

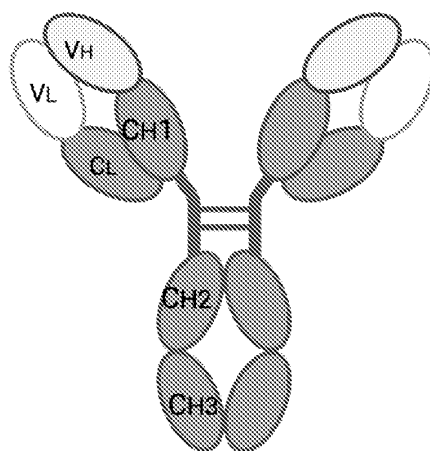


Figure 1A

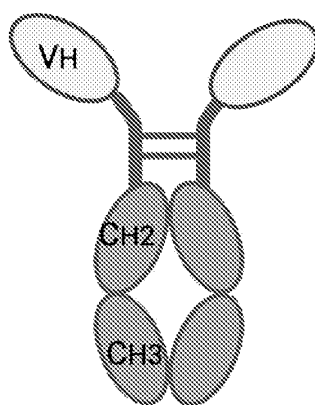


Figure 1B



Figure 1C

[illegible]

Figure 2A

F12	QVQLQESGGDLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G1	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G2	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G3	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G4	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G5	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G7	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G8	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G9	QVQLXESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EXTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G10	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
G12	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H3	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H4	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H5	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H6	QVQLQESGGDLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H7	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H8	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H9	QVQLXESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H10	QVQLQESGGDLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS
H11	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSAITWSAGSTYYADSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCAADSLSAGYESSWLEAFGSWGQGTQVTVSS

Figure 2A Continued

Experiment 2	Sequence
R2_B5	QVQLQESGGGLVQAGGSLRLSCAASGFTDDYAIGWFRQAPGKEREGVSCISSSDGSTYYADSVKGRFTMSSDNAKNTVYLQMNSLKPE DTAVYYCAADHDGSSWLSCQALLPFGSWGQGTQVTVSS
R2_B6	QVQLQESGGGLVQFGGSLRLSCSASGFTVDNRAIGWYRQAPGKAREGISCIGSSSRQTHYSDSVKGRFTISRDSAKNTVFLQKNLTPDDT GIYYCAAPTWFPPCTTVGGRGDVWGQGTQVTVSS
R2_B8	QVQLQESGGGLVQAGGSLRLSCAASGRTFSINAMGWYRQAPGKQRDLVAIEHLSGSTQHADSIDKRFISIRDNKNTVYLRMSALQPED TAVYYCNAEVRTSGGQYWLPLYWGQGTQVTVSS
R2_B9	QVQLQESGGGSVQAGGSLRLSCEASGFTRDDYAIGWFRQAPGKEREGVACIENGFNKTVYEDSVQGRFTISSDNAKNTLYLQMNNLKP DTAIYYCAASNEYVSGYCLLGASSWGQGTQVTVSS
R2_B10	QVQLQESGGGVVQAGGSLRLSCVVSGLSFDSDNIGWFRQAPGKEREAIVSCISSDGSSTFYGDSAKGRFTIARNNAKNTVFLEMNNLKSE DTAVYYCAADVDRSLWCKTGDYDYWGQGTQVTVSS
R2_B11	QVQLQESGGGLAQPGGSLRLSCVVSISVSDTMGWYRQVPGQERELVAEINKDGTINYADSVKGRFTVSGDTRDVDHLAVYLLMNSL NFEDTAVYYCHAGLEAWGSLADYDFWGQGTQVTVSS
R2_B12	QVQLQESGGGLVQTGGSLRLSCVVSFTLDDYSIGWFRQVPGKEREGIVCFSSKNGFMYYADSVKGRFTISSDNAKNTVYLQMNNLKSE DTAVYYCAADPIHLDEYCSRWNLMMEYWGKGQTQVTVSS
R2_C1	QVQLQESGGGLVQPGGSLRLSCEASGFTDDYAIGWFRQAPGKEREGVSCISAGARSTFYADSVKGRFTISSDRAKNTVYLQMNSLSPED TARYYYCAARVWEVGHCTPAEYDYWGQGTQVTVSS
R2_C3	QVQLQESGGGLVQAGGSLRLSCVASGFTDDYAIGWFRQAPGKEREGVSCIRFSDGKTYKDSVKGRFTISSDNAKNTVYLQMNNLKPE DTAVYYCAADPAGFLAIATMEFDYWGQGTQVTVSS
R2_C5	QVQLQESGGGLVQPGGSLRLSCEASGFTFYQNAWCRQAPGKQRELVAIVTAEGSPHYADSVKAHFTISRDKSNILYLMENLKPED TAVYYCNLGTIYSGSLYSLDDWGQGTQVTVSS
R2_C6	QVQLQESGGGLVHAGGSLRLSCAVTRISFTTIDIMEWYRQAPGKQRELVASITNSGSTTYSDAVKGRFAISRDDAKNTGYLQMNSLKPEDT AIYSCRCVLDARYVFWGQGTQVTVSS
R2_C7	QVQLQESGGGLVQAGGSLRLSCAASGFASAYYIGWFRQAPGKEREGVACINTCDGDTYYLESVKGRFTISSDNAKNTVYLQMNSLAPE DAVYYCAADEILRRCLYYSNNGNFHTEYLGRTQVTVSS
R2_C9	QVQLQESGGGLVQAGGSLRLSCAVSLGSLFDDGAVGWFRQAPGKEREGVACLNRDRGTYIDSVKGRFTISSDNAKNTVYLQNLGLEP EDTAVYYCSATYIKCWPNGVYDSWGQGTQVTVSS
R2_C11	QVQLQESGGGLVQAGGSLRLSCAASGRTFSYAMGWFRQAPGKEREGVSGIRGSDGVTFYADSVKGRFTISRDTENTVYLQMNSLKPE DTAVYYCAALGSPYSSYYTQSVWPRVAIYSYWQGTQVTVSS
R2_C12	QVQLQESGGGLVPRGGSLRLSCEASGFTFSTYAMSWVRQAAGKLEWISVINGGSDKIKYSDSMKGRVTCSDNAKNTLWLQMDNLR PEDTAVYYCVRELRPAAGWVLGDFWGQGTQVTVSS
R2_D4	QVQLQESGGGLVQAGGSLRLSCAASGFTDDYAIGWFRQAPGKEREGVSCISVSDGSTSYADSVKGRFTISSDNAKNTVYLQMNSLKPED TAVYYCAAASSYGLGYLGCFAHGLDYYGMDYWGKGQTQVTVSS
R2_D5	QVQLQESGGESVQPGGSLRLSCEASGFTIFSMNVMGWYRQAPREERELVAHITSNGTITYANSVKGRFTISRGVAKTIVYLQMNSLKPED TAVYYCYADAWARTGKGFEDYWGQGTQVTVSS
R2_D6	QVQLQESGGGLVQPGGSLRLSCVSGSFGSDVTMGWVRQAPGKLEWVAISWDGGSTYYKDSMKGRFTISRDNKNTVALQMISV ESEDVAVYYCVDEALSRFSWGQGTQVTVSS
R2_D7	VQLQESGGGLVQPGGSLRLSCEASGVTGFNTYWMYVVRHVPRKGLEWVFSINSGGDITDTPSVKGRFIISRDNAKNTLYLQMDSLKSE DTAAYYCVASLSGRHYCSGSGCYASDYWGPGTQVTVSS
R2_D8	QVQLQESGGGLVQAGGSLRLSCATSGFTDDYAIGWFRQAPGKEREGVSCISVSDGSTYYEDSVKGRFTVSSDNAENTVYLQMNSLKPE DTAVYYCAADAVGIGCYQYEDYWGGGTQVTVSS
R2_D9	QVQLQESGGGLVQAGDSLRLSCEASGRTFSTYSMGWFRQAPGKEREFVSAITYSGGTTSYADSVKGRFTISRDNKNTVYLQMNSLKSE DTARYYCNADDPHLPGMPLNYWGQGTQVTVSS
R2_D11	QVQLQESGGGNVQPGGSLRLSCEASGVSGLNAMGWYRQADDKERKFVAITRSGTPVYADSVKGRFTIAGDAAKHTSDQLQMDNLNT EDTAVYYCAKRQYYSYSGYSEEDYWGGGTQVTVSS
R2_D12	QVQLQESGGGLVQPGESLTLSVSGSFPDDYALAWFRQAPGKEREGVSCISTSDGSTYYADSVKGRFTISSDNAKNTVYLQMNSLKVED TAVYYCAASLIPTVFPWPWYDYWGQGTQVTVSS
R2_E1	QVQLQESGGGLVQAGGSLRLSCEASGFTDDYAIGWFRQAPGKEREGVSCISSSGSTYYADSVKGRFTISSDNAKNTVYLQMNSLKPED TAVYYCAATLLSGSSWYYPFLFYDRGQGTQVTVSS
R2_E2	QVQLQESGGGLVQAGDSLRLSCEASGRTFSFTMGWFRQAPGKEREFVAAIVWSGSSTVYTDVSKGRFTISRDNKNTVYLQMNSLKPE DTAVYYCAAMDTIATISSPWSYDYWGQGTQVTVSS
R2_E4	QVQLQESGGGLVQPGGSLRLSCEASGTSRLTSMGWYRQAPGNQRDFVAAISTGGGTNLADSVKGRFTISLDSVKNTMYLQMDSLKSE DTAVYYCNAVGPTRGEQYWGQGTQVTVSS
R2_E6	QVQLQESGGGLVQTGGSLRLSCEASGATFDDYIGWFRQAPGKERERVSCAMFSDGSTFYSDTVKGRFTISSDNAKNTAYLQMNSLEPE DTAVYYCAVTKSAERLCQPVWFETWGQGTQVTVSS
R2_E7	QVQLQESGGGLVQPGGSLRLSCEASGDFIVIHDMGWYRQSPGKQREMAVLIKSDGRTNYADSVKGRFTISRDNKNTISLQMNSLEPED TAIYSCYADVTSATSHVGDRLDFRSMGYWGSQGTQVTVSS
R2_E8	QVQLQESGGGLVQPGGSLRLSCEASGFILDDKHIGWFRQAPGKEREGVSCISSGDSSTYYTDSVKGRFTISRDNKNTVYLQMNSLEPED TAIYYCATDRTPYDGSCLPLVYEDYWGGGTQVTVSS
R2_E9	QVQLQESGGGLVQPGGSLRLSCEASGSDTSDYYAIGWFRQAPGKEREGITCISRDGGSTVYAVAVKGRFTISKEHANHTVYLDMRSLKPED TATYYCAAFGDTWHCGQPAYSGMKYWGRGTQVTVSS

Figure 2B

Nanobody	CDR3	Enrichment	MW (Da)	Ext coeff (M ⁻¹ cm ⁻¹)
Nb_C8	NLIGLRVGPENKY	1	13115	31065
Nb_G6	AADSLSAGYESSWLEAFGS	82	13536	32555

Figure 3

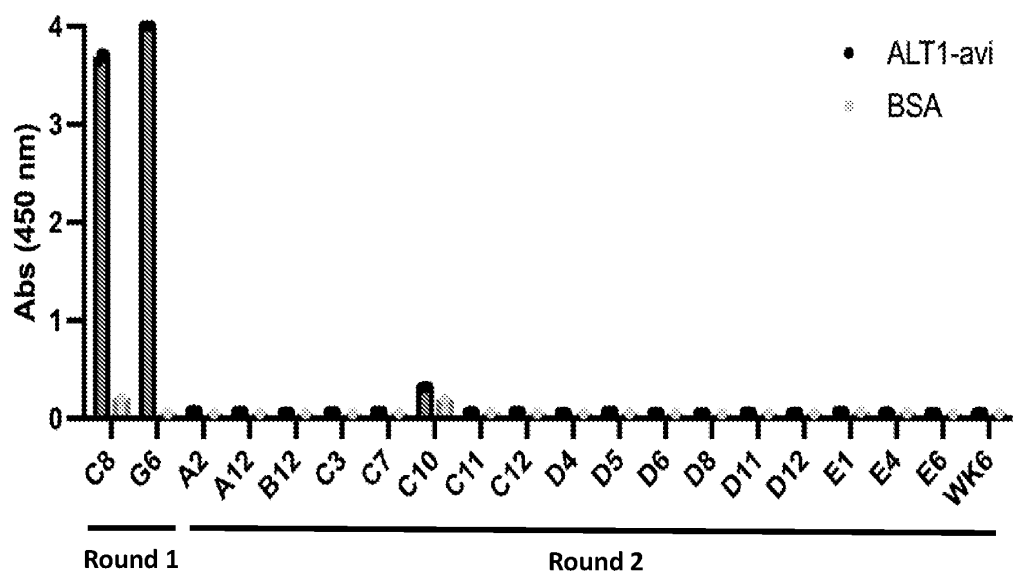


Figure 4

Nb_C8

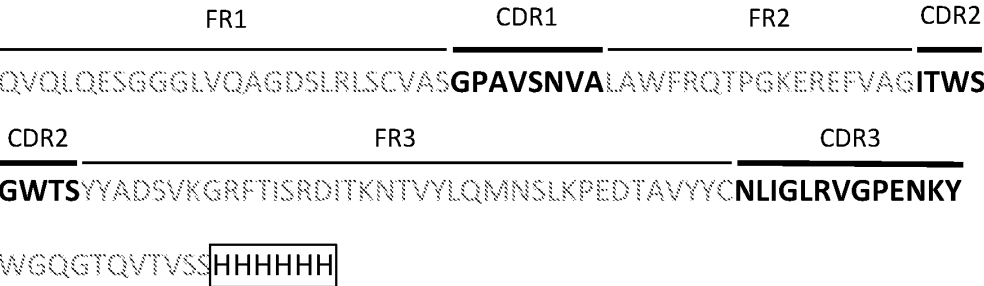


Figure 5A

QVQLQESGGGLVQAGDSLRLSCVAS**GPAVSNVALAWFRQTPGKERE**FVAGITWS
GWTSYYADSVKGRFTISRDIKNTVYLQMNSLKPEDTAVYYC**NLIGLRVGPENKY**
WGQGTQVTVSS**DDYKDDDDKHHHHHH**

Figure 5B

Nb_G6

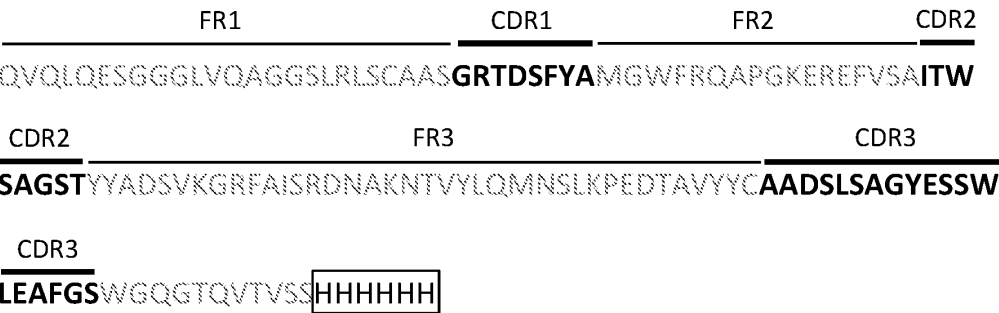


Figure 6A

QVQLQESGGGLVQAGGSLRLSCAAS**GRTD**SFYAMGWFRQAPGKERE**FVSAITW**
AGSTYYADSVKGRFAISRDNKNTVYLQMNSLKPEDTAVYYC**AADSL**SAGYESSW
EAFGSWGQGTQVTVSS**DDYKDDDDKHHHHHH**

Figure 6B

Nb_C10

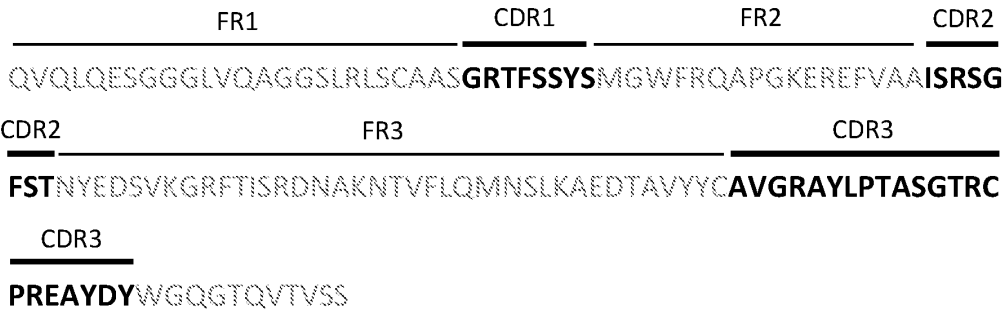


Figure 7

% Identity	Nb_C8	Nb_G6	Nb_C10
Nb_C8		76	71
Nb_G6			77

Figure 8

Nanobody	V-gene	J-gene	D-gene
G6	IGHV3-3*01F	IGHJ6*01 F	IGHD6*01 F
Nucleotides/Identity (%)	276/288 nt/95.83	42/47 nt/89.36	RF2
C8	IGHV3-3*01F	IGHJ4*01 F	IGHD6*01 F
Nucleotides/Identity (%)	251/288 nt/87.15	42/47 nt/89.36	RF1
C10	IGHV3-3*01	IGHJ4*01	IGHD3*01
Nucleotides/Identity (%)	270/288 nt/93.75	45/47 nt /95.74	RF2

Figure 9

Nb_G6	1	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSA	50
NB_C8	1	QVQLQESGGGLVQAGDSLRLSCVASGPAVSNVALAWFRQTPGKEREFVAG	50
Nb_G6	51	ITWSAGSTYYADSVKGRFAISRDNKNTVYLMNSLKPEDTAVYYCAADS	100
NB_C8	51	ITWSGWTSTYYADSVKGRFTISRDKNTVYLMNSLKPEDTAVYYCNLIG	100
Nb_G6	101	LSAGYESSWLEAFGSWGQGTQVTVSS	126
NB_C8	101	LRVGPENKY-----WGQGTQVTVSS	120

Figure 10

NB_C8	1	QVQLQESGGGLVQAGDSLRLSCVASGPAVSNVALAWFRQTPGKEREFVAG	50
Nb_C10	1	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYSMGWFRQAPGKEREFVAA	50
NB_C8	51	ITWSGWTSTYYADSVKGRFTISRDKNTVYLMNSLKPEDTAVYYC----	96
Nb_C10	51	ISRSGFSTNYEDSVKGRFTISRDNKNTVFLQMSLKAEDTAVYYCAVGR	100
NB_C8	97	----NLIGLRVGPE-NKYWGQGTQVTVSS	120
Nb_C10	101	AYLPTASGTRCPREAYDYWGQGTQVTVSS	129

Figure 11

Nb_G6	1	QVQLQESGGGLVQAGGSLRLSCAASGRTDSFYAMGWFRQAPGKEREFVSA	50
Nb_C10	1	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYSMGWFRQAPGKEREFVAA	50
Nb_G6	51	ITWSAGSTYYADSVKGRFAISRDNKNTVYLMNSLKPEDTAVYYCAADS	100
Nb_C10	51	ISRSGFSTNYEDSVKGRFTISRDNKNTVFLQMSLKAEDTAVYYCAVGR	100
Nb_G6	101	L---SAGYESSWLEAFGSWGQGTQVTVSS	126
Nb_C10	101	AYLPTASGTRCPREAYDYWGQGTQVTVSS	129

Figure 12

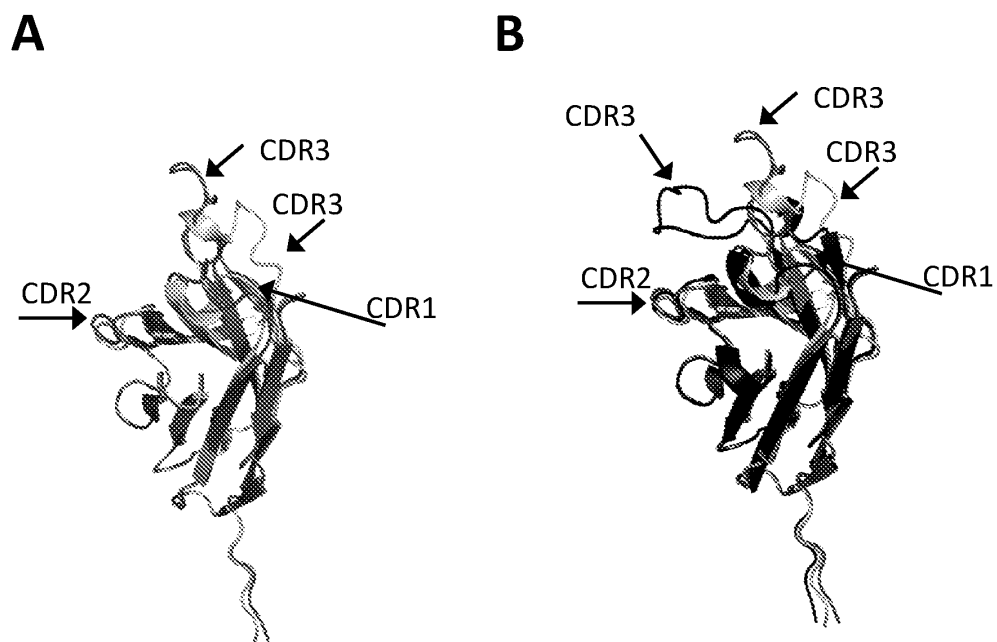


Figure 13

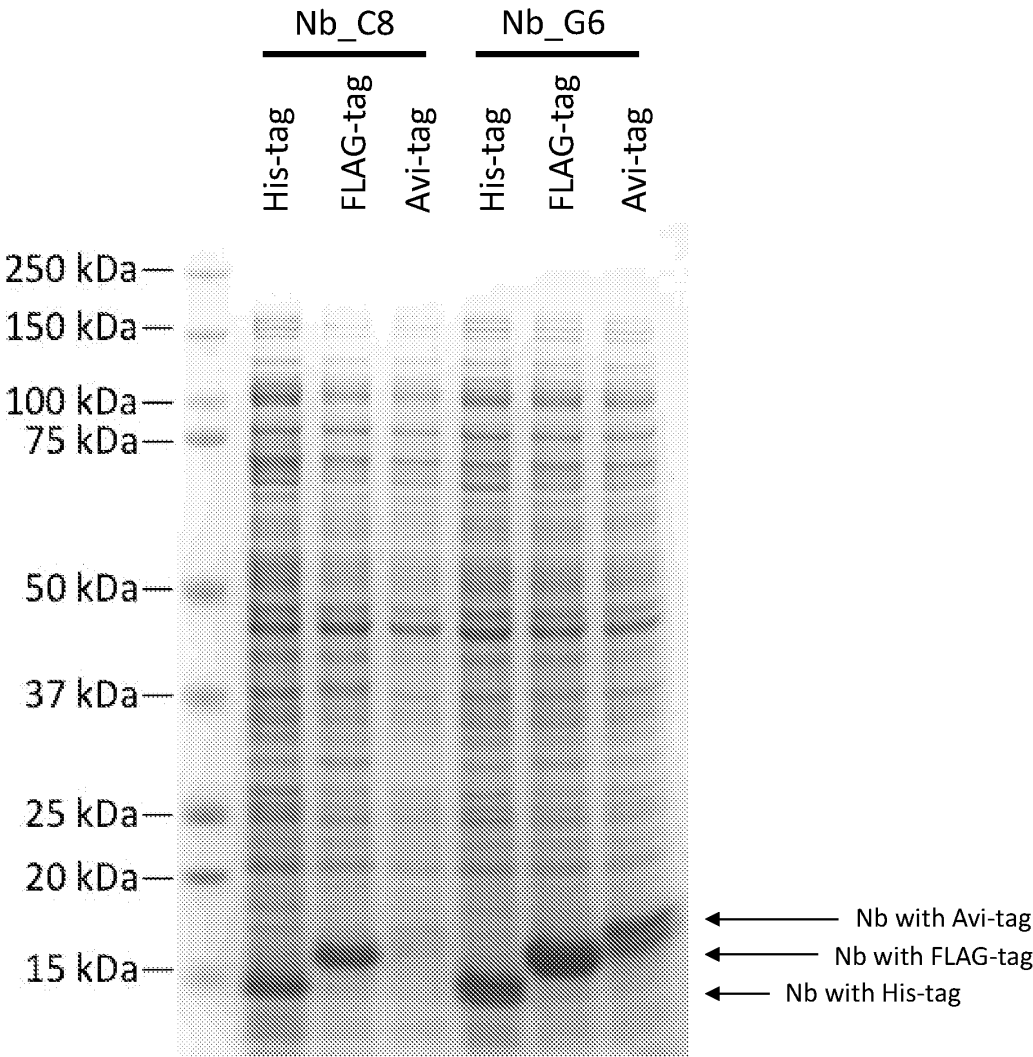


Figure 14

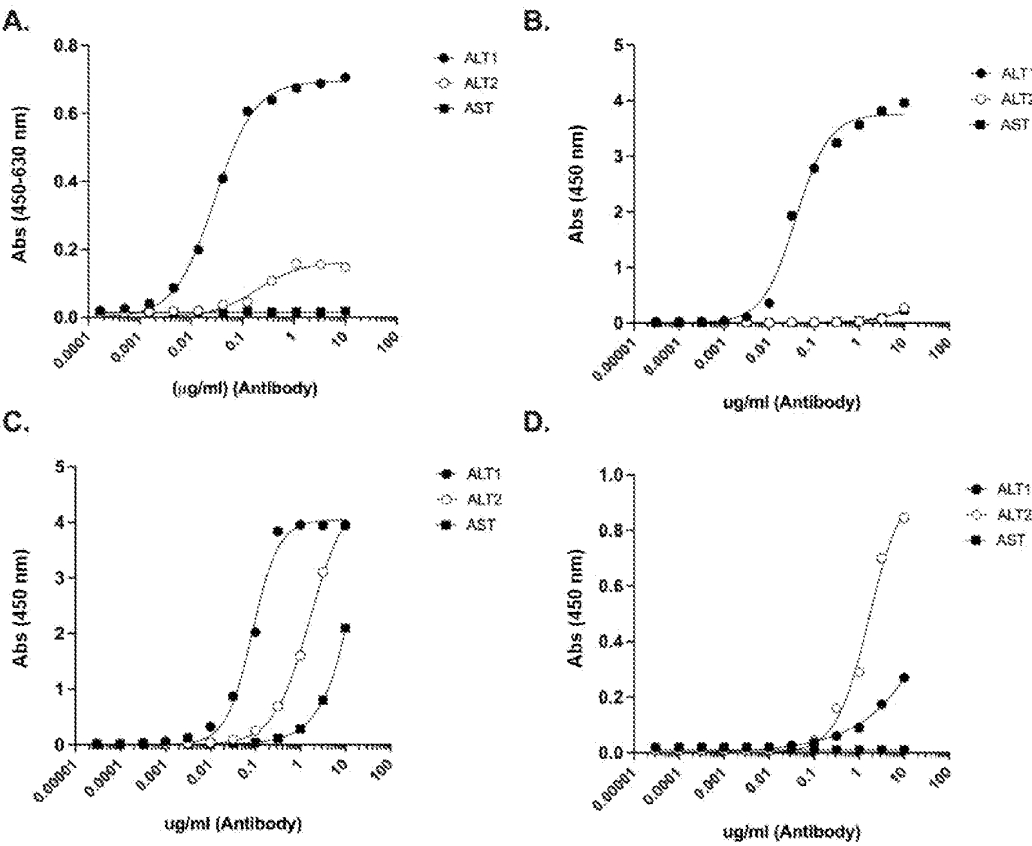


Figure 15

	µg/mL antibody for 10x background		
	ALT1	ALT2	AST
Nb_C8	0.003	6.515	6.975
Nb_G6	0.008	1.153	>10
Polyclonal Rb	0.011	0.084	0.569
Monoclonal Rb	3.786	0.477	>10

Figure 16

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CLUSTAL O(1.2.4) multiple sequence alignment

ALT1	-----MASSTGDRSQAVRHGLRAKVLTLDGMNPRVRRV	33
ALT2iso1	MQRAAALVRRGCGPRTTPSSWGRSQSSAAAEASAVLKVRPERSRRERILTLESMPNQVKAV	60
	*.:.: . .: . * :.:***.:***:*. *	
ALT1	EYAVRGPIVQRALELEQELRQGVKKPFTEVIRANIGDAQAMGQRPITFLRQVLALCVNPD	93
ALT2iso1	EYAVRGPIVLKAGEIELELQRGIKKPFTEVIRANIGDAQAMGQQPITFLRQVMAICTYPN	120
	***** :* *: * *: :*:*****:*****:***. *:	
ALT1	LLSSPNFPDDAKKRAERILQACGGHSLGAYSVSSGIQLIREDVARYIERRDGGIPADPN	153
ALT2iso1	LLDSPSPFEDAKKRARRILQACGGNSLGSYSASQGVNCIREDDVAAYITRRDGGVPADPDN	180
	.*.:*****.*****:***:*. *.: ***** ** *****:***:*	
ALT1	VFLSTGASDAIVTVLKLKVAGEGHTRTGVLIPQYPLYSATLAEAGVQVDYYLDEERA	213
ALT2iso1	IYLTGASDGIISTILKILVSGGGKSRGTGVMIPIQYPLYSAVISLDAIQVNYLDEENC	240
	:*:*****.* *:***:*. * *:***:*****.:.*:.**:*****.:	
ALT1	WALDVAELHRLGQARDHCRPRALCVINPGNPTGQVQTRECIEAVIRFAFEERLFLLADE	273
ALT2iso1	WALNVNELRRVQAEAKDHCDPKVLCIINPGNPTGQVQSRKCIEDVIHFAWEEKLFLLADE	300
	:* *:: :*:*** *:.**:*****:*.*** *:***:*.*****	
ALT1	VYQDNVYAAGSQFHSFKKVLMMGPYPAGQQLASFHSTSKGYMGECGFRGGYVEVVNMD	333
ALT2iso1	VYQDNVYSPDCRFHSFKKVLVYEMGPYSSNVELASFHSTSKGYMGECGYRGGYMEVINLH	360
	*****: .:***** ***** *:.: *****:*****:***:*. *:	
ALT1	AAVQQQMLKLMSVRLCPPVPGQALLDLVVSPPAPTDPSPFAQFQAEKQAVLAELAAKAKLT	393
ALT2iso1	PEIKGQLVKLLSVRLCPPVSGQAAMDIVVNPVAGEESFEQFSREKESVLGNLAKKAKLT	420
	:* :*:***:***** ***** :*:***. : ** *. *:***:*** *****	
ALT1	EQVFNEAPGISCNPVQGAMYSFPRVQLPPRAVERAQELGLAPDMFFCLRLLLEETGICVVP	453
ALT2iso1	EDLFNQVPGIHCNPLQGAMYAFPRIFIPAKAVEAAQAHQMAPDMFYCMKLEETGICVVP	480
	*:***:*** *****:*****:***: :* :*** ** :*****:***:*****	
ALT1	GSGFGQREGTYHFRMTILPPEKLRLLEKLSRFHAKFTLEY-	495
ALT2iso1	GSGFGQREGTYHFRMTILPPVEKLKTVLQKVDFHINFLEKYA	523
	*****:***: :*:.: ** :* :*	

Figure 17

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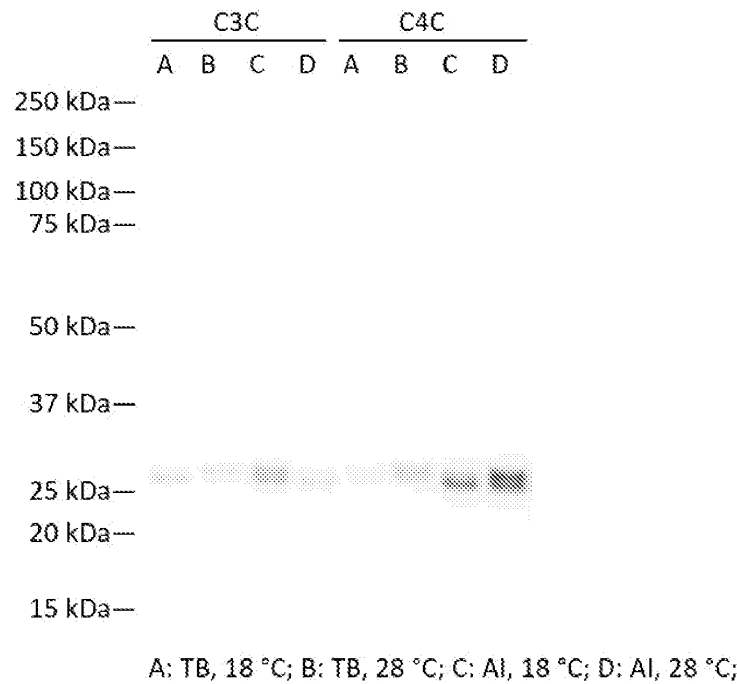
CLUSTAL O(1.2.4) multiple sequence alignment		
AST	-----MAPPVFA	8
ALT1	-----MASSTGDRSQAVRHGLRAKVLTLDGMNPRVRRV	33
ALT2iso1	MQRAAALVRRGCGPRTSSWGRSQSSAAAEASAVLKVRPERSRRERILTLESMNPQVKAV	60
ALT2iso2	-----	0
AST	EVPQAQPVLVFKLT--ADFRE---DPDPRKVNLGVGAYRTDDCHPWVLPVVKKEQKIAN	63
ALT1	EYAVRGPIVQRALELEQELRQGVKKPFTEVIRANIGDAQAMGQRPI--TFLRQVLALCVN	91
ALT2iso1	EYAVRGPIVLKAGEIELELQRGIKKPFTEVIRANIGDAQAMGQQPI--TFLRQVMALCTY	118
ALT2iso2	-----MGQQPI--TFLRQVMALCTY	18
	. : * . : : *	
AST	DNSLNHEYLP-----ILG---LAEFRSCASRLALGDDSPALKEKRVGGVQSLG	108
ALT1	PDLLSSPNFPDDAKKRAERILQACGGHSLGAYSVSSGIQLIREDVARYIERDGGIPADP	151
ALT2iso1	PNLLDSPFPEDAKKRARRILQACGNSLGSYSASQGVNCIREDVAAYITRRDGGVPADP	178
ALT2iso2	PNLLDSPFPEDAKKRARRILQACGNSLGSYSASQGVNCIREDVAAYITRRDGGVPADP	78
	: * . : * * . : . : : * : * * : :	
AST	GTGALRI-----GADFLARWYNGTNNKNTPVYVSSPTWENHNAVFSAGFKDIRSYRYWD	163
ALT1	NNVFLSTGASDAIVTVLKLLVAGEGHTRTGVLIPIQYPLYSATLAELGAVQVD---YYL	208
ALT2iso1	DNIYLTGTASDGISTILKILVSGGKSRTGVMIPIQYPLYSAVISELDAIQVN---YYL	235
ALT2iso2	DNIYLTGTASDGISTILKILVSGGKSRTGVMIPIQYPLYSAVISELDAIQVN---YYL	135
	. * . * . : . : * : : * : : * :	
AST	AEKR--GLDLQGFNDLENAPEFSIVVLHACAH---NPTGIDPTPEQWKQIASVMKHRFL	218
ALT1	DEERAWALDVAELHRAALGQARDHC-RPRALCVINPGNPTGQVQTRECI EAVIRFAFEERL	267
ALT2iso1	DEENCWALNVNELRRAVQEAKDHC-DPKVLCIINPGNPTGQVQSRKCI EDVIHFAWEEKL	294
ALT2iso2	DEENCWALNVNELRRAVQEAKDHC-DPKVLCIINPGNPTGQVQSRKCI EDVIHFAWEEKL	194
	* : . . * : : . : * : * * * : : : : . . *	
AST	FPPFDSAYQGFASGNLERDAWAIRYFVSEGEFFFC-----AQSFSSK-NFGLYNERVGNL	271
ALT1	FLLADEVYQDNVYAAGSQFHSFKKVLMMEMGPPYAGQQELASFHSTSKGYMGECGFRGGYV	327
ALT2iso1	FLLADEVYQDNVYSPDCRFHSFKKVLVEMGPEYSSNVELASFHSTSKGYMGECGYRGGYM	354
ALT2iso2	FLLADEVYQDNVYSPDCRFHSFKKVLVEMGPEYSSNVELASFHSTSKGYMGECGYRGGYM	254
	* : * . * . . : : : . * : : * * : * . * * :	
AST	TVVGKEPESILQVLSQMEKIVRITWSNPPAQGARIVASTLSN---PELFEEWTGNVKTM	327
ALT1	EVVNMDAAVQQQ---MLKLMSVRL-CPPVPGQALLDLVVSPPAPTDP SFAQFQAEKQAV	382
ALT2iso1	EVINLHPEIKGQ---LVKLLSVRL-CPPVSGQAAMDIVVNPPVAGEESFEQFSREKESV	409
ALT2iso2	EVINLHPEIKGQ---LVKLLSVRL-CPPVSGQAAMDIVVNPPVAGEESFEQFSREKESV	309
	* : . . * : * : : * . * : . . * : : : :	
AST	ADRILTRMSELRARLEALKTPGTWNHITDQIGMFSFTGL--NPKQVEY-----	373
ALT1	LAELA-AKAKLTEQVF-NEAPGIS-CNPVQGAMYSFPRVQLPPRAVERAQELGLAPDMFF	439
ALT2iso1	LGNLA-KKAKLTEDLF-NQVPGIH-CNPLQGAMYAFPRIFIPAKAVEAAQAHQMAPDMFY	466
ALT2iso2	LGNLA-KKAKLTEDLF-NQVPGIH-CNPLQGAMYAFPRIFIPAKAVEAAQAHQMAPDMFY	366
	. : : : * : : . * * . * : : : *	
AST	---LVNEKHIYLLPSGRINVSGLTTKNLDYV-ATSIHEAVTKIQ-----	413
ALT1	CLRLLEETGICVVPGS GF-----GQREGTYHFRMTILPPEKLRLLLEKLSRFHAKFTLE	494
ALT2iso1	CMKLLLEETGICVVPGS GF-----GQREGTYHFRMTILPPVEKLRLLLEKLSRFHAKFTLE	521
ALT2iso2	CMKLLLEETGICVVPGS GF-----GQREGTYHFRMTILPPVEKLRLLLEKLSRFHAKFTLE	421
	* : : * . * : : * . : : * : * :	
AST	-- 413	
ALT1	Y- 495	
ALT2iso1	YA 523	
ALT2iso2	YA 423	

Figure 18

Nanobody	Code	Linker	Description
C8-3-C8	C3C	GGGGSGGGGSGGGGS	Nb_C8 joined via 3 repeat (GGGGS) linker to Nb_C8
C8-4-C8	C4C	GGGGSGGGGSGGGGSGGGGS	Nb_C8 joined via 4 repeat (GGGGS) linker to Nb_C8
G6-3-G6	G3G	GGGGSGGGGSGGGGS	Nb_G6 joined via 3 repeat (GGGGS) linker to Nb_G6
G6-4-G6	G4G	GGGGSGGGGSGGGGSGGGGS	Nb_G6 joined via 4 repeat (GGGGS) linker to Nb_G6
C8-3-G6	C3G	GGGGSGGGGSGGGGS	Nb_C8 joined via 3 repeat (GGGGS) linker to Nb_G6
C8-4-G6	C4G	GGGGSGGGGSGGGGSGGGGS	Nb_C8 joined via 4 repeat (GGGGS) linker to Nb_G6
G6-3-C8	G3C	GGGGSGGGGSGGGGS	Nb_G6 joined via 3 repeat (GGGGS) linker to Nb_C8
G6-4-C8	G4C	GGGGSGGGGSGGGGSGGGGS	Nb_G6 joined via 4 repeat (GGGGS) linker to Nb_C8

Figure 19

A



B

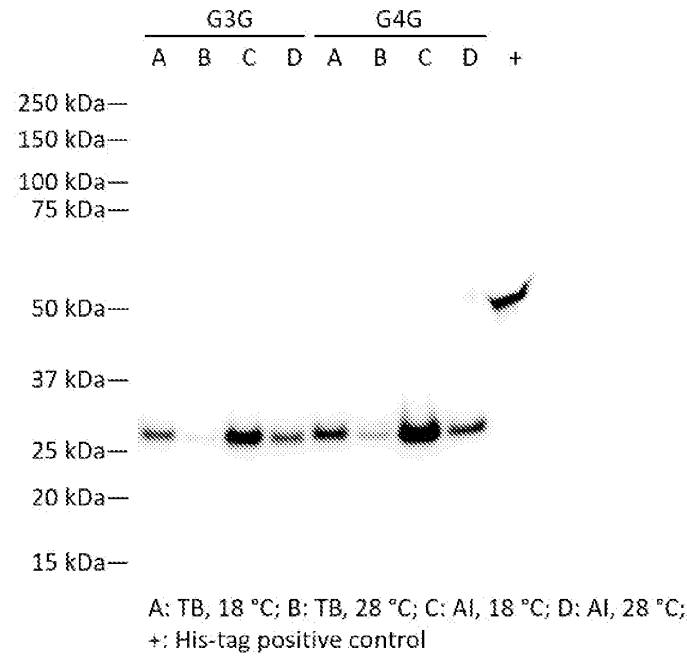


Figure 20

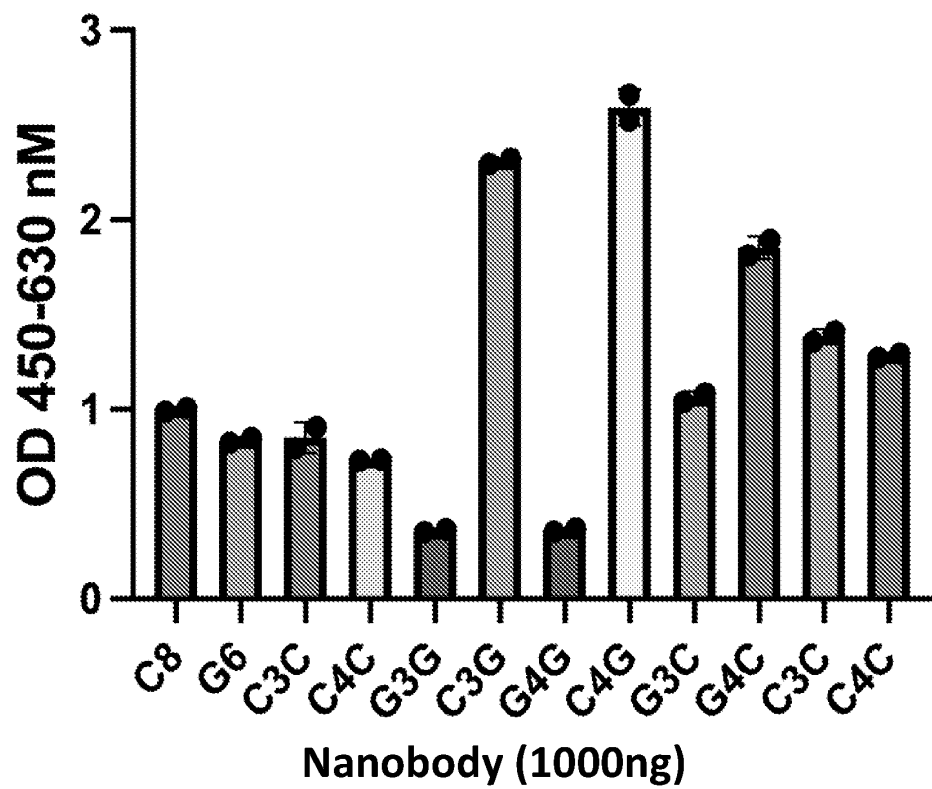


Figure 21

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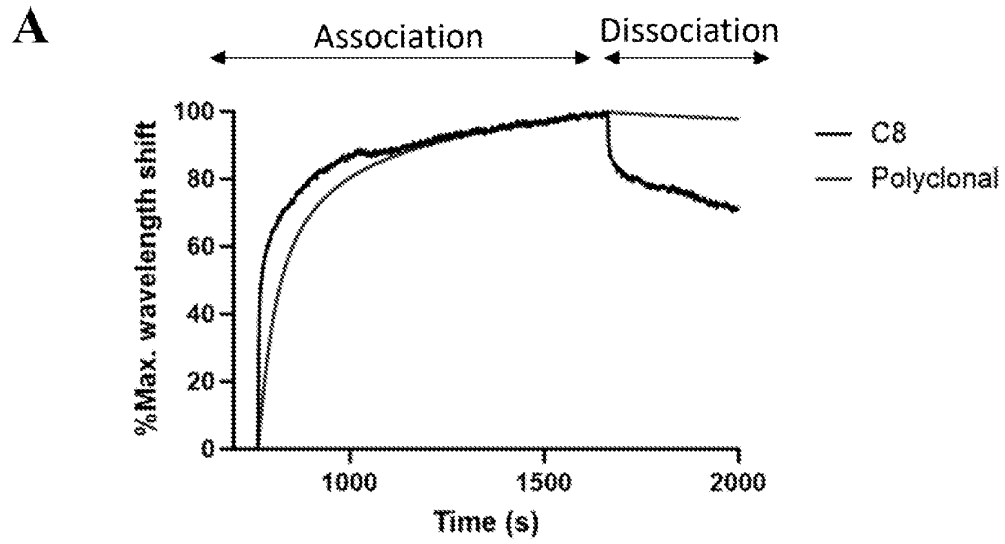


Figure 22

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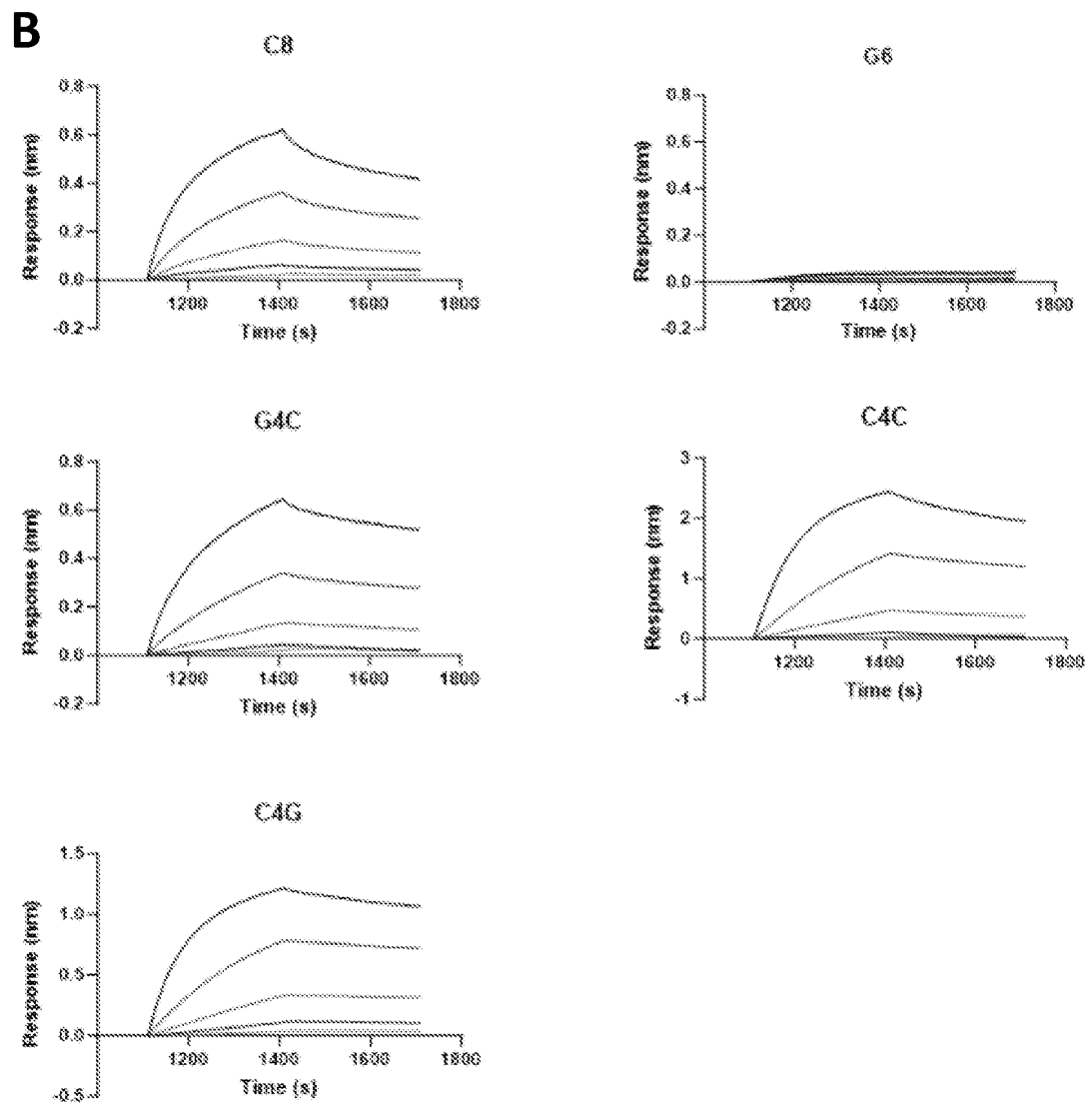


Figure 22 Continued

A

Antibody	K_{on} (1/Ats)	K_{off} (1/s)	K_D (M)	R^2
C8	1.09E+04	1.35E-03	1.34E-07	0.9979
G6	nd	nd	nd	nd
G4C	8.12E+03	3.83E-04	8.41E-08	0.9992
C4C	9.54E+03	6.82E-04	7.15E-08	0.9997
C4G	1.09E+04	3.43E-04	3.15E-08	0.9991

B

Antibody	fold improvement compared to C8		
	K_{on} (1/Ats)	K_{off} (1/s)	K_D (M)
G4C	1.34	3.52	1.59
C4C	1.14	1.98	1.87
C4G	1.00	3.94	4.25

Figure 23

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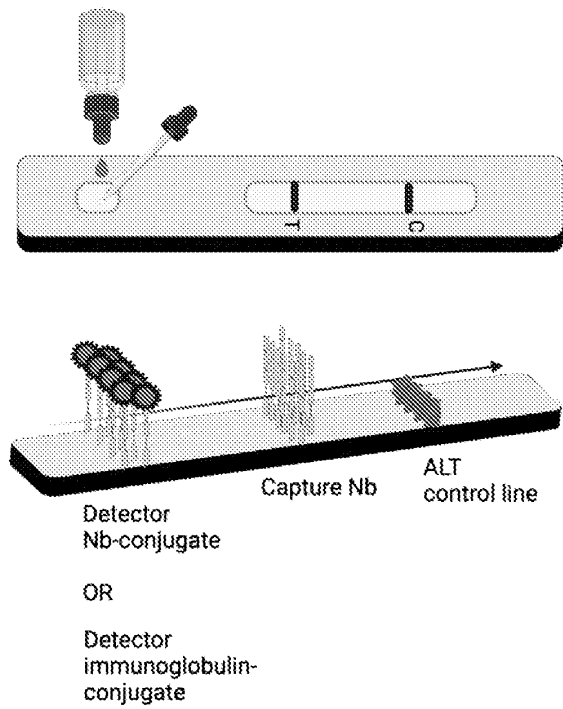


Figure 24

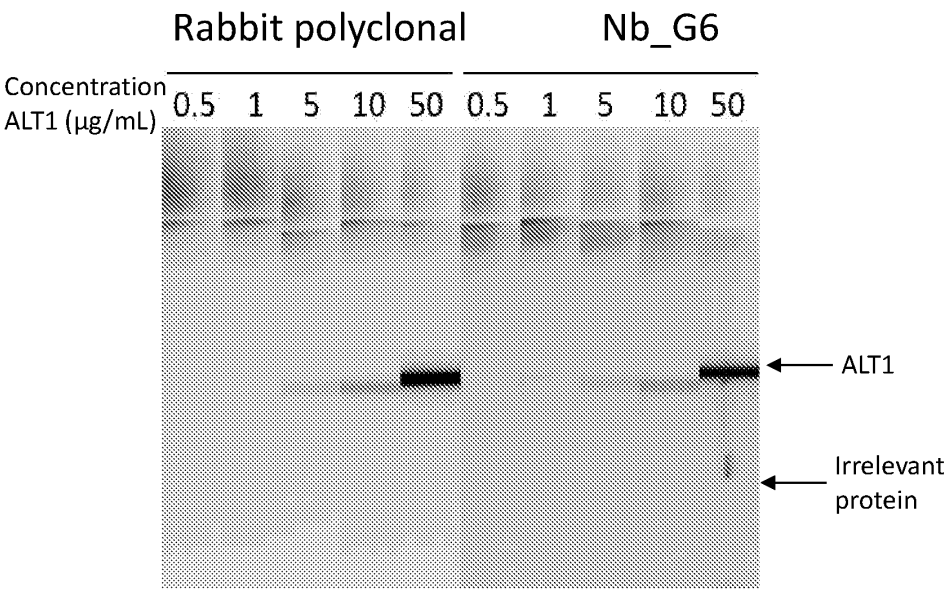


Figure 25

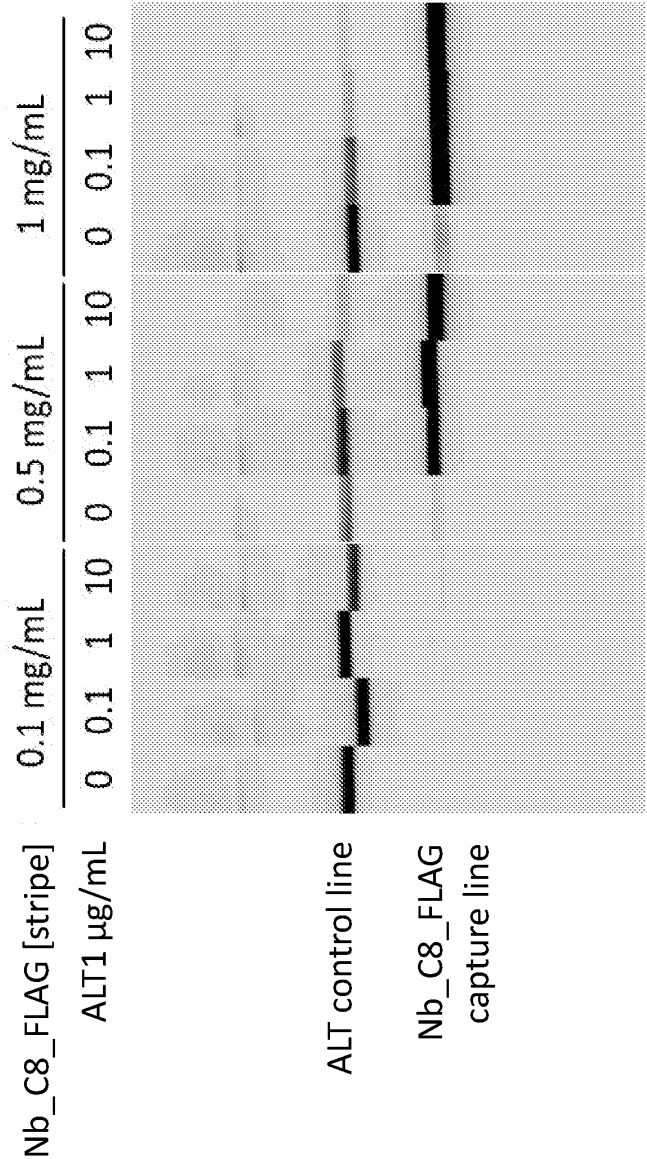


Figure 26

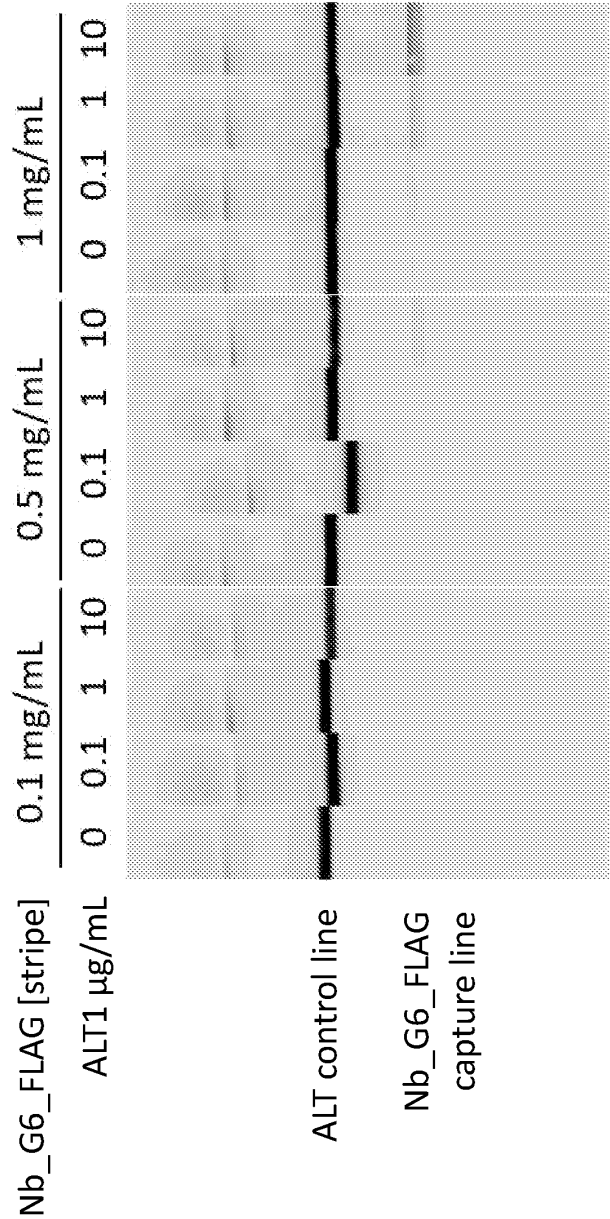


Figure 27

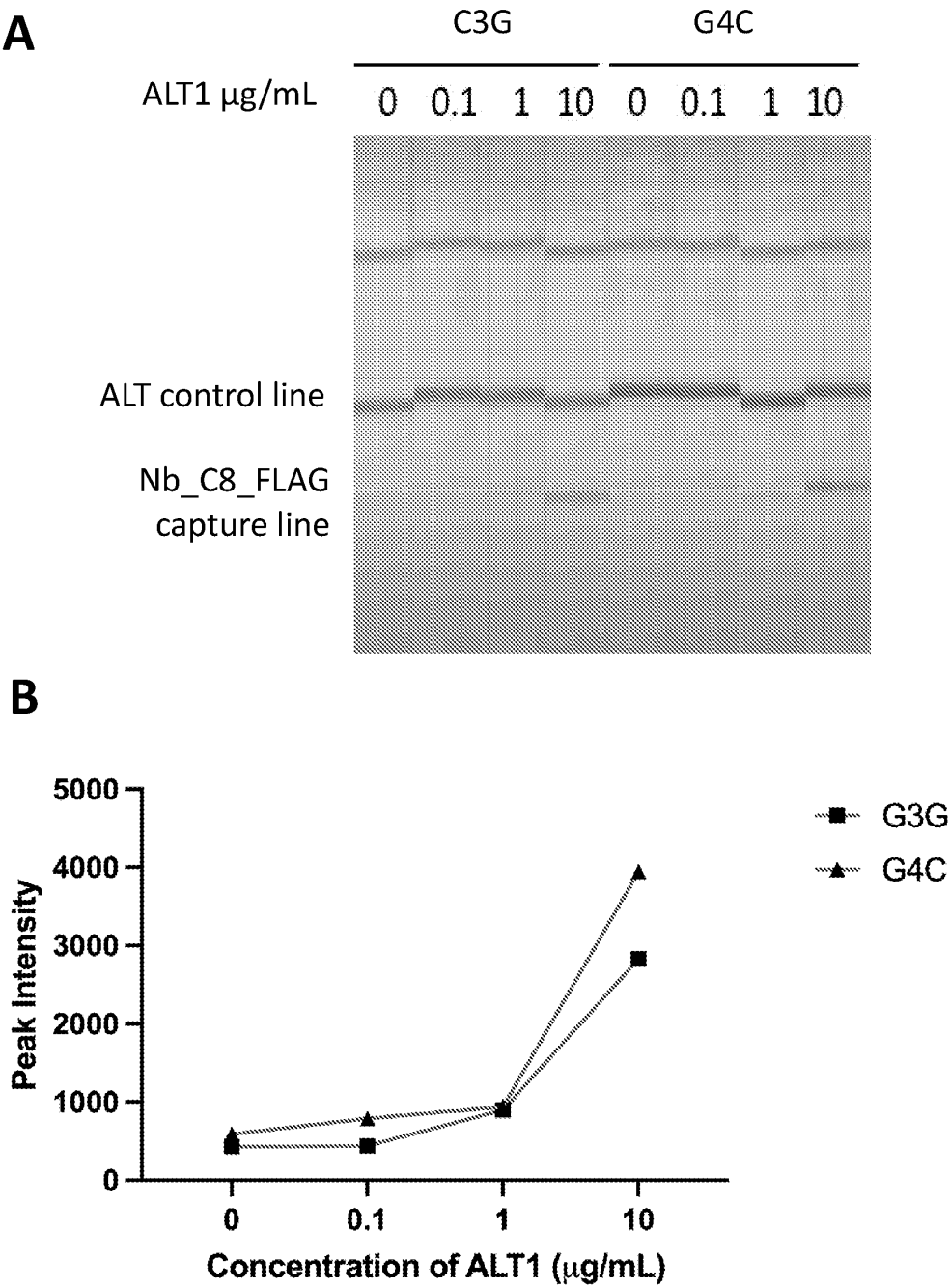


Figure 28

A

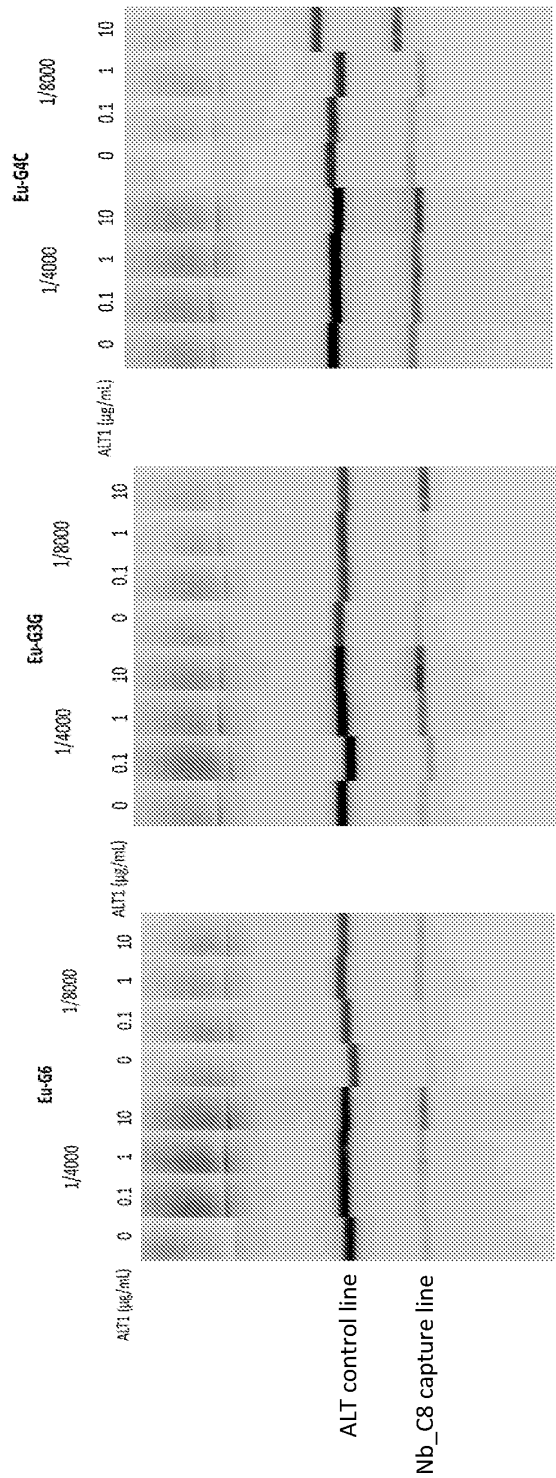
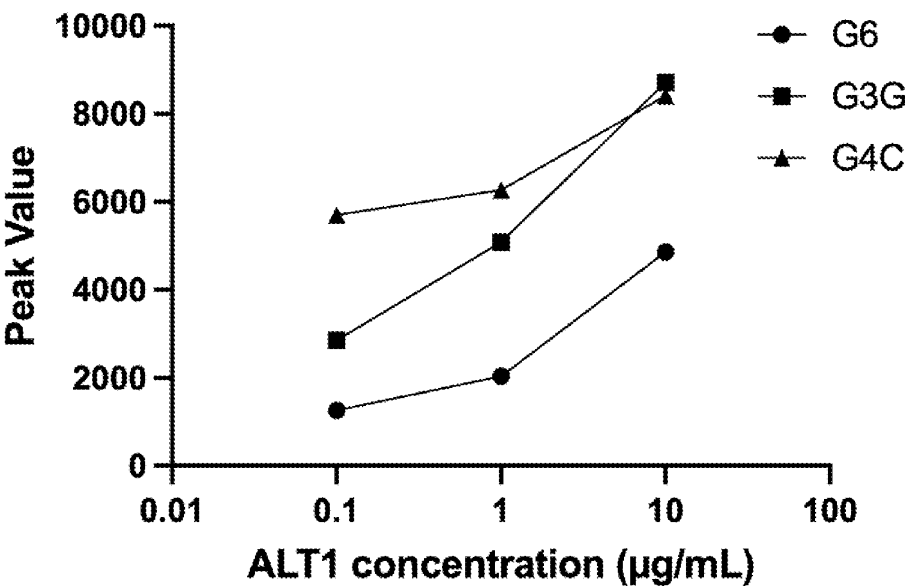


Figure 29

B



C

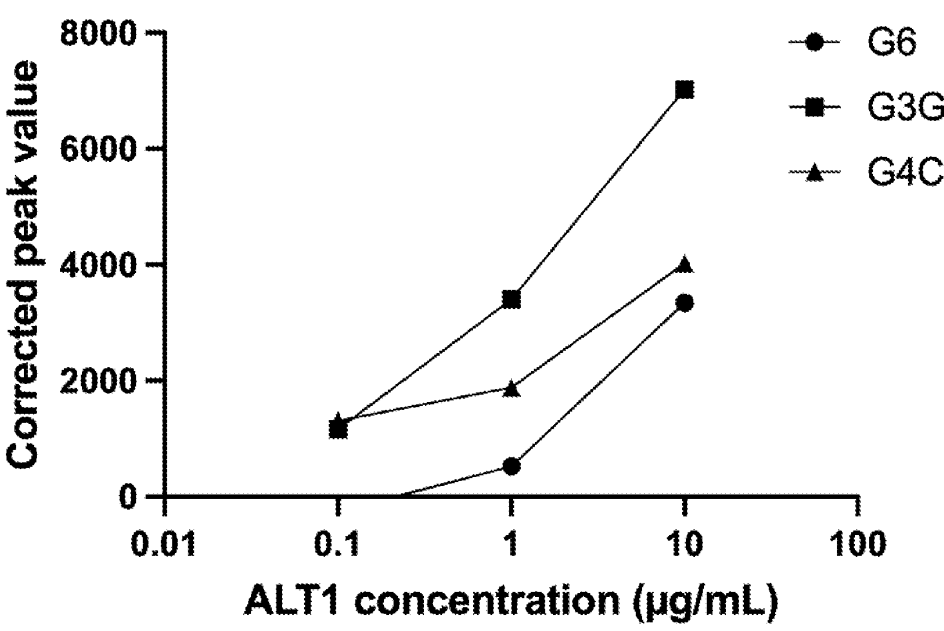


Figure 29 Continued

A Gold nanoshells conjugated to G4C

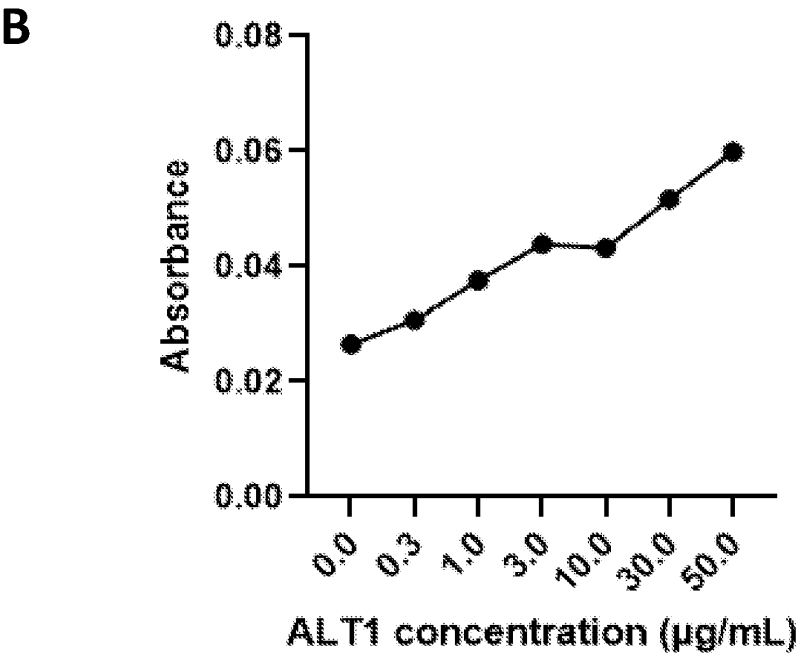
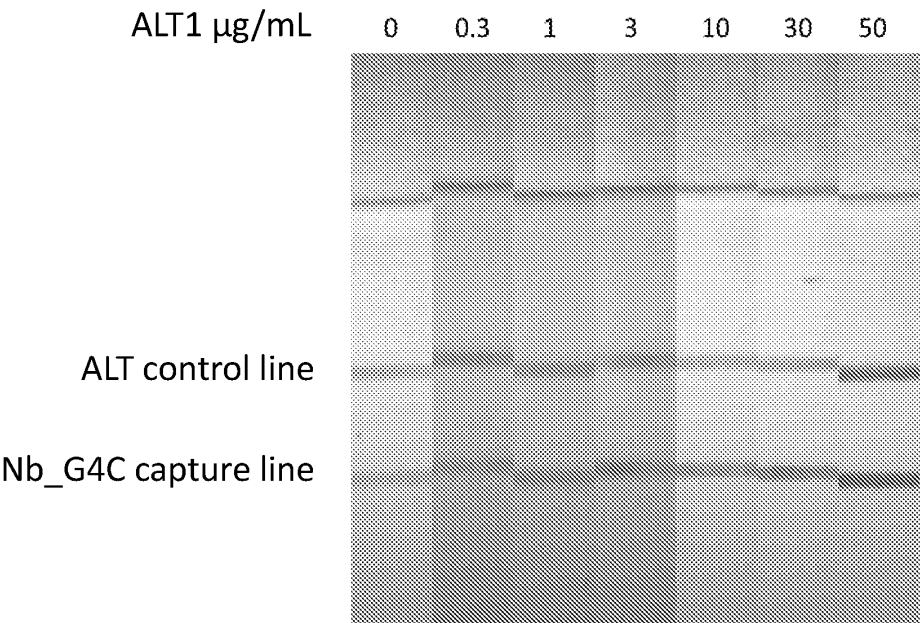


Figure 30

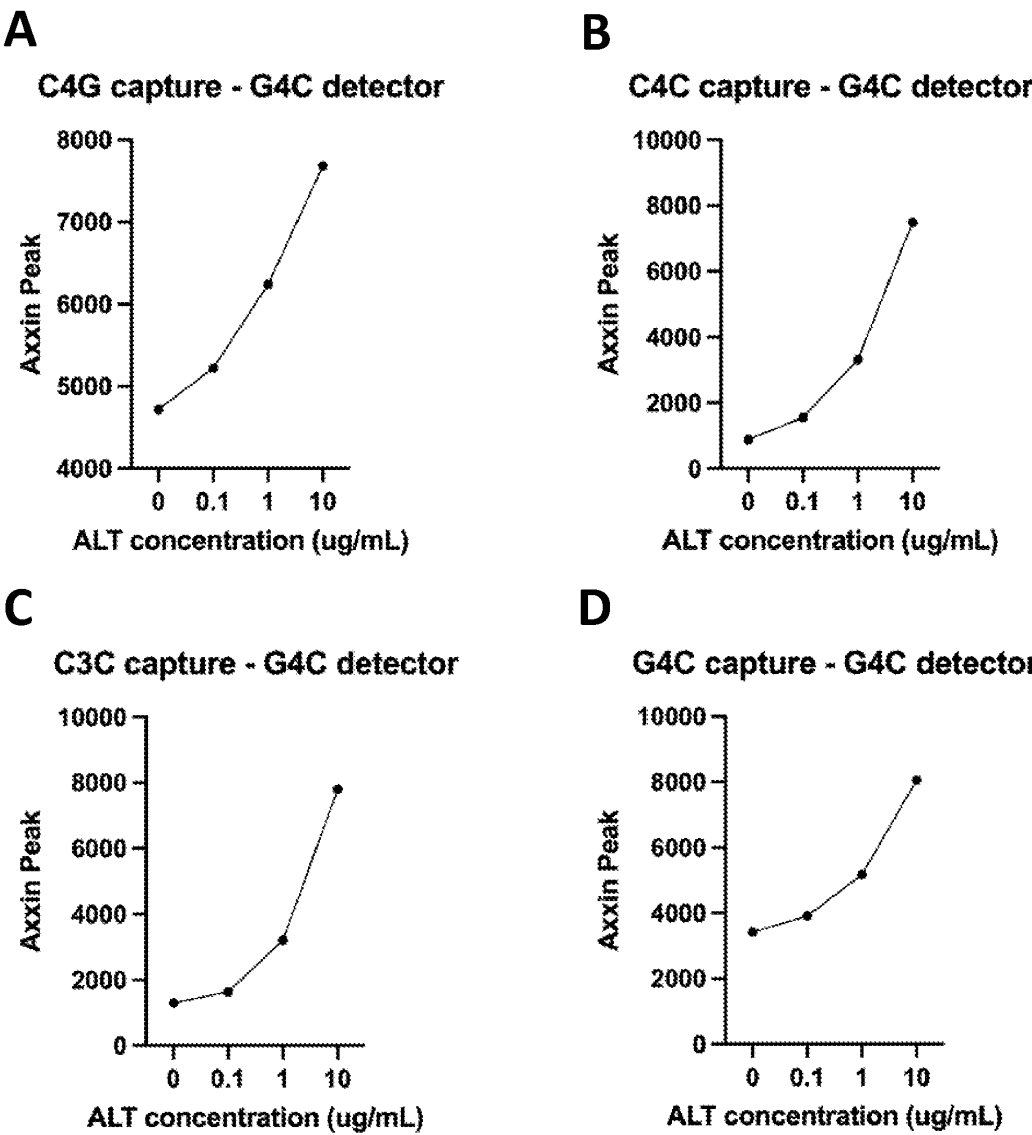


Figure 31

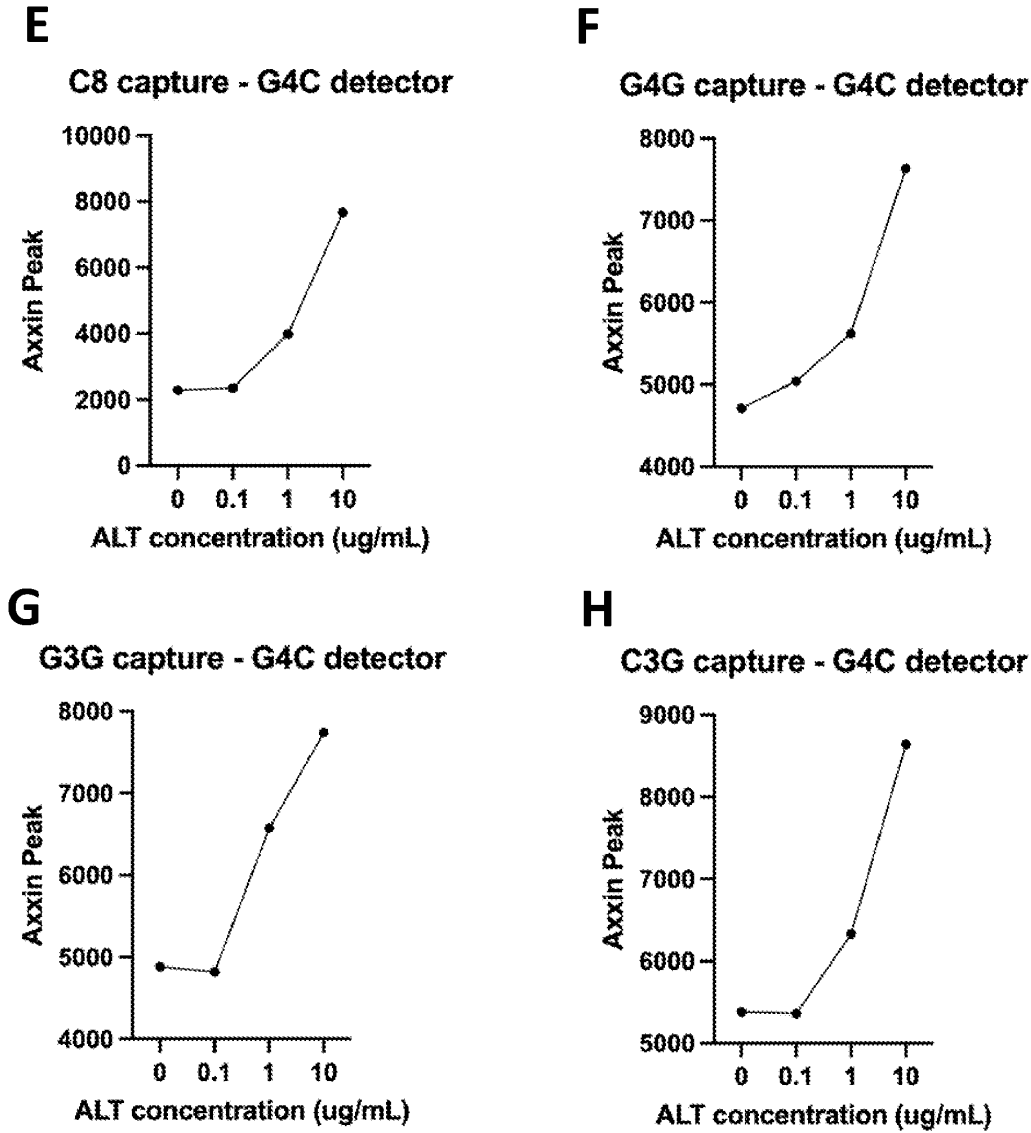


Figure 31 Continued

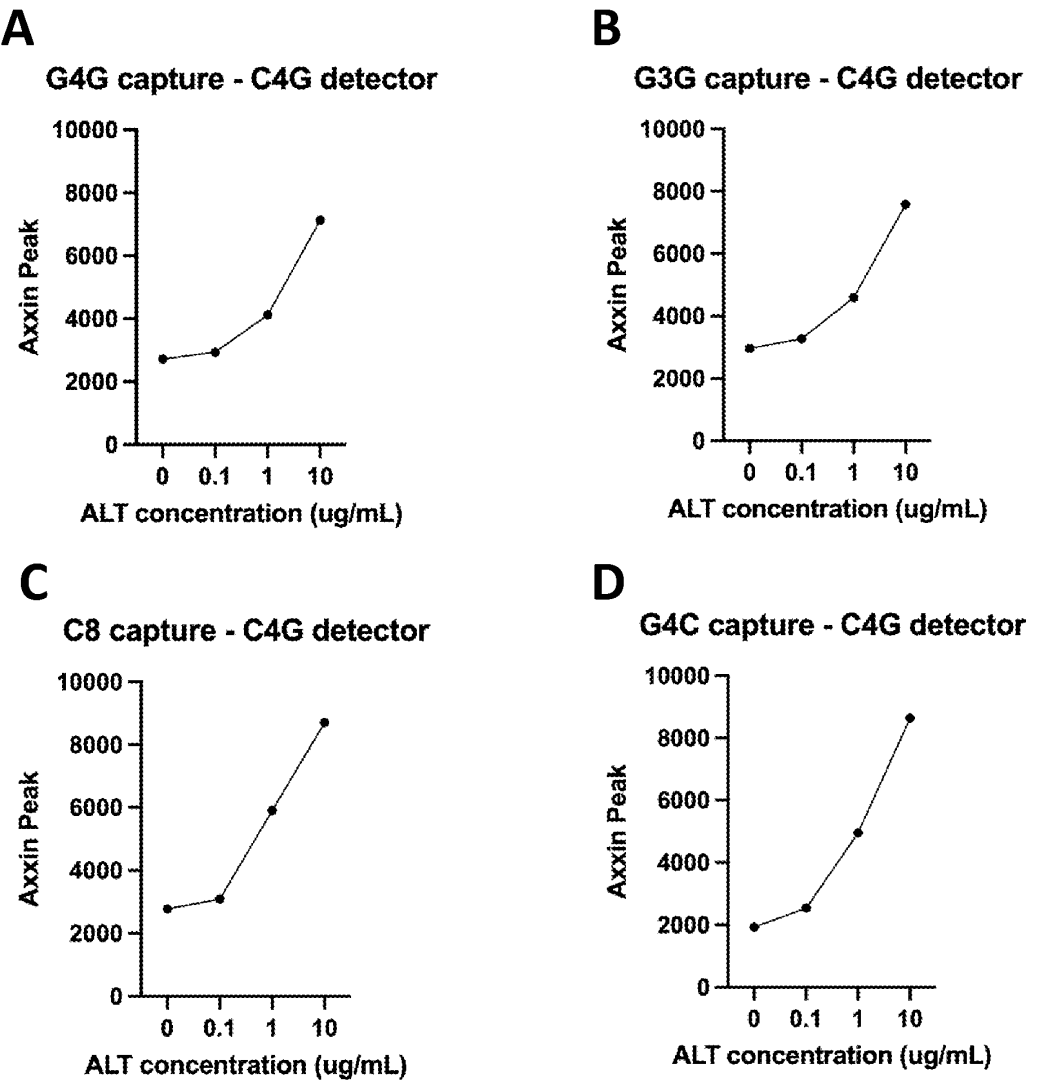


Figure 32

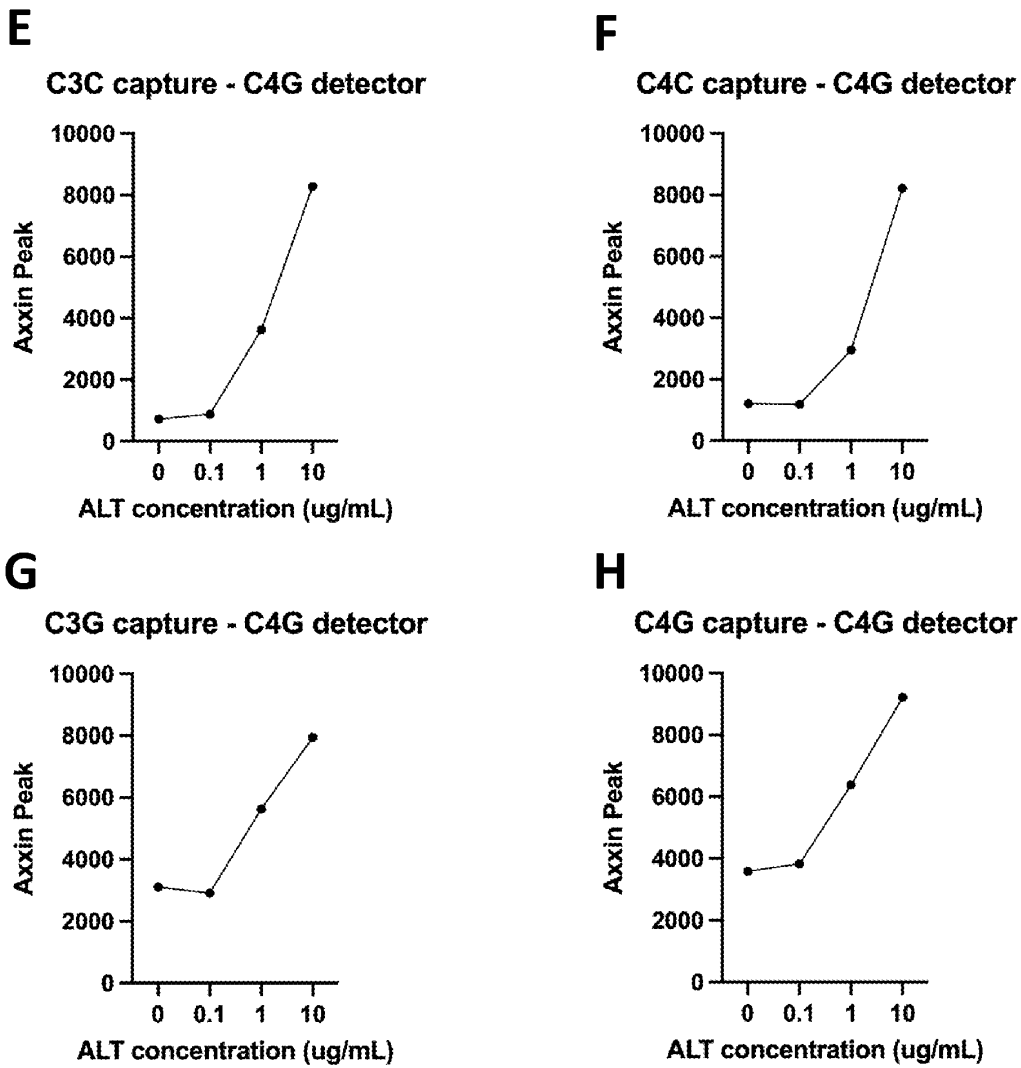


Figure 32 Continued

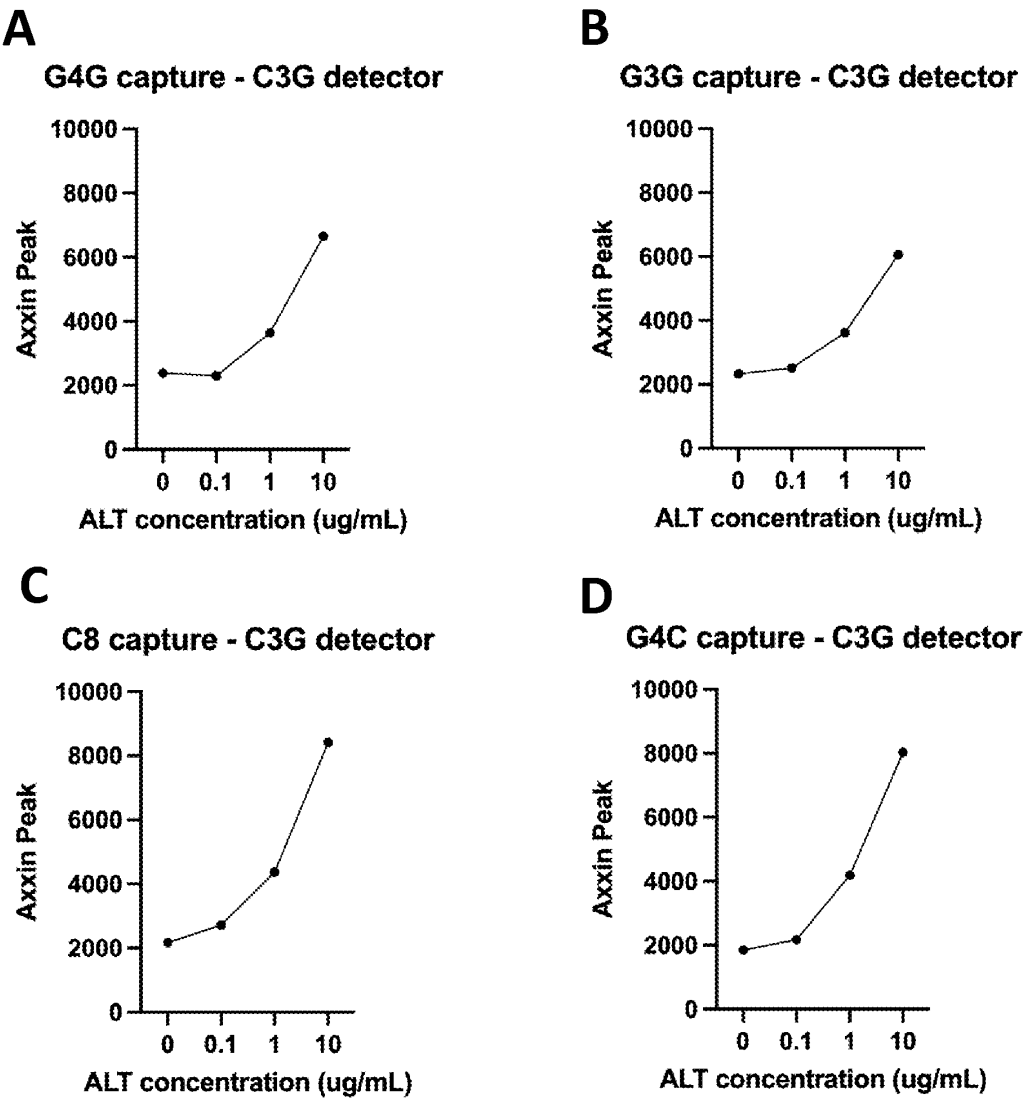


Figure 33

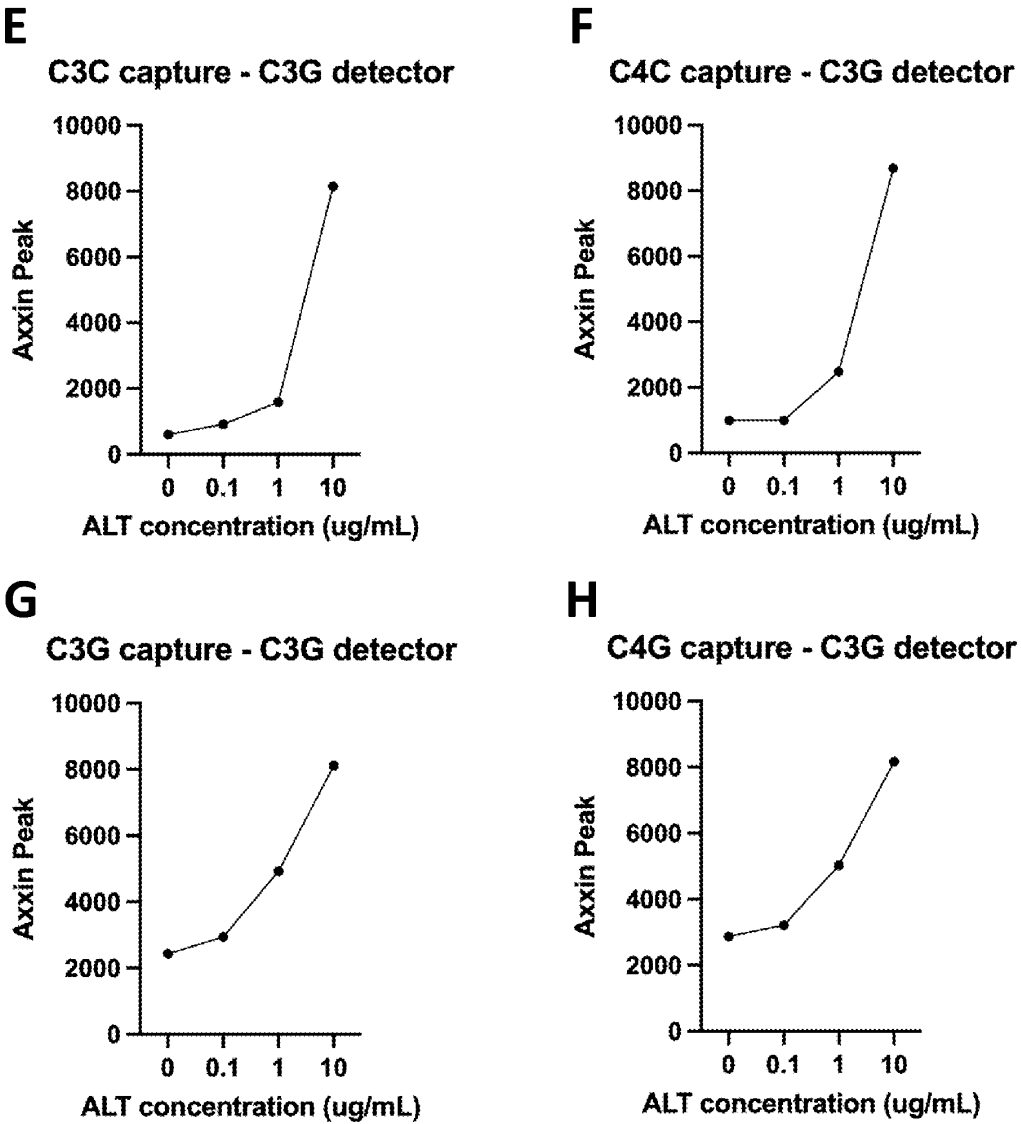


Figure 33 Continued

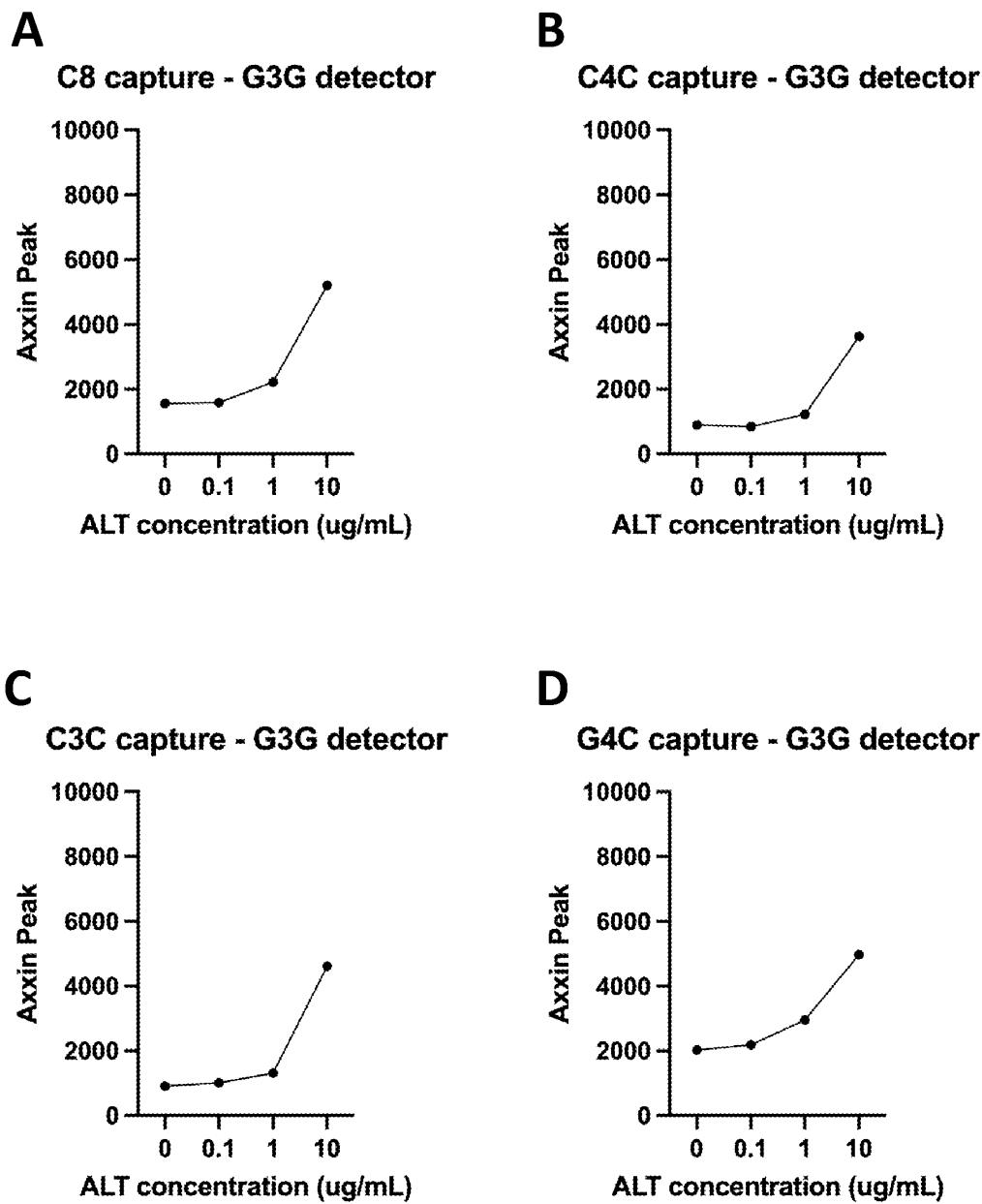


Figure 34

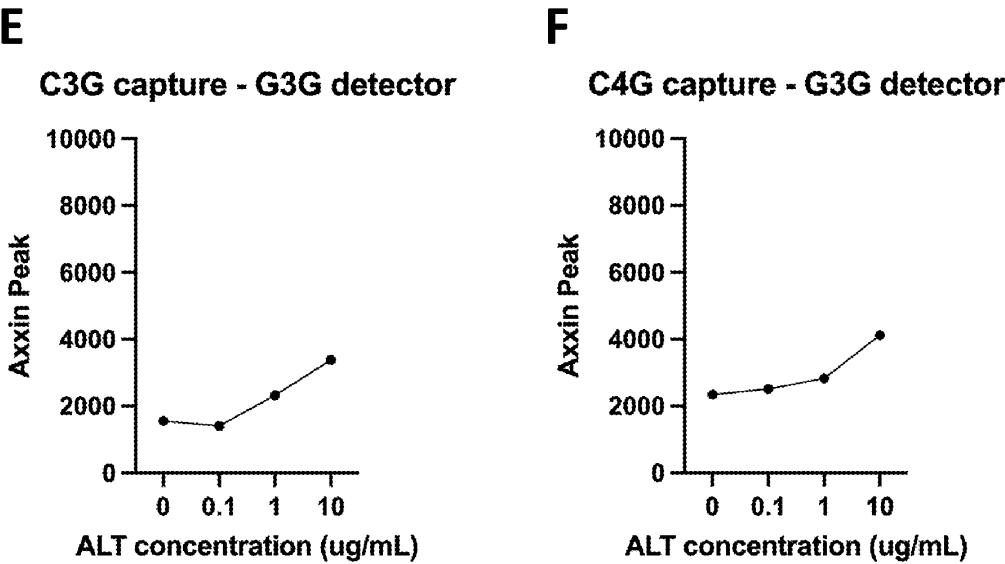


Figure 34 Continued

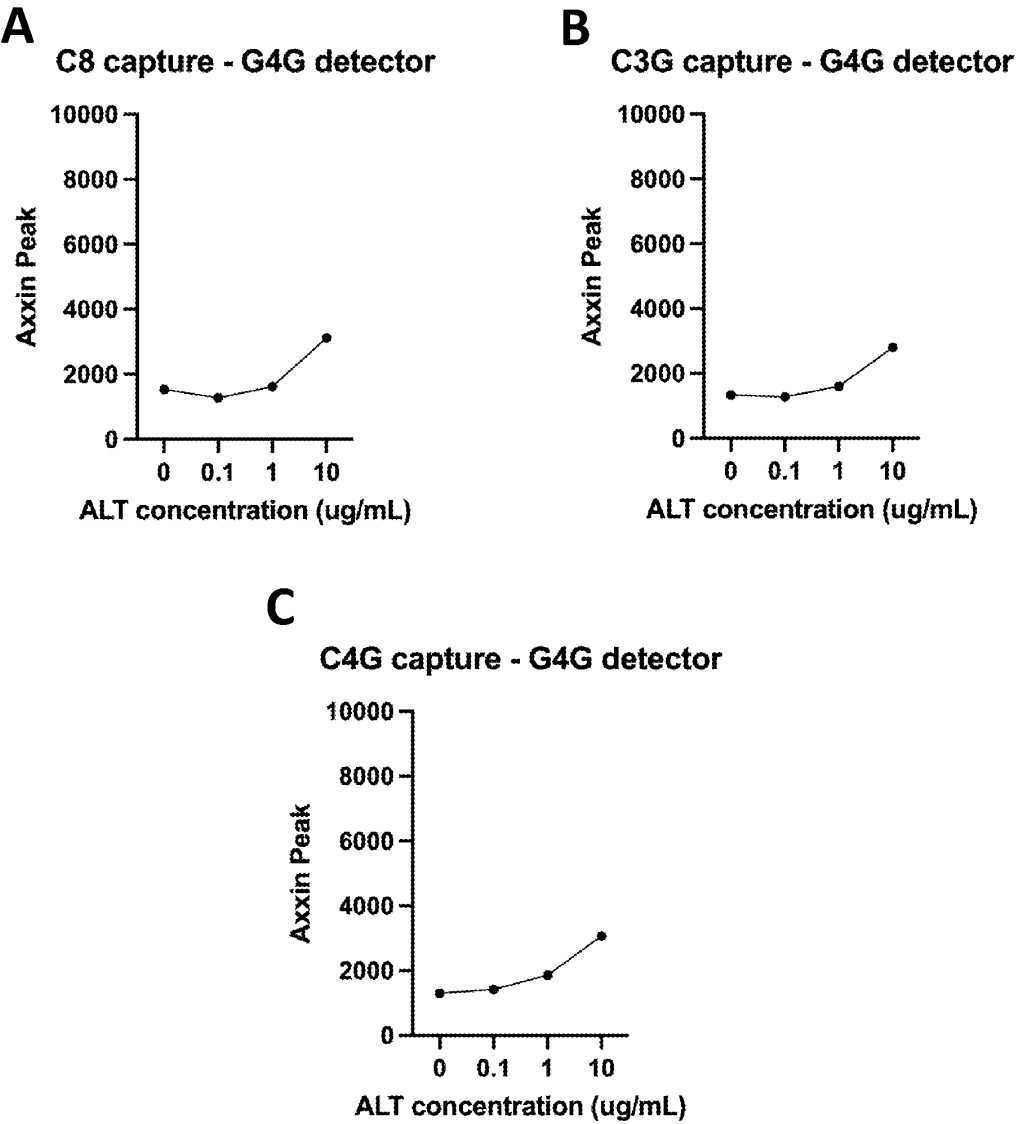


Figure 35

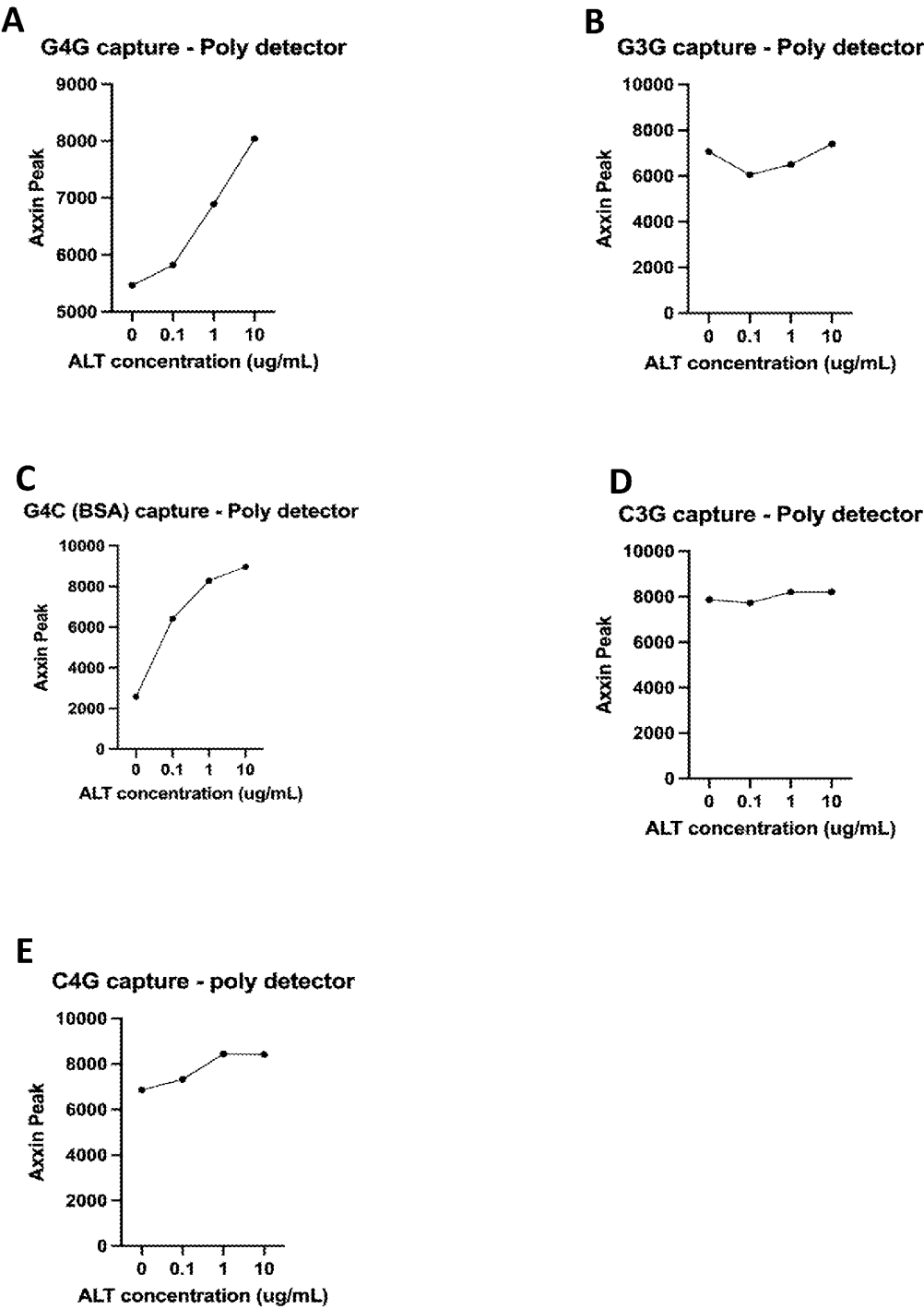


Figure 36

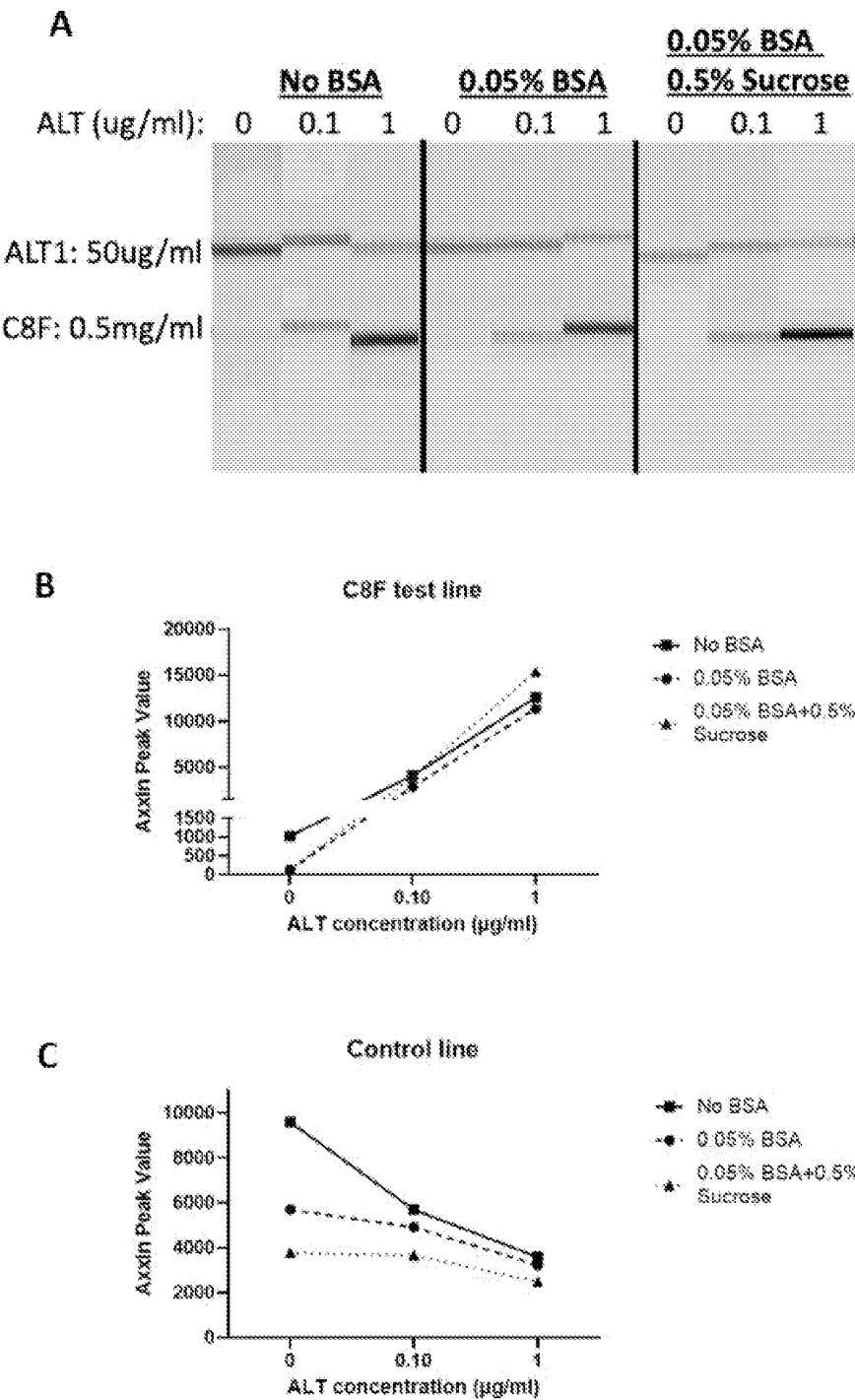


Figure 37

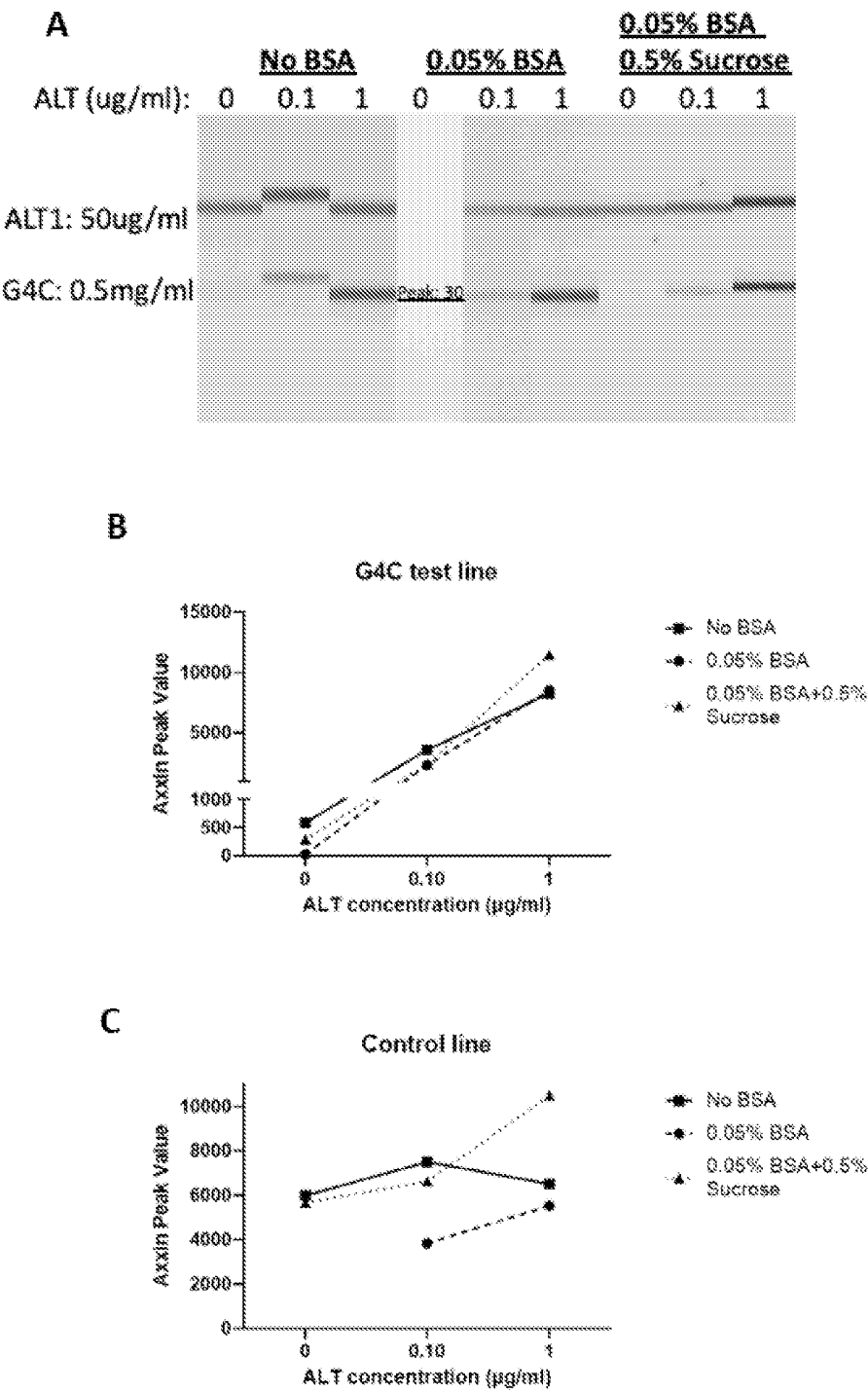


Figure 38

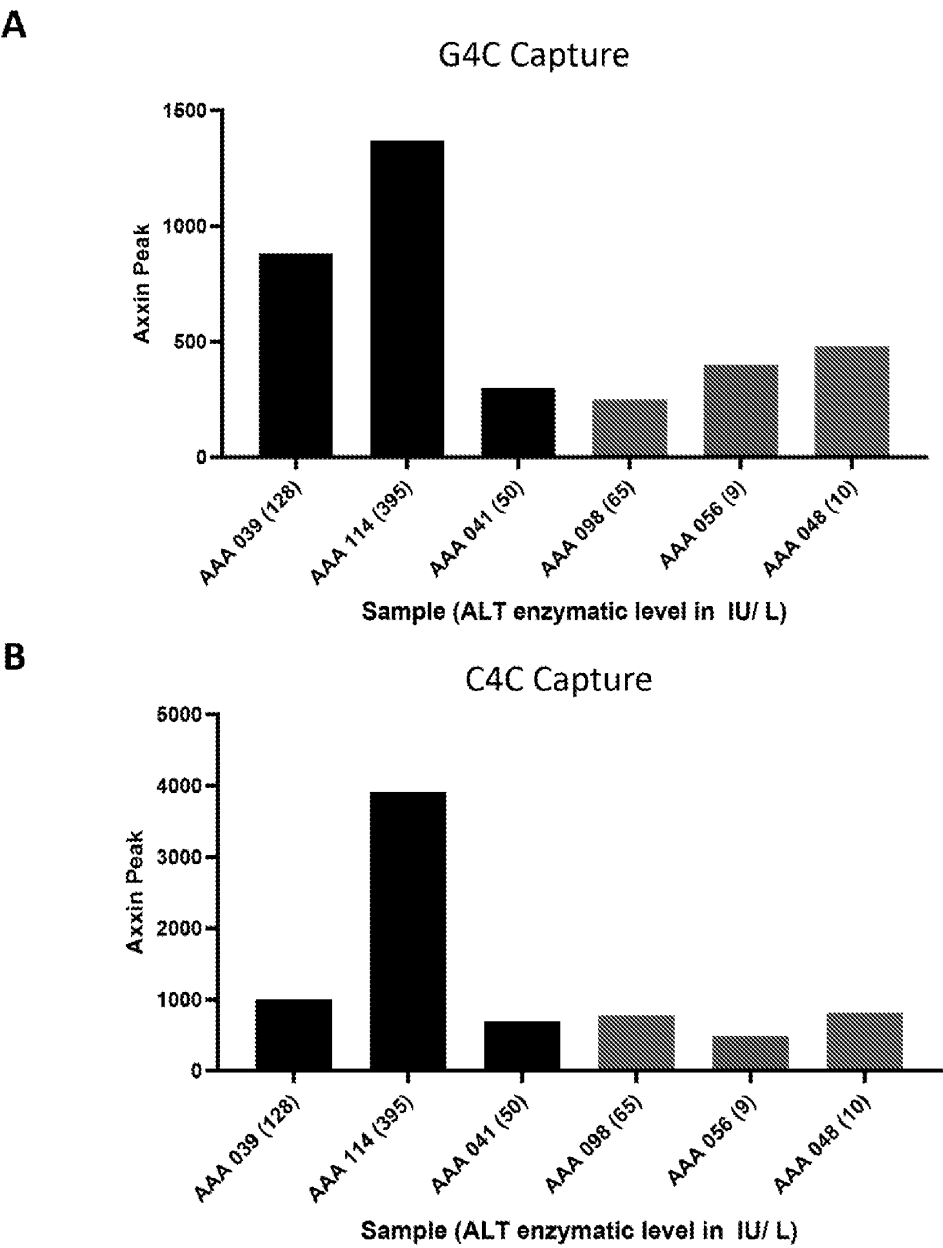
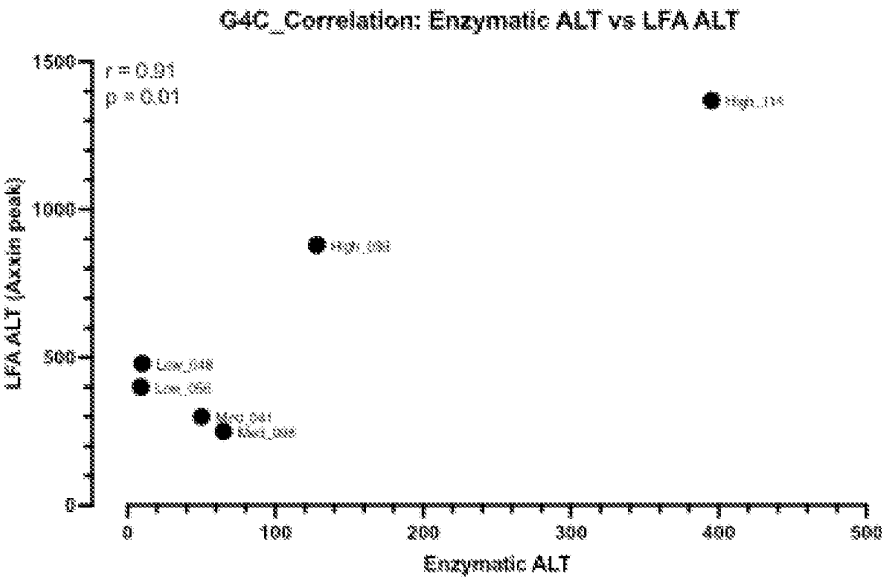


Figure 39

A



B

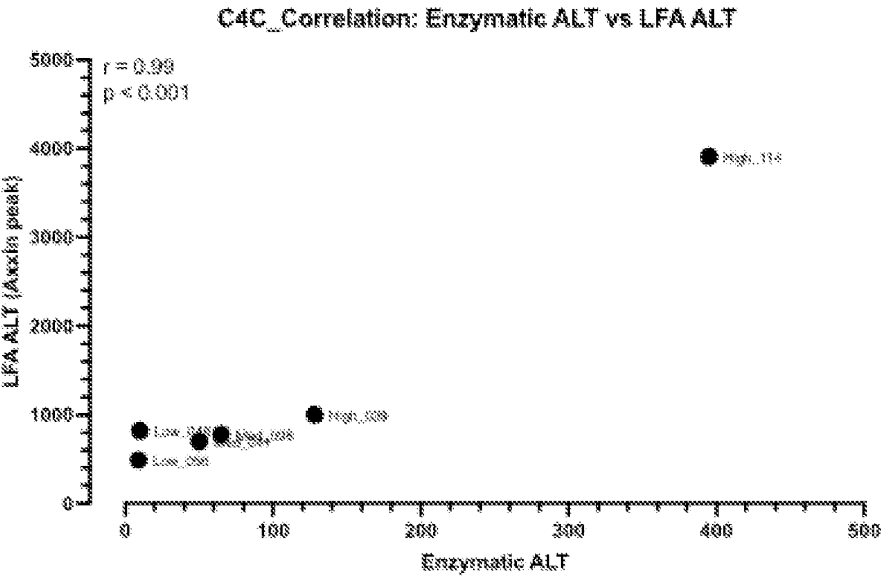
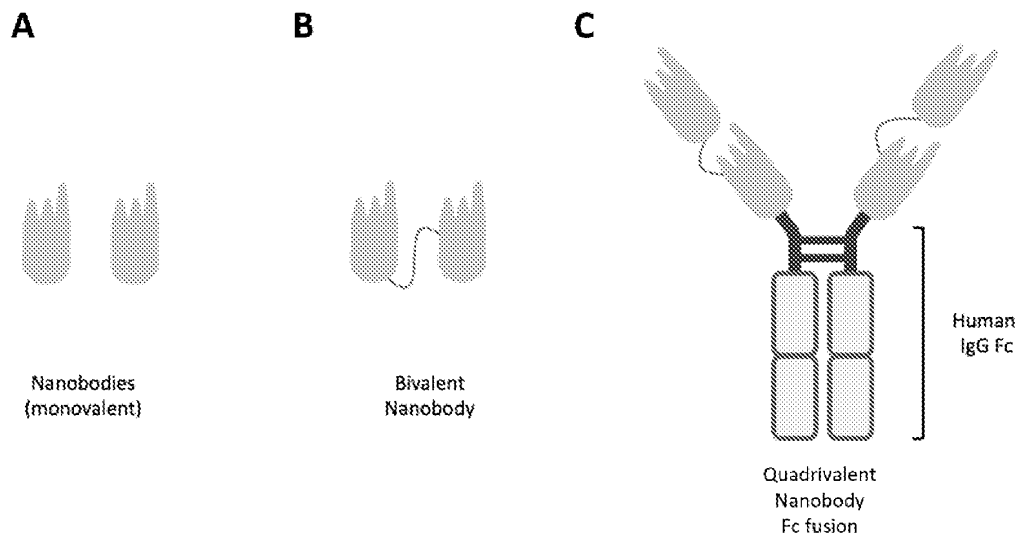


Figure 40

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**Figure 41**

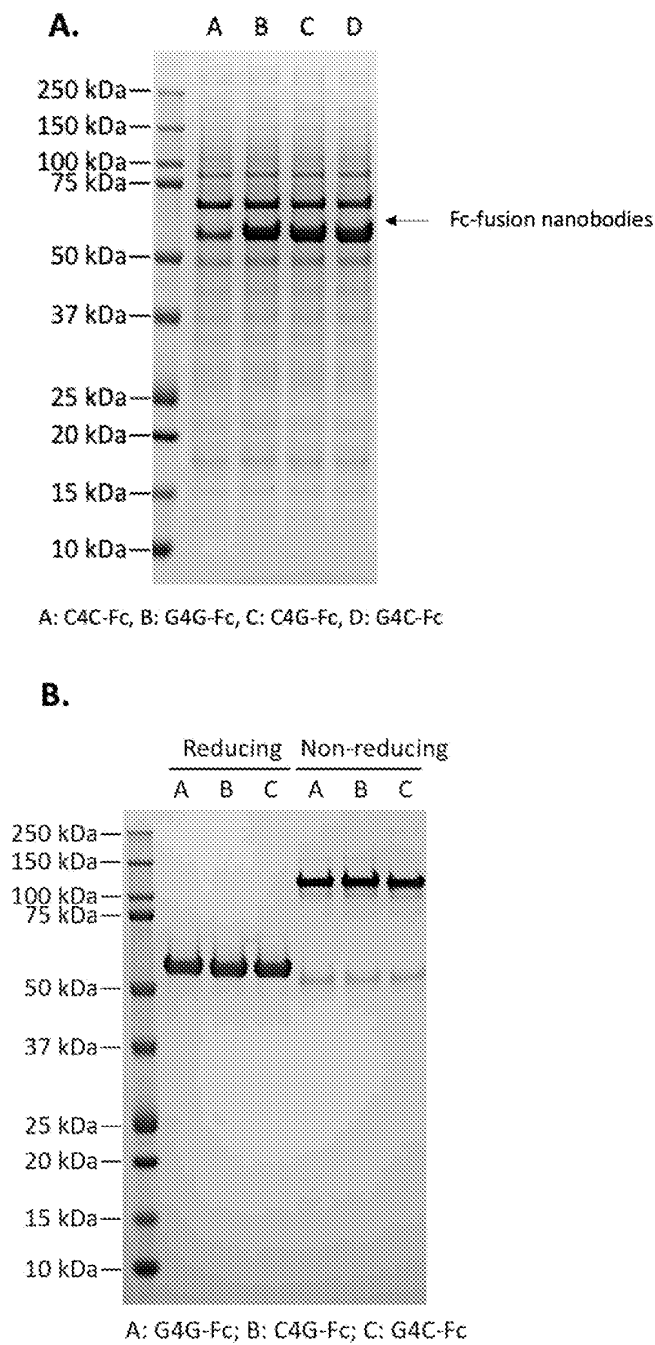


Figure 42

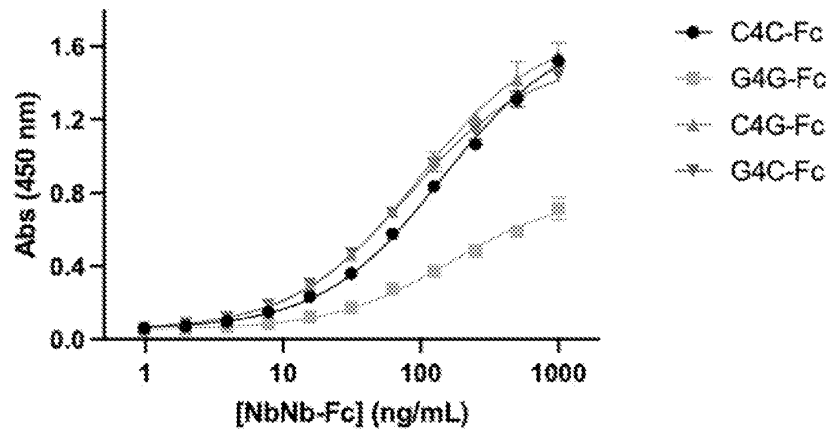


Figure 43

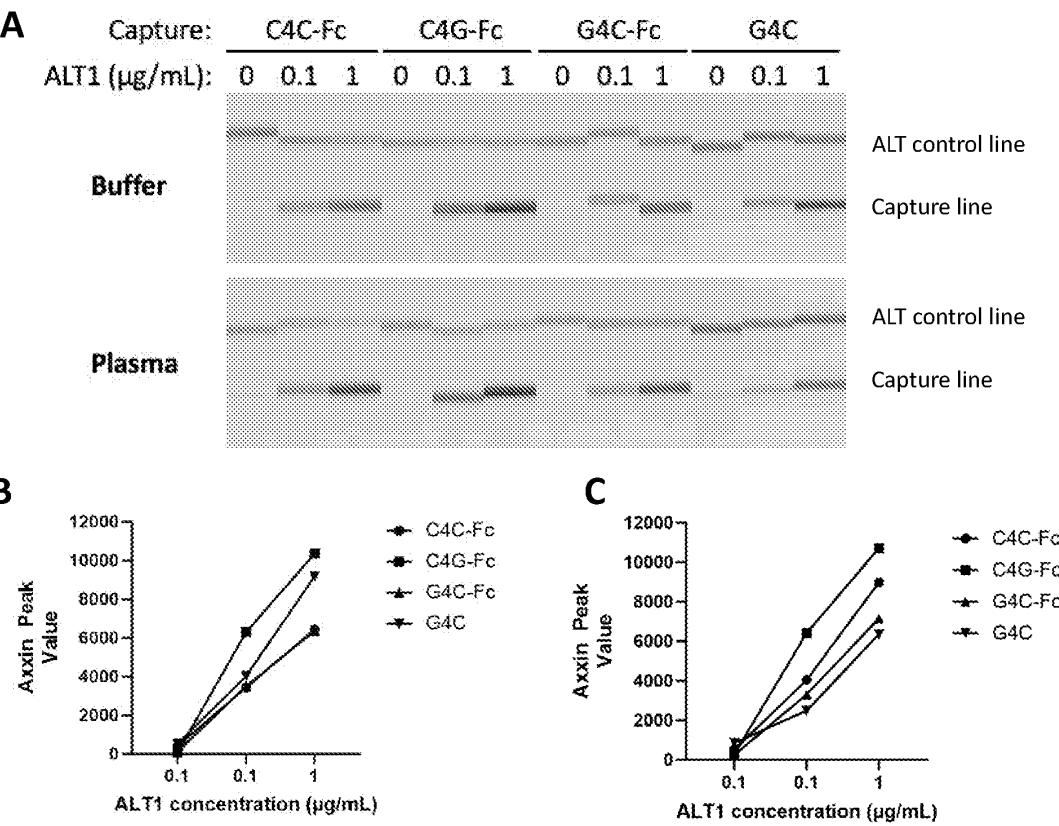


Figure 44

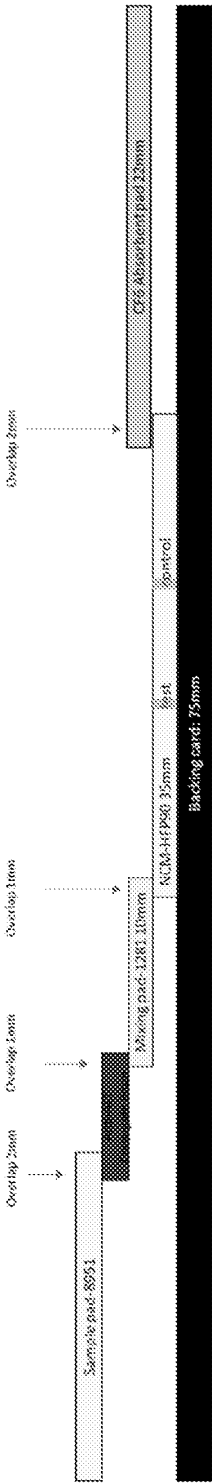


Figure 45

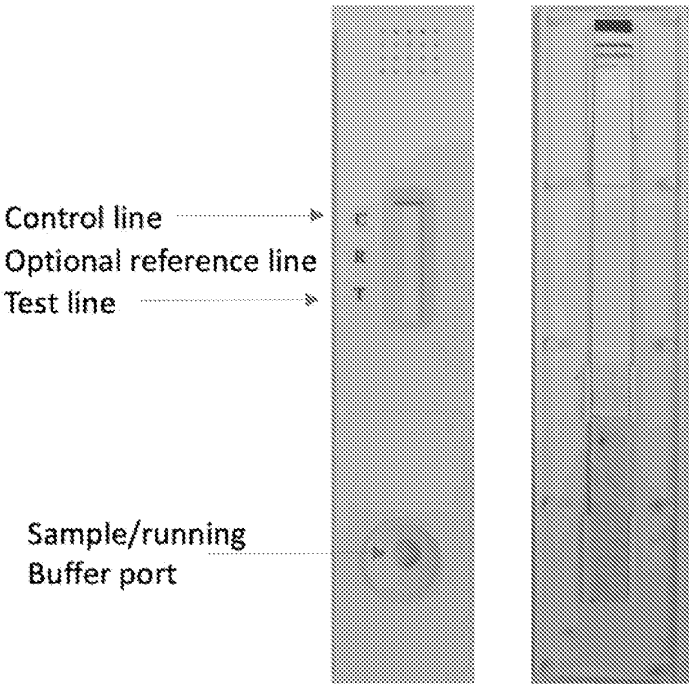


Figure 46

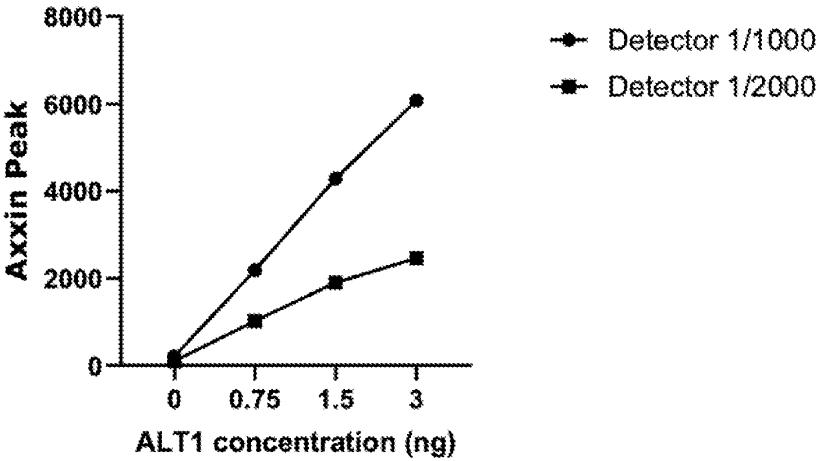


Figure 47

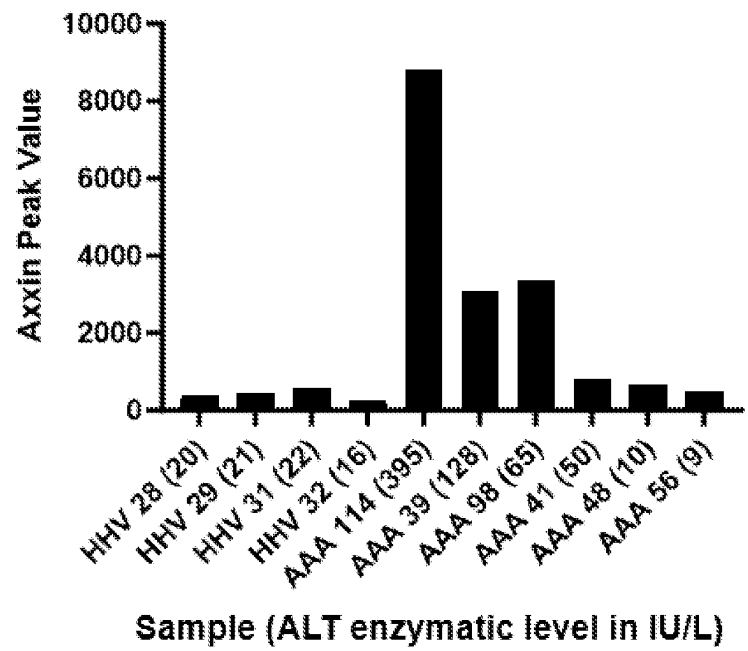


Figure 48

Construct	Nucleotide sequence
Nb_C8 full length	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCCGGGACTCCCTGAGACTCTCCTGTGTTGCCTCTGGGCCC GCCGTGAGCAACGTTGCCTTGGCTGGTTCCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACG TGGAGTGGTTGGACGTCATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAAC ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGG TTGGGCCCAGATAAGTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCACACCACCATCACCATCACTAGTA A
Nb_G6 full length	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCTGGGGCTCTCTGAGACTCTCCTGTGCAGCCTCTGGACGC ACCGACAGTTTCTATGCCATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGTATTACCT GGAGTCTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCCATCTCCAGAGACAACGCCAAGAACA CGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGC GGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTACCGTCTCCTCACACCA CCATCACCATCACTAGTAA
Nb_C10 full length	ATGAAATATTTACTACCCACAGCAGCTGCGGGACTGTTGCTGTTGGCTGCCAGCCAGCAATGGCGCAAGTTCAA CTGCAAGAAAGCGGTGGCGGCTTGGTGAAGCGGGCGGTTTCGTTACGTCTGAGCTGCGCGGCTCCGCGCCGAC CTTCTCCAGCTACAGCATGGGTTGGTTTCGCCAGGCTCCGGGTAAGAAGCTGAGTTTCGTGGCCGCGATTCTCGT AGCGGCTTTTCGACCAACTATGAGGACAGCGTTAAAGGTGTTTTACCATCAGCAGAGATAATGCAAAGAACC GTTTTCTCGCAGATGAACAGTCTGAAGGCGGAAGACACGGCTGTGTATTACTGCGCGGTTGGTCCGCGCATACCTG CCGACTGCGTCTGGCACCCGTTGCCGCGTGAAGCATACGATTATGGGGTACAGGTACCGTACCGTGAGC TCCATCATCACACCACCAC
C3C	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCCGGGACTCCCTGAGACTCTCCTGTGTTGCCTCTGGGCCC GCCGTGAGCAACGTTGCCTTGGCTGGTTCCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACG TGGAGTGGTTGGACGTCATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAAC ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGG TTGGGCCCAGATAAGTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCAGGAGTGGTGGATCCGCGCGT GGCGGTTCTGGTGGAGTGGATCTCAGGTGCAACTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCCGGGGACT CCCTGAGACTCTCCTGTGTTGCCTCTGGGCCCCGCGTCAGCAACGTTGCTTGGCCTGGTTCCGCCAGACTCCAGG GAAGGAACGTGAGTTTGTGGCAGGAATTACGTGGAGTGGTTGGACGTCATATTATGCGGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACATTACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG CCGTCTATTACTGTAATCTTATAGGACTACGGGTTGGGCCGAGAATAAGTACTGGGGCCAGGGGACCCAGGTCA CCGTCTCCTCACACCACCATCACCATCACTAGTAA
C4C	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCCGGGACTCCCTGAGACTCTCCTGTGTTGCCTCTGGGCCC GCCGTGAGCAACGTTGCCTTGGCTGGTTCCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACG TGGAGTGGTTGGACGTCATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAAC ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGG TTGGGCCCAGATAAGTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCAGGTGGTGGTGGTTCTGTTGGT GGTGGTTCTGGCGGCGGCGCTCCGTTGGTGGTGGATCCAGGTGCAACTGCAGGAGTCTGGAGGAGGATTGGT GCAGGCCGGGACTCCCTGAGACTCTCCTGTGTTGCCTCTGGGCCCCGCGTCAGCAACGTTGCCTTGGCTGGTT CGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACGTGGAGTGGTTGGACGTCATATTATGCGGA CTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAA CCTGAGGACACGGCGCTATTACTGTAATCTTATAGGACTACGGGTTGGGCCGAGAATAAGTACTGGGGCCAG GGGACCCAGGTACCGTCTCCTCACACCACCATCACCATCACTAGTAA
C4C codon optimized	ATGAAATATTTACTACCCACAGCAGCTGCGGGCCTATTATTGCTTGGCGGCACAACCCGCTATGGCGCAGGTGCAA CTGCAAGAGAGCGGTGGCGGCTTGGTTACGGCGGGCGACTCCTTGCGGCTGAGTTGCGTTGCGAGCGGTCCGGC AGTTTCAAGCTGGCGCTGGCATGTTTCGTGACAGCCCCGGGTAAGAGCGCGAATTCGTGGCTGGCATCACCTG GTCAGGCTGGACGAGCTATTACGCCGATTCTGTTAAGGGTCGCTTACCATTAGCCGTGATATTACTAAGAACC GTGTATCTGCAGATGAATAGCTTGAAGCCGGAAGATACCGCGGTGTAATACTGCAACCTGATTGGTCTGCGTGTG GTCCGGAACAAATACTGGGGTCAGGGAACGCAAGTACCCGTGAGCAGCGGCGGTGGTGGCTCTGGCGGTGGC GGTAGCGGCGGTGGTGGTTCCGGCGGTGGCGGGTCTCAGGTTACGCTTCAAGAATCCGGTGGCGGCTGGTTCA AGCGGGTGACTCCTTGCCTGAGCTGTGTCGCTCTGGCCAGCTGTGAGCAATGTTGCTCTGGCTGGTTTCGC CAGACTCCGGGTAAAGAAGCTGAGTTCGTTGCCGGATTACCTGGAGCGGCTGGACCAGCTACTATGCAGATTCC GTGAAAGGTGTTTTACCATCAGCGTGACATACCAAAAATACGGTATATCTGCAAATGAACCTCGCTCAAGCCGG AGGACACCGCGGTGTTACTGCAATTTAATCGGCTGCGCTGGGTCCGGAGAACAAGTACTGGGGTCAAGGCA CGCAGGTACCGTTTTCTCTACACCACCATCACCATCACTAG

Figure 49

G3G	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGACGGCTGGGGGCTCTGAGACTCTCCTGTGCAGCCTCTGGACGC ACCGACAGTTTCTATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGATCAGCTATTACCT GGAGTGCTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACA CGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGC GGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCAGGAG GTGGTGGATCCGGCGGTGGCGTTCTGGTGGAGGTGGATCTCAGGTGCAACTGCAGGAGTCTGGAGGAGGATTG GTGCAGGCTGGGGGCTCTGAGACTCTCCTGTGCAGCCTCTGGACGCACCGACAGTTTCTATGCCATGGGCTGGT TCCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCTGGAGTGCTGGTAGCACATACTATGCAG ACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACACGGGTGTATCTGCAAATGAACAGCCTGA AACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGCGGGGTACGAAAGTAGCTGGTTGGAGG CGTTTGGTTCCTGGGGCCAGGGGACCCAGGTACCCGTCTCTCACACCACCATCACCATCACTAGTAA
G4G	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGACGGCTGGGGGCTCTGAGACTCTCCTGTGCAGCCTCTGGACGC ACCGACAGTTTCTATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCT GGAGTGCTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACA CGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGC GGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCAGGTG GTGGTGGTCTGGTGGTGGTGGTCTGGCGGCGCGGCTCCGTTGGTGGTGGTATCCAGGTGCAACTGCAGGAG TCTGGAGGAGGATTGGTGACGGCTGGGGGCTCTGAGACTCTCCTGTGCAGCCTCTGGACGCACCGACAGTTTC TATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCTGGAGTGCTGGT AGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTG CAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCTCGCGGGGTACGAA AGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTACCCGTCTCTCACACCACCATCACCATC ACTAGTAA
G4G codon optimized	ATGAAATATTTACTACCCACAGCAGCTGCGGGCCTTCTATTGTTAGCGGCACAACCCGCTATGGCGCAGGTCCAG CTGCAGGAGAGCGGTGGCGGTCTGGTTCAAGCGGGTGGCTCCCTTCGTCTGTCATGTGCGGTAGCGGTGCGACC GATTCGTTCTATGCCATGGGTTGGTTTCGTCAAGCACCGGGTAAAGAGCGCGAATTTGTTCCGCGATCACCTGGA GCGCGGGTAGCACCTATTACGCCGATTCCGTGAAGGGTCCGCTTCGCGATCAGCCGTGACAACGCAAAAAACACGG TTTATCTGCAGATGAACAGCCTGAAGCCAGAAGATACCGCTGTGTACTACTGCGCTGCGGATAGCTTGAGCGCCG GCTATGAGTCCTCTGGCTGGAAGCGTTTGGCAGCTGGGGCCAGGGCACGCAAGTGACCGTCTCGAGCGGGGT GGTGGTCCGGTGGCGGCGCTCTGGAGGCGGCGTTCTGGCGGCGGCGGAGCCAGGTACAGCTGCAAGAGA GTGGGGGTGGTTGGTTCAAGCGGGTGGCTCGTTACGTCTCAGCTGCGCTGCGAGCGGCGGTACCGACAGCTTCT ATGCAATGGGTTGGTTCCGCCAAGCTCCGGGTAAAGAAAGAGAATTCGTGAGCGCGATTACCTGGTCTGCGGGT CTACGTACTACGCGGACAGCGTTAAGGGTCGTTTTGCAATTTCCCGTGATAATGCCAAGAACACCGTTTACCTGCA AATGAATAGCCTGAAACCGGAGGACACCGCTGTGTACTACTGCGCCGACAGACGTTGTCCGACGGCTATGAAAG TAGCTGGCTGGAGGCGTTCCGGCTCTGGGGTCAAGGTACACAGGTGACTGTGTCGAGCCACCACCATCACCATCA CTAG
C3G	ATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTGCAG CTGCAGGAGTCTGGAGGAGGATTGGTGACGGCCGGGACTCCCTGAGACTCTCCTGTGTTGCCTCTGGGCCCCGCC GTCAGCAACGTTGCCCTGGCTGGTTCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACGTGG AGTGGTTGGACGTATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAACACG GTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGCTATTACTGTAATCTTATAGGACTACGGGTTG GGCCCCGAGAATAAGTACTGGGGCCAGGGGACCCAGGTACCCGTCTCCTCAGGAGGTGGTGGATCCGGCGGTGGC GGTTCGGTGGAGGTGGATCTCAGGTGCAACTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCTGGGGGCTCTCT GAGACTCTCCTGTGCAGCCTCTGGACGCACCGACAGTTTCTATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAA GGAGCGTGAGTTTGTATCAGCTATTACCTGGAGTGCTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATT CGCCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGT TTATTACTGTGCAGCAGACTCTCTCCGCGGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCA GGGGACCCAGGTACCCGTCTCTCACACCACCATCACCATCACTAG

Figure 49 Continued

C4G	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGACGGCCGGGACTCCCTGAGACTCTCTGTGTTGCCCTCTGGGCC GCCGTGAGCAACGTTGCCCTTGGCTGGTTCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACG TGGAGTGGTTGGACGTATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAAC ACGGTGTATCTGCAAATGAACAGCTGAAACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGG TTGGGCCCGAGAATAAGTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGGTGGTGGTGGTCTGTGGT GGTGGTCTGTGGCGCGCGGCTCCGGTGGTGGTGGATCCAGGTGCAACTGCAGGAGTCTGGAGGAGGATTGGT GCAGGCTGGGGGCTCTCTGAGACTCTCTGTGCAGCTCTGGACGCACCGACAGTTTCTATGCCATGGGCTGGTTC CGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCTGGAGTGTGGTAGCACATACTATGCAGAC TCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCTGAAA CCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCTCCGCGGGGTACGAAAGTAGCTGGTGGAGGCG TTGGTCTCTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACACCACCATCACCATCACTAGTAA
C4G codon optimized	ATGAAATATTTACTACCCACAGCAGCTGCGGGCTATTGCTACTTGCAGCACAAACCCGCTATGGCGCAGGTCCAA CTGCAGGAGAGCGGGGGCGGGTGGTTCAGCGGGTGATAGCTTACGCTGTCTTGTGTGCCAGCGGCCCGGC AGTTAGCAATGTTGCGCTGGCATGGTTCGCCAGACCCCGGTAAGGAGCGCGAATTCGTAGCGGGTATTACCTG GTCTGGCTGGACAGCTATTACGCGGATTCCGTGAAGGGTCGCTTCACCATTAGCCGTGACATCAACAAAAATACC GTGTACCTGCAGATGAATAGCCTCAAGCCGGAAGACACGGCTGTGTATTACTGCAACCTGATTGGTTTGCCTGTTG GCCCAGAGAACAAGTATTGGGGTCAGGTCAGCAGGTAACCTGTTTCGAGTGGTGGCGGAGGCTCGGGTGGCGGT GGCTCCGGTGGCGCGGATCCGGCGCGCGGCTCCCAAGTGCAGCTGCAAGAGTCCGGTGGTGGTCTGTGCA AGCGGGCGGCTCTTTCGTCTGAGCTGCGCTGCGAGCGGTGTCACCGATAGCTTTATGCCATGGGTTGGTTTCGT CAGGCTCCGGGTAAAGAAAGAGAGTTCTGTGCAGCCATCAGCTGGTCCGACGGCTCGACCTATTACGCCGACAGC GTGAAGGGTCGTTTTCGATCAGCCGTGATAACGCGAAAAACACCGTCTACCTGCAGATGAACAGCCTGAAACCG GAGGACACTCGGTTTACTACTGCGCTGCTGACAGCTTGTCTGCGGGTTATGAATCCAGCTGGCTGGAAGCATTTG GTAGCTGGGGTCAAGGCACCCAAGTACGGTTAGCTCTCACACCATCACCATCACTAG
G3C	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGACGGCTGGGGGCTCTCTGAGACTCTCTGTGCAGCCTCTGGACGC ACCGACAGTTTCTATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCT GGAGTGTCTGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACA CGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGC GGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGGAG GTGGTGGATCCGGCGGTGGCGTTCTGGTGAGGTGGATCTCAGGTGCAACTGCAGGAGTCTGGAGGAGATTG GTGCAGGCCGGGACTCCCTGAGACTCTCTGTGTTGCCTCTGGGCCCGCGTCAGCAACGTTGCCTTGGCTGGT TCCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACGTGGAGTGGTGGACGTATATTATGCGG ACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAA ACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGGTTGGGCCCGAGAATAAGTACTGGGGCCA GGGAGCCAGGTACCGTCTCCTCACACCACCATCACCATCACTAGTAA
G4C	ATGATGAAATACCTATTACCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCAGCCGGCCATGGCCAGGTG CAGCTGCAGGAGTCTGGAGGAGGATTGGTGACGGCTGGGGGCTCTCTGAGACTCTCTGTGCAGCCTCTGGACGC ACCGACAGTTTCTATGCCATGGGCTGGTTCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTATCAGCTATTACCT GGAGTGTCTGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCCGCATCTCCAGAGACAACGCCAAGAACA CGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCAGACTCTCTCCGC GGGGTACGAAAGTAGCTGGTTGGAGGCGTTTGGTTCCTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGGTG GTGGTGGTCTGGTGGTGGTGGTCTGGCGGCGCGGCTCCGGTGGTGGTGGATCCAGGTGCAACTGCAGGAG TCTGGAGGAGGATTGGTGAGGCCGGGACTCCCTGAGACTCTCTGTGTTGCCTCTGGGCCCGCGTCAGCAAC GTTGCCCTGGCTGGTTCGCCAGACTCCAGGGAAGGAACGTGAGTTTGTGGCAGGAATTACGTGGAGTGGTGG ACGTATATTATGCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACATTACCAAGAACACGGTGTATCTGCA AAATGAACAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTAATCTTATAGGACTACGGGTTGGGCCCGAGA ATAAGTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACACCACCATCACCATCACTAGTAA
G4C codon optimized	ATGAAATATTTACTACCCACAGCAGCTGCGGGCTACTTTTGTAGCGGCACAACCCGCTATGGCGCAGGTTACGTTCCAAGAG AGCGGTGGCGGATTGGTTCAAGCCGGTGGCAGCCTGCGCCTGAGCTGCGCCGTAGCGGCCGTACCGATTCTTTTATGCTATGG GTTGGTTCCGTACGGCTCCGGGTAAAGAACGTGAATTCGTGAGTGCATCAGTGGTCAAGCGGGCTCGACCTATTACGCGGACT TGTTAAGGGTCGTTTGAATCAGCGTGACAACGCCAAAAATACCGTCTATTGCAAATGAACAGCCTTAAGCCGGAGGACACC GCGGTGTACTACTGCGCGCTGATAGCTTAAGCGCGGGTTATGAATCCAGCTGGCTGGAAGCATTGGTTTCATGGGGTCAGGGT ACGCAAGTTACGGTGAAGTCCGGCGCGCGGCAAGTGGTGGCGGTGGCTGGCGGCGGTGGCTGGCGGCGGTGGTGGTCTCA GGTGCAACTGCAAGAGTCCGGTGGTGGCTGGTGAAGCGGGAGATAGCTTGCCTGAGCTGTGTGCTGTGGCCAGCAGT GTCCAACGTGGCTCTGGCATGGTTCCGCCAGACCCCGGTAAAGAGCGCGAGTTCTGGCTGGTATTACCTGGAGCGGTTGGAC CTCTATTACGCGGACAGCGTTAAGGGTCGTTTACCATTAGCCGTGACATCACGAAAAACACCGTCTACCTGCAAATGAACAGCT TGAAGCCGGAGGATACTGCGGTTTACTACTGCAATCTGATTGGTCTGAGAGTTGGTCCGAAAAATAAATTGGGGTCAAGGGCA CCCAGGTAAGTGTGAGCAGCCACCACCATCACCATCACTAG

Figure 49 Continued

C4C-Fc	ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGTGGAGCAGTCTTCGTTTCGGCTAGCCAAGT GCAGCTGCAAGAGTCCGGCGGCGGCTGGTCCAGGCTGGCGACAGTCTGCGGCTGAGCTGCGTCGCTCTGGAC CAGCCGTGAGCAATGTGGCCCTGGCCTGGTTCGGGCAGACACCTGGCAAAGAGAGAGATTCTGTGGCCGGAATC ACCTGGAGCGGCTGGACAAGCTACTACGCCGATAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACATCACCAA GAACACAGTGTATCTGCAGATGAACAGCCTGAAGCCTGAGGACACCGCCGTGTATTCTGTAATCTGATCGGACT GAGAGTGGGCCCCGAGAACAAGTACTGGGGACAGGGCACCAGGTGACCGTGTCCAGTGGCGGCGGCGGCTCC GGAGGCGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGTGGCAGCCAAGTGCAGCTGCAAGAGAGCGGCGGG GGCCTGGTGAGGCGGCGGATTCTCTGAGACTGTCTGCGTGGCTTCTGGCCCTGCCGTGCCAACGTGGCTCTGG CTTGTTTATAGGCAGACCCCTGGCAAAGAAAGAGAATTCTGTGTGGCATCACCTGGTCCGGCTGGACCTCTACTA CGCCGACTCCGTGAAGGGCAGATTACAATCTCTAGAGACATCACCAGAACACCGTGTACCTGCAGATGAATCC CTCAAGCCCGAAGATACAGCCGTGTACTACTGCAACCTGATTGGCCTGAGAGTGGGCCCTGAGAACAACTACTGG GGCCAGGGCACACAGGTGACCGTGTCCAGCGGATCCAAGACACACCTGTCTCCATGTCTGCTCCAGAGCTG CTCGGAGGCGCTTCCGTGTTTCTGTTCCCTCAAAGCCTAAGGACACCTGATGATCAGCAGAACCCTGAAGTGA CCTGCGTGGTGGTGGATGTGTCTACGAGGACCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTG CACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCCGTGCTGACCGTGCTG CACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCGTCTATCGAGAAA ACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACACTGCCTCCAAGCAGGGACGAGCTGACC AAGAATCAGGTGTCCCTGACCTGCCGTGTCAGGGCTTCTACCTTCCGATATCGCCGTGGAATGGGAGAGCAAT GGCCAGCCTGAGAACAACTACAAGACAACCCCTCTGTGCTGGACAGCGACGGCTCATTCTCTGTACAGCAAGC TGACAGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTACAGCTGCAGCGTATGCACAGGCGCTGCACAAC CACTACACCCAGAAGTCCCTGAGCCTGTCTCTGGCAAGTAA
G4G-Fc	ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGTGGAGCAGTCTTCGTTTCGGCTAGCCAACC GACAGTCTTACGCTATGGGCTGGTTCAGACAGGCTCCTGGCAAGGAAAGAGAGTTCGTGTCTGTATCACCTGG AGCGCCGGCTCTACATACTATGCCGACTCCGTGAAGGCGAGATTGCCATCAGCCGGGACAACGCCAAGAACACC GTGTACCTGCAGATGAACCTCCTGAAGCCCGAGGACACCGCCGTGTACTACTGCGCCGTGACTCTGTCCGCCG GCTACGAGAGTCTCTGGCTGGAAGCCTTCGGCAGCTGGGGACAGGGCACACAGGTGACCGTGTCCAGCGGATCC AAGACACACACCTGTCTCCATGTCTGCTCCAGAGTGTCTCGGAGGCCCTTCCGTGTTTCTGTTCCCTCAAAGCC TAAGGACACCTGATGATCAGCAGAACCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCTCACGAGGACCCGGA AGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACA ACAGCACCTACAGAGTGGTGTCCGTGCTGACCGTGTGCACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGCA AGGTGTCCAACAAGGCCCTGCCTGCTCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAAACCCC AGGTTTACACACTGCCTCCAAGCAGGGACGAGCTGACCAAGAATCAGGTGTCCCTGACCTGCCTGGTCAAGGGCT TCTACCCTTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCTGT GCTGGACAGCGACGGCTCATTCTCTGTACAGCAAGCTGACAGTGGACAAGAGCAGATGGCAGCAGGGCAACG TGTTACAGCTGCAGCGTATGCACGAGGCCCTGCACAACCACTACACCAGAAGTCCCTGAGCCTGTCTCTGGCAA GTAA
C4G-Fc	ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGTGGAGCAGTCTTCGTTTCGGCTAGCCAAGT GCAGCTGCAAGAGTCCGGCGGCGGCTGGTCCAGGCGGCGACAGCCTGCGGCTGTCTTGCCTGCCAGCGGCC CAGCCGTGTCCAACGTGGCCCTGGCTGTTTATAGACAGACCCCTGGCAAAGAGAGAGATTCTGTGGCTGGCATCA CCTGGTCCGGCTGGACAAGCTACTACGCTGATTCTGTGAAGGGCCGGTTCACCATCAGCCGGGACATCACCAAGA ATACCGTGTACCTGCAGATGAACCTCCTGAAGCCTGAAGATACCGCCGTGTACTACTGCAACCTGATCGGCCTCAG AGTGGGACCTGAGAACAAGTACTGGGGACAGGGCACCAGGTGACAGTGTCTCCGGCGGCGGAGGCTCCGGC GGTGGAGGCTCTGGAGGCGGCGGCTCCGGCGGCGGAGGCAGCCAAGTGCAGCTGCAAGAGTCTGGCGGCGGCC TGGTGACGGCCGGAGGCGAGCTGAGACTGAGCTGCGCCGCTCTGGCAGAACCCGACAGCTTCTACGCCATGGGCT GGTTCCGGCAGGCTCCTGGAAGAAAGAGAATTTGTGTCTGCTATCACCTGGTCTGCTGGCAGCACCTACTACGC CGATTCTGTGAAGGGCAGATTCCGCATCTCCAGGACAACGCCAAGAACAAGTGTACCTGCAGATGAACAGCCT GAAGCCCGAGGACACAGCCGTTTATTACTGTGTGCTGTGACAGCCTGTCCGCGGCTACGAGTCTCTTGGCTGGAA GCCTTCGGCAGCTGGGGCCAGGGCACACAGGTGACCGTGTCCAGCGGATCCAAGACACACCTGTCTCCATGT CCTGTCTCAGAGCTGCTCGAGGCGCCTTCCGTGTTTCTGTTCCCTCAAAGCCTAAGGACACCTGATGATCAGCA GAACCCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCTCACGAGGACCCGAAGTGAAGTTCAATTGGTACGTGG ACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCC GTGCTGACCGTGTGCACCAAGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCT GCTCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACACTGCCTCCAAGC AGGGACGAGCTGACCAAGAATCAGGTGTCCCTGACCTGCCTGGTCAAGGGCTTCTACCTTCCGATATCGCCGTG GAATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCTGTGCTGGACAGCGACGGCTCATT TTCTGTACAGCAAGCTGACAGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTACAGCTGCAGCGTATGCA CGAGGCCCTGCACAACCACTACACCAGAAGTCCCTGAGCCTGTCTCTGGCAAGTAA

Figure 49 Continued

G4C-Fc	ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTCGGCTAGCCAAGT GCAGCTGCAAGAGTCCGGCGGCGGCCTGGTGCAGGCCGGCGGAAGCCTGAGACTGAGCTGCGCCGCCAGCGGC AGAACAGATAGCTTCTACGCCATGGGCTGTTTAGACAGGCCCCAGGCAAGGAAAGAGAGTTCTGTGTCTGCTATC ACATGGTCCGCGGGAAGCACCTACTACGCCGACTCCGTGAAGGGACGCTTCGCCATCTCTCGGGACAACGCCAAG AATACCGTCTACCTGCAGATGAACTCCCTGAAGCCTGAAGATACCGCGTGTACTACTGTGCCGTGATTCTGTCTGTC TGCTGGCTACGAGAGCAGCTGGCTGGAAGCCTTCGGCTCTTGGGGCCAGGGCACCCAGGTGACCGTGTCTCCGG TGGAGGCGGCTCTGGTGGCGGAGGCTCCGGCGGGGGCGGCTCTGGCGGCGGCGGCAGCCAAGTGCAGCTGCAA GAGTCTGGCGGCGGCTGGTCCAGGCTGGCGACTCTCTGCGGCTGTCTGCGTGGCTTCCGGCCCTGTGTGTCCA ACGTGGCCCTGGCTGGTTCGGGCAGACCCCTGGCAAAGAGCGGGAATTTGTGGCCGGCATCACCTGGAGCGGA TGGACCACTACTATGCCGACAGCTGAAGGGCAGATTACCATCTCCAGAGACATACCAAGAACACCGTGTAC CTGCAGATGAACAGCCTGAAACCCGAGGACACAGCCGTGTACTACTGCAACCTGATCGGCCCTCAGAGTGGGACCT GAGAACAGTACTGGGGCCAGGGCACACAGGTGACCGTGTCCAGCGGATCCAAGACACACACCTGTCTCCATGT CCTGTCCAGAGTGTCTCGGAGGCCCTCCGTGTTCTGTTCCCTCAAAGCCTAAGGACACCCCTGATGATCAGCA GAACCCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCTCAGGAGACCCCGAAGTGAAGTTCAATTGGTACGTGG ACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCC GTGCTGACCGTGTGCACCAAGGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCT GCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACACTGCCTCCAAGC AGGGACGAGTGACCAAGAATCAGGTGTCCCTGACCTGCCTGGTCAAGGGCTTCTACCTTCCGATATCGCCGTG GAATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCTGTGCTGGACAGCGACGGCTCATT TTCTGTACAGCAAGCTGACAGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTAGCTGCAGCGTGATGCA CGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGTCTCTGGCAAGTAA
Fc region	GGATCCAAGACACACACCTGTCTCCATGTCTGCTCCAGAGCTGCTCGGAGGCCCTTCCGTGTTTCTGTTCCCTCC AAAGCCTAAGGACACCCCTGATGATCAGCAGAACCCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCTCAGAGGA CCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGAAGTGCAACGCCAAGACCAAGCCTAGAGAGGAAC AGTACAACAGCACCTACAGAGTGGTGTCCGTGCTGACCGTGTGCAACAGGATTGGCTGAACGGCAAAGAGTACA AGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGG AACCCAGGTTTACACACTGCCTCCAAGCAGGGACGAGCTGACCAAGAATCAGGTGTCCCTGACCTGCCTGGTCAA GGGCTTCTACCTTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCC TCCTGTGCTGGACAGCGACGGCTATTCTTCTGTACAGCAAGCTGACAGTGGACAAGAGCAGATGGCAGCAGGG CAACGTGTTAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGTCTCCT GGCAAGTAA

Figure 49 Continued

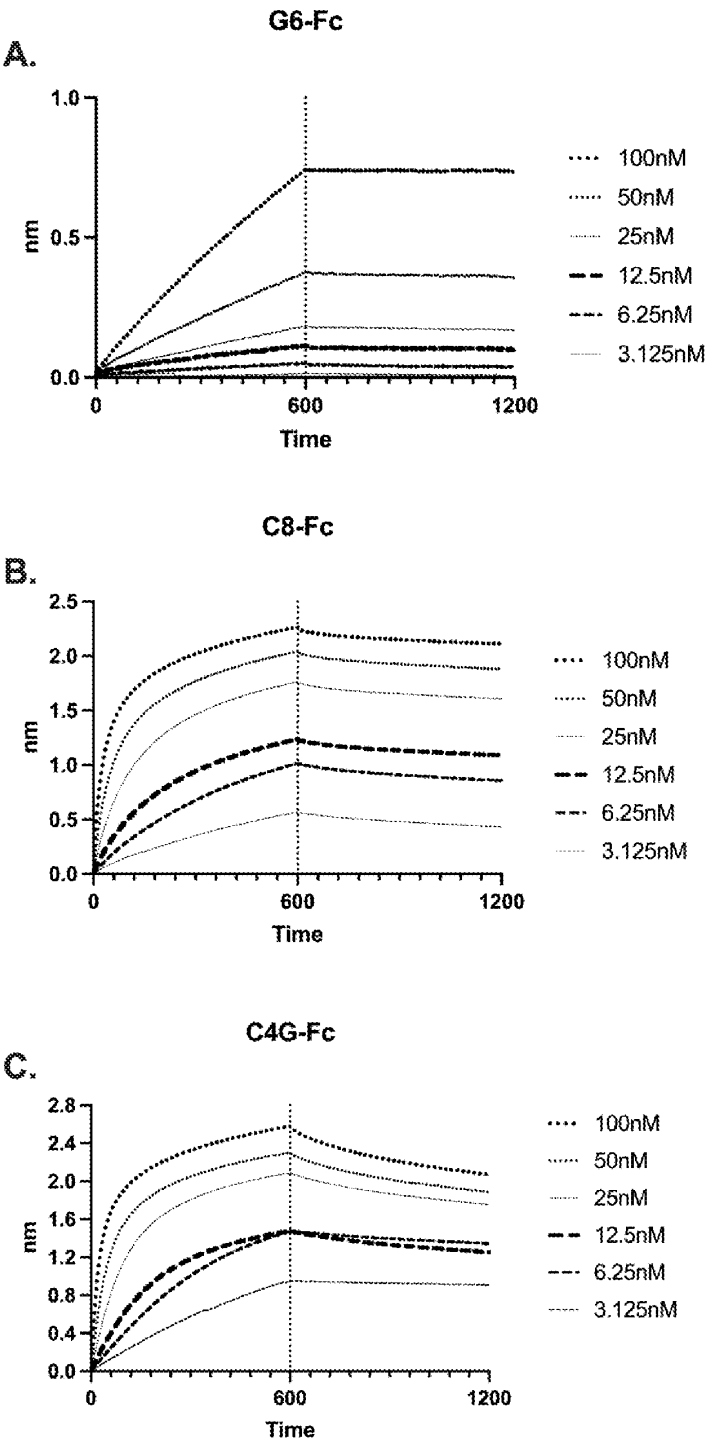


Figure 50

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>RmAb1_15B5_Heavy Chain

QSVEESGGRLVTPGTPLTLTCTVSGFSLNNYNMGWVRQAPGKGLEWIGYITAGGNIYYATWARGRF
TISKTSTTVDLKITSPTTEDTATYFCARDLAGNVYYDFDLWGQGTLTVSS

>rMab1_15B5_Light Chain

LVMTQTPASVSAAVGGTVTINCQASENIYSGLAWYQQKPGQRPKLLIYKASTLASGVPSRFKSGSGT
EFTLTISDLECADAAATYYCQGGTYSSGADISFGGGTKVVVE**Figure 51**

>RmAb2_20C12_Heavy chain

EQVEESGGGLVQPGGSLTLTKASGFDLSSYYMTWIRQAPGKGLEWIGVIWLGSGNIDYASWVNGR
FTISSDNAQNTVDLKMSTLTVSDTATYFCARGWLDDSFDPWGPGLTVTVSS

>RmAb2_20C12_Light chain

AVLTQTPSPVSAAVGGTVSINCQSSSVHYNKWLWSWFQQKPGQPPKLLIYGASTLASGVPSRFKSGSGS
GTQFTLTISDLQCDDAATYYCAGGYSSGSDKFAFGGGTEVVVK**Figure 52**

>RmAb3_22G10_Heavy chain

QSVEESGGRLVTPGTPLTLTCTVSGFSLITYSMGWVRQAPGKGLEWIGAIASGTAFYATWAEGRFT
ISKSTTVDLRITGPTTEDTATYFCARGSGPSGIESYKLWGQGTLTVTVSS

>RmAb3_22G10_Light chain

FELTQTPSSVEAAVGGTVTIKCQASQSIGNYLAWYQQKPGQPPKLLISRSTLESVPSRFKSGSGT
QFTLTISDLECADAAATYYCQGYGIHITFGGGTEVVVK**Figure 53**

>RmAb4_36D4_Heavy Chain

QSLEESGGRLVTPGTPLTLTCTVSGIDLSVNAVAWVRQAPGKGLEWIGIHTYDVTIDYASWATGRFTIS
KSSTTVDLKITSPTTEDTATYFCARKDWTSGDSFNPWGPGLTVTVSS

>RmAb4_36D4_Light Chain

FELTQTPSPVSGAVGGTVTIKCQASQSISTALAWYQKRPQPPKLLIYSASTLASGVSSRFKGSASGTEF
TLTISDLECADAAATYYCQCTYHSSSTGYAFGGGTEVVVK**Figure 54**

>RmAb5_42F12_Heavy chain

QSVKESEGGLFKPTDTLTLTCTVSGFSLNDAISWVRQAPGNGLWIGAISSAGRPHYASWARSRS
TITRNTNENTVTLKMTSLTAADTATYFCARDKGYYSYHYAYDTRLDLWGQGTLTVTVSS

>RmAb5_42F12_Light chain

DPVLTQTPSPVTAAGGGTVTISCQSSQSISSYLSWYQQKPGQPPKLLIYRVSTLASGVPSRFKSGSGS
GAEFTLTISDLECADAAIYYCQGTYGSGSSSYGNAFGGGTEVVVK**Figure 55**

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	CDR1	CDR2
15B5_HC	QSVEESGGRLVTPGTPLTLTCTVSGFSLNNYMGWVRQAPGKGLEWIGYITAG-GNIYYA	
22G10_HC	QSVEESGGRLVTPGTPLTLTCTVSGFSLITYSMGWVRQAPGKGLEWIGAI SAS-GTAFYA	
36D4_HC	QSLEESGGRLVTPGTPLTLTCTVSGIDLSVNAVAVVRQAPGKGLEWIGIHTY-DVTIDYA	
20C12_HC	EQVEESGGGLVQPGGSLTLTCKASGFDLSSYYMTWIRQAPGKGLEWIGIWLGSGNIDYA	
42F12_HC	QSVKESEGGFLFKPTDTLTCTVSGFSLSDNAISWVRQAPGNLEWIGAISSA-GRPHYA	
	: : : * * * . * . * * * * . * * : : * * * * : * * * * * * * . * * *	
		CDR3
15B5_HC	TWARGRFTIS--KTSTTVDLKITSPTTEDTATYFCARDL-----AGNVYYDFDLNGQGTL	
22G10_HC	TWAEGRFTIS--KTSTTVDLRITGPTTEDTATYFCARGS-----GFGSIESYKLNQGTL	
36D4_HC	SWATGRFTIS--KSSTTVDLKITSPTTEDTATYFCARKD-----WTS-GDSFNPWPGTL	
20C12_HC	SWVNGRFTISSDNAQNTVDLKMTSLTVSDTATYFCARG-----WLDSDFDNPWPGTL	
42F12_HC	SWARSRSTITRNTNENTVTLKMTSLTAADTATYFCARDKGYYSYHYAYDTRLDLNGQGTL	
	: * . * * * : . . . * * * : * . * . * * * * * * * * * * * * * * *	
15B5_HC	VTVSS	
22G10_HC	VTVSS	
36D4_HC	VTVSS	
20C12_HC	VTVSS	
42F12_HC	VTVSS	

Figure 56

	CDR1	CDR2
22G10_LC	-FELTQTPSSVEAAVGGTVTIKCQASQSIGN--YLAWYQQKPGQPPKLLISPASTLESQV	
36D4_LC	-FELTQTPSPVSGAVGGTVTIKCQASQSIST--ALAWYQKRPQPPKLLIYSASTLASQV	
15B5_LC	-LVMTQTPASVSAAVGGTVTINCQASENIYS--GLAWYQQKPGQPPKLLIYKASTLASQV	
42F12_LC	DPVLTQTPSPVTAAVGGTVTISCQSSQSISSS-YLSWYQQKPGQPPKLLIYRVSTLASQV	
20C12_LC	-AVLTQTPSPVSAAVGGTVSINCQSSVSVHYNKWLSWFQQKPGQPPKLLIYGASTLASQV	
	: * * * * : * . * * * * : * * * * : : : * * * * : * * * * * * * . * * * *	
		CDR3
22G10_LC	PSRFKSGSGTQFTLTISDLECAAAATYYCGGYGIHIT-----FGGGTEVVVK	
36D4_LC	SSRFKGSASGTEFTLTISDLECAAAATYYCCTYHSSSTGY--AFGGGTEVVVK	
15B5_LC	PSRFKSGSGTEFTLTISDLECAAAATYYCGGTYSSGADI--SFGGGTEVVVK	
42F12_LC	PSRFKSGSGAEFTLTISDLECAAAIYYCGGTYGSGSSSYGNAFGGGTEVVVK	
20C12_LC	PSRFKSGSGTQFTLTISDLQCDAAATYYCAGGYSSGSDKF--AFGGGTEVVVK	
	. * * * * . * * : : * * * * * : *	

Figure 57

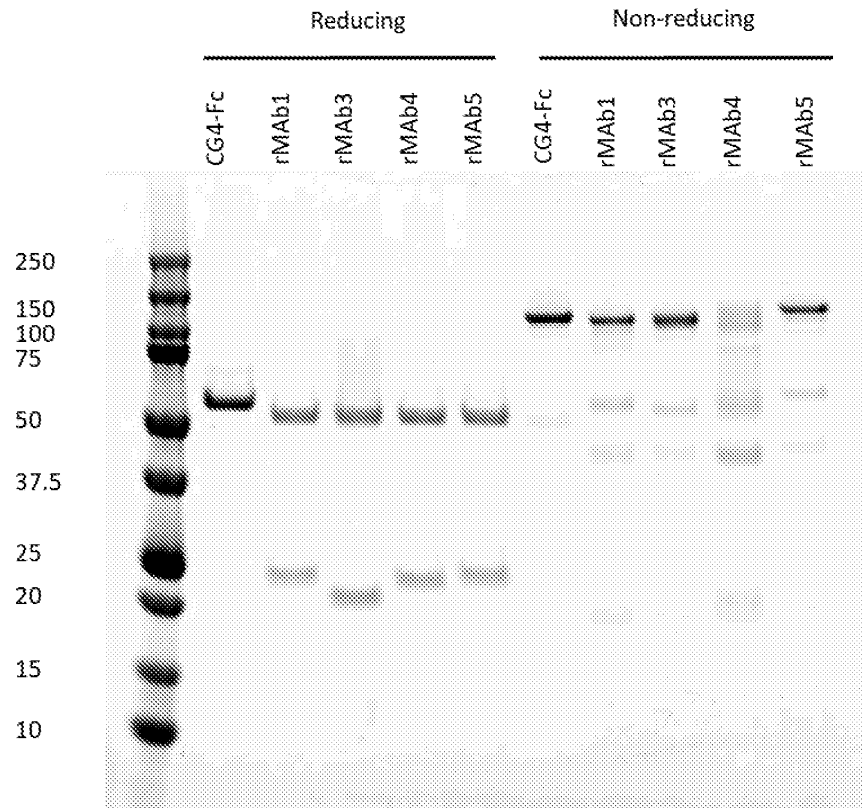


Figure 58

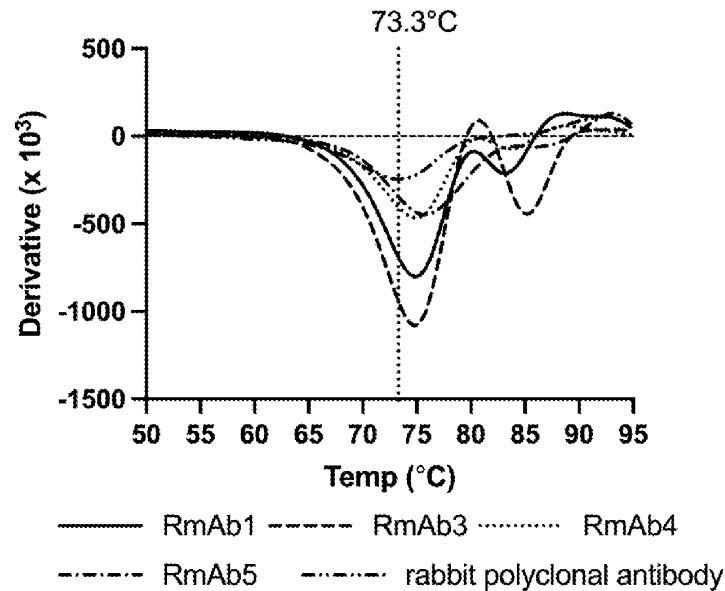
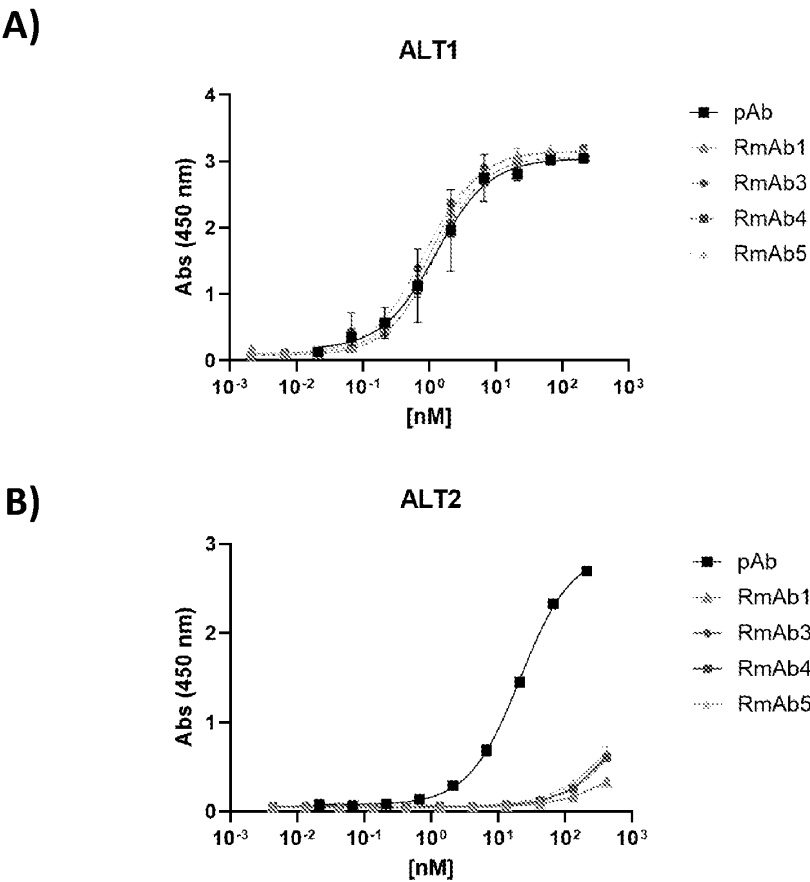


Figure 59



C)	nM Ab for 10x background	
	ALT1 (nM)	ALT2 (nM)
pAb	0.30	7.2
Rmab1	0.30	>420
RmAb3	0.23	>420
RmAb4	0.38	>420
RmAb5	0.38	>420

Figure 60

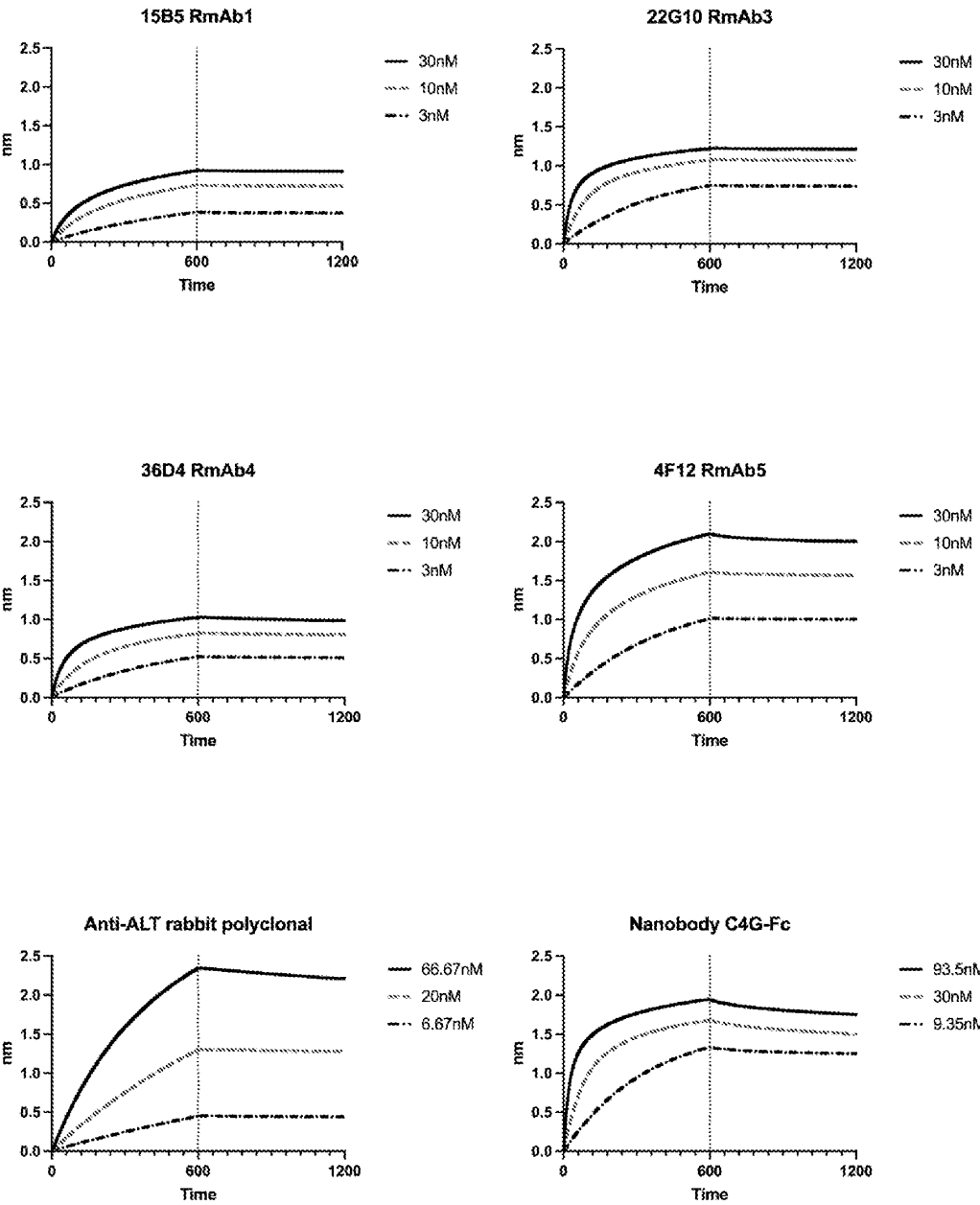


Figure 61

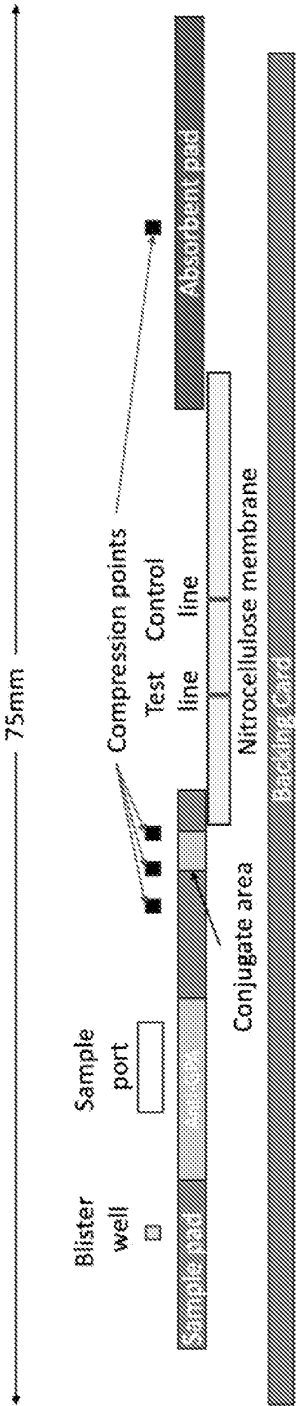


Figure 62

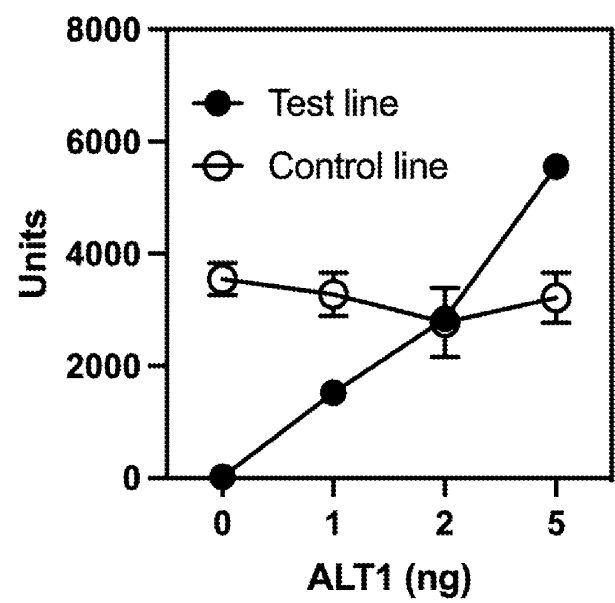


Figure 63

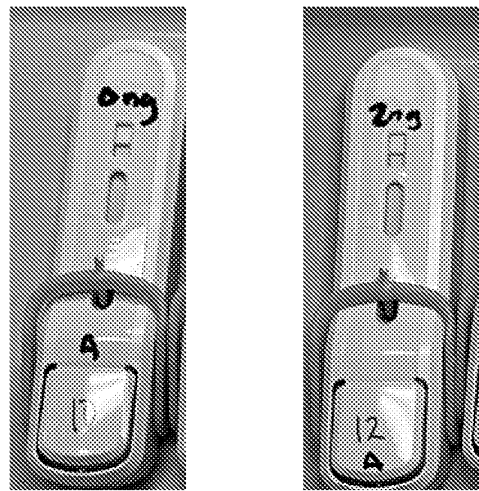


Figure 64

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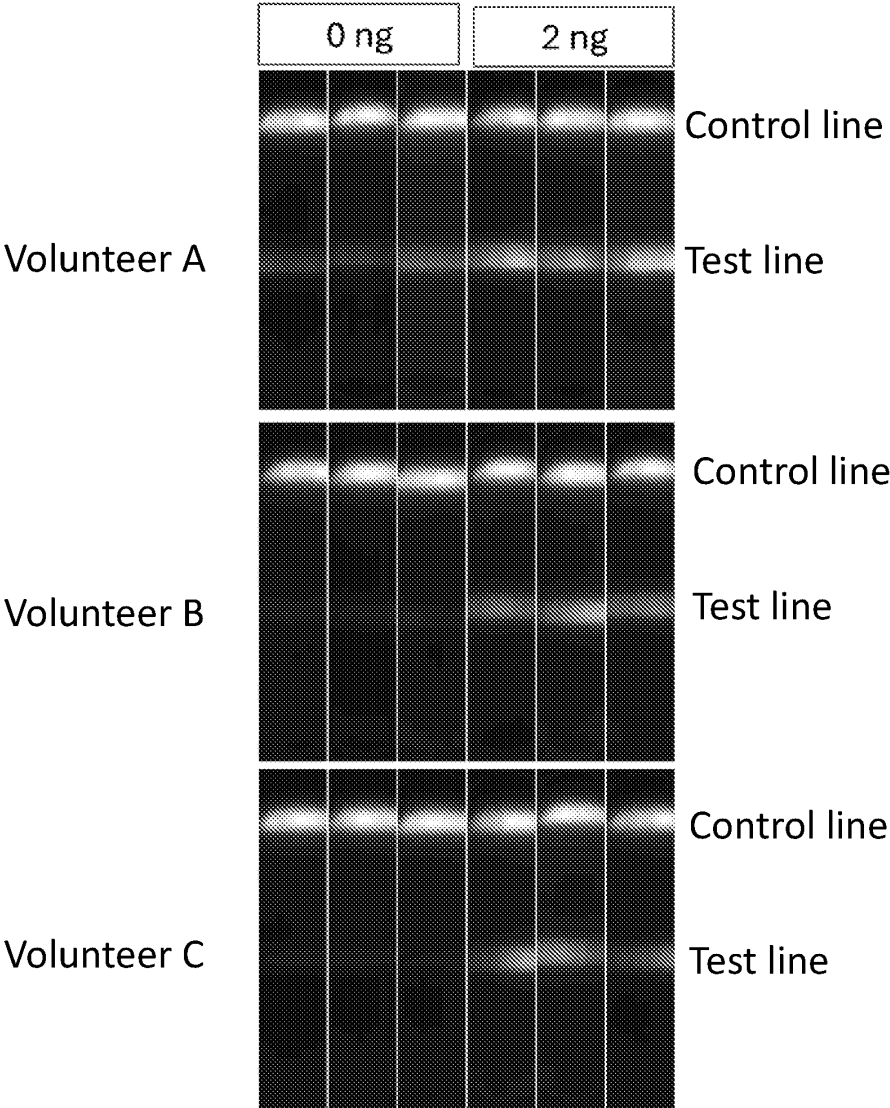


Figure 65

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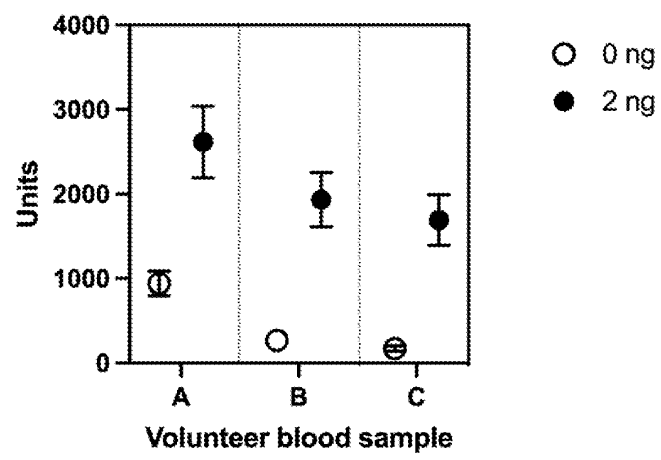


Figure 66

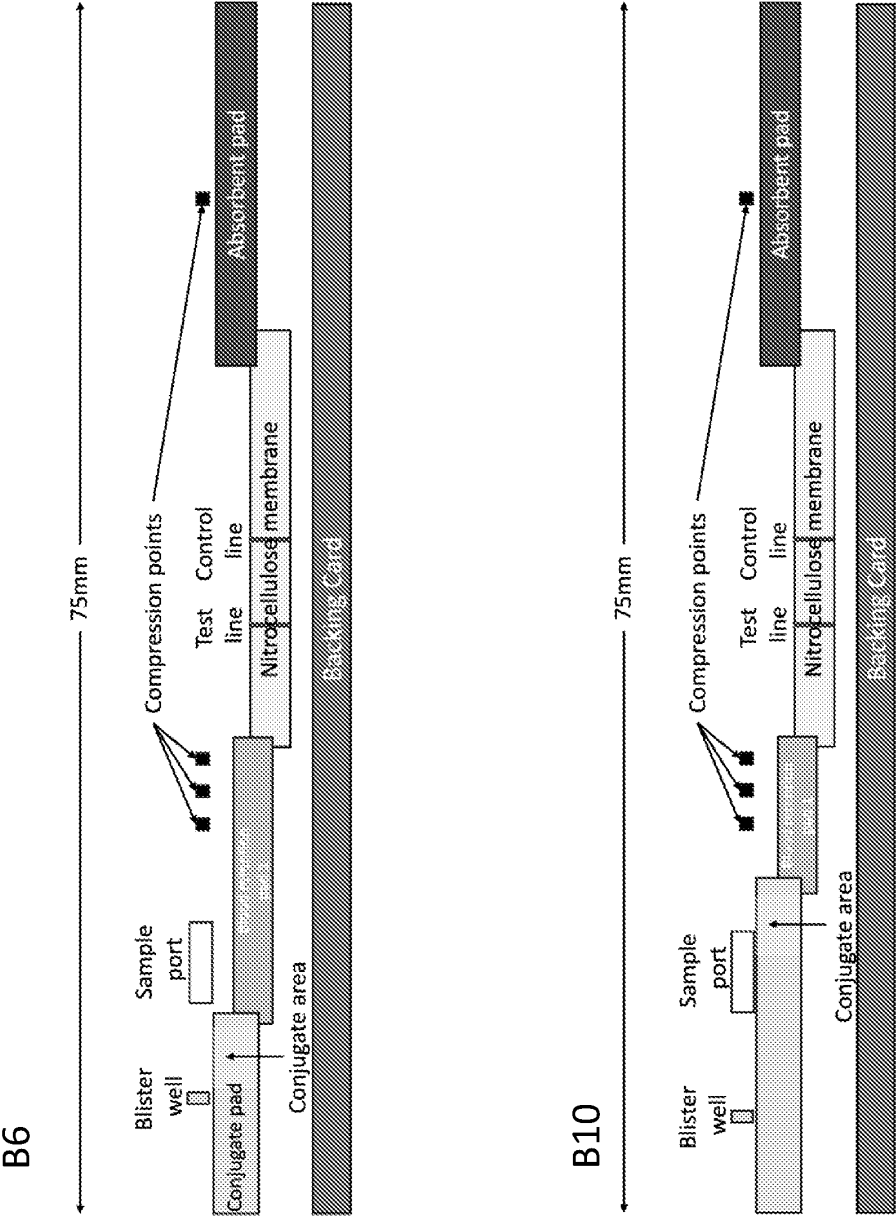


Figure 67

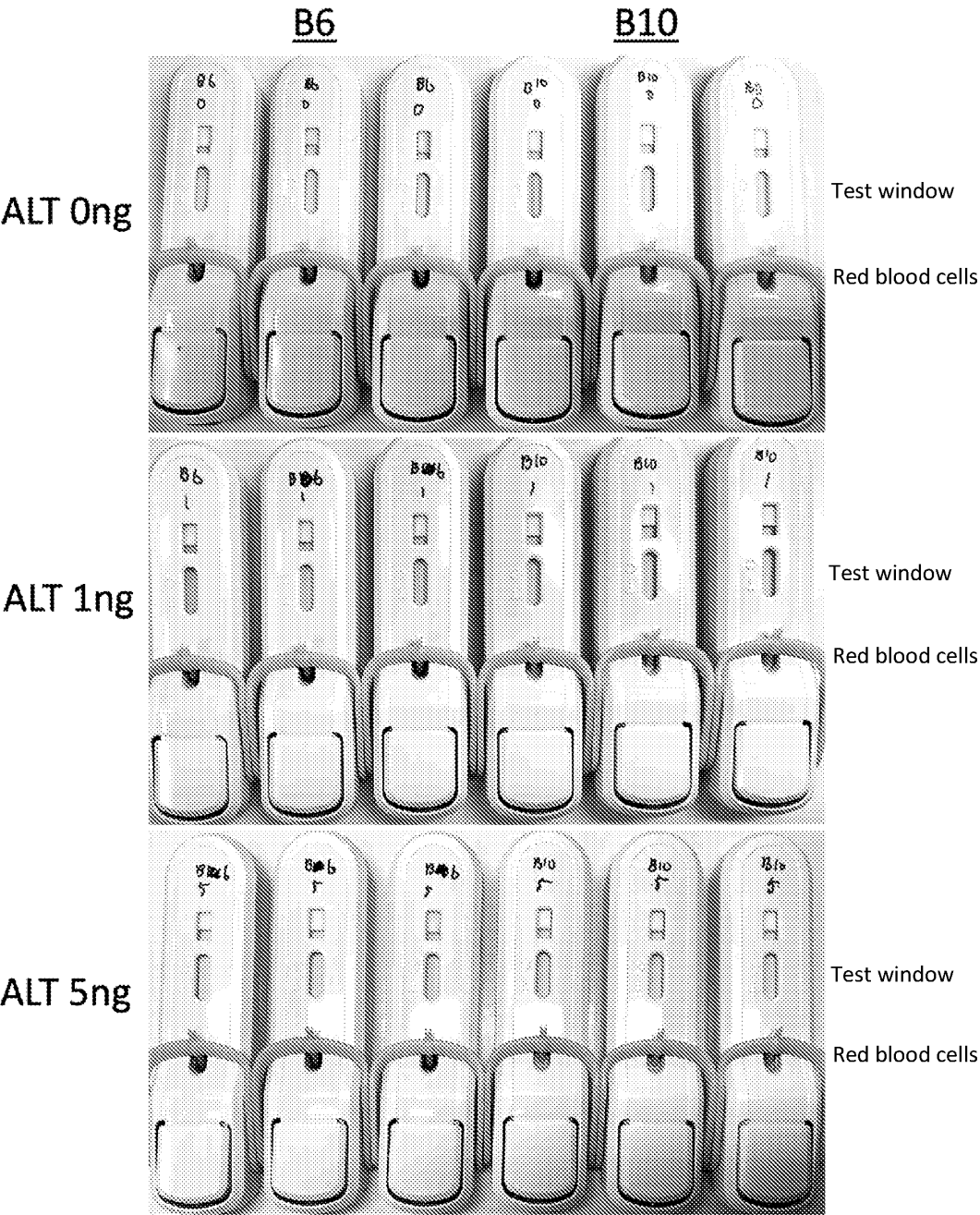


Figure 68

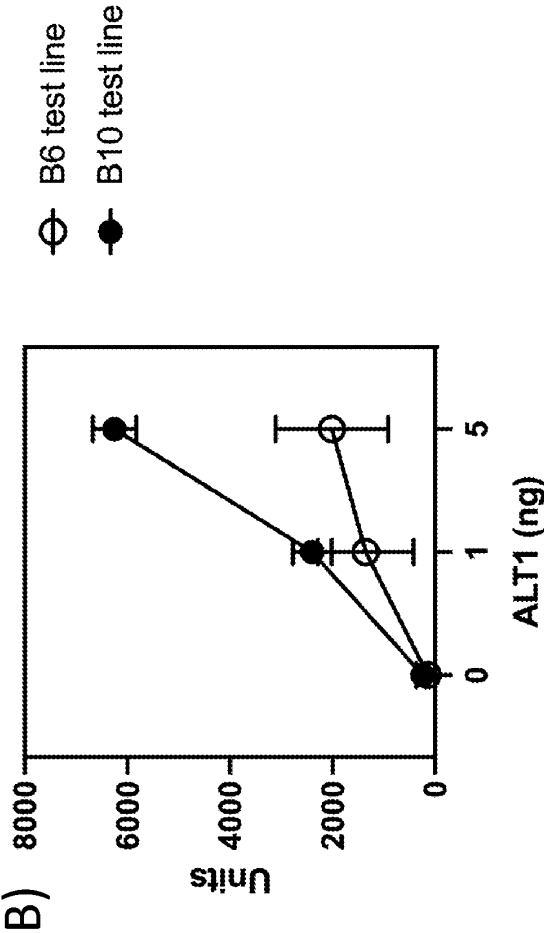
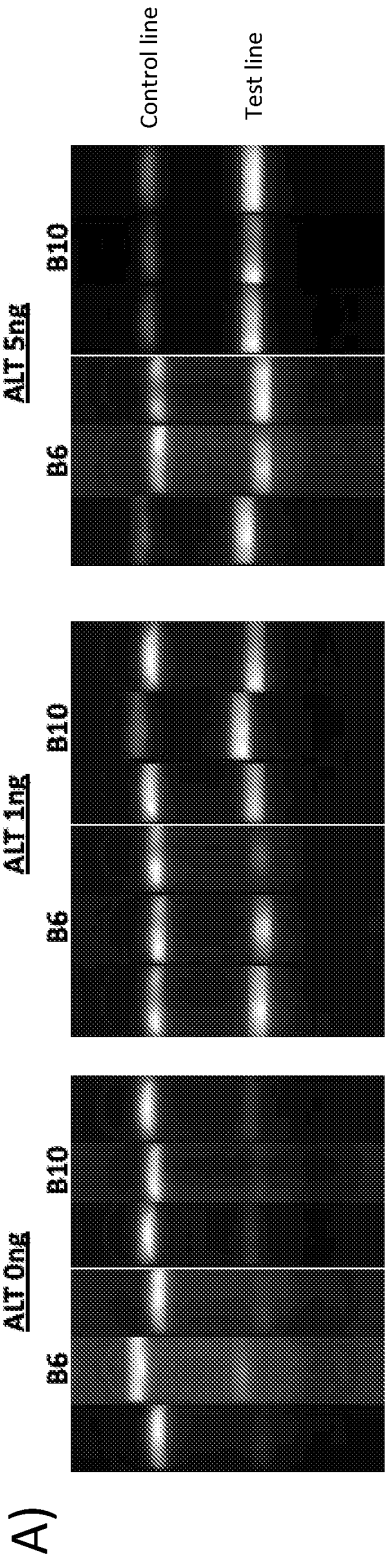


Figure 69

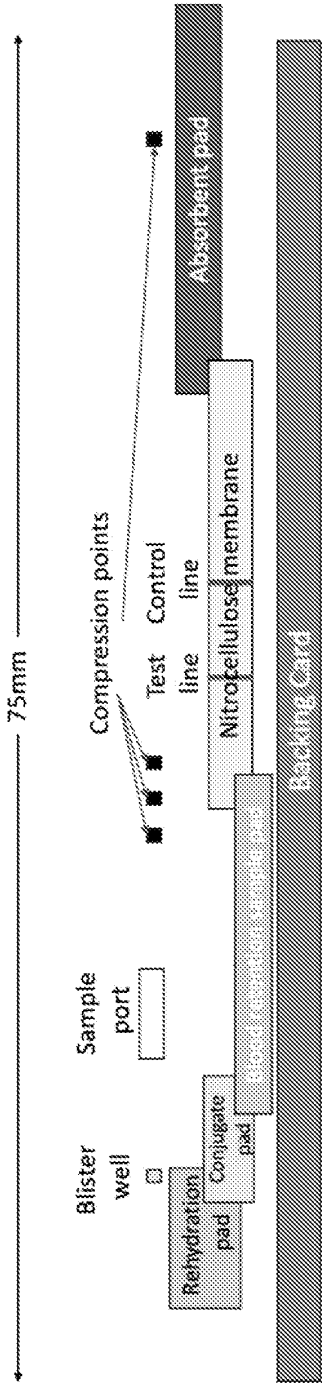


Figure 70

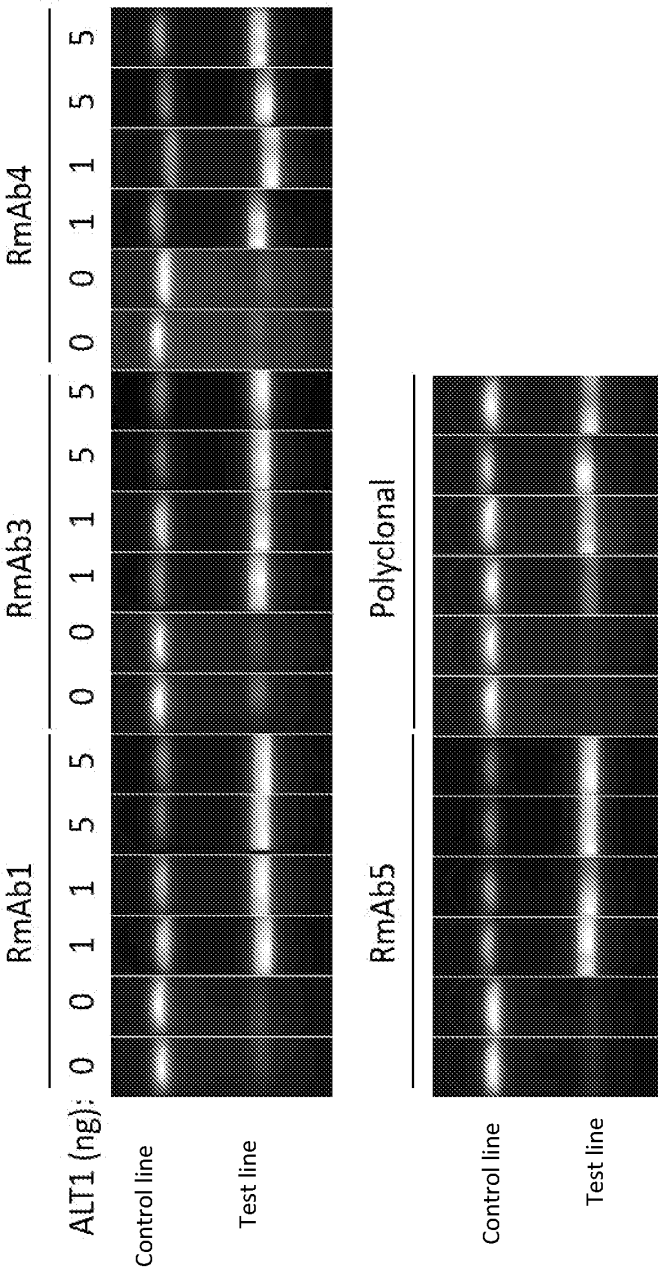


Figure 71

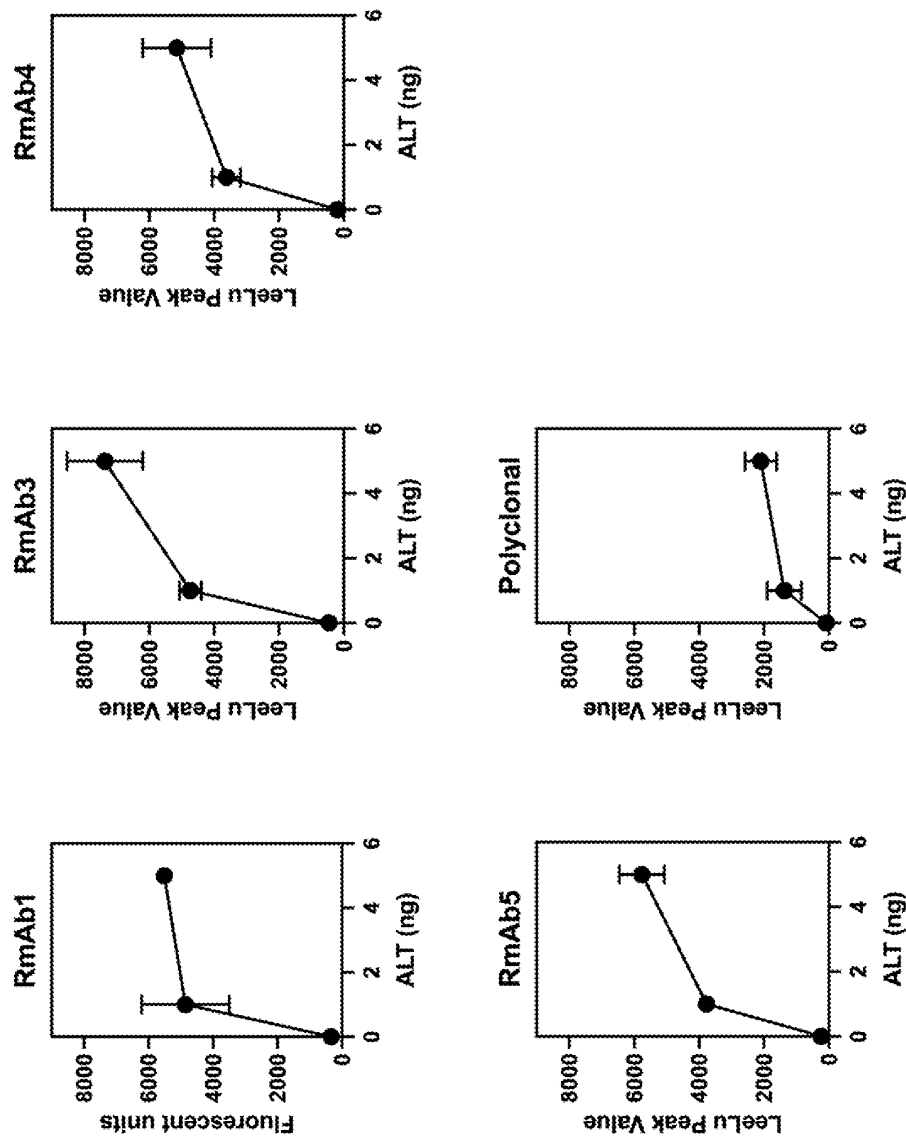


Figure 72

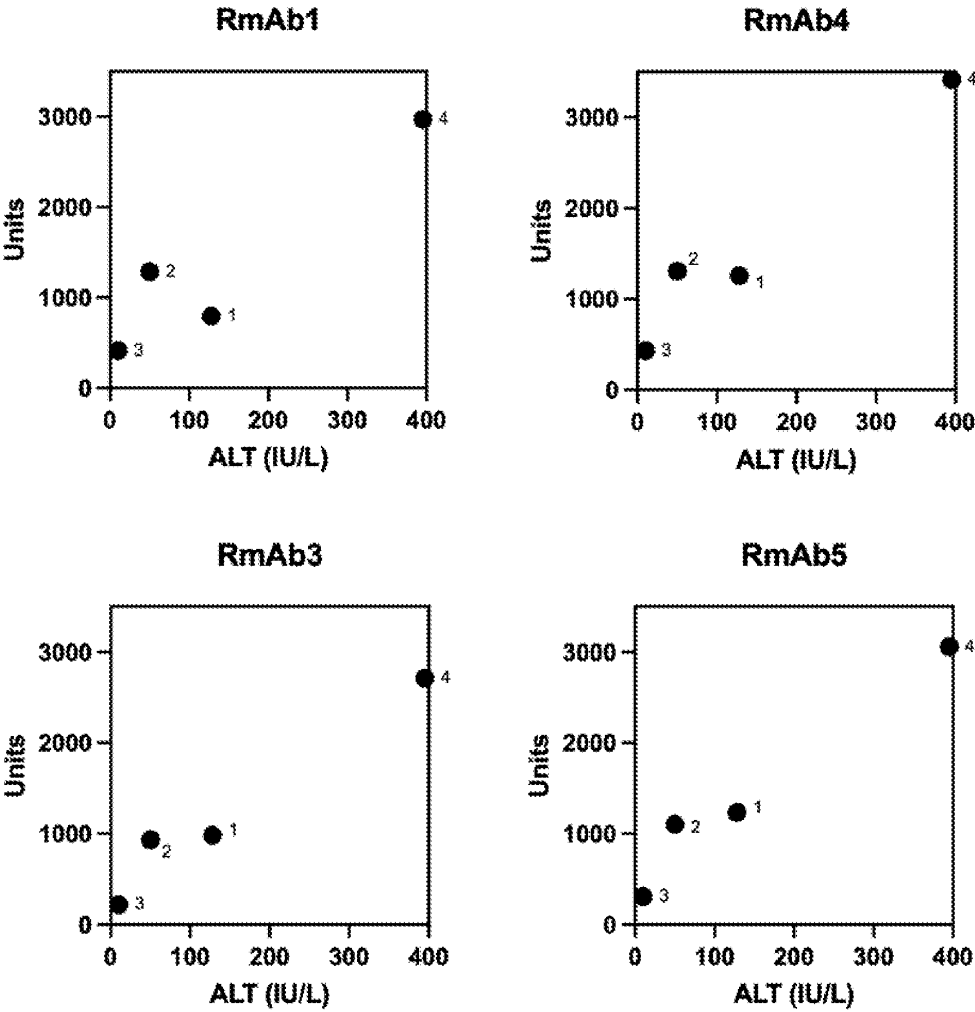


Figure 73

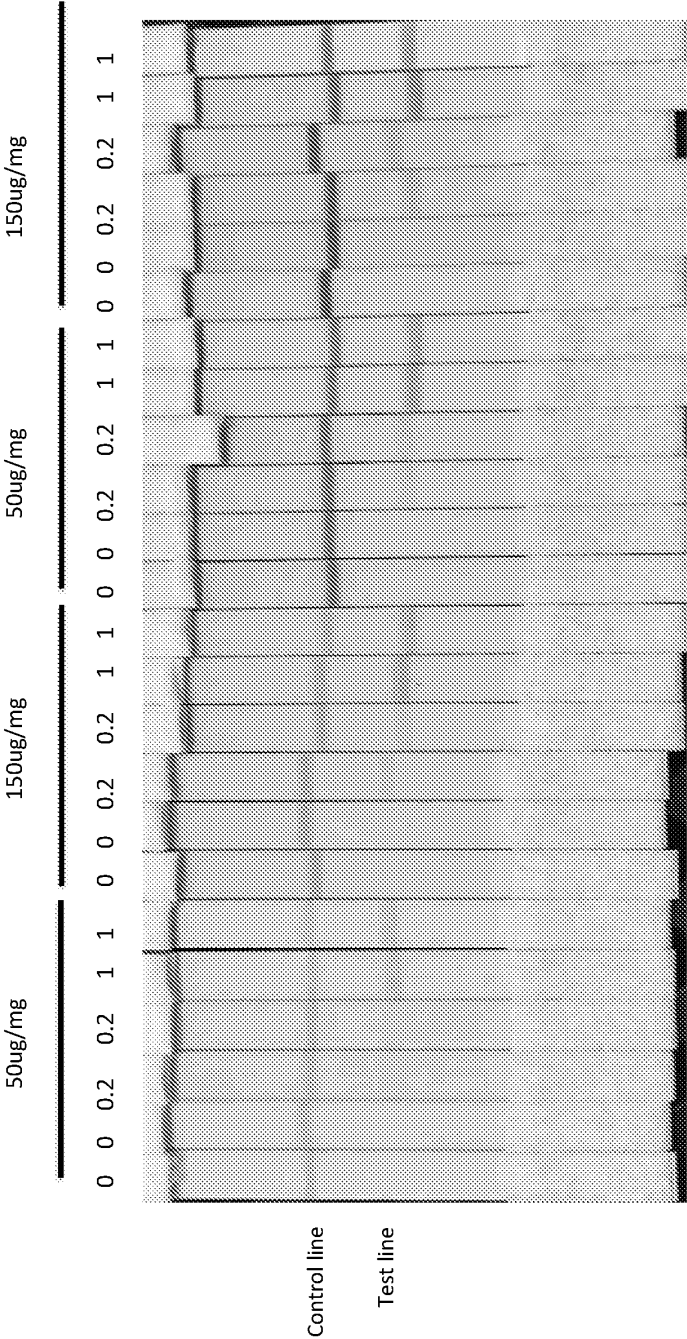


Figure 74

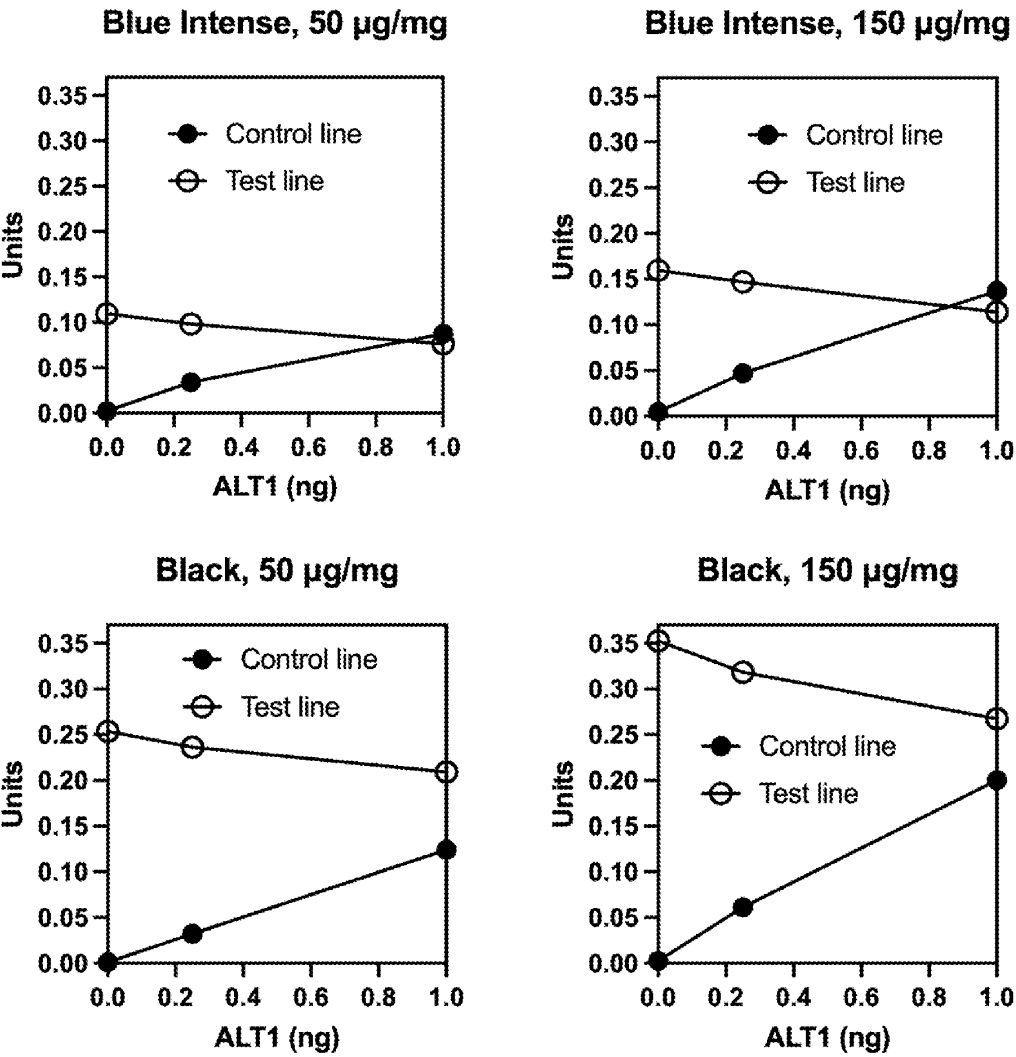


Figure 75

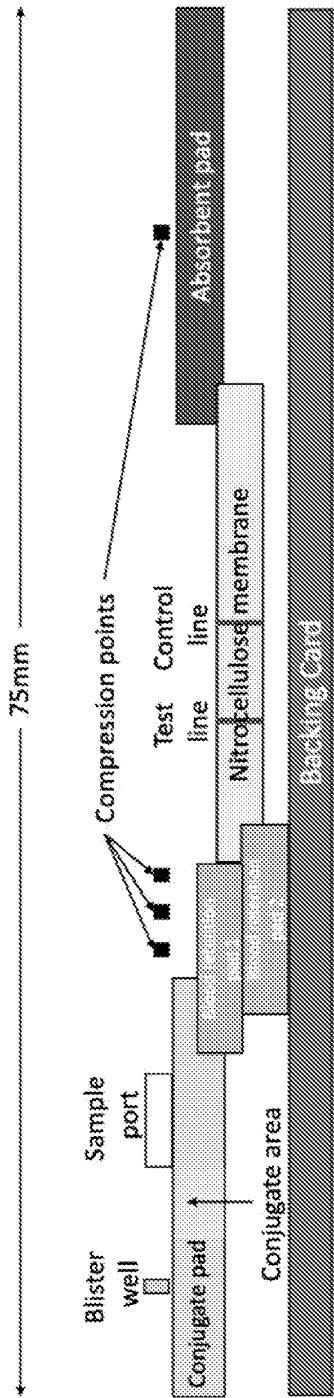


Figure 76

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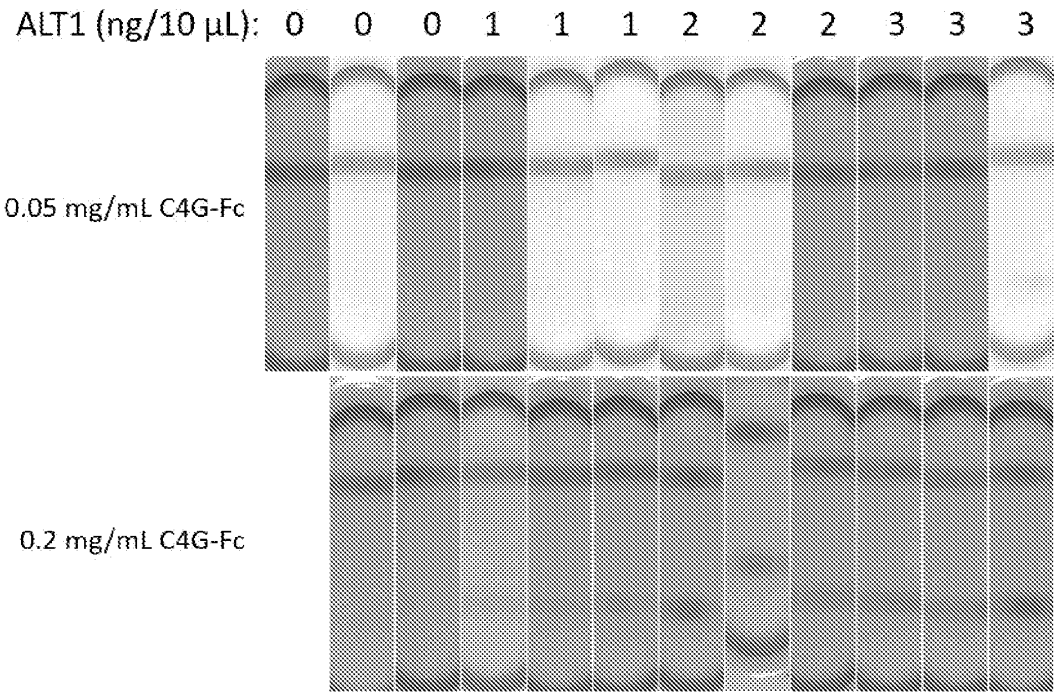


Figure 77

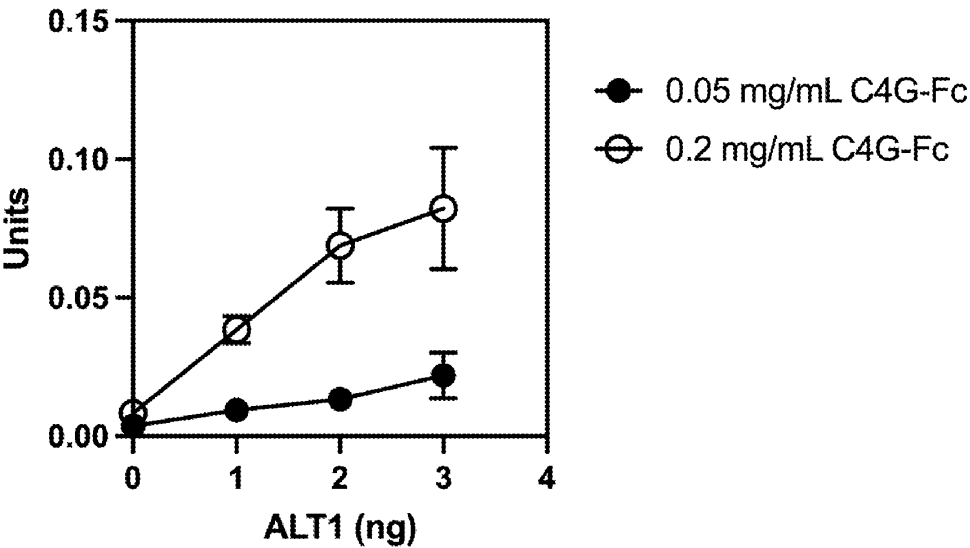


Figure 78

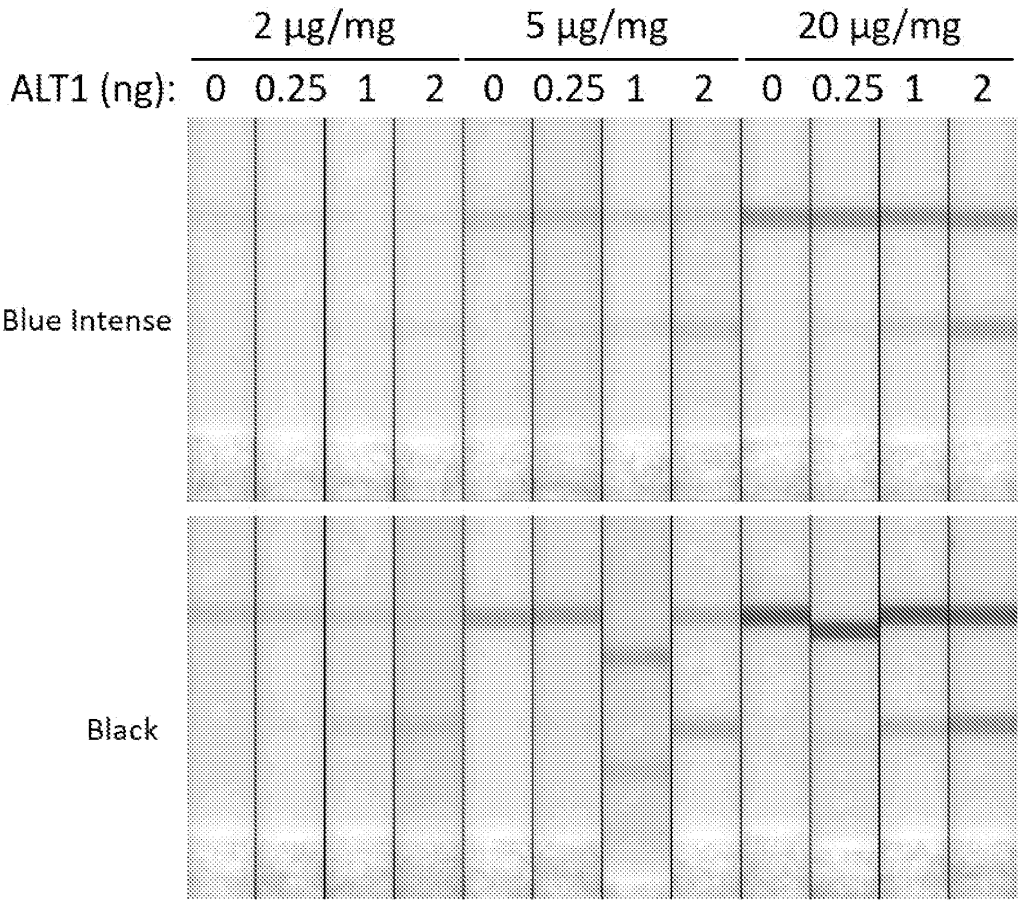


Figure 79

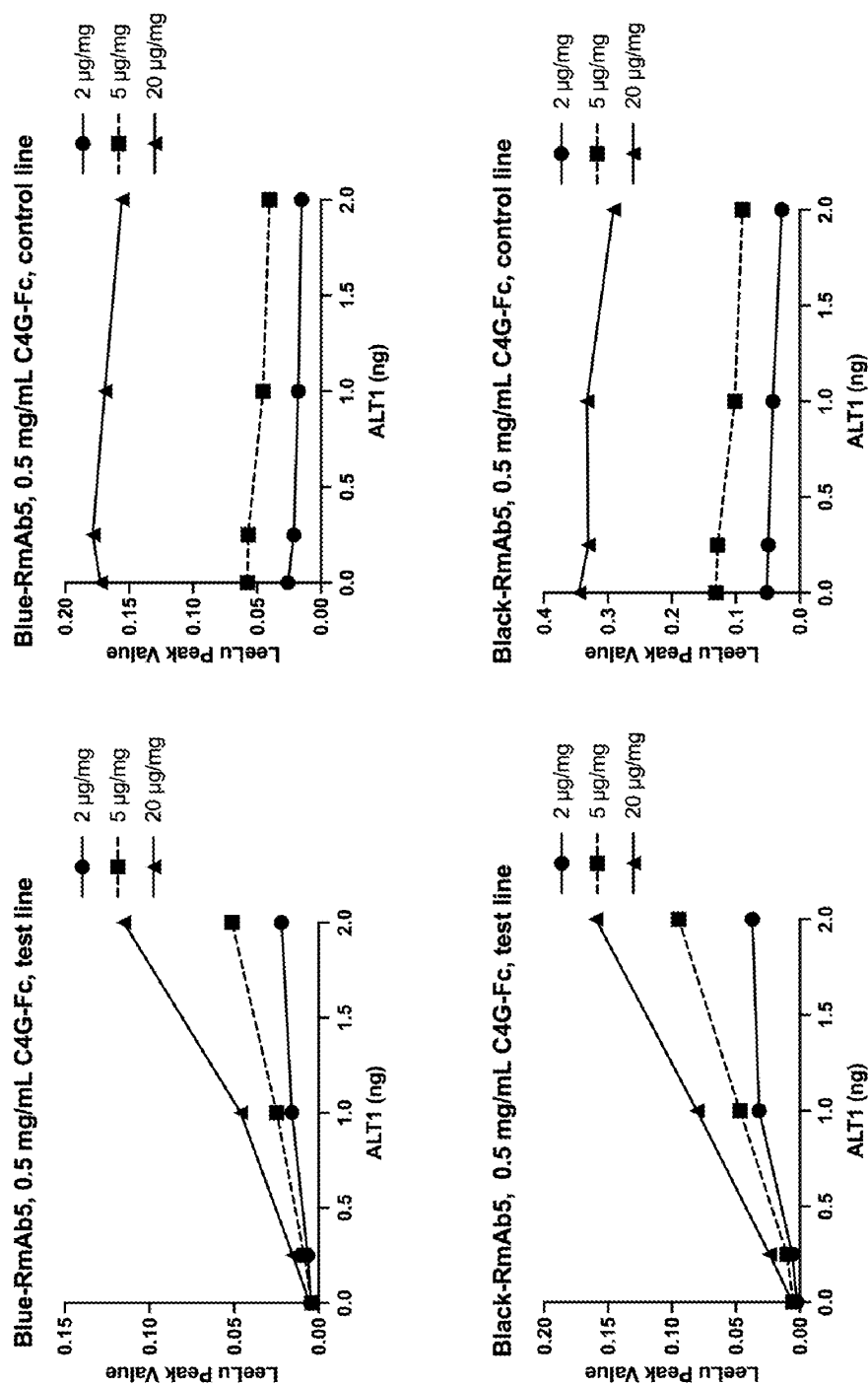


Figure 80

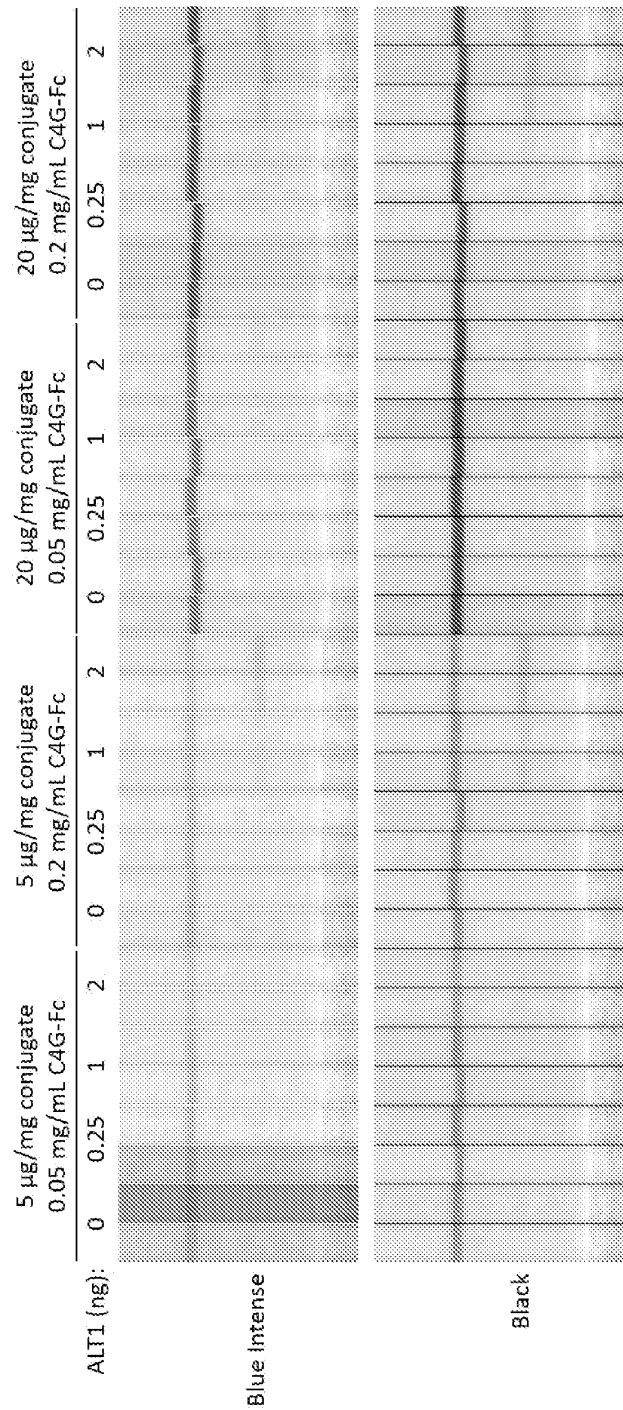


Figure 81

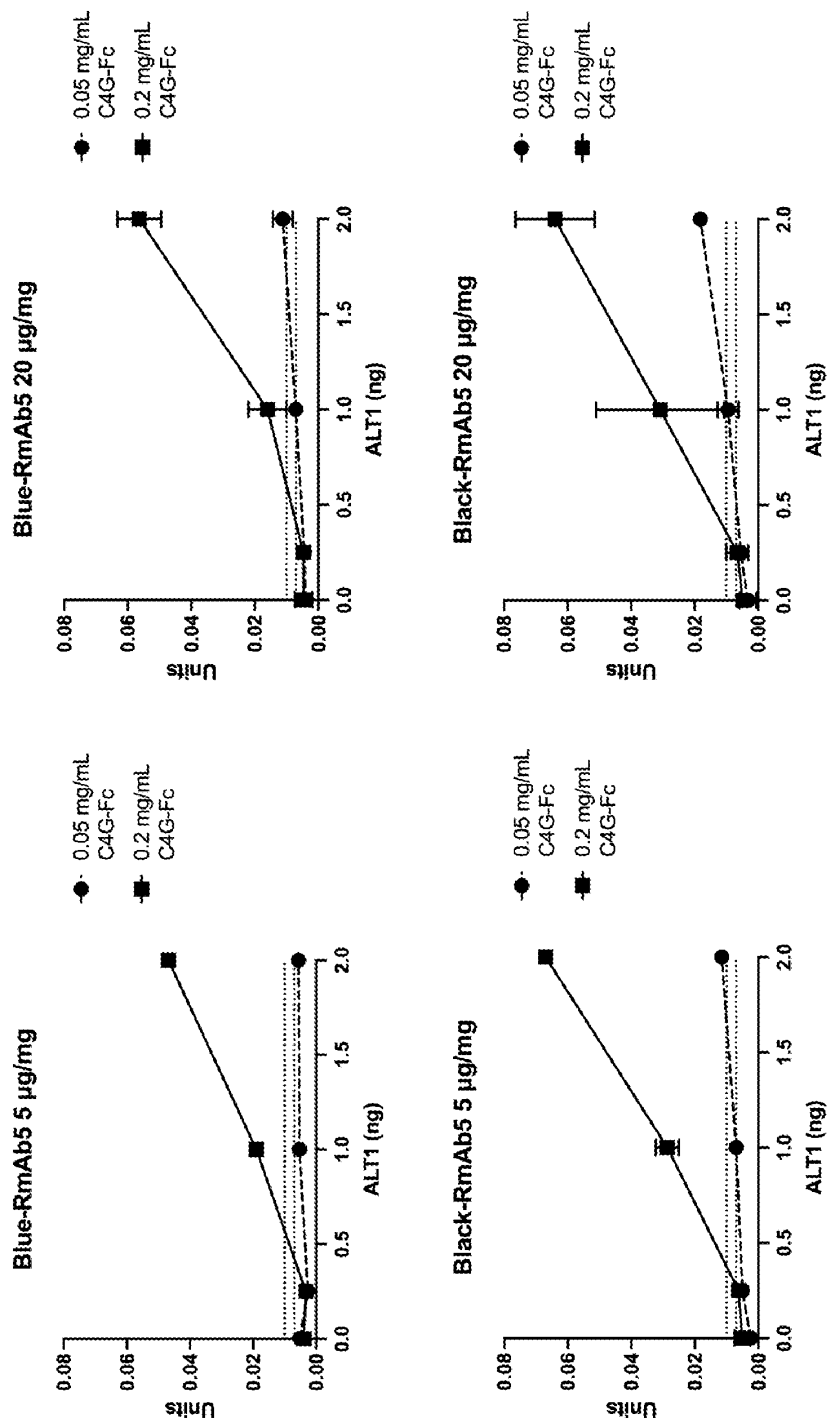


Figure 82

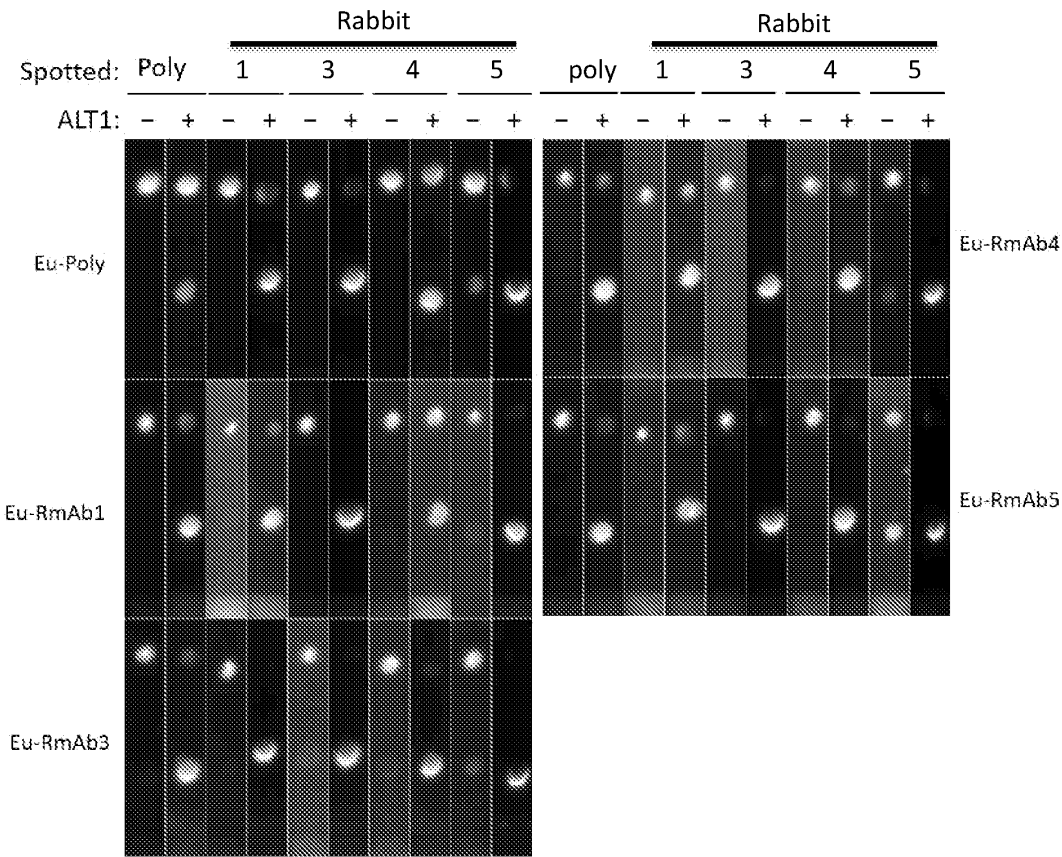


Figure 83

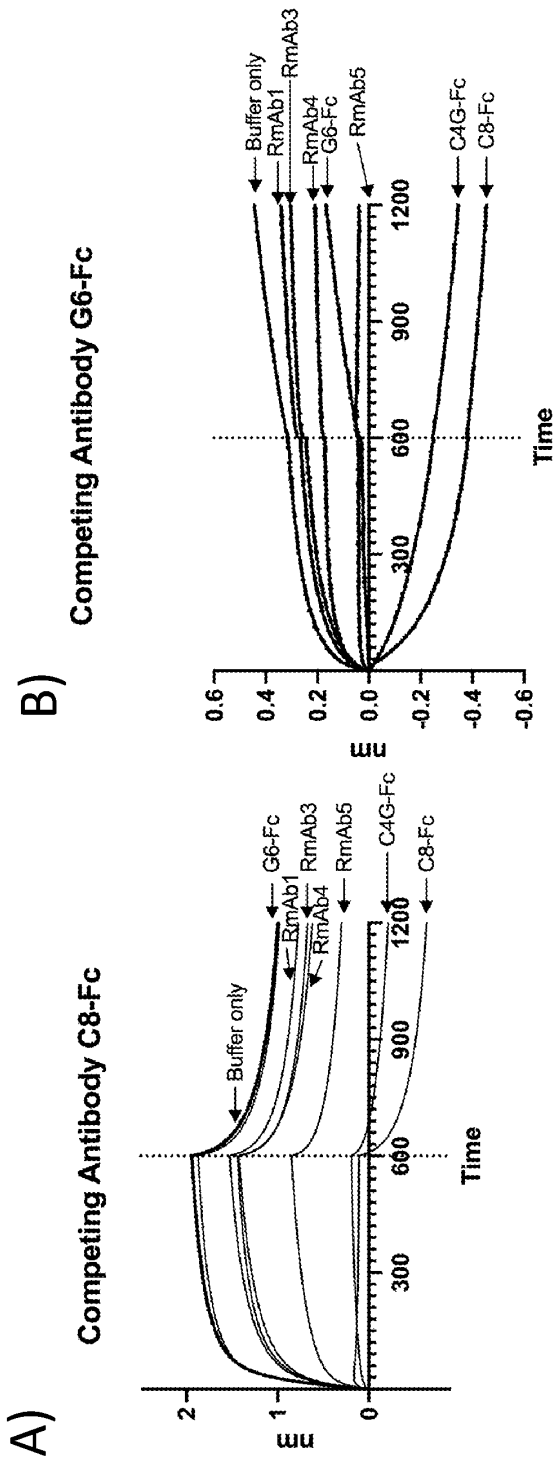


Figure 84

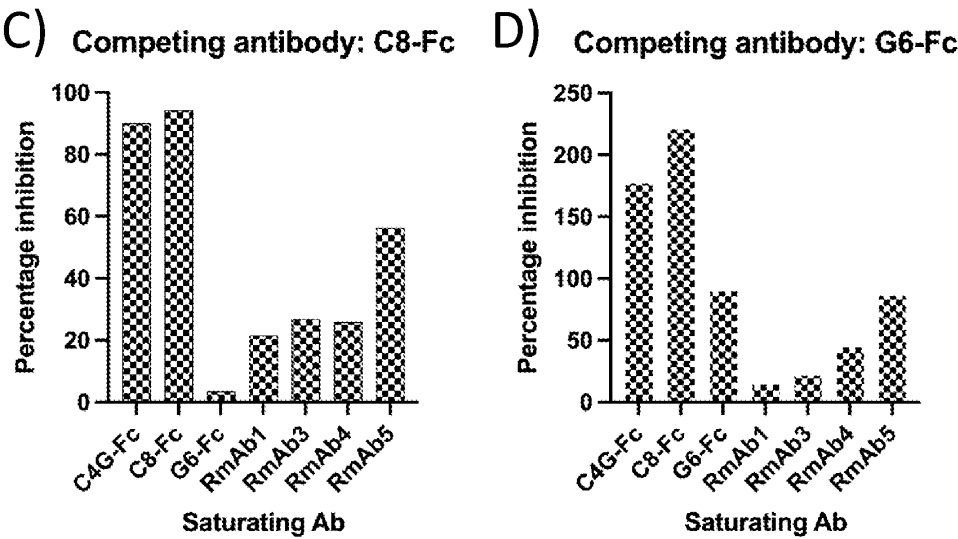
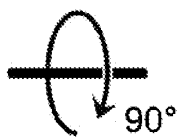
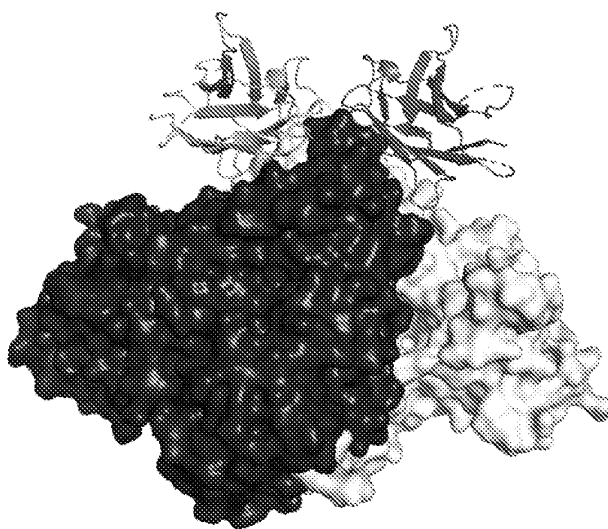


Figure 84 Continued

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A)



B)

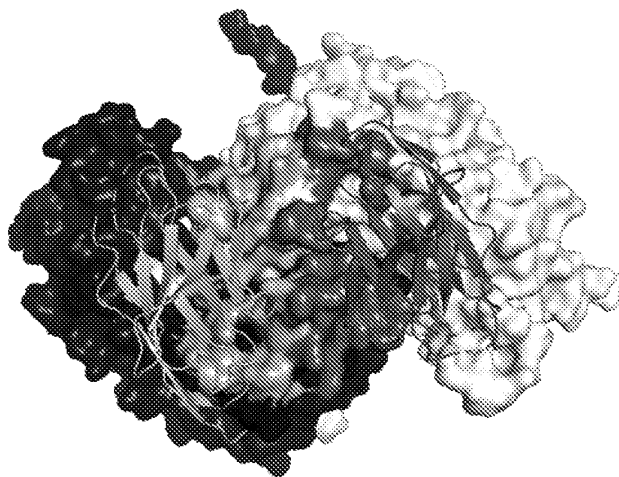


Figure 85

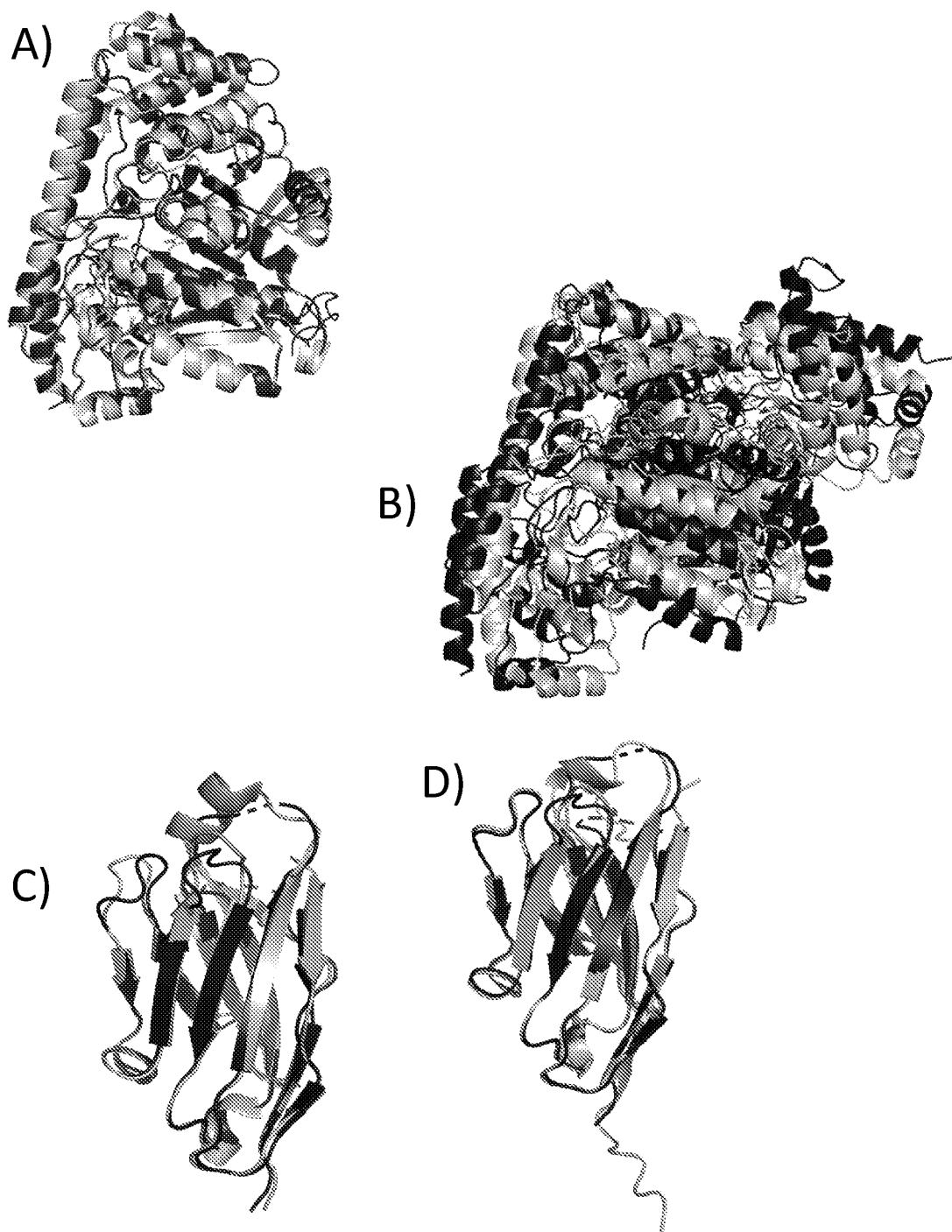


Figure 86

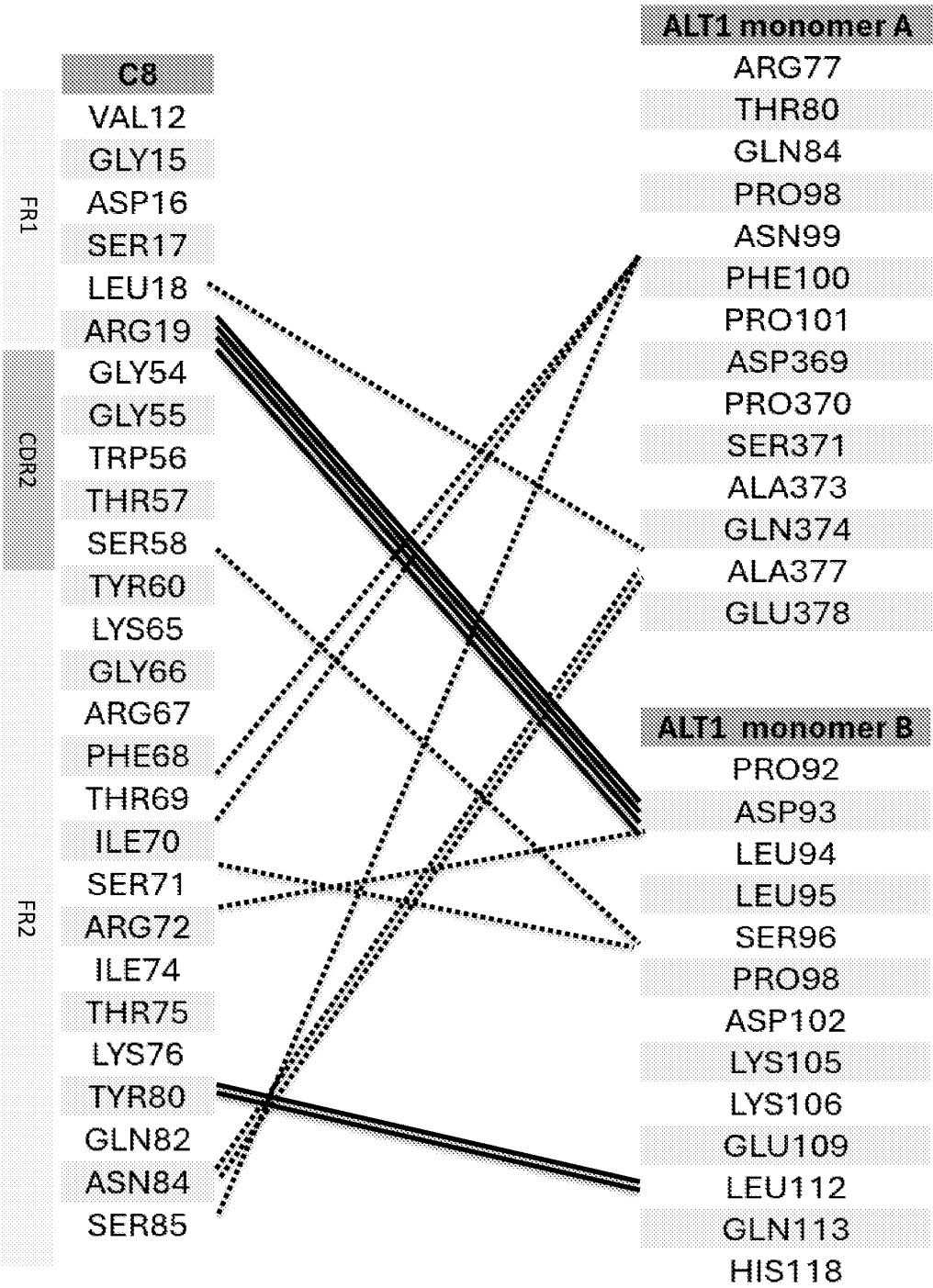


Figure 87

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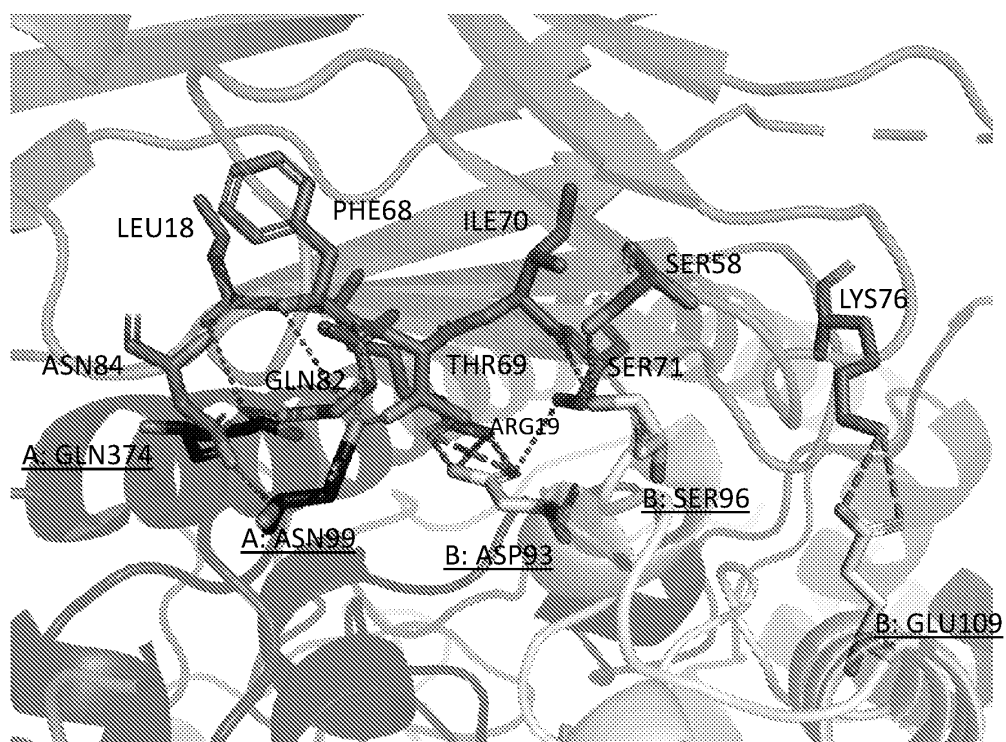


Figure 88

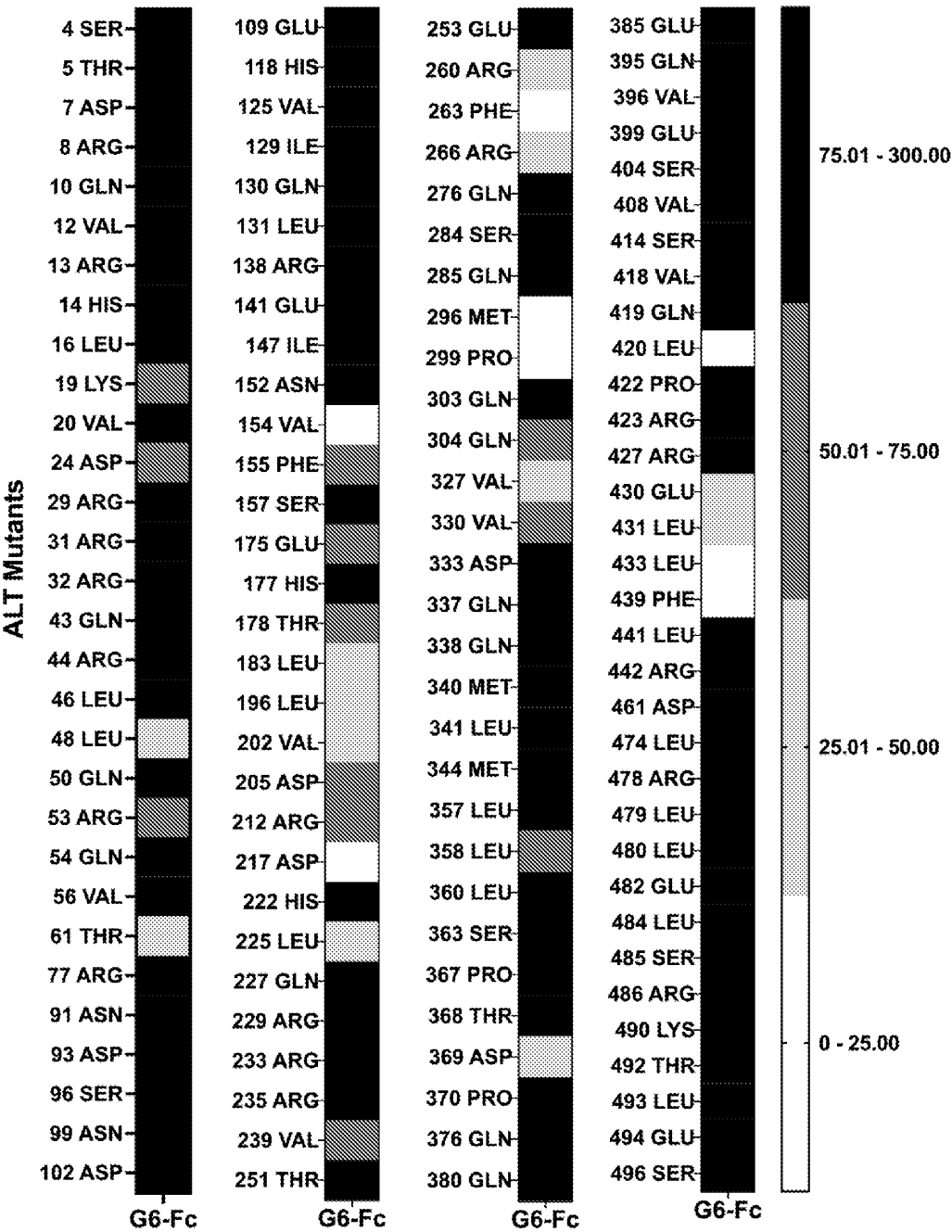


Figure 89

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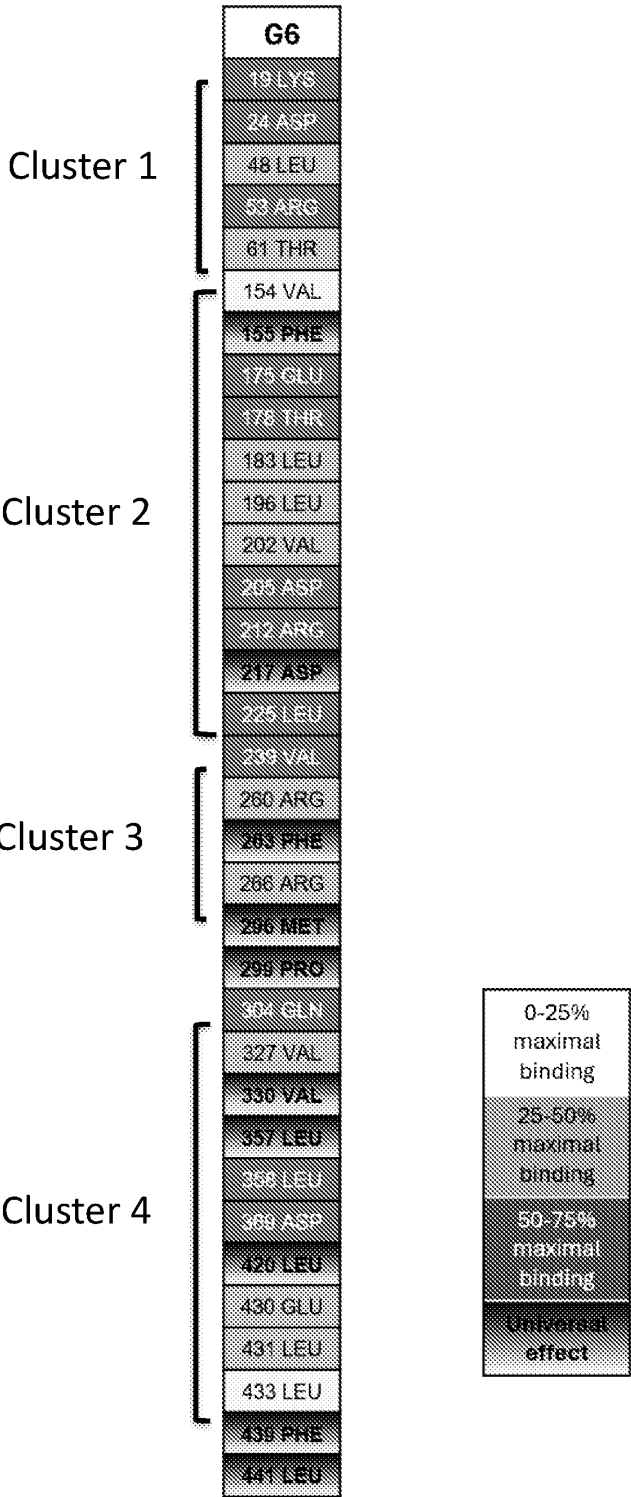


Figure 90

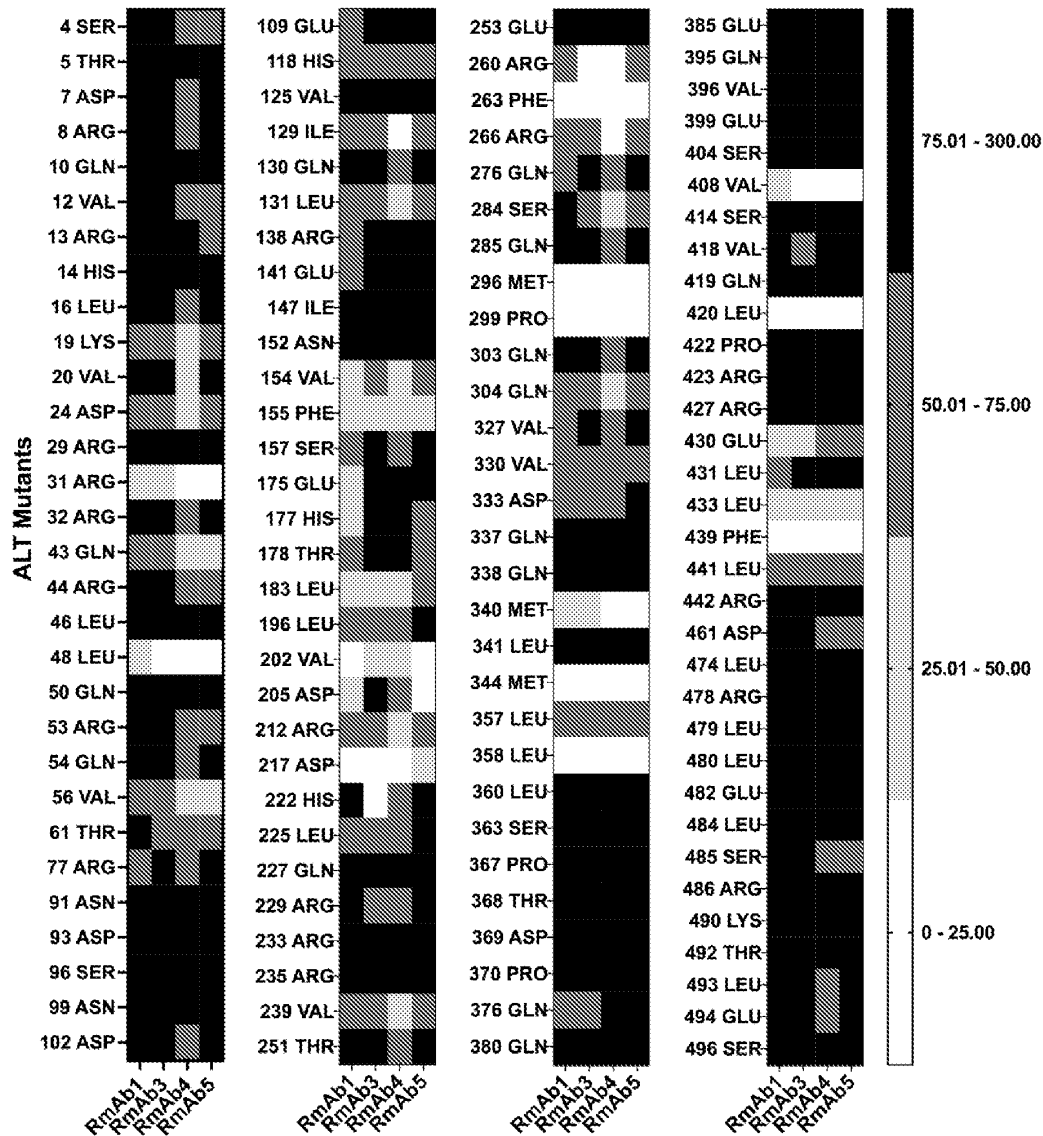


Figure 91

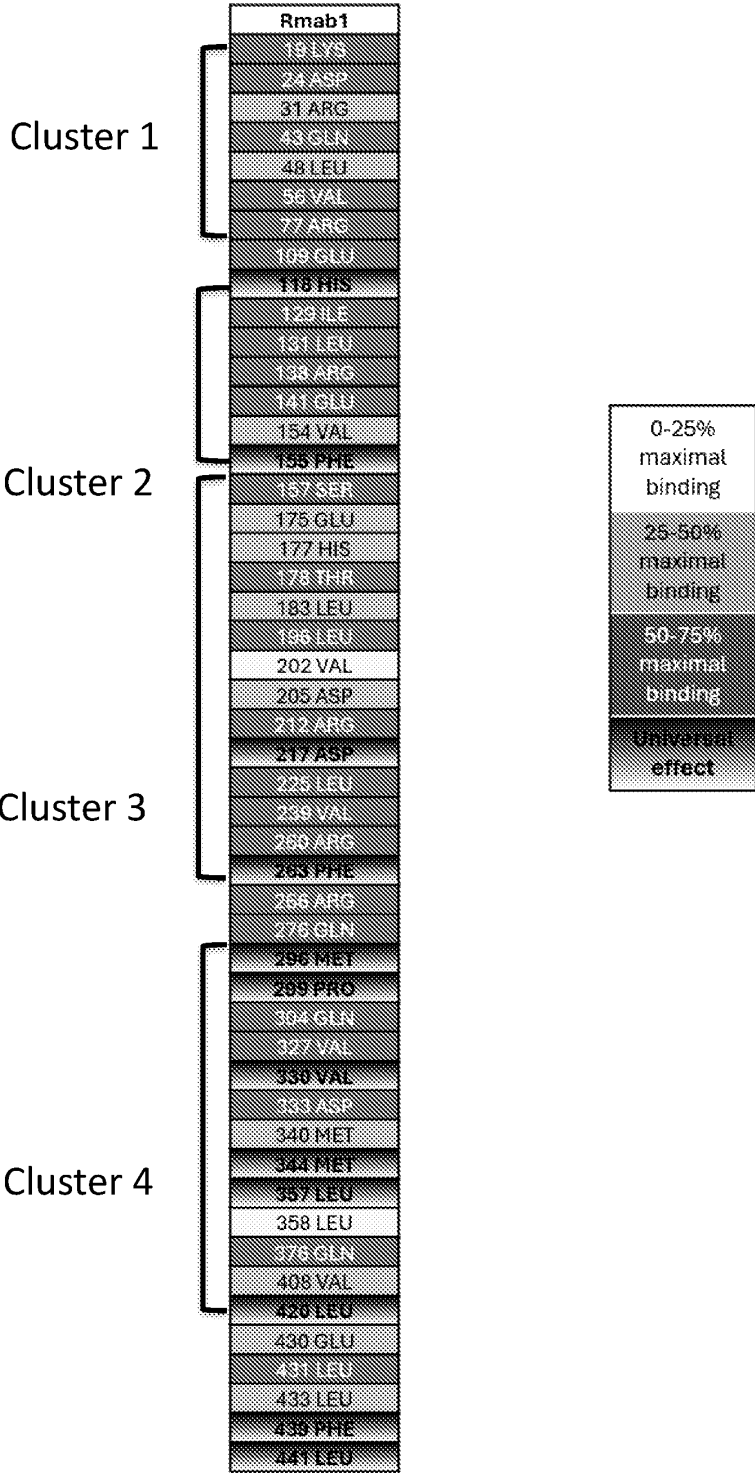


Figure 92

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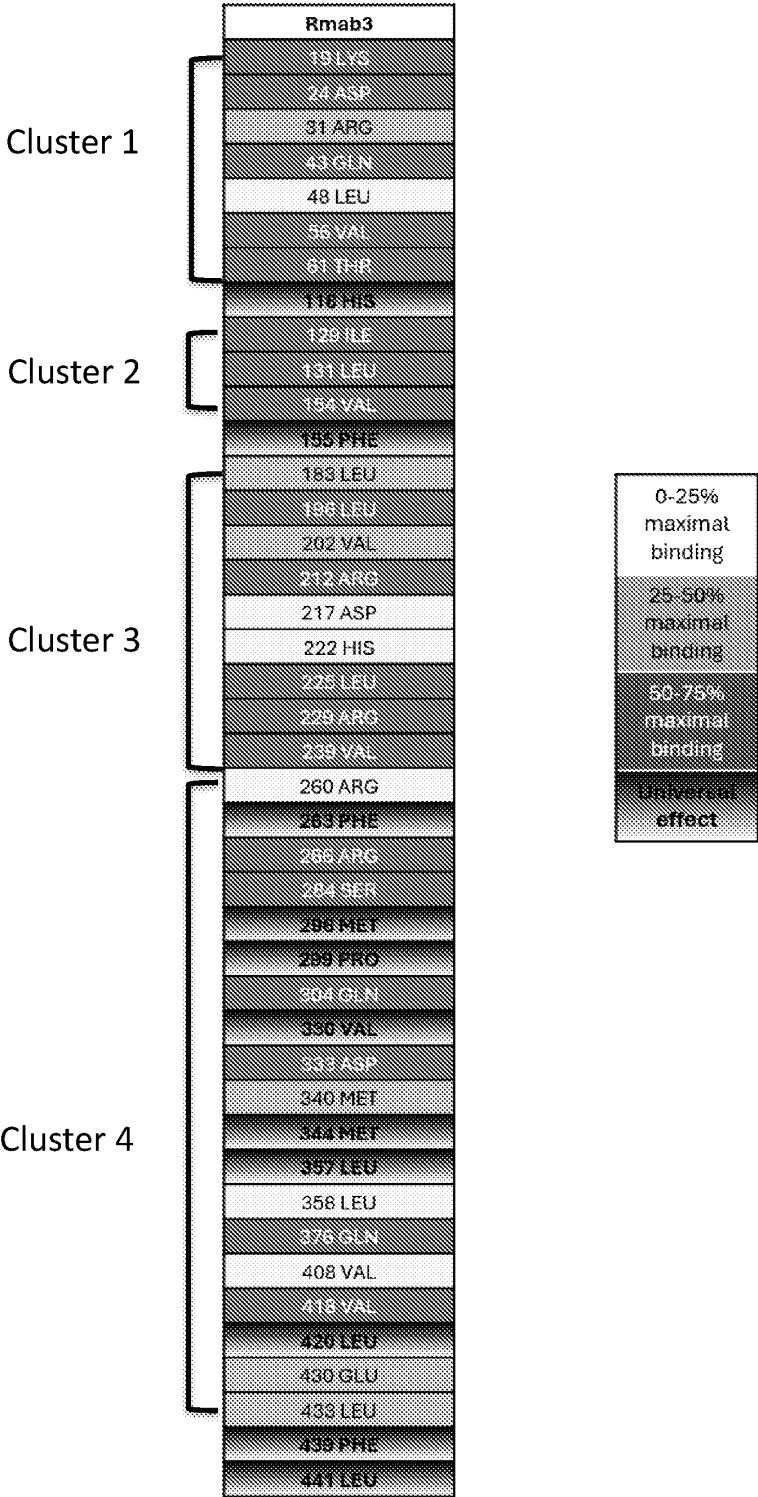


Figure 93

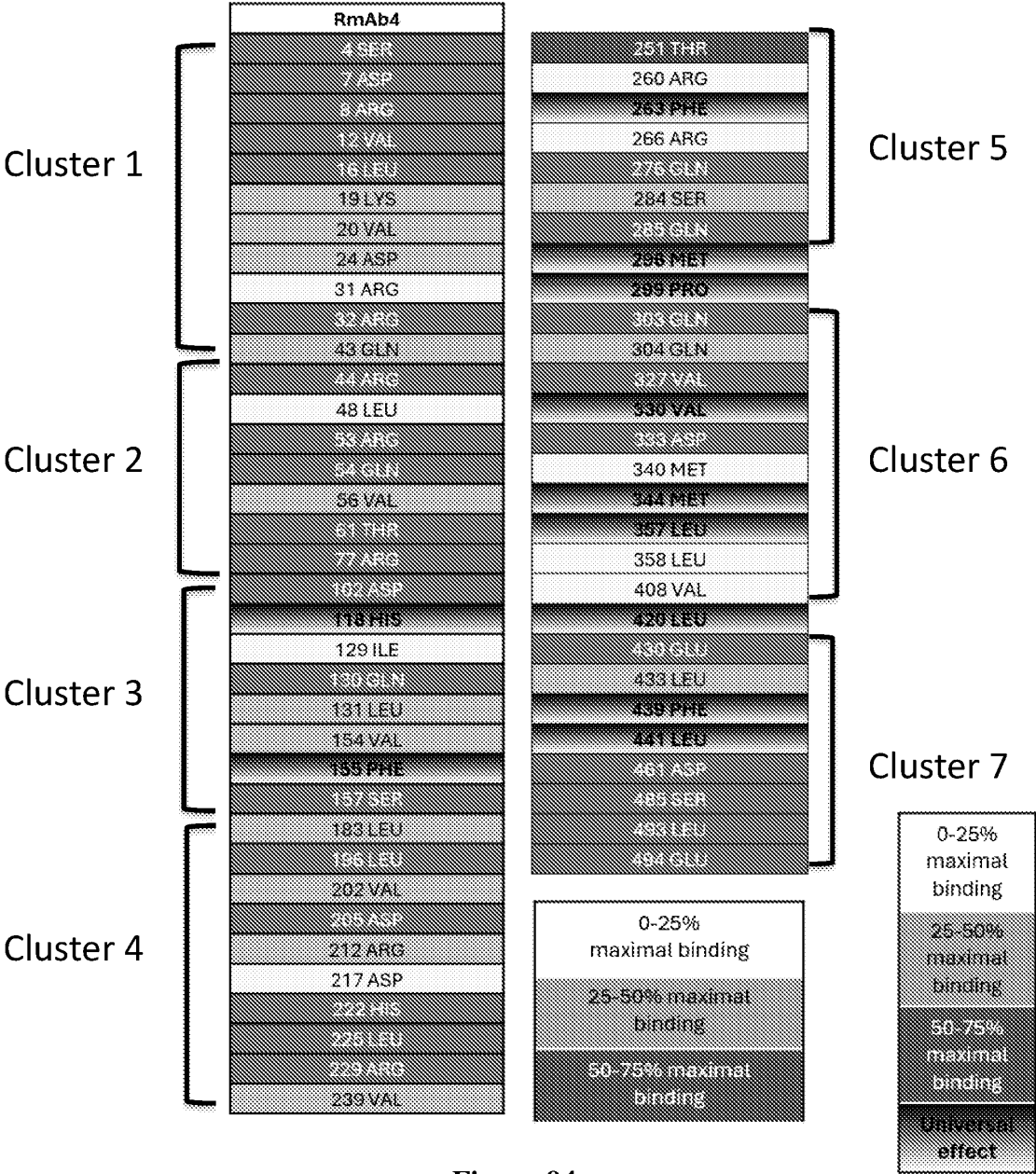


Figure 94

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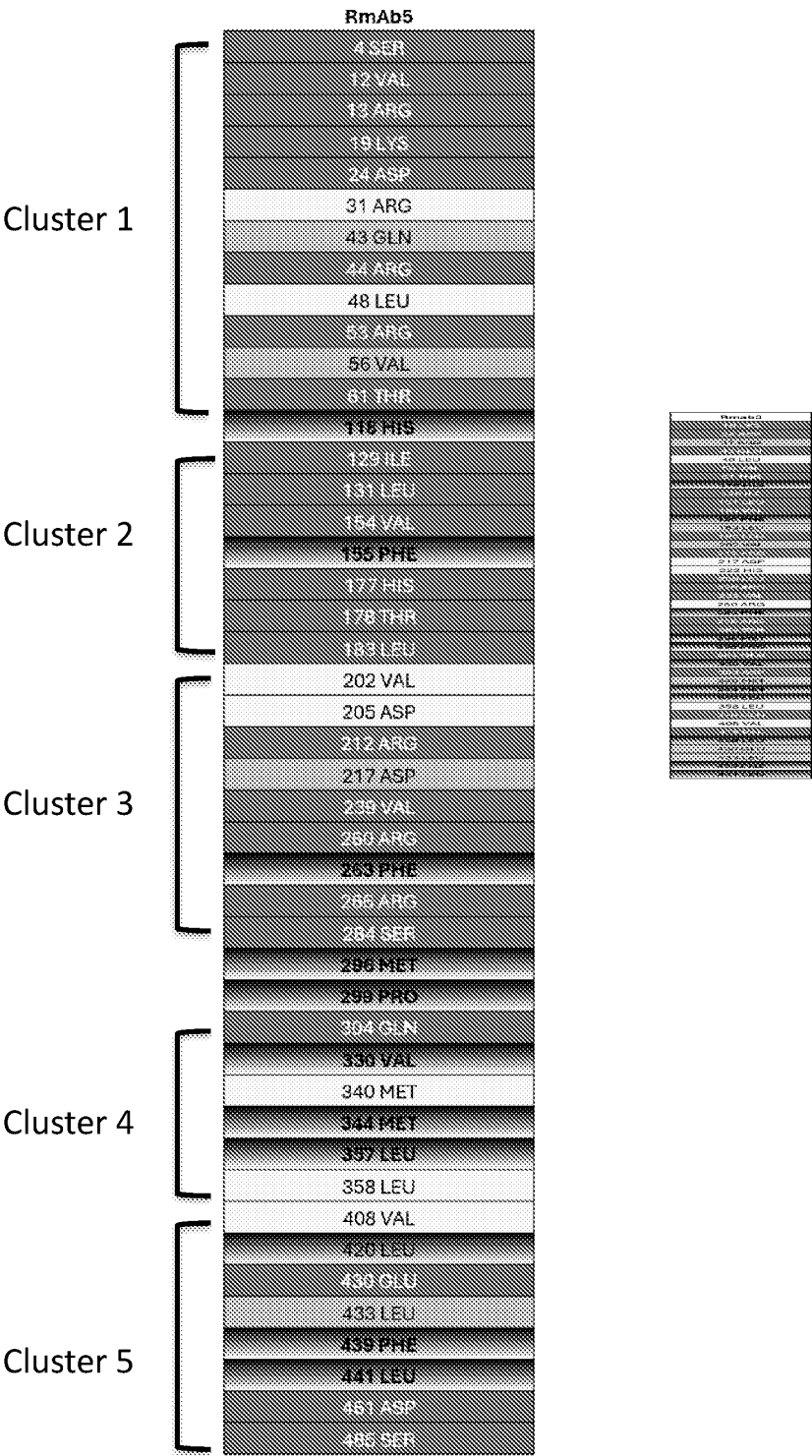


Figure 95

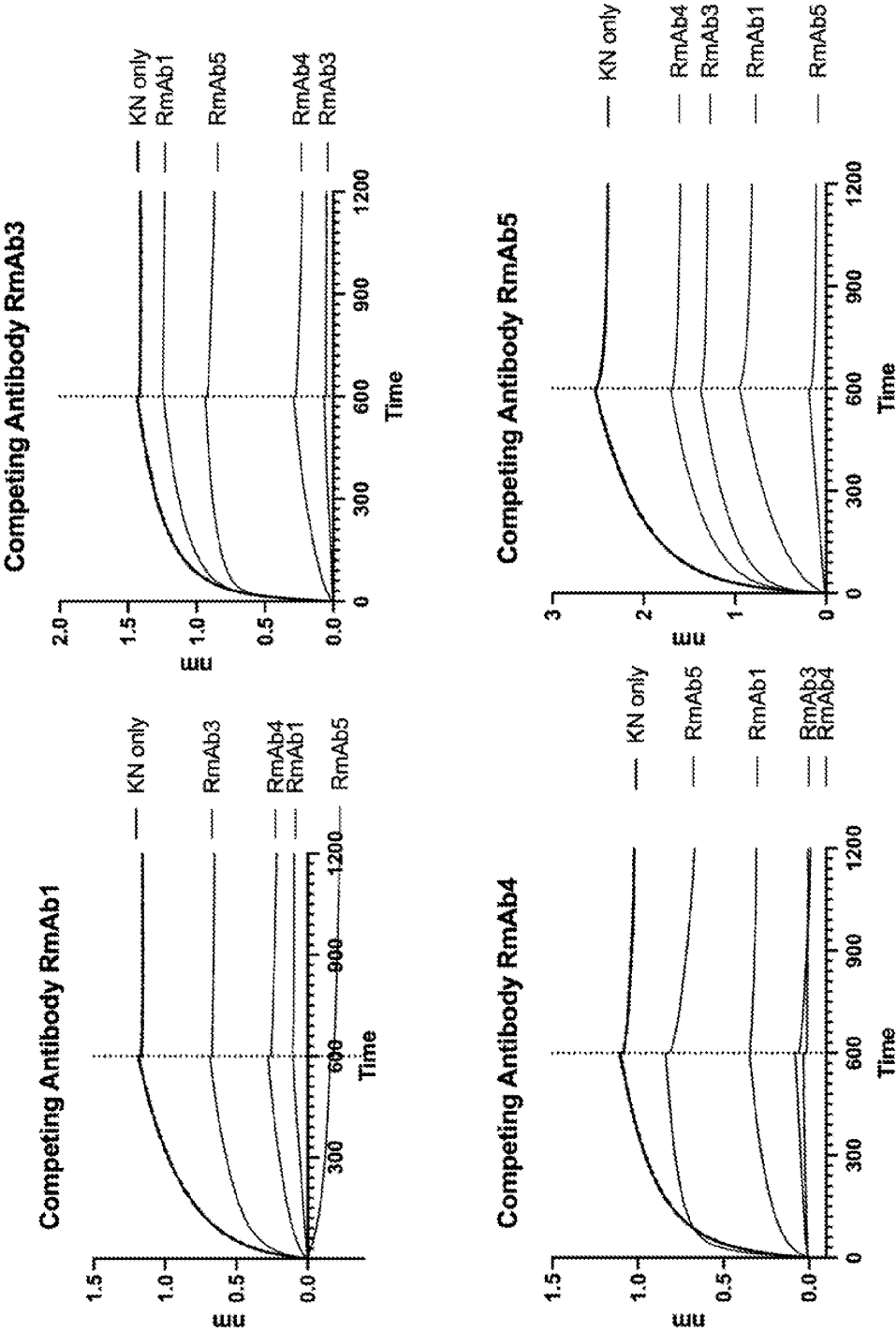


Figure 96

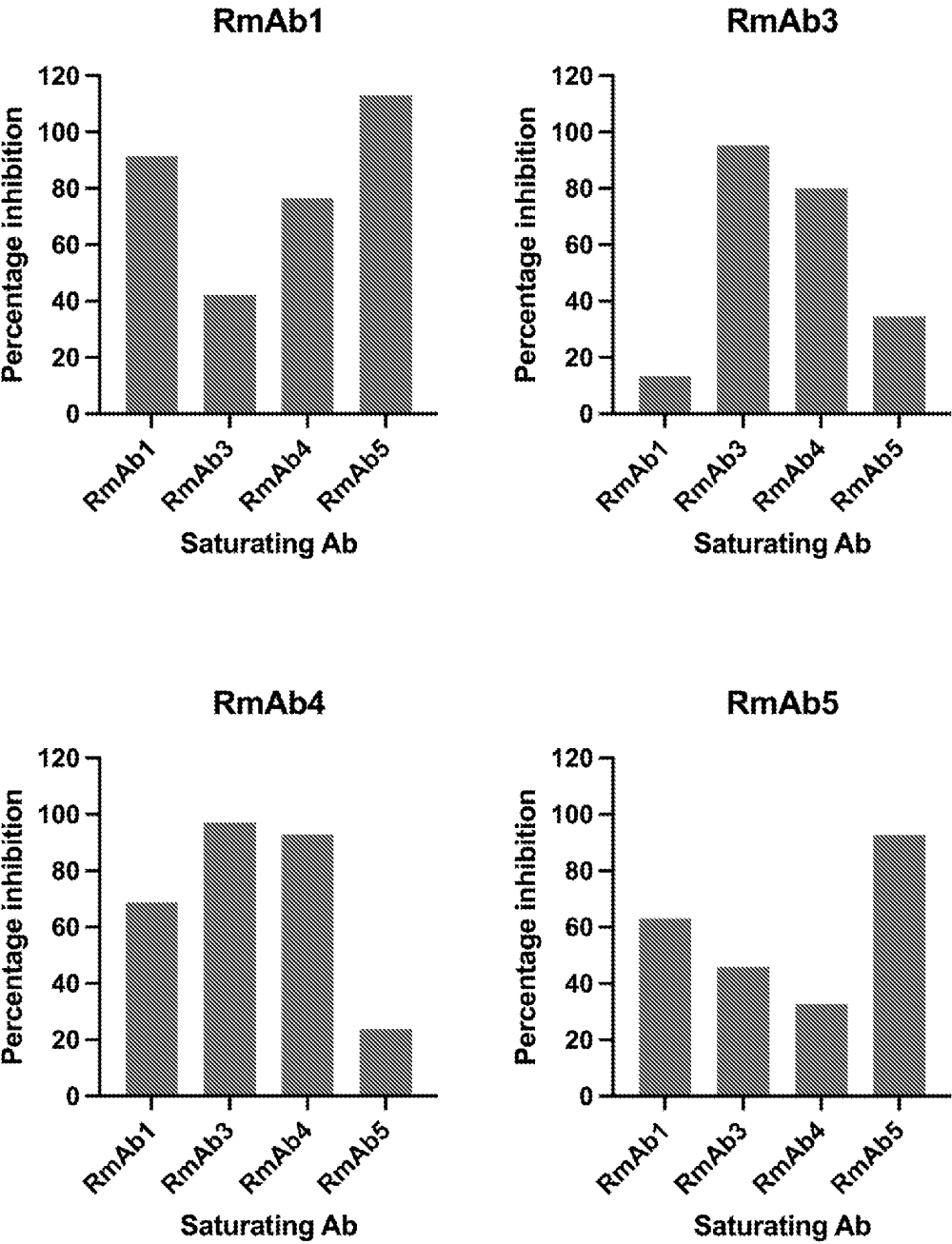


Figure 97

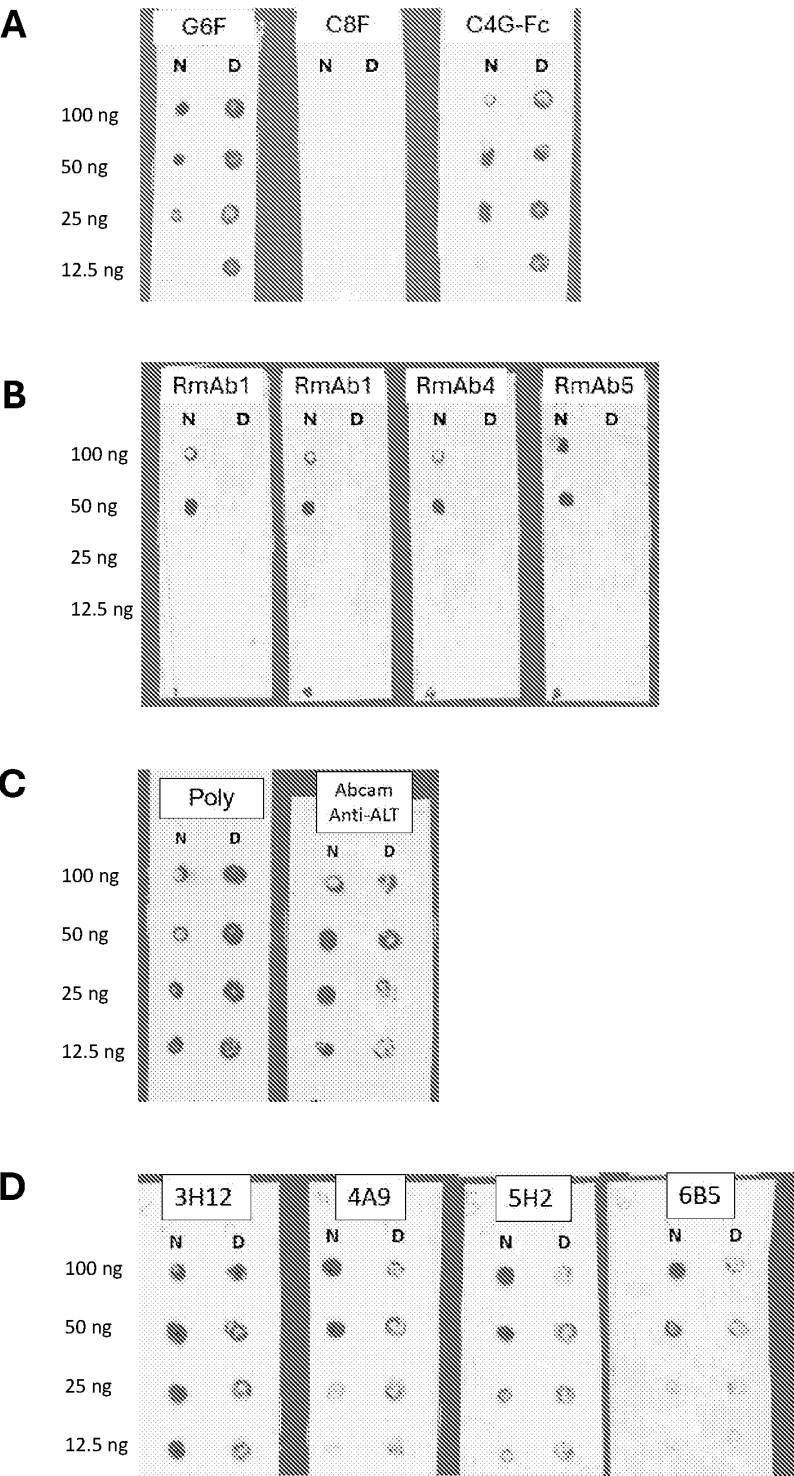


Figure 98

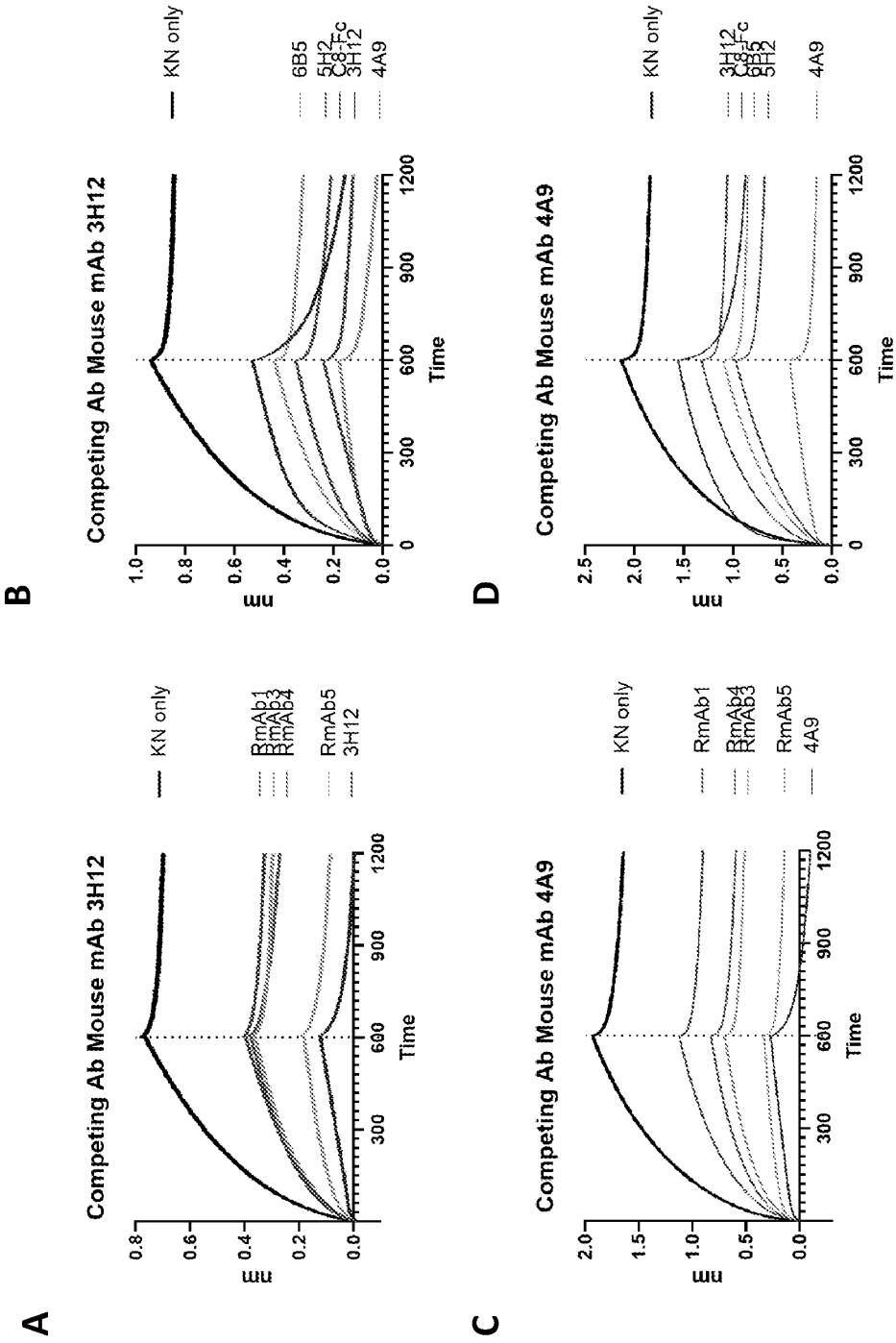


Figure 99

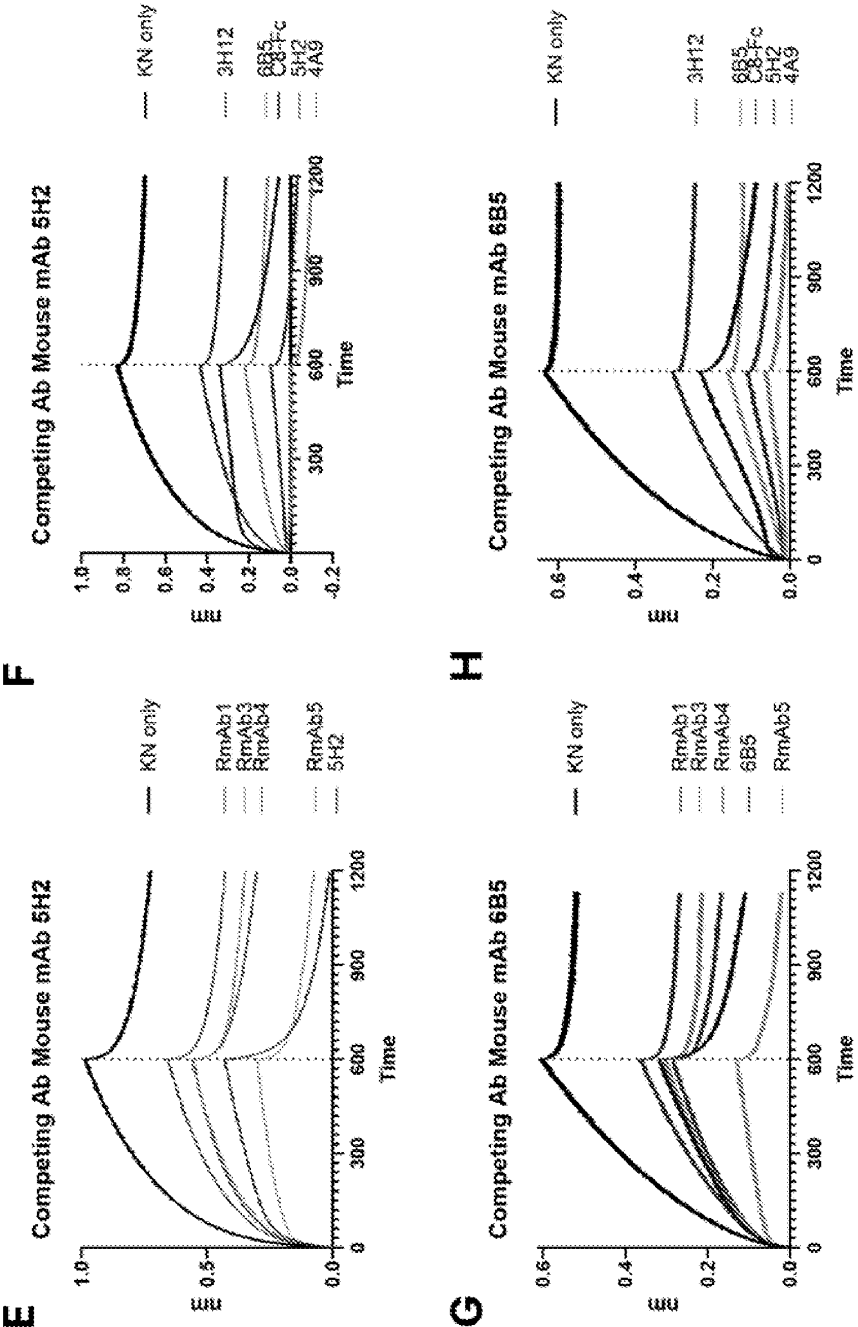
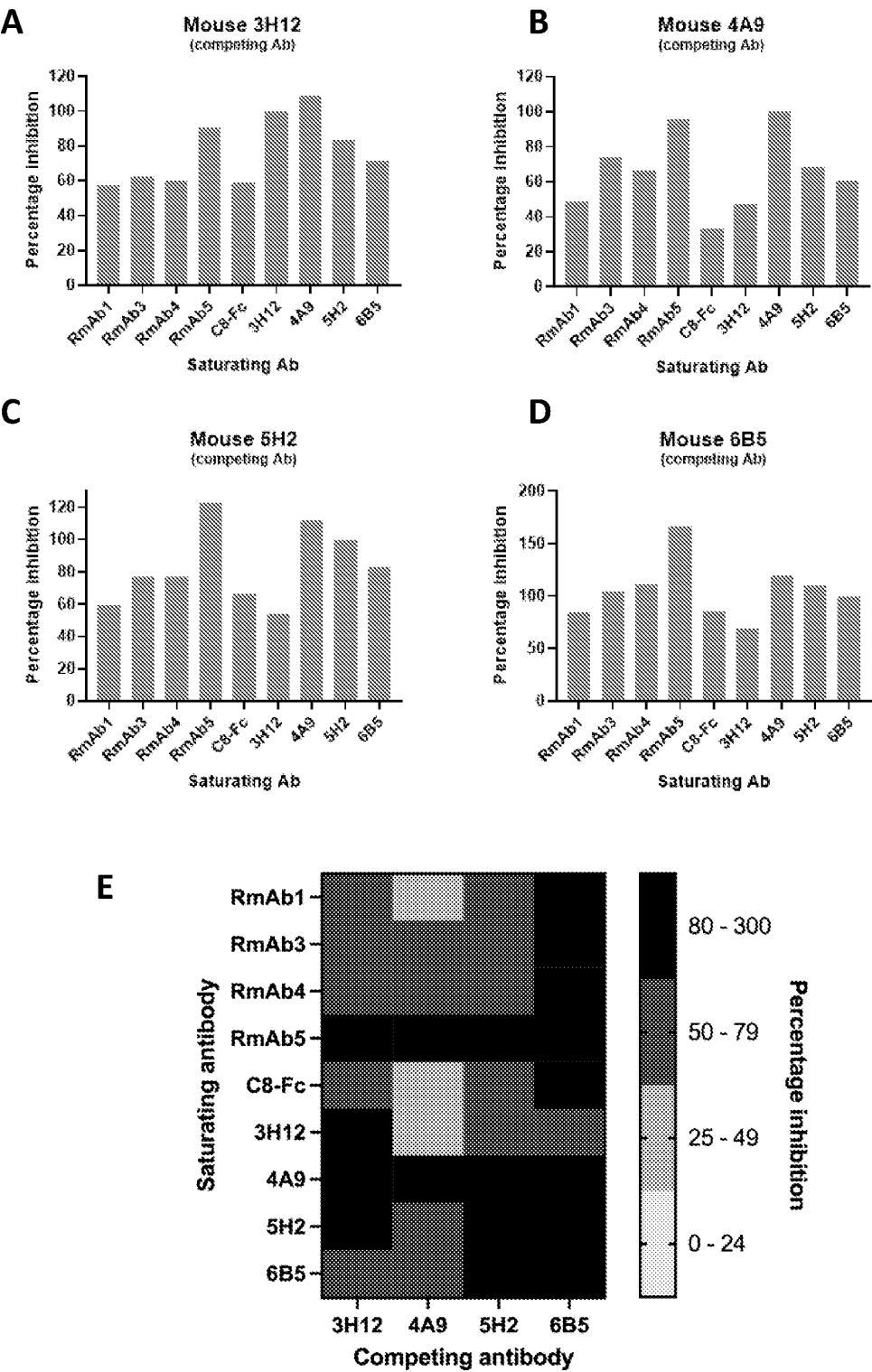
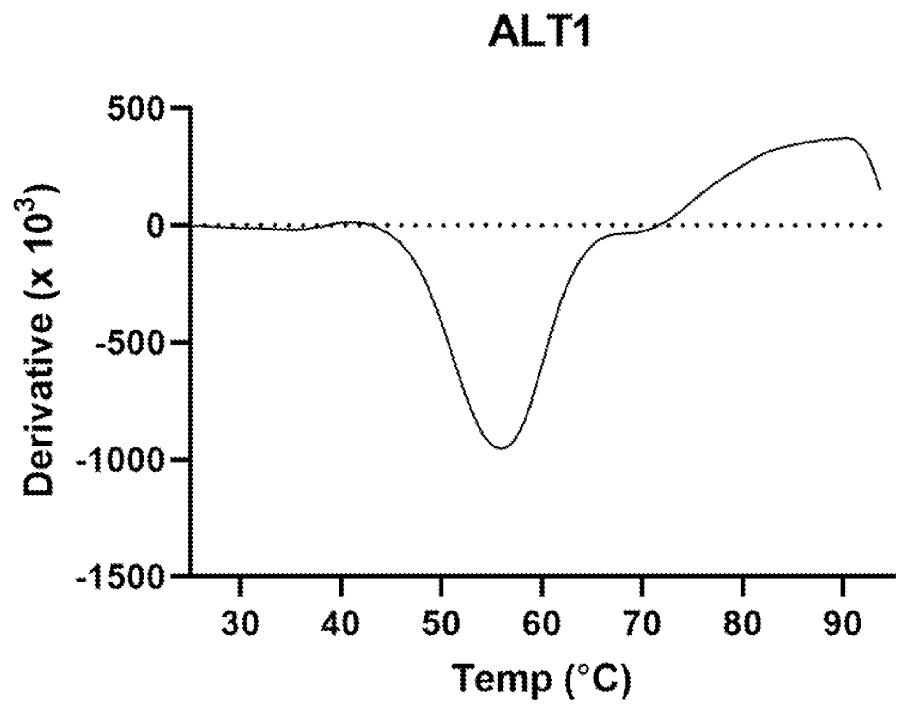


Figure 99 Continued



	Detection																			
	C8	G6	Poly	C4G-Fc	G4C-Fc	C4C-Fc	G4G-Fc	C4G-Fc	C4C-Fc	RmAb1	RmAb3	RmAb4	RmAb5	G3C	G4C	C3G	C4C	G3G	G4G	
Capture	C8																			
	G6																			
	Poly																			
	C4G-Fc																			
	G4C-Fc																			
	C4C-Fc																			
	G4G-Fc																			
	RmAb1																			
	RmAb3																			
	RmAb4																			
	RmAb5																			
	G3C																			
	G4C																			
	C3G																			
	C4G																			
	C3C																			
	C4C																			
	G3G																			
	G4G																			

Figure 101



Protein	Inflection point (T _m , °C)
ALT1	56.0

Figure 102