F	L	423
hu37D3-H9.v30.8	31.4	105%	-	D	D	L	H	S	Y	G	N	T	Y	F	L	424
hu37D3-H9.v30.9	36.4	63%	-	D	D	L	H	S	H	G	N	T	Y	F	L	425
hu37D3-H9.v30.10	16.1	84%	Yes	D	D	L	H	S	K	G	N	T	Y	F	L	426
hu37D3-H9.v30.11	20.9	86%	Yes	D	D	L	H	S	R	G	N	T	Y	F	L	427
hu37D3-H9.v31.1	41.2	72%	-	D	D	L	H	S	N	A	G	T	Y	F	L	428
hu37D3-H9.v31.2	10.6	90%	Yes	D	D	L	H	S	N	A	V	T	Y	F	L	429
hu37D3-H9.v31.3	9.8	93%	Yes	D	D	L	H	S	N	A	I	T	Y	F	L	430
hu37D3-H9.v31.4	0.8	533%	-	D	D	L	H	S	N	A	P	T	Y	F	L	431
hu37D3-H9.v31.5	15.2	85%	Yes	D	D	L	H	S	N	A	F	T	Y	F	L	432
hu37D3-H9.v31.6	15.5	90%	Yes	D	D	L	H	S	N	A	Y	T	Y	F	L	433
hu37D3-H9.v31.7	6.9	83%	Yes	D	D	L	H	S	N	A	R	T	Y	F	L	434
hu37D3-H9.v31.8	10.9	78%	Yes	D	D	L	H	S	N	A	N	V	Y	F	L	435
hu37D3-H9.v31.9	7.5	81%	Yes	D	D	L	H	S	N	A	N	I	Y	F	L	436
hu37D3-H9.v31.10	5.5	261%	-	D	D	L	H	S	N	A	N	P	Y	F	L	437
hu37D3-H9.v31.11	22.7	126%	-	D	D	L	H	S	N	A	N	F	Y	F	L	438
hu37D3-H9.v31.12	41.6	99%	-	D	D	L	H	S	N	A	N	Y	Y	F	L	439
hu37D3-H9.v31.13	48.1	83%	-	D	D	L	H	S	N	A	N	N	Y	F	L	440
hu37D3-H9.v31.14	35.5	86%	-	D	D	L	H	S	N	A	N	R	Y	F	L	441

FIG. 8D

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**FIG. 9****FIG. 10**

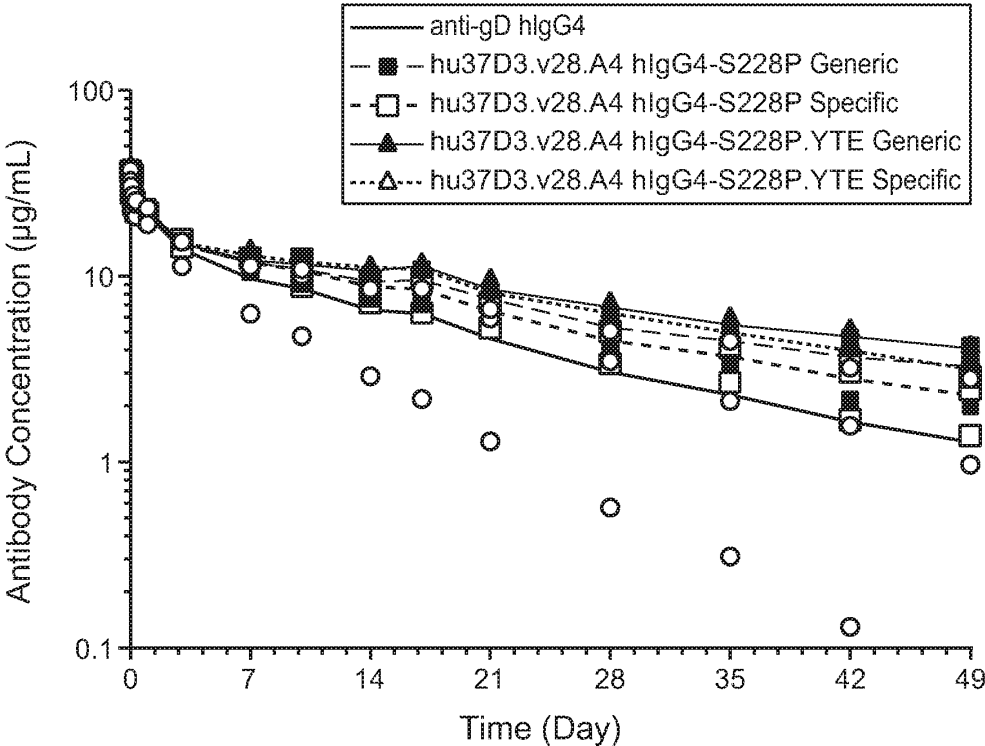


FIG. 11

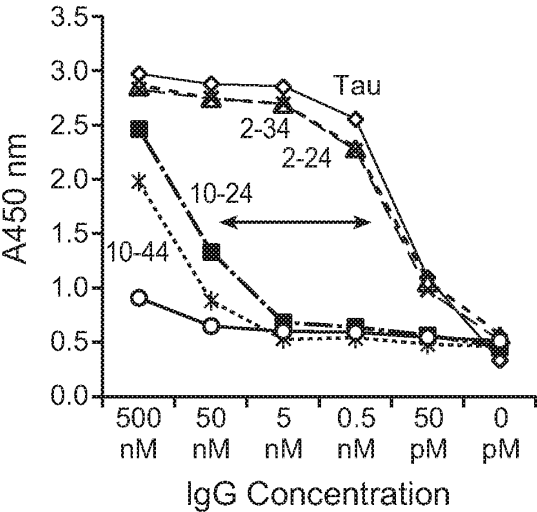


FIG. 12B

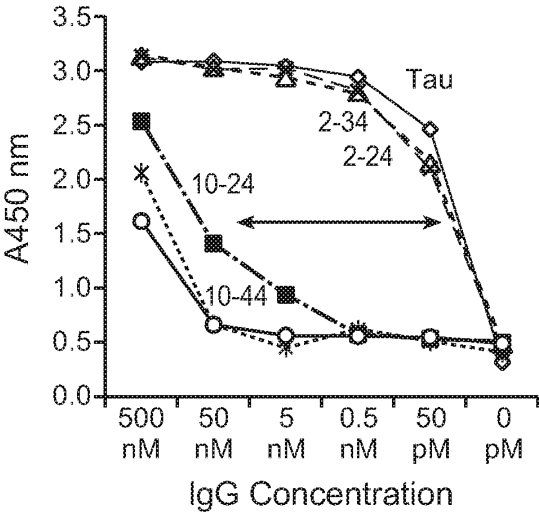


FIG. 12C

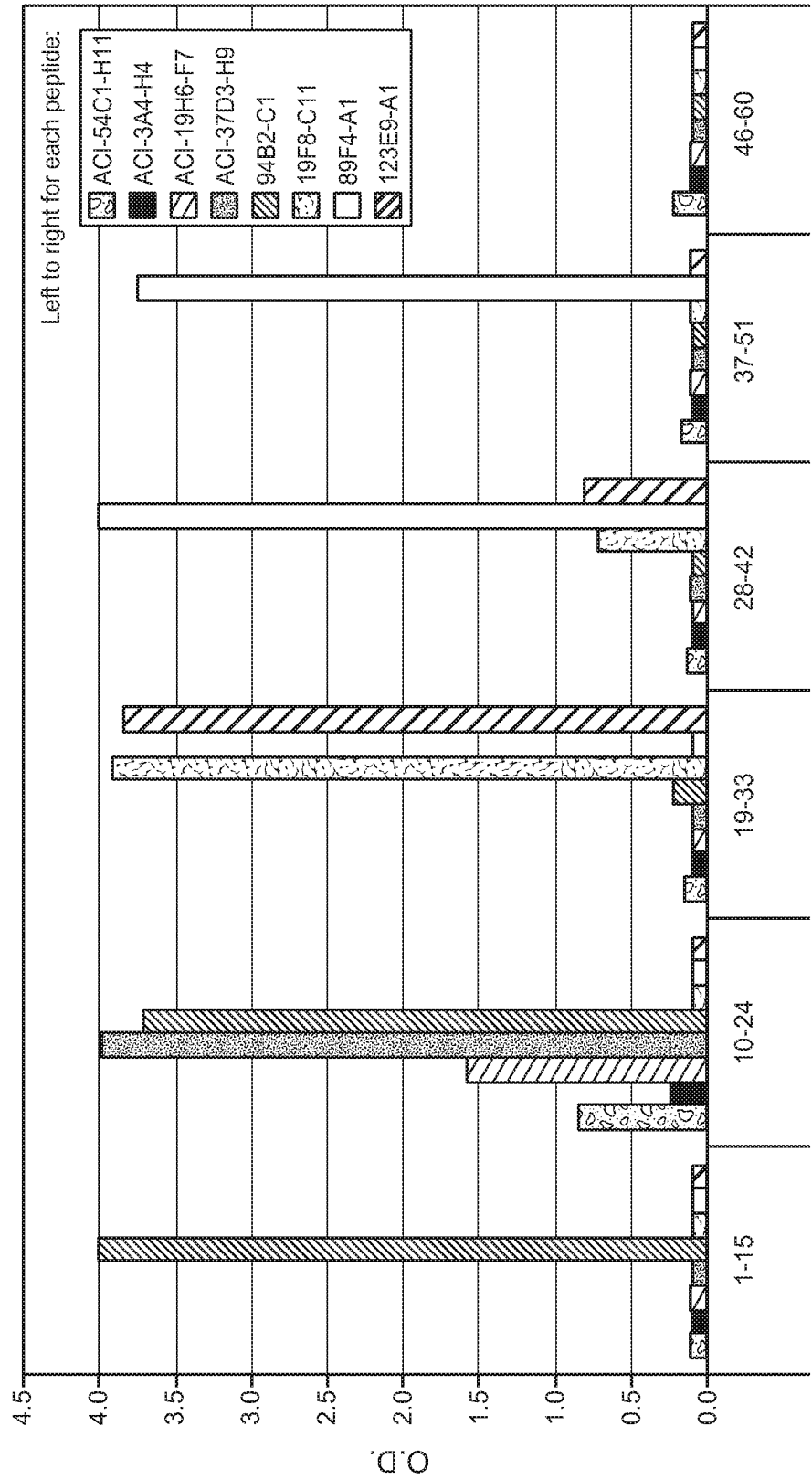


FIG. 12A

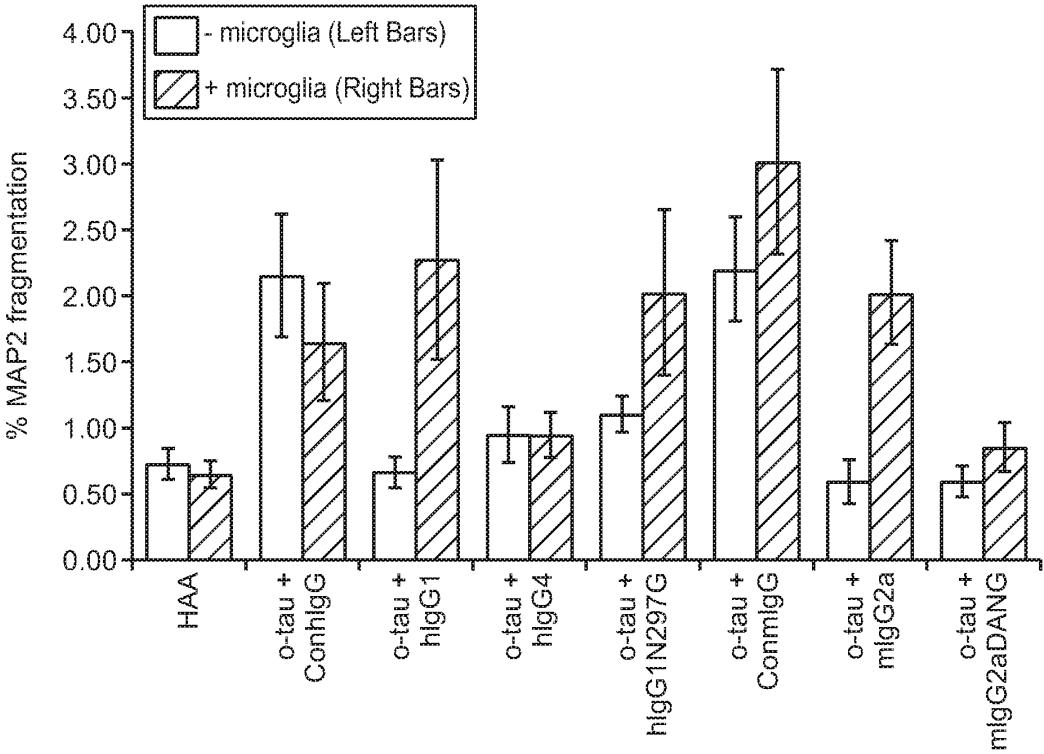


FIG. 13A

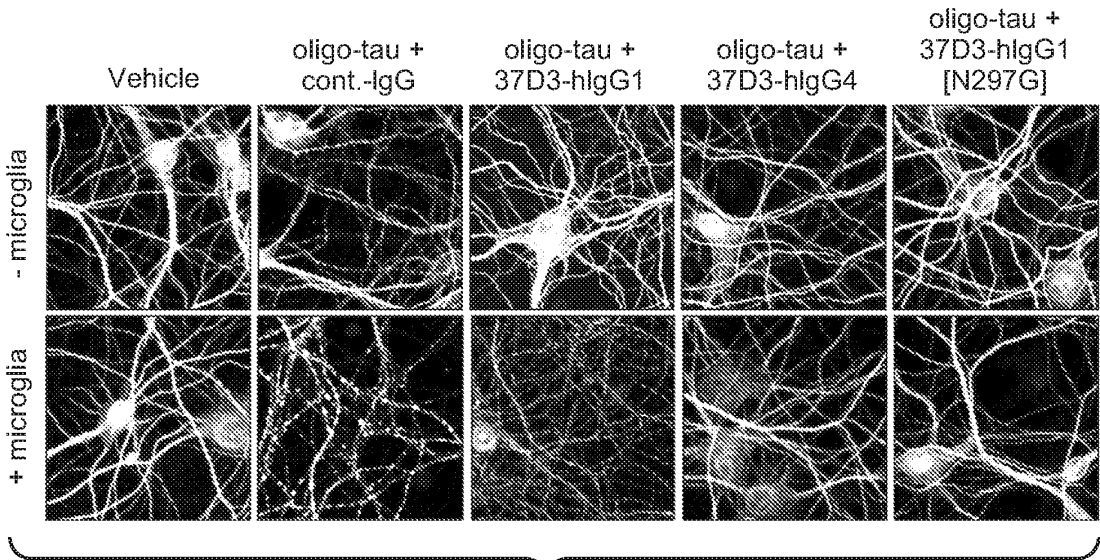


FIG. 13B

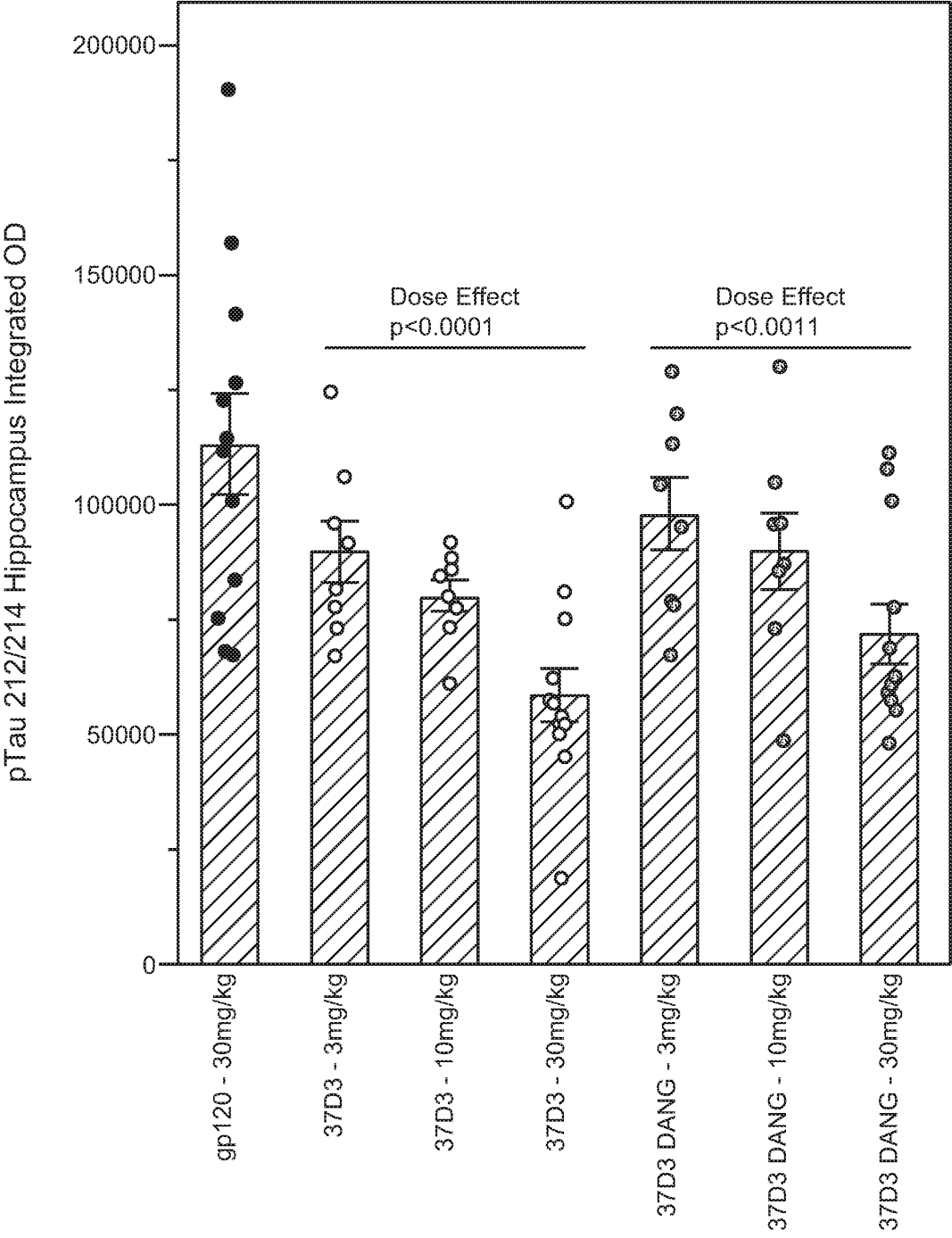


FIG. 14

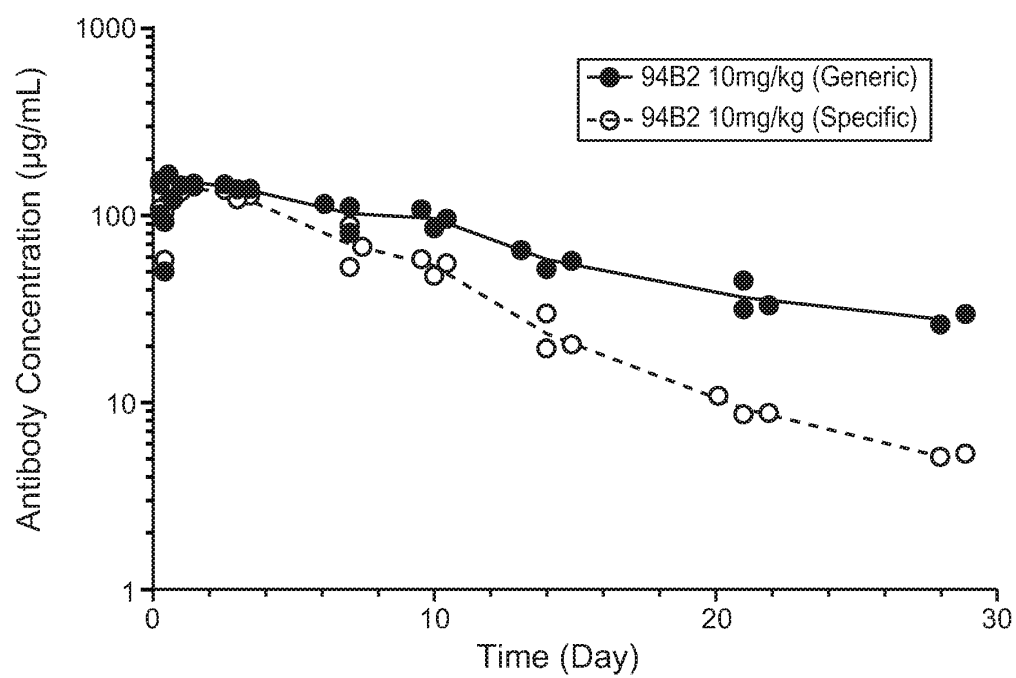
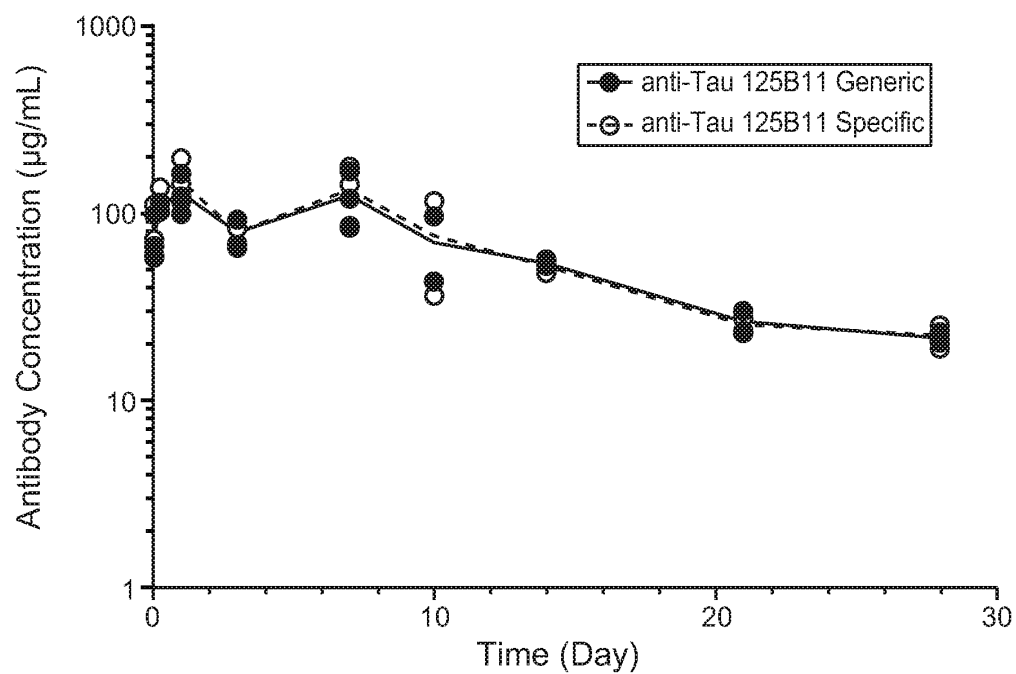
Native Tau Position 2		37D3 Epitope (2-24)	
		↓	
PRO364486.HU	1	MHHHHHHG	ENLYFQGS
PRO378546.CYNO	1	MHHHHHHG	ENLYFQGS
PRO364486.HU	51	EGD	TDAGLKE
PRO378546.CYNO	51	EGD	TDAGLKE
PRO364486.HU	101	GKQ	AAQPH
PRO378546.CYNO	101	GEQ	AAQPH
PRO364486.HU	151	GSD	DKKAKG
PRO378546.CYNO	151	GSD	DKKAKG
PRO364486.HU	201	GEP	PKSGDR
PRO378546.CYNO	201	GEP	PKSGDR
PRO364486.HU	251	PSS	AKSRLQ
PRO378546.CYNO	251	PSS	AKSRLQ
PRO364486.HU	301	NVQ	SKCGSK
PRO378546.CYNO	301	NVQ	SKCGSK
PRO364486.HU	351	QVE	VKSEKL
PRO378546.CYNO	351	QVE	VKSEKL
PRO364486.HU	401	TDH	GAEIVYK
PRO378546.CYNO	401	TDH	GAEIVYK
PRO364486.HU	451	LAK	QGL
PRO378546.CYNO	451	LAK	QGL

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1 MHHHHHHG ENLYFQGS AEP RQEF E V MEDHAGTYGLGDRKDQ GGYTM HQDQ 50
 1 MHHHHHHG ENLYFQGS AEP RQEF D V MEDHAGTYGLGDRKDQ EGYTM LQDQ 50
 51 EGD TDAGLKE SP LQ T P T E D G S E E P G S E T S D A K S T P T A E D V T A P L V D E G A P 100
 51 EGD TDAGLKE SP LQ T P A E D G S E E L G S E T S D A K S T P T A E D V T A P L V D E R A P 100
 101 G K Q A A A Q P H T E I P E G T T A E E A G I G D T P S L E D E A A G H V T Q A R M V S K S K D G T 150
 101 G E Q A A A Q P H M E I P E G T T A E E A G I G D T P S L E D E A A G H V T Q A R M V S K S K D G T 150
 151 G S D D K K A K G A D G K T K I A T P R G A A P P G Q K G Q A N A T R I P A K T P P A P K T P P S S 200
 151 G S D D K K A K G A D G K T K I A T P R G A A P P G Q K G Q A N A T R I P A K T P P A P K T P P S S 200
 201 G E P P K S G D R S G Y S S P G S P G T P G S R S R T P S L P T P P T R E P K K V A V V R T P P K S 250
 201 G E P P K S G D R S G Y S S P G S P G T P G S R S R T P S L P T P P A R E P K K V A V V R T P P K S 250
 251 P S S A K S R L Q T A P V P M P D L K N V K S K I G S T E N L K H Q P G G K V Q I I N K K L D L S 300
 251 P S S A K S R L Q T A P V P M P D L K N V K S K I G S T E N L K H Q P G G K V Q I I N K K L D L S 300
 301 N V Q S K C G S K D N I K H V P G G S V Q I V Y K P V D L S K V T S K C G S L G N I H H K P G G G 350
 301 N V Q S K C G S K D N I K H V P G G S V Q I V Y K P V D L S K V T S K C G S L G N I H H K P G G G 350
 351 Q V E V K S E K L D F K D R V Q S K I G S L D N I T H V P G G G N K K I E T H K L T F R E N A K A K 400
 351 Q V E V K S E K L D F K D R V Q S K I G S L D N I T H V P G G G N K K I E T H K L T F R E N A K A K 400
 401 T D H G A E I V Y K S P V S G D T S P R H L S N V S S T G S I D M V D S P Q L A T L A D E V S A S 450
 401 T D H G A E I V Y K S P V S G D T S P R H L S N V S S T G S I D M V D S P Q L A T L A D E V S A S 450
 451 L A K Q G L 456 S E Q I D N O: 1
 451 L A K Q G L 456 S E Q I D N O: 3

FIG. 15

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**FIG. 16****FIG. 17**

Light Chain Variable Region

			CDR L1 - Chothia										CDR L1 - Kabat										CDR L1 - Contact																			
			CDR L2 - Contact										CDR L2 - Chothia										CDR L2 - Kabat																			
			CDR L3 - Contact										CDR L3 - Chothia										CDR L3 - Kabat																			
Kabat number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	28	29	30	31	32	33	34	35	36	37
hu37D3.v1 hlgG1	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q
hu37D3.v1 hlgG4	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q
hu37D3.v39 hlgG4.YTE	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q
hu37D3.v40 hlgG4.YTE	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q
hu37D3.v41 hlgG4.YTE	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q
hu37D3.v41 hlgG4.YTE	E	D	Q	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	F	E	W	Y	Q

			CDR L2 - Contact										CDR L2 - Chothia										CDR L2 - Kabat																			
Kabat number	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79
hu37D3.v1 hlgG1	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q
hu37D3.v1 hlgG4	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q
hu37D3.v39 hlgG4.YTE	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q
hu37D3.v40 hlgG4.YTE	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q
hu37D3.v41 hlgG4.YTE	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q

			CDR L3 - Contact										CDR L3 - Chothia										CDR L3 - Kabat															
Kabat number	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107										
hu37D3.v1 hlgG1	P	E	D	F	A	T	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	SEQ ID NO: 281									
hu37D3.v1 hlgG4	P	E	D	F	A	T	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	SEQ ID NO: 281									
hu37D3.v39 hlgG4.YTE	P	E	D	F	A	T	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	SEQ ID NO: 561									
hu37D3.v40 hlgG4.YTE	P	E	D	F	A	T	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	SEQ ID NO: 571									
hu37D3.v41 hlgG4.YTE	P	E	D	F	A	T	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	SEQ ID NO: 581									

FIG. 18

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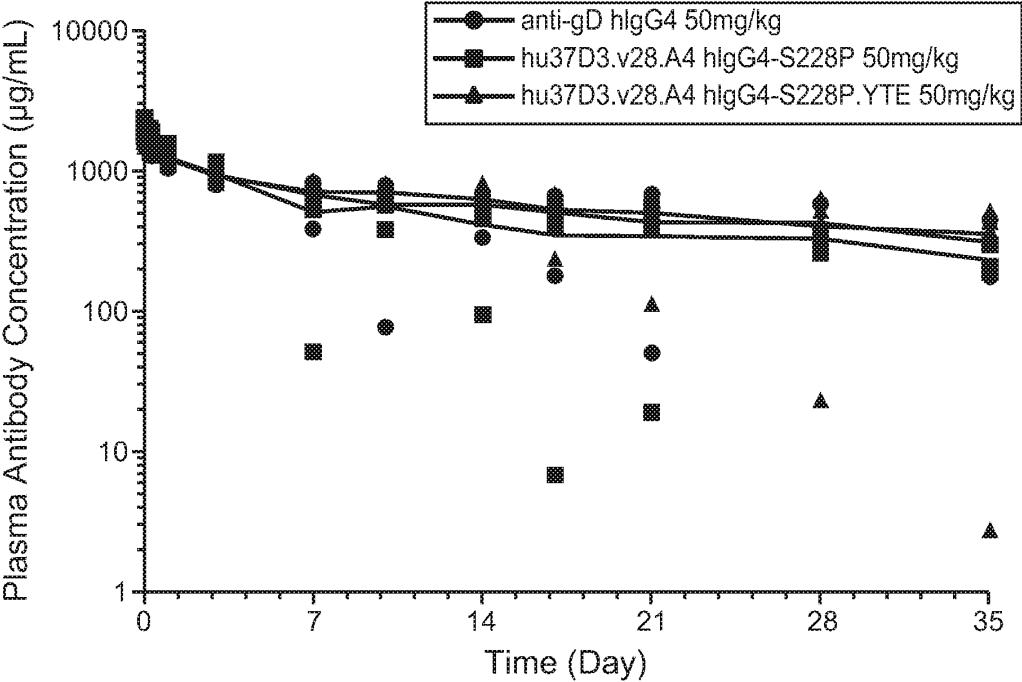


FIG. 19A

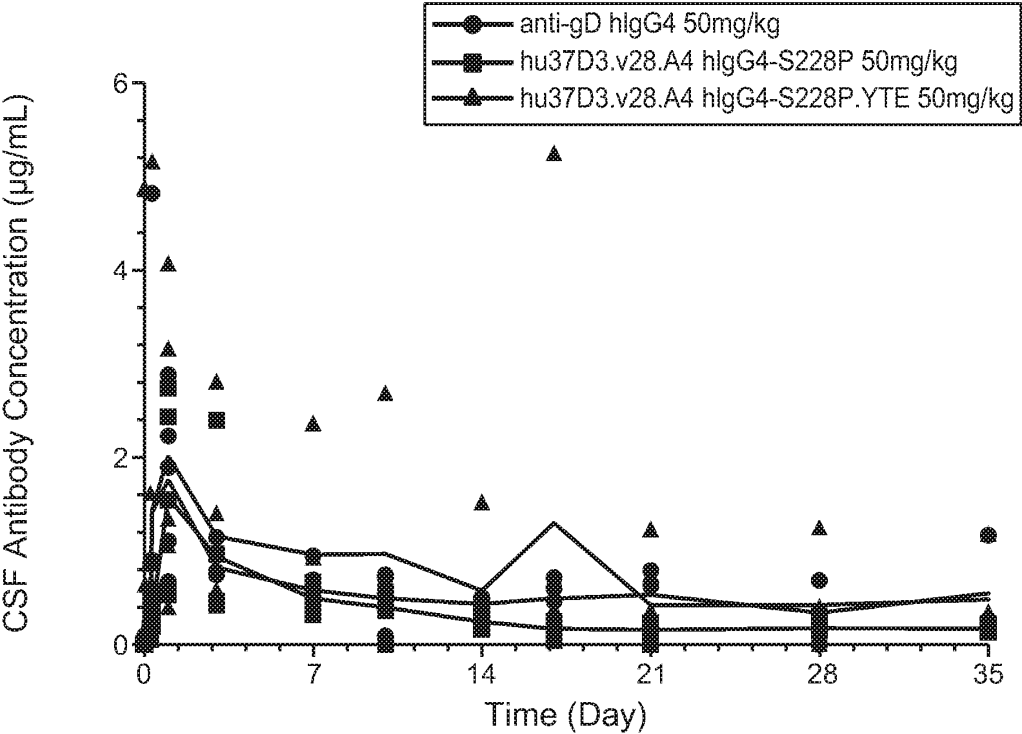


FIG. 19B

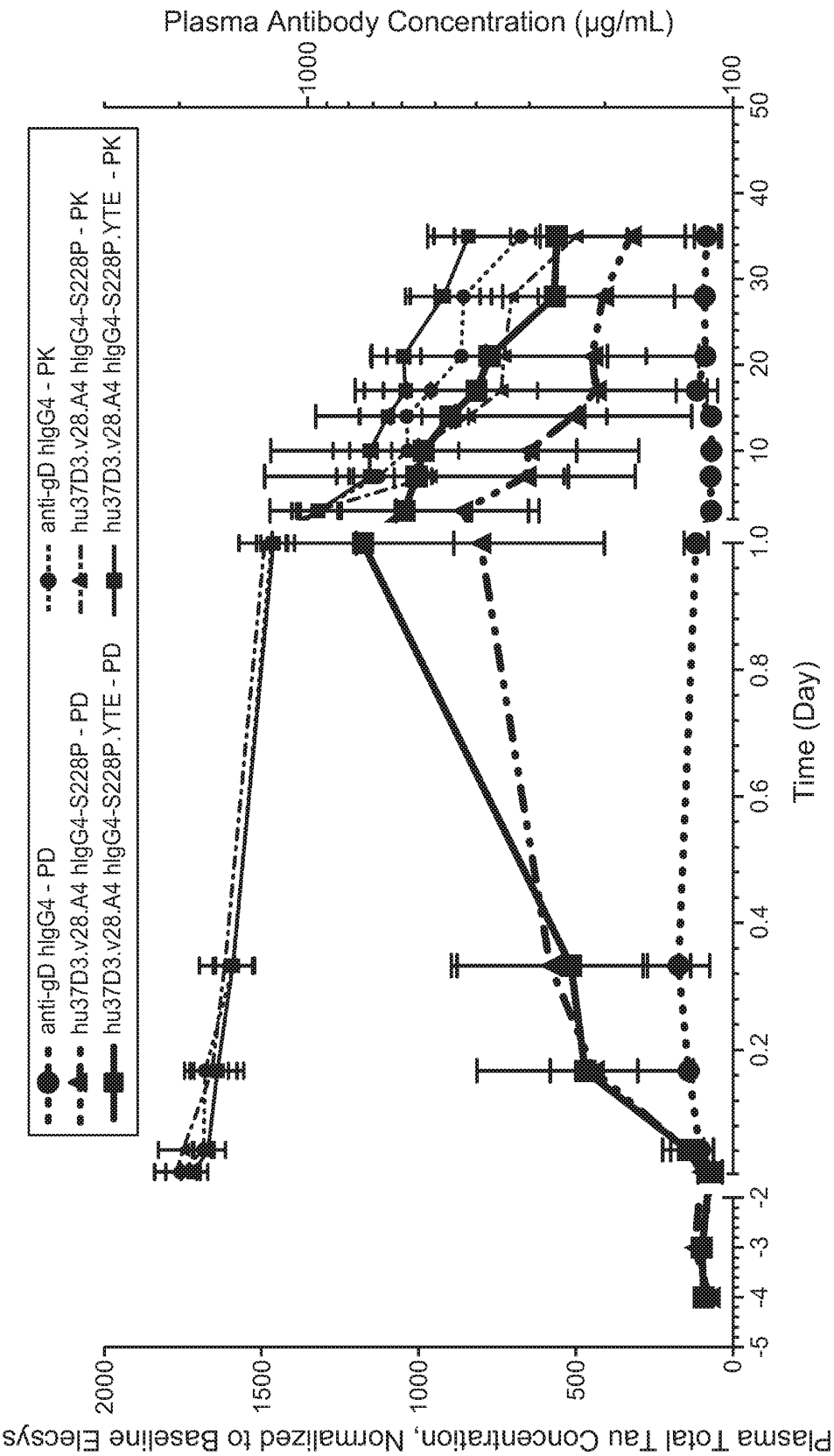
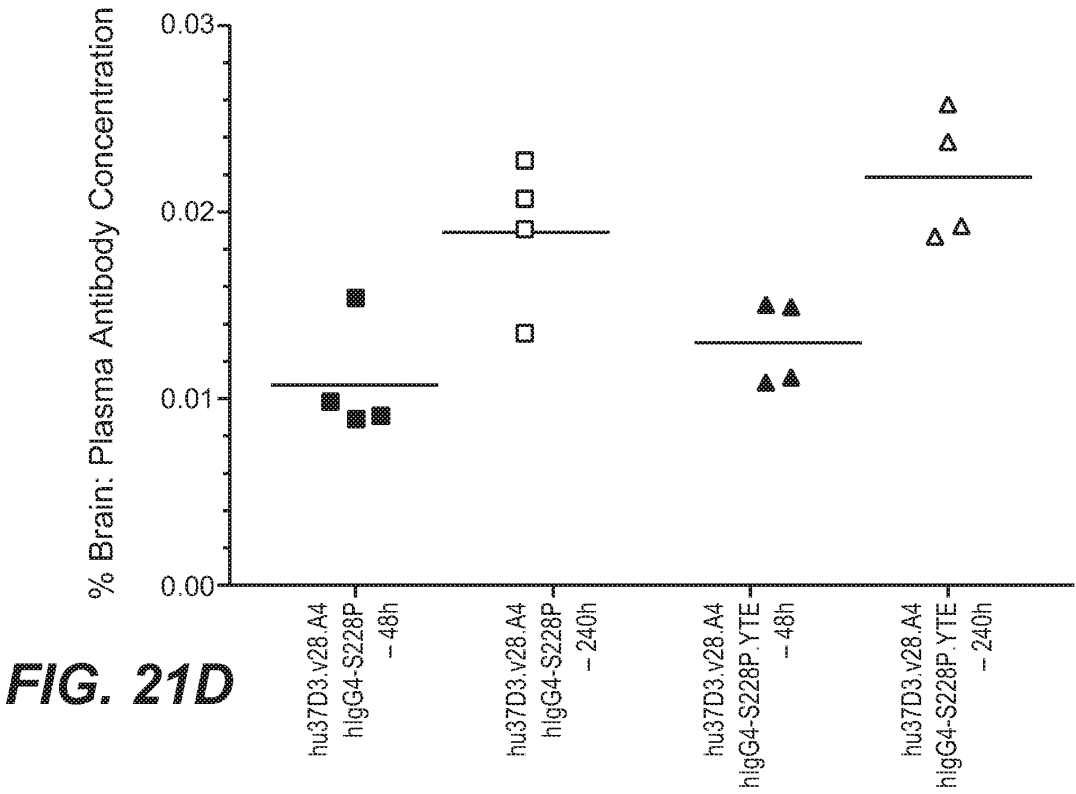
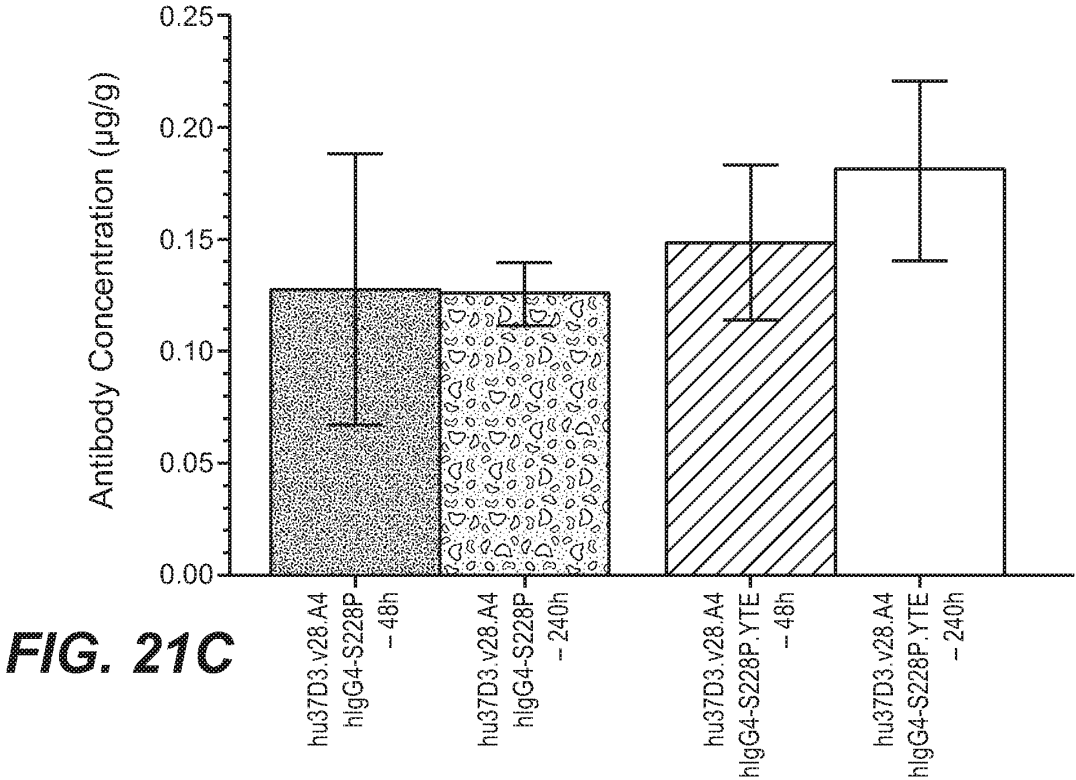


FIG. 20





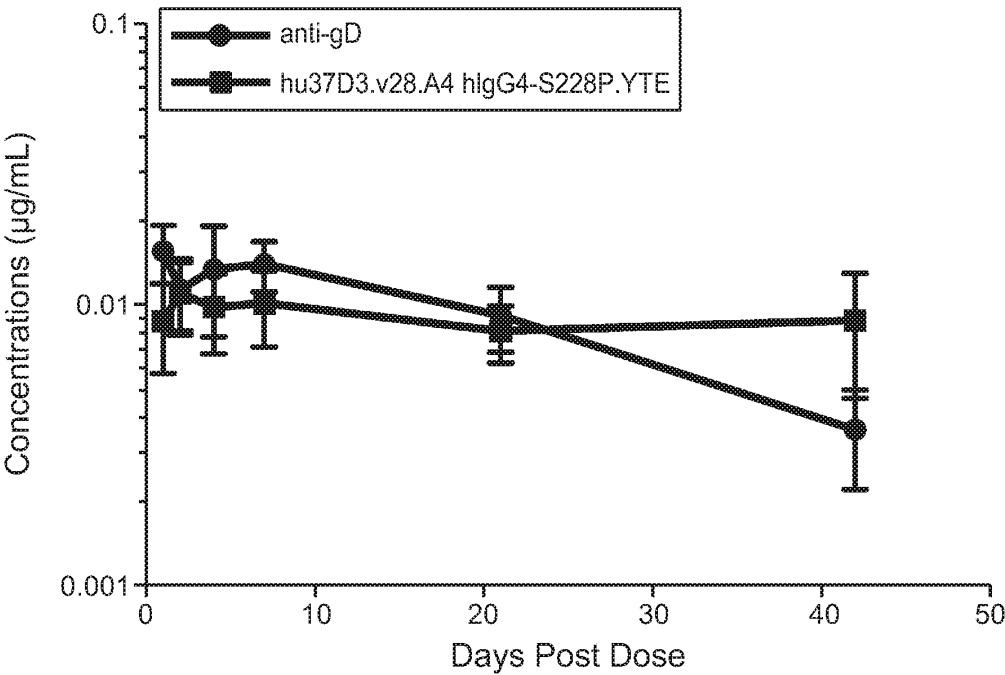


FIG. 22A

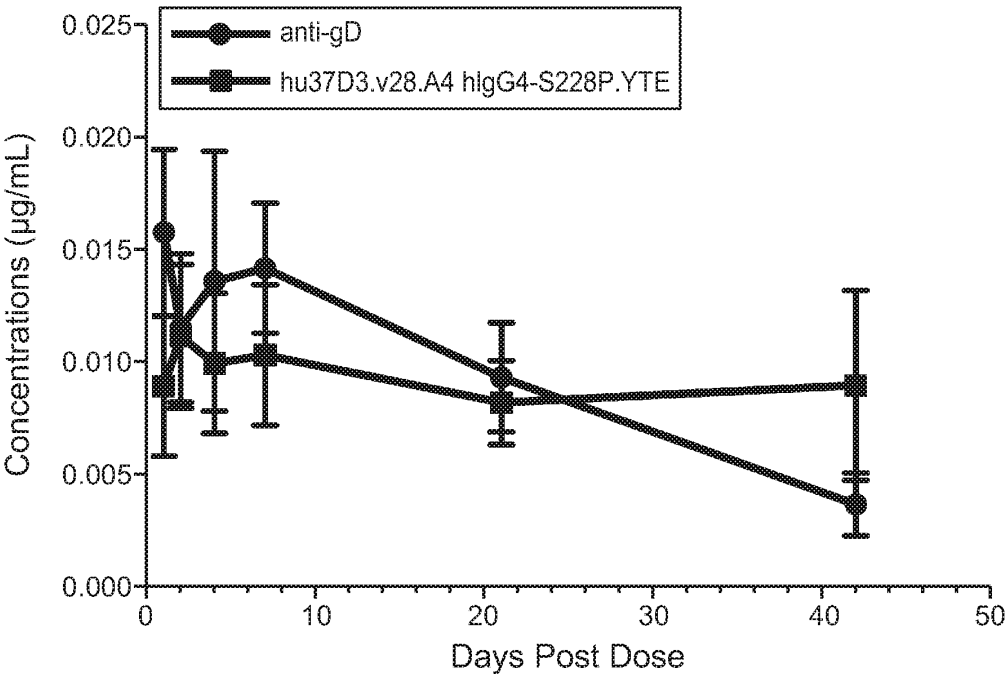


FIG. 22B

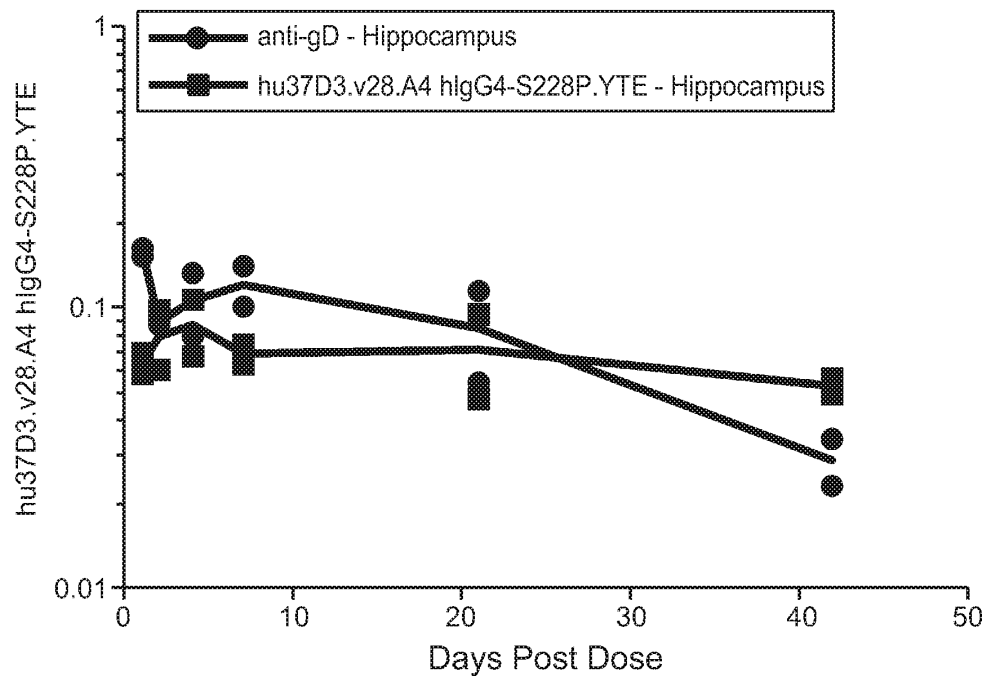


FIG. 23A

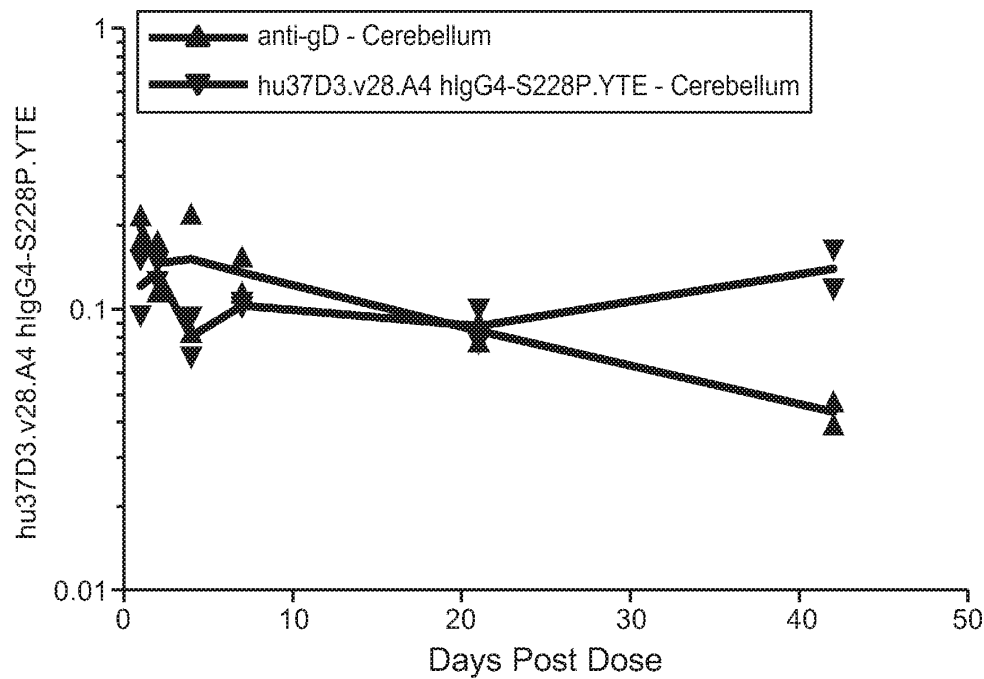


FIG. 23B

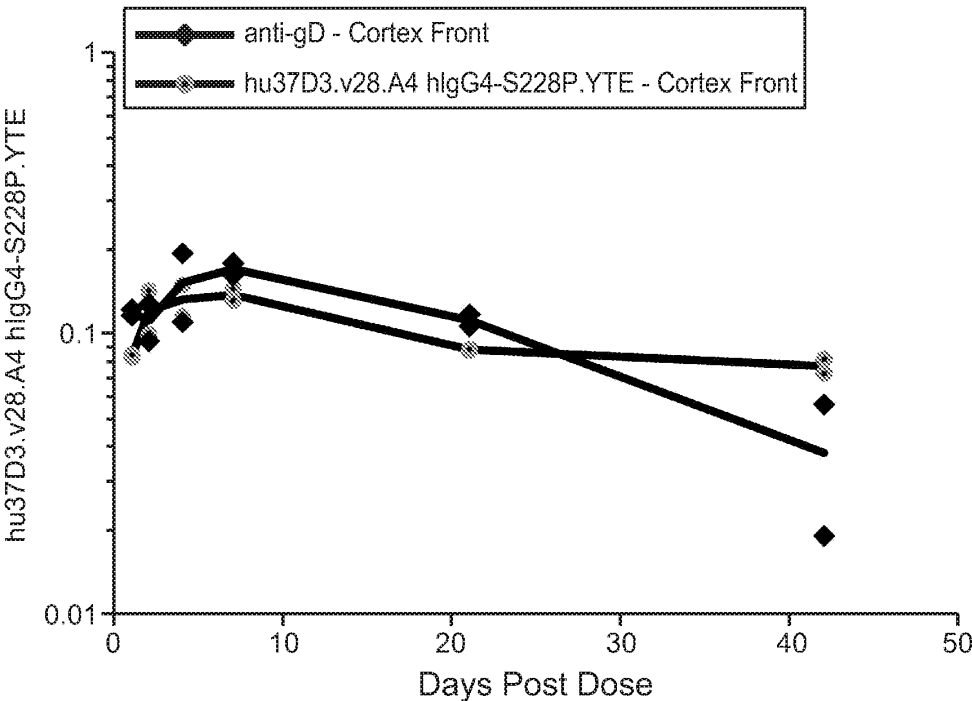


FIG. 23C

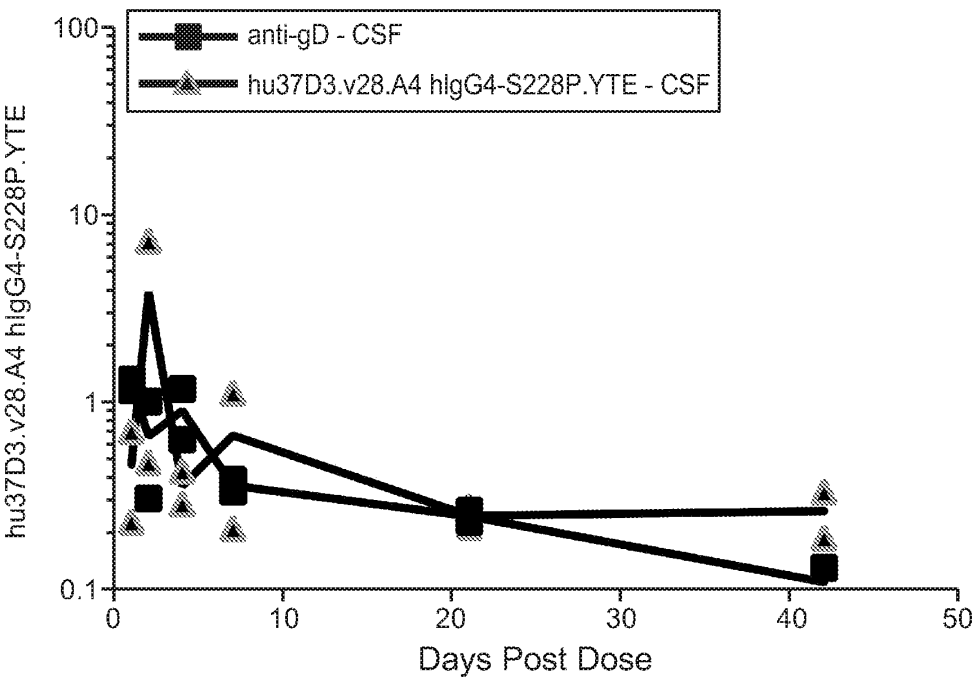
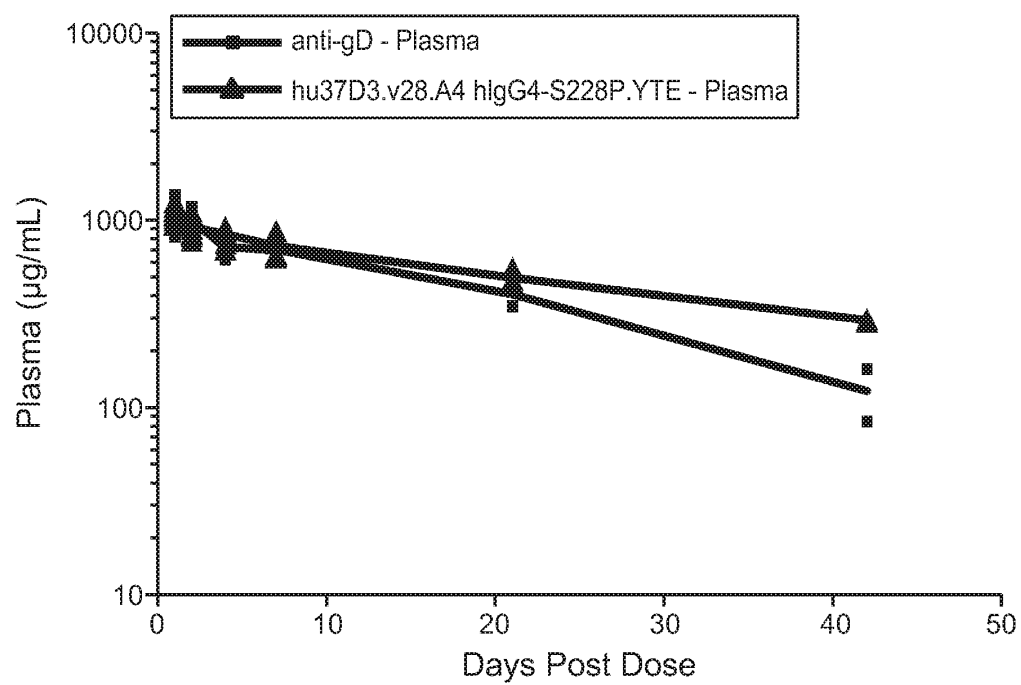


FIG. 23D

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**FIG. 23E**

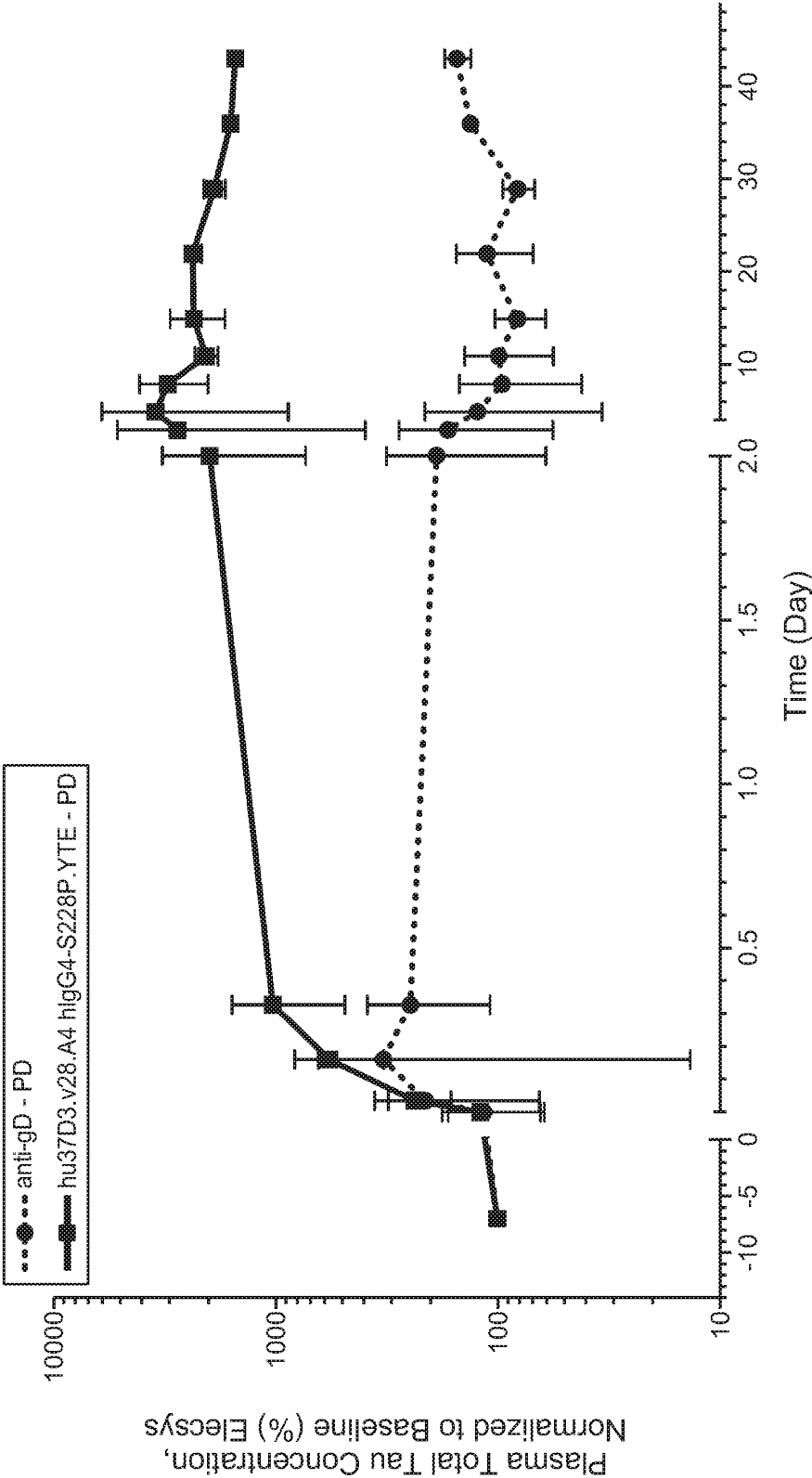


FIG. 24A

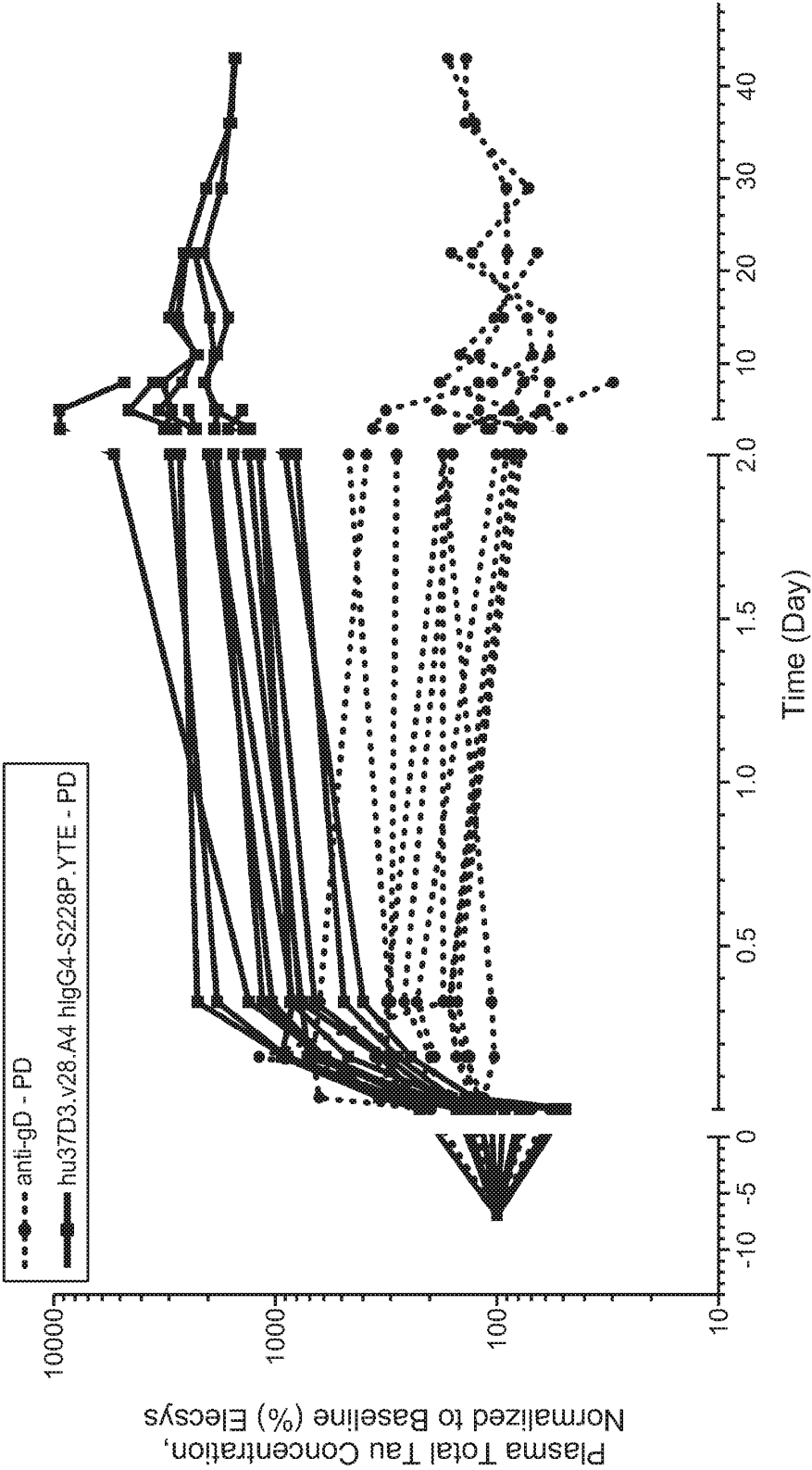


FIG. 24B

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Light Chain Variable Region

Kabat number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	28	29	30	31	32	33	34	35	36	37
hu37D3.v28.A4.hlgG4.YTE	D	D	V	L	T	Q	T	P	L	S	L	P	V	T	P	G	Q	P	A	S	I	S	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	L
hu37D3.v76.hlgG1	D	D	L	L	T	Q	T	P	L	S	L	P	V	T	P	G	Q	P	A	S	I	S	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	L
hu37D3.v76.hlgG4.YTE	D	D	L	L	T	Q	T	P	L	S	L	P	V	T	P	G	Q	P	A	S	I	S	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	L
hu37D3.v83.hlgG1	D	D	L	L	T	Q	S	P	L	S	L	P	V	T	L	G	Q	P	A	S	I	S	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	Q
hu37D3.v83.hlgG4.YTE	D	D	L	L	T	Q	S	P	L	S	L	P	V	T	L	G	Q	P	A	S	I	S	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	Q
hu37D3.v93.hlgG1	E	D	L	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	Q
hu37D3.v93.hlgG4.YTE	E	D	L	L	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	S	S	Q	S	I	V	H	S	N	G	N	T	Y	L	E	W	Y	Q

Kabat number	CDR L2 - Chothia																											CDR L2 - Contact														
	CDR L2 - Kabat																																									
	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79
hu37D3.v28.A4.hlgG4.YTE	Q	K	P	G	Q	S	P	Q	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E
hu37D3.v76.hlgG1	Q	K	P	G	Q	S	P	Q	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E
hu37D3.v76.hlgG4.YTE	Q	K	P	G	Q	S	P	Q	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E
hu37D3.v83.hlgG1	Q	R	P	G	Q	S	P	R	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E
hu37D3.v83.hlgG4.YTE	Q	R	P	G	Q	S	P	R	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E
hu37D3.v93.hlgG1	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q
hu37D3.v93.hlgG4.YTE	Q	K	P	G	K	S	P	K	L	L	I	Y	K	V	S	N	R	F	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q

Kabat number	CDR L3 - Kabat																											SEQ ID NO:	
	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106		107
hu37D3.v28.A4.hlgG4.YTE	A	E	D	V	G	V	Y	Y	C	F	Q	G	S	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	341
hu37D3.v76.hlgG1	A	E	D	V	G	V	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	604
hu37D3.v76.hlgG4.YTE	A	E	D	V	G	V	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	604
hu37D3.v83.hlgG1	A	E	D	V	G	V	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	615
hu37D3.v83.hlgG4.YTE	A	E	D	V	G	V	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	615
hu37D3.v93.hlgG1	P	E	D	F	A	T	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	620
hu37D3.v93.hlgG4.YTE	P	E	D	F	A	T	Y	Y	C	F	Q	G	T	L	V	P	W	T	F	G	Q	G	T	K	V	E	I	K	620

FIG. 25A

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Heavy Chain Variable Region

Kabat number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
hu37D3.v28.A4.hlgG4.YTE	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v76.hlgG1	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v76.hlgG4.YTE	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v83.hlgG1	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v83.hlgG4.YTE	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v93.hlgG1	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G
hu37D3.v93.hlgG4.YTE	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	L	I	F	R	S	Y	G	M	S	W	V	R	Q	A	P	G

FIG. 25B

