

Figure 1A**Version 1: 66650 lineage (VH1-03; VL-kappa-1-5)**

What	Sequence	SEQ ID NO:
CDR-H1	Y-T-F-X-X2-Y-A-X3-H, wherein X is N, R, D, G or K; X2 is S, H, I or Q; X3 is M or V	1
CDR-H2	W-I-H-A-G-T-G-X-T-X2-Y-S-Q-K-F-Q-G, wherein X is N, A or V; X2 is K or L	2
CDR-H3	A-R-G-L-G-X-V-G-P-T-G-T-S-W-F-D-P wherein X is S or E	3
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	4
CDR-L2	E-A-S-S-L-E-S	5
CDR-L3	Q-Q-Y-R-X-X2-P-F-T, wherein X is S, V, Y, L or Q; X2 is F; S or G	6

Figure 1B**Version 1: 66670 lineage (VH1-69; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-T-F-X-X2-Y-X3-I-S wherein X is S or N; X2 is E or S; X3 is V or P	7
CDR-H2	G-I-I-P-X-X2-G-T-A-X3-Y-A-Q-K-F-Q-G wherein X is G or Y, X2 is A or S; X3 is N, I, or V	8
CDR-H3	A-R-G-R-H-X-H-E-T wherein X is S, G or F	9
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	10
CDR-L2	A-A-S-S-L-Q-S	11
CDR-L3	Q-Q-V-Y-X-X2-P-W-T wherein X is S or R; X2 is L, I or F	12

Figure 1C**Version 1: 66692 lineage (VH3-23, VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	F-T-F-X-N-X2-A-M-S wherein X is G or D or S; X2 is T or V or Y	13
CDR-H2	A-I-S-X-X1-X2-G-S-T-Y-Y-A-D-S-V-K-G, wherein X is G or A; X2 is N or S; X3 is A or G	14
CDR-H3	A-K-G-P-D-R-Q-V-F-D-Y	15
CDR-L1	R-A-S-Q-G-I-X-S-W-L-A wherein X is S or D	16
CDR-L2	A-A-S-S-L-Q-S	17
CDR-L3	Q-H-A-X-X1-F-P-Y-T, wherein X is Y or L; X1 is S or F	18

Figure 1D**Version 1: 66716 lineage (VH1-39; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-S-I-S-S-X-X2-Y-X3-W-G wherein X is S or P; X2 is E or D; X3 is G, Y, or P	19
CDR-H2	S-I-X-X2-X3-G-X4-T-Y-Y-N-P-S-L-K-S, wherein X is Y or V; X2 is Y or N; X3 is Q or S; X4 is S or A	20
CDR-H3	A-R-G-P-X-R-Q-X2-F-D-Y, wherein X is Y or H, X2 is V or L	21
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	22
CDR-L2	A-A-S-S-L-Q-S	23
CDR-L3	Q-Q-G-X-X2-F-P-Y-T, wherein X is S or F; X2 is S or V	24

Figure 1E**Version 2: 66650 lineage (VH1-03; VL-kappa-1-5)**

What	Sequence	SEQ ID NO:
CDR-H1	Y-T-F-X-X2-Y-A-X3-H, wherein X, X2 and/or X3 is any amino acid	25
CDR-H2	W-I-H-A-G-T-G-X-T-X2-Y-S-Q-K-F-Q-G wherein X and/or X2 is any amino acid	26
CDR-H3	A-R-G-L-G-X-V-G-P-T-G-T-S-W-F-D-P wherein X is any amino acid	27
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	28
CDR-L2	E-A-S-S-L-E-S	29
CDR-L3	Q-Q-Y-R-X-X2-P-F-T, wherein X and/or X2 is any amino acid	30

Figure 1F**Version 2: 66670 lineage (VH1-69; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-T-F-X-X2-Y-X3-I-S, wherein X, X2 and/or X3 is any amino acid	31
CDR-H2	G-I-I-P-G-X2-G-T-A-X3-Y-A-Q-K-F-Q-G, wherein X, X2 and/or X3 is any amino acid	32
CDR-H3	A-R-G-R-H-X-H-E-T, wherein X is any amino acid	33
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	34
CDR-L2	A-A-S-S-L-Q-S	35
CDR-L3	Q-Q-V-Y-X-X2-P-W-T, wherein X and/or X2 is any amino acid	36

Figure 1G**Version 2: 66692 lineage (VH3-23, VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	F-T-F-X-N-X2-A-M-S, wherein X and/or X2 is any amino acid	37
CDR-H2	A-I-S-X-X1-X2-G-S-T-Y-Y-A-D-S-V-K-G, wherein X, X2 and/or X3 is any amino acid	38
CDR-H3	A-K-G-P-D-R-Q-V-F-D-Y	39
CDR-L1	R-A-S-Q-G-I-X-S-W-L-A , wherein X is any amino acid	40
CDR-L2	A-A-S-S-L-Q-S	41
CDR-L3	Q-H-A-X-X1-F-P-Y-T, wherein X and/or X1 is any amino acid	42

Figure 1H**Version 2: 66716 lineage (VH1-39; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-S-I-S-S-X-X2-Y-X3-W-G wherein X, X2 and/or X3 is any amino acid	43
CDR-H2	S-I-X-X2-X3-G-X4-T-Y-Y-N-P-S-L-K-S, wherein X, X2 , X3 and/or X4 is any amino acid	44
CDR-H3	A-R-G-P-X-R-Q-X2-F-D-Y, wherein X is any amino acid; X2 is any amino acid	45
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	46
CDR-L2	A-A-S-S-L-Q-S	47
CDR-L3	Q-Q-G-X-X2-F-P-Y-T, wherein X is any amino acid, X2 is any amino acid	48

Figure 1I**Version 3: 66650 lineage (VH1-03; VL-kappa-1-5)**

What	Sequence	SEQ ID NO:
CDR-H1	Y-T-F-X-X2-Y-A-X3-H wherein X is N, R, D, G, T, Q, S, A or K; X2 is S, H, I, N, L, Y or Q; X3 is M or V	844
CDR-H2	X-I-X2-A-G-X3-X4-X5-T-X6-Y-S-Q-K-F-Q-G wherein X is W or Y; X2 is H or N; X3 is S,T or A; X4 is G or A; X5 is N, A, T or V; X6 is E, K or L	845
CDR-H3	A-R-G-L-G-X-V-G-P-T-G-T-S-W-F-D-P wherein X is S, L, A, K or E	846
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	847
CDR-L2	E-A-S-S-X-E-S wherein X is L or S	848
CDR-L3	Q-Q-Y-R-X-X2-P-F-T wherein X is S, V, Y, L, T or Q; X2 is F, S, Y or G	849

Figure 1J**Version 3: 66670 lineage (VH1-69; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-T-F-X-X2-Y-X3-I-S wherein X is S or N; X2 is E or S; X3 is V or P	850
CDR-H2	G-I-I-P-X-X2-G-T-A-X3-Y-A-Q-K-F-Q-G wherein X is G, S, I or Y; X2 is A, V or S; X3 is N, I or V	851
CDR-H3	A-R-G-R-H-X-H-E-T wherein X is S, G or F	852
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	853
CDR-L2	A-A-S-S-L-Q-S	854
CDR-L3	Q-Q-X-Y-X2-X3-P-W-T wherein X is V or L; X2 is S or R; X3 is L, I or F	855

Figure 1K**Version 3: 66692 lineage (VH3-23, VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	F-T-F-X-X2-X3-X4-M-S wherein X is G, S, P or D or S; X2 is N, S or P; X3 is T, V or Y; X4 is A, H or I	856
CDR-H2	A-I-S-X-X2-X3-X4-X5-T-X6-Y-A-D-S-V-K-G wherein X is G or A; X2 is N, T, E or S; X3 is A or G; X4 is A or G; X5 is S or G; X6 is Y or F	857
CDR-H3	A-K-G-P-D-R-Q-V-F-D-Y	858
CDR-L1	R-A-S-Q-G-I-X-S-W-L-A wherein X is S or D	859
CDR-L2	A-A-S-S-L-Q-S	860
CDR-L3	Q-H-X-X2-X3-F-P-Y-T wherein X is A or G; X2 is Y, R or L; X3 is S, R, L or F	861

Figure 1L**Version 3: 66716 lineage (VH1-39; VL-kappa-1-12)**

What	Sequence	SEQ ID NO:
CDR-H1	G-S-I-X-S-X2-X3-Y-X4-W-X5 wherein X is S or F; X2 is S or P; X3 is E or D; X4 is G, P or Y; X5 is G or S	862
CDR-H2	X-I-X2-X3-X4-G-X5-T-Y-Y-N-P-S-L-K-S wherein X is S or V; X2 is Y, V, F or A; X3 is Y, F or N; X4 is Q, A or S; X5 is S, A or N	863
CDR-H3	A-R-G-P-X-R-Q-X2-F-D-Y wherein X is Y, H or F, X2 is V or L	864
CDR-L1	R-A-S-Q-G-I-S-S-W-L-A	865
CDR-L2	A-A-S-S-L-Q-S	866
CDR-L3	Q-Q-G-X-X2-F-P-Y-T wherein X is S, N, W or F; X2 is S or V	867

Figure 1M**IgG1:**

ASTKGPSVFP	LAPSSKSTSG	GTAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSSLGTQT	YICNVNHKPS	NTKVDKKVEP	KSCDKHTTCP	PCPAPELLGG	120
PSVFLFPPKP	KDTLMISRT	EVTCTVVVDVS	HEDPEVKFNV	YVDGVEVHNA	KTKPREEQYN	180
STYRVSVLT	VLHQDWLNGK	EYKCKVSNKA	LPAPIEKTIS	KAKGQPREPQ	VYTLPPSRDE	240
LTKNQVSLT	LVKGFYPSDI	AVEWESNGQP	ENNYKTTTPV	LDSDGSFFLY	SKLTVDKSRW	300
QQGNVFSCSV	MHEALHNHYT	QKSLSLSPGK				330

(SEQ ID NO:49)

IgG2:

ASTKGPSVFP	LAPCSRSTSE	STAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSNFGTQT	YTCNVNHHKPS	NTKVDKTVET	KCCVECPPCP	APPVAGPSVF	120
LFPPKPKDTL	MISRTPEVTC	VVVDVSHEDP	EVQFNWYVDG	VEVHNAKTKP	REEQFNSTFR	180
VVSVLTVVHQ	DWLNGKEYKC	KVSNKGLPAP	IEKTISKTKG	QPREPQVYTL	PPSREEMTKN	240
QVSLTCLVKG	FYPSTIAVEW	ESNGQPENNY	KTTTPMMLDS	GSFFLYSKLT	VDKSRWQQGN	300
VFSCSVMHEA	LHNHYTQKSL	SLSPGK				326

(SEQ ID NO:50)

IgG3:

ASTKGPSVFP	LAPCSRSTSG	GTAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSSLGTQT	YTCNVNHHKPS	NTKVDKRVEL	KTPLGDTTHT	CPRCPEPKSC	120
DTPPPCPRCP	EPKSCDTPPP	CPRCPEPKSC	DTPPPCPRCP	APELLGGPSV	FLFPPKPKDT	180
LMISRTPEVT	CVVVDVSHED	PEVQFKWYVD	GVEVHNAKTK	PREEQYNSTF	RVVSVLTVLH	240
QDWLNGKEYK	CKVSNKALPA	PIEKTISKTK	GQPREPQVYT	LPPSREEMTK	NQVSLTCLVK	300
GFYPSDIAVE	WESSGQPENN	YNTTPMMLDS	DGSFFLYSKL	TVDKSRWQQG	NIFSCVMHE	360
ALHNRFTQKS	LSLSPGK					377

(SEQ ID NO:51)

IgG4:

ASTKGPSVFP	LAPCSRSTSE	STAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSSLGTKT	YTCNVNHHKPS	NTKVDKRVES	KYGPCCPPCP	APEFLGGPSV	120
FLFPPKPKDT	LMISRTPEVT	CVVVDVSHED	PEVQFNWYVD	GVEVHNAKTK	PREEQFNSTY	180
RVVSVLTVLH	QDWLNGKEYK	CKVSNKGLPS	SIEKTISKAK	GQPREPQVYT	LPPSQEEMTK	240
NQVSLTCLVK	GFYPSDIAVE	WESNGQPENN	YKTTTPVLDS	DGSFFLYSRL	TVDKSRWQEG	300
NVFSCVMHE	ALHNRFTQKS	LSLSLKG				327

(SEQ ID NO:52)

IgG4:

ASTKGPSVFP	LAPCSRSTSE	STAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSSLGTKT	YTCNVNHHKPS	NTKVDKRVES	KYGPCCPPCP	APEFLGGPSV	120
FLFPPKPKDT	LMISRTPEVT	CVVVDVSHED	PEVQFNWYVD	GVEVHNAKTK	PREEQFNSTY	180
RVVSVLTVLH	QDWLNGKEYK	CKVSNKGLPS	SIEKTISKAK	GQPREPQVYT	LPPSQEEMTK	240
NQVSLTCLVK	GFYPSDIAVE	WESNGQPENN	YKTTTPVLDS	DGSFFLYSRL	TVDKSRWQEG	300
NVFSCVMHE	ALHNRFTQKS	LSLSPGK				327

(SEQ ID NO:53)

IgG4:

ASTKGPSVFP	LAPCSRSTSE	STAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	60
GLYSLSSVVT	VPSSSLGTKT	YTCNVNHHKPS	NTKVDKRVES	KYGPCCPPCP	APEFLGGPSV	120
FLFPPKPKDT	LMISRTPEVT	CVVVDVSHED	PEVQFNWYVD	GVEVHNAKTK	PREEQFNSTY	180
RVVSVLTVLH	QDWLNGKEYK	CKVSNKGLPS	SIEKTISKAK	GQPREPQVYT	LPPSQEEMTK	240
NQVSLTCLVK	GFYPSDIAVE	WESNGQPENN	YKTTTPVLDS	DGSFFLYSRL	TVDKSRWQEG	300
NVFSCVMHE	ALHNRFTQKS	LSLSG				327

(SEQ ID NO:868)

Figure 2A: ADI-71709 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71709 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCEASGYTFDIYAVHWVRQAPGQRLEWMGWIHAGTGATKYSQ</u> <u>KFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGPTGTSWFDPWGQGLVTVSS</u>	54
vhCDR1 ADI-71709 hlgG4 S228P kappa	<u>YTFDIYAVH</u>	55
vhCDR2 ADI-71709 hlgG4 S228P kappa	<u>WIHAGTGATKYSQKFQG</u>	56
vhCDR3 ADI-71709 hlgG4 S228P kappa	<u>ARGLGEVGPTGTSWFDP</u>	57
Full length heavy chain sequence ADI-71709 hlgG4 S228P kappa	QVQLVQSGAEVKKPGASVKVSCEASGYTFDIYAVHWVRQAPGQRLEWMGWIHAGTGATKYSQ KFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGPTGTSWFDPWGQGLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	58
Variable light (vl) domain ADI-71709 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES</u> <u>SGSGSGTEFTLTISSLQPDDFATYYCQQYRQSPFTFGGGTKVEIK</u>	59
vlCDR1 ADI-71709 hlgG4 S228P kappa	<u>RASQSISSWLA</u>	60
vlCDR2 ADI-71709 hlgG4 S228P kappa	<u>EASSLES</u>	61
vlCDR3 ADI-71709 hlgG4 S228P kappa	<u>QQYRQSPFT</u>	62
Full length light chain sequence ADI-71709 hlgG4 S228P kappa	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES SGSGSGTEFTLTISSLQPDDFATYYCQQYRQSPFTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	63

Figure 2B: ADI-71719 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71719 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGSSSVKVSCKASGGTFNSYVISWVRQAPQGLEWMGGIIPGAGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHSSETWGQGTTLTVSS</u>	64
vhCDR1 ADI-71719 hlgG4 S228P kappa	<u>GTFNSYVIS</u>	65
vhCDR2 ADI-71719 hlgG4 S228P kappa	<u>GIIPGAGTANYAQKFQG</u>	66
vhCDR3 ADI-71719 hlgG4 S228P kappa	<u>ARGRHSSET</u>	67
Full length heavy chain sequence ADI-71719 hlgG4 S228P kappa	QVQLVQSGAEVKKPGSSSVKVSCKASGGTFNSYVISWVRQAPQGLEWMGGIIPGAGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHSSETWGQGTTLTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	68
Variable light (vl) domain ADI-71719 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> FSGSGSGTDFTLTISSLQPEDFATYYCQQVYSLPWTFGGGTKVEIK	69
vlCDR1 ADI-71719 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	70
vlCDR2 ADI-71719 hlgG4 S228P kappa	<u>AASSLQS</u>	71
vlCDR3 ADI-71719 hlgG4 S228P kappa	<u>QQVYSLPWT</u>	72
Full length light chain sequence ADI-71719 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQVYSLPWTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	73

Figure 2C: ADI-71720 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71720 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYVISWVRQAPGGLEWMGGIIPGAGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHSSETWGQGT</u> LVTVSS	74
vhCDR1 ADI-71720 hlgG4 S228P kappa	<u>GTFSEYVIS</u>	75
vhCDR2 ADI-71720 hlgG4 S228P kappa	<u>GIIPGAGTANYAQKFQ</u>	76
vhCDR3 ADI-71720 hlgG4 S228P kappa	<u>ARGRHSSET</u>	77
Full length heavy chain sequence ADI-71720 hlgG4 S228P kappa	QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYVISWVRQAPGGLEWMGGIIPGAGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHSSETWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	78
Variable light (vl) domain ADI-71720 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIGSLQPEDFATYYCQQVYSLPWTFGGGTKVEIK</u>	79
vlCDR1 ADI-71720 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	80
vlCDR2 ADI-71720 hlgG4 S228P kappa	<u>AASSLQS</u>	81
vlCDR3 ADI-71720 hlgG4 S228P kappa	<u>QQVYSLPWT</u>	82
Full length light chain sequence ADI-71720 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIGSLQPEDFATYYCQQVYSLPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	83

Figure 2D: ADI-71722 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71722 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYPISWVRQAPGQGLEWMGGIIPGAGTAIYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHFHETWGQGT</u> LTVTSS	84
vhCDR1 ADI-71722 hlgG4 S228P kappa	<u>GTFSEYPI</u> S	85
vhCDR2 ADI-71722 hlgG4 S228P kappa	<u>GIIPGAGTAIYAQKFQ</u> G	86
vhCDR3 ADI-71722 hlgG4 S228P kappa	<u>ARGRHFHET</u>	87
Full length heavy chain sequence ADI-71722 hlgG4 S228P kappa	QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYPISWVRQAPGQGLEWMGGIIPGAGTAIYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHFHETWGQGT LTVTSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	88
Variable light (vl) domain ADI-71722 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLA</u> WYQQKPGKAPKLLIYA <u>AASSLQ</u> SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC <u>QQVYRFPWT</u> FGGGTKVEIK	89
vlCDR1 ADI-71722 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	90
vlCDR2 ADI-71722 hlgG4 S228P kappa	<u>AASSLQ</u> S	91
vlCDR3 ADI-71722 hlgG4 S228P kappa	<u>QQVYRFPWT</u>	92
Full length light chain sequence ADI-71722 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYA <u>AASSLQ</u> SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYRFPWTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	93

Figure 2E: ADI-71701 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71701 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYAMHWVRQAPGQRLEWMGWIHAGTGNTKYSQ</u> <u>KFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGP</u> <u>TGTSWFD</u> <u>PWGQGTLVTVSS</u>	94
vhCDR1 ADI-71701 hlgG4 S228P kappa	<u>YTFNSYAMH</u>	95
vhCDR2 ADI-71701 hlgG4 S228P kappa	<u>WIHAGTGNTKYSQKFQG</u>	96
vhCDR3 ADI-71701 hlgG4 S228P kappa	<u>ARGLGEVGP</u> <u>TGTSWFD</u> <u>P</u>	97
Full length heavy chain sequence ADI-71701 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYAMHWVRQAPGQRLEWMGWIHAGTGNTKYSQ</u> <u>KFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGP</u> <u>TGTSWFD</u> <u>PWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHREALHNHYTQKSLSLSLG	98
Variable light (vl) domain ADI-71701 hlgG4 S228P kappa	<u>DIQMTQSPPTLSASVGD</u> <u>RVITITCRASQSISSWLA</u> <u>WYQQKPGKAPKLLIYEASSLES</u> <u>GVPSRF</u> <u>SGSGSGTEFTLTIS</u> <u>SLQPDDFATYYCQYRVFPFT</u> <u>FGGGTKVEIK</u>	99
vlCDR1 ADI-71701 hlgG4 S228P kappa	<u>RASQSISSWLA</u>	100
vlCDR2 ADI-71701 hlgG4 S228P kappa	<u>EASSLES</u>	101
vlCDR3 ADI-71701 hlgG4 S228P kappa	<u>QYRVFPFT</u>	102
Full length light chain sequence ADI-71701 hlgG4 S228P kappa	<u>DIQMTQSPPTLSASVGD</u> <u>RVITITCRASQSISSWLA</u> <u>WYQQKPGKAPKLLIYEASSLES</u> <u>GVPSRF</u> <u>SGSGSGTEFTLTIS</u> <u>SLQPDDFATYYCQYRVFPFT</u> <u>FGGGTKVEIK</u> RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	103

Figure 2F: ADI-71663 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71663 hlgG4 S228P kappa	<u>EVQLLES</u> GGGLVQPGGSLRLSCAASGFTFGNTAMSWVRQAPGKGLEWVSAISANAGSTYYA <u>DSVKGRFTISR</u> DNSKNTLYLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLLVTVSS	104
vhCDR1 ADI-71663 hlgG4 S228P kappa	<u>FTFGNTAMS</u>	105
vhCDR2 ADI-71663 hlgG4 S228P kappa	<u>AISANAGSTYYADSVKG</u>	106
vhCDR3 ADI-71663 hlgG4 S228P kappa	<u>AKGPDRQVFDY</u>	107
Full length heavy chain sequence ADI-71663 hlgG4 S228P kappa	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNTAMSWVRQAPGKGLEWVSAISANAGSTYYA DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLSLG	108
Variable light (vl) domain ADI-71663 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASV</u> GDRVTTITCRASQGISSWLAWYQQKPGKAPKLLIYA <u>AASSLQ</u> SGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQHALLFPYTFGGGTKVEIK	109
vlCDR1 ADI-71663 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	110
vlCDR2 ADI-71663 hlgG4 S228P kappa	<u>AASSLQS</u>	111
vlCDR3 ADI-71663 hlgG4 S228P kappa	<u>QHALLFPYT</u>	112
Full length light chain sequence ADI-71663 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRTTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQHALLFPYTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	113

Figure 2G: ADI-71662 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71662 hlgG4 S228P kappa	<u>EVQLLES</u> GGGLVQPGGSLRLSCAASGFTFDNVAMSWVRQAPGKGLEWVSAISGNAGSTYYA <u>DSVKGRFTISR</u> DNSKNTLHLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLLVTSS	114
vhCDR1 ADI-71662 hlgG4 S228P kappa	<u>FTFDNVAMS</u>	115
vhCDR2 ADI-71662 hlgG4 S228P kappa	<u>AISGNAGSTYYADSVKG</u>	116
vhCDR3 ADI-71662 hlgG4 S228P kappa	<u>AKGPDRQVFDY</u>	117
Full length heavy chain sequence ADI-71662 hlgG4 S228P kappa	EVQLLESGGGLVQPGGSLRLSCAASGFTFDNVAMSWVRQAPGKGLEWVSAISGNAGSTYYA DSVKGRFTISRDNKNTLHLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLLVTSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLSLG	118
Variable light (vl) domain ADI-71662 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASV</u> GDRVTTITCRASQGISSWLAWYQQKPGKAPKLLIYA <u>AASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> ISSLPEDFATYYCQHAYSFPYTFGGGTKVEIK	119
vlCDR1 ADI-71662 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	120
vlCDR2 ADI-71662 hlgG4 S228P kappa	<u>AASSLQS</u>	121
vlCDR3 ADI-71662 hlgG4 S228P kappa	<u>QHAYSFPYT</u>	122
Full length light chain sequence ADI-71662 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRTTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLPEDFATYYCQHAYSFPYTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	123

Figure 2H: ADI-66692 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-66692 hlgG4 S228P kappa	<u>EVQLLES</u> GGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYA <u>DSVKGRFTISR</u> DNSKNTLYLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLVTVSS	124
vhCDR1 ADI-66692 hlgG4 S228P kappa	<u>FTFSNYAMS</u>	125
vhCDR2 ADI-66692 hlgG4 S228P kappa	<u>AISGSGGSTYYADSVKG</u>	126
vhCDR3 ADI-66692 hlgG4 S228P kappa	<u>AKGPDRQVFDY</u>	127
Full length heavy chain sequence ADI-66692 hlgG4 S228P kappa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYA DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGPDRQVFDYWGQGTLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	128
Variable light (vl) domain ADI-66692 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASV</u> GDRVTTITCRASQGIDSWLAWYQQKPGKAPKLLIYA <u>AASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> ISSLPEDFATYYCQHAYSFPYTFGGGTKVEIK	129
vlCDR1 ADI-66692 hlgG4 S228P kappa	<u>RASQGIDSWLA</u>	130
vlCDR2 ADI-66692 hlgG4 S228P kappa	<u>AASSLQS</u>	131
vlCDR3 ADI-66692 hlgG4 S228P kappa	<u>QHAYSFPYT</u>	132
Full length light chain sequence ADI-66692 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRTTITCRASQGIDSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLPEDFATYYCQHAYSFPYTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	133

Figure 2I: ADI-71710 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71710 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFGIYAMHWVRQAPGQRLEWMGWIHAGTGVTKYSQ</u> <u>KFQGRVTITRDTSASTAYMELSSLRSEDAVYYCARGLGEVGP</u> <u>TGTSWFD</u> <u>PWGQGT</u> <u>LVTVSS</u>	134
vhCDR1 ADI-71710 hlgG4 S228P kappa	<u>YTFGIYAMH</u>	135
vhCDR2 ADI-71710 hlgG4 S228P kappa	<u>WIHAGTGVTKYSQKFQG</u>	136
vhCDR3 ADI-71710 hlgG4 S228P kappa	<u>ARGLGEVGP</u> <u>TGTSWFD</u> <u>P</u>	137
Full length heavy chain sequence ADI-71710 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFGIYAMHWVRQAPGQRLEWMGWIHAGTGVTKYSQ</u> <u>KFQGRVTITRDTSASTAYMELSSLRSEDAVYYCARGLGEVGP</u> <u>TGTSWFD</u> <u>PWGQGT</u> <u>LVTVSS</u> <u>ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP</u> <u>TVSWNSGALTSGVHTFPAVLQSS</u> <u>GLYSLSSVTVPS</u> <u>SSLG</u> <u>TKTYTCNV</u> <u>DHKPSNTKVDKRVESKYGPPCP</u> <u>PCPAPEFLGGPSV</u> <u>FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY</u> <u>RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK</u> <u>TISKAKGQPREPQVYTLPPS</u> <u>QEEMTK</u> <u>NQVSLTCLVKGFYPSDIAVEWESNGQPENNYK</u> <u>TPPVLDSDGSFFLYSRLTVDKSRWQEG</u> <u>NVFSCSVMEALHNHYTQKSLSL</u> <u>SLG</u>	138
Variable light (vl) domain ADI-71710 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES</u> <u>GVPSRF</u> <u>SGSGSGTEFTLTIS</u> <u>SLQ</u> <u>PDDFATYYCQQYRYS</u> <u>PFT</u> <u>FGGGTKVEIK</u>	139
vlCDR1 ADI-71710 hlgG4 S228P kappa	<u>RASQSISSWLA</u>	140
vlCDR2 ADI-71710 hlgG4 S228P kappa	<u>EASSLES</u>	141
vlCDR3 ADI-71710 hlgG4 S228P kappa	<u>QQYRYS</u> <u>PFT</u>	142
Full length light chain sequence ADI-71710 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES</u> <u>GVPSRF</u> <u>SGSGSGTEFTLTIS</u> <u>SLQ</u> <u>PDDFATYYCQQYRYS</u> <u>PFT</u> <u>FGGGTKVEIK</u> <u>RTVAAPS</u> <u>VFIFPPSDEQLKSGTASV</u> <u>VCLLNNFY</u> <u>PREAKVQWKVDNALQSGNSQES</u> <u>VTEQDSK</u> <u>DSTYSL</u> <u>SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR</u> <u>GEC</u>	143

Figure 2J: ADI-71717 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71717 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFKQYAMHWVRQAPGQRLEWMGWIHAGTGNTKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGSVGPTGTSWFDPWGQGT</u> <u>LVTVSS</u>	144
vhCDR1 ADI-71717 hlgG4 S228P kappa	<u>YTFKQYAMH</u>	145
vhCDR2 ADI-71717 hlgG4 S228P kappa	<u>WIHAGTGNTKYSQKFQG</u>	146
vhCDR3 ADI-71717 hlgG4 S228P kappa	<u>ARGLGSVGPTGTSWFDP</u>	147
Full length heavy chain sequence ADI-71717 hlgG4 S228P kappa	QVQLVQSGAEVKKPGASVKVSCKASGYTFKQYAMHWVRQAPGQRLEWMGWIHAGTGNTKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGSVGPTGTSWFDPWGQGT LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	148
Variable light (vl) domain ADI-71717 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES</u> <u>GVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYRSGPFTFGGGTKVEIK</u>	149
vlCDR1 ADI-71717 hlgG4 S228P kappa	<u>RASQSISSWLA</u>	150
vlCDR2 ADI-71717 hlgG4 S228P kappa	<u>EASSLES</u>	151
vlCDR3 ADI-71717 hlgG4 S228P kappa	<u>QQYRSGPFT</u>	152
Full length light chain sequence ADI-71717 hlgG4 S228P kappa	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLES GVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYRSGPFTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	153

Figure 2K: ADI-71739 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71739 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSSETLSLTCTVSGGSISSPDYPWGWI</u> <u>RQPPGKGLEWIGSIYYQGATYY</u> <u>NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC</u> <u>ARGPYRQLFDYWGQGT</u> <u>LVTVSS</u>	154
vhCDR1 ADI-71739 hlgG4 S228P kappa	<u>GSISSPDYPWG</u>	155
vhCDR2 ADI-71739 hlgG4 S228P kappa	<u>SIYYQGATYYNPSLKS</u>	156
vhCDR3 ADI-71739 hlgG4 S228P kappa	<u>ARGPYRQLFDY</u>	157
Full length heavy chain sequence ADI-71739 hlgG4 S228P kappa	QLQLQESGPGLVKPSSETLSLTCTVSGGSISSPDYPWGWI RQPPGKGLEWIGSIYYQGATYY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC ARGPYRQLFDYWGQGT LVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGKTITCNVDHKPSNTKVDKRVES KYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWY VDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD SDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	158
Variable light (vl) domain ADI-71739 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQG</u> <u>ISSWLAWYQQKPGKAPKLLIYA</u> <u>AASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> <u>ISSLPEDFATYYCQQGSVFPYT</u> <u>FGGGTKVEIK</u>	159
vlCDR1 ADI-71739 hlgG4 S228P kappa	<u>RASQG</u> <u>ISSWLA</u>	160
vlCDR2 ADI-71739 hlgG4 S228P kappa	<u>AASSLQS</u>	161
vlCDR3 ADI-71739 hlgG4 S228P kappa	<u>QQGSVFPYT</u>	162
Full length light chain sequence ADI-71739 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQG ISSWLAWYQQKPGKAPKLLIYA AASSLQSGVPSR FSGSGSGTDFTLT ISSLPEDFATYYC QQGSVFPYT FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP PREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	163

Figure 2L: ADI-71736 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71736 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSSETLSLTCTVSGGSISSEYGWGWIRQPPGKGLEWIGSIVNSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGLVTVSS</u>	164
vhCDR1 ADI-71736 hlgG4 S228P kappa	<u>GSISSEYGWG</u>	165
vhCDR2 ADI-71736 hlgG4 S228P kappa	<u>SIVNSGSTYYNPSLKS</u>	166
vhCDR3 ADI-71736 hlgG4 S228P kappa	<u>ARGPHRQVFDY</u>	167
Full length heavy chain sequence ADI-71736 hlgG4 S228P kappa	QLQLQESGPGLVKPSSETLSLTCTVSGGSISSEYGWGWIRQPPGKGLEWIGSIVNSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	168
Variable light (vl) domain ADI-71736 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKHLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGFSFPYTFGGGTKVEIK</u>	169
vlCDR1 ADI-71736 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	170
vlCDR2 ADI-71736 hlgG4 S228P kappa	<u>AASSLQS</u>	171
vlCDR3 ADI-71736 hlgG4 S228P kappa	<u>QQGFSFPYT</u>	172
Full length light chain sequence ADI-71736 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKHLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGFSFPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	173

Figure 2M: ADI-71707 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71707 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFRHYAMHWVRQAPGQRLEWMGWIHAGTGNTLYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGPTGTSWFDPWGQGTLLTVVSS</u>	174
vhCDR1 ADI-71707 hlgG4 S228P kappa	<u>YTFRHYAMH</u>	175
vhCDR2 ADI-71707 hlgG4 S228P kappa	<u>WIHAGTGNTLYSQKFQ</u>	176
vhCDR3 ADI-71707 hlgG4 S228P kappa	<u>ARGLGEVGPTGTSWFDP</u>	177
Full length heavy chain sequence ADI-71707 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGASVKVSCKASGYTFRHYAMHWVRQAPGQRLEWMGWIHAGTGNTLYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGLGEVGPTGTSWFDPWGQGTLLTVVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	178
Variable light (vl) domain ADI-71707 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYRLGPFTFGGGTKVEIK</u>	179
vlCDR1 ADI-71707 hlgG4 S228P kappa	<u>RASQSISSWLA</u>	180
vlCDR2 ADI-71707 hlgG4 S228P kappa	<u>EASSLES</u>	181
vlCDR3 ADI-71707 hlgG4 S228P kappa	<u>QQYRLGPFT</u>	182
Full length light chain sequence ADI-71707 hlgG4 S228P kappa	<u>DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYRLGPFTFGGGTKVEIK</u> RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSLSLTLLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	183

Figure 2N: ADI-66716 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-66716 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSDYYWGWI</u> <u>RQPPGKGLEWIGSIYYSGSTYY</u> <u>NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGLVTVSS</u>	184
vhCDR1 ADI-66716 hlgG4 S228P kappa	<u>GSISSSDYYWG</u>	185
vhCDR2 ADI-66716 hlgG4 S228P kappa	<u>SIYYSGSTYYNPSLKS</u>	186
vhCDR3 ADI-66716 hlgG4 S228P kappa	<u>ARGPHRQVFDY</u>	187
Full length heavy chain sequence ADI-66716 hlgG4 S228P kappa	QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSDYYWGWI RQPPGKGLEWIGSIYYSGSTYY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	188
Variable light (vl) domain ADI-66716 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLTISSLQPEDFATYYCQQGSSFPYTFGGGTKVEIK</u>	189
vlCDR1 ADI-66716 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	190
vlCDR2 ADI-66716 hlgG4 S228P kappa	<u>AASSLQS</u>	191
vlCDR3 ADI-66716 hlgG4 S228P kappa	<u>QQGSSFPYT</u>	192
Full length light chain sequence ADI-66716 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQGSSFPYTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	193

Figure 20: ADI-71728 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71728 hlgG4 S228P kappa	<u>QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYPISWVRQAPGQGLEWMGGIIPYSGTAVYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHGHETWGQGT</u> LVTVSS	194
vhCDR1 ADI-71728 hlgG4 S228P kappa	<u>GTFSEYPI</u> S	195
vhCDR2 ADI-71728 hlgG4 S228P kappa	<u>GIIPYSGTAVYAQKFQ</u> G	196
vhCDR3 ADI-71728 hlgG4 S228P kappa	<u>ARGRHGHET</u>	197
Full length heavy chain sequence ADI-71728 hlgG4 S228P kappa	QVQLVQSGAEVKKPGSSVKVSKASGGTFSEYPISWVRQAPGQGLEWMGGIIPYSGTAVYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRHGHETWGQGT LVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLG	198
Variable light (vl) domain ADI-71728 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> FSGSGSGTDFTLTISLQPEDFATYYC <u>QQVYSIPWT</u> FGGGTKVEIK	199
vlCDR1 ADI-71728 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	200
vlCDR2 ADI-71728 hlgG4 S228P kappa	<u>AASSLQ</u> S	201
vlCDR3 ADI-71728 hlgG4 S228P kappa	<u>QQVYSIPWT</u>	202
Full length light chain sequence ADI-71728 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> FSGSGSGTDFTLTISLQPEDFATYYCQQVYSIPWTFGGGTKVEIK RTVAAPSVPFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	203

Figure 2P: ADI-71741 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71741 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSDYPWGWIQQPGKLEWIGSIYYSGSTYY</u> <u>NPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGPYRQVFDYWGQGLVTVSS</u>	204
vhCDR1 ADI-71741 hlgG4 S228P kappa	<u>GSISSSDYPWG</u>	205
vhCDR2 ADI-71741 hlgG4 S228P kappa	<u>SIYYSGSTYYNPSLKS</u>	206
vhCDR3 ADI-71741 hlgG4 S228P kappa	<u>ARGPYRQVFDY</u>	207
Full length heavy chain sequence ADI-71741 hlgG4 S228P kappa	QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSDYPWGWIQQPGKLEWIGSIYYSGSTYY NPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGPYRQVFDYWGQGLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	208
Variable light (vl) domain ADI-71741 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLTISLQPEDFATYYCQQGNSFPYTFGGGTKVEIK</u>	209
vlCDR1 ADI-71741 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	210
vlCDR2 ADI-71741 hlgG4 S228P kappa	<u>AASSLQS</u>	211
vlCDR3 ADI-71741 hlgG4 S228P kappa	<u>QQGNSFPYT</u>	212
Full length light chain sequence ADI-71741 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISLQPEDFATYYCQQGNSFPYTFGGGTKVEIK RTVAAPSVPFIAPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	213

Figure 2Q: ADI-71742 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71742 hlgG4 S228P kappa	<u>QLQLQESSPGLVKPSETLSLTCTVSGGSISSPDYPGWIRQPPGKGLEWIGSIFYSGNTYY</u> <u>NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGT</u> <u>LVTVSS</u>	214
vhCDR1 ADI-71742 hlgG4 S228P kappa	<u>GSISSPDYPWG</u>	215
vhCDR2 ADI-71742 hlgG4 S228P kappa	<u>SIFYSGNTYYNPSLKS</u>	216
vhCDR3 ADI-71742 hlgG4 S228P kappa	<u>ARGPHRQVFDY</u>	217
Full length heavy chain sequence ADI-71742 hlgG4 S228P kappa	QLQLQESSPGLVKPSETLSLTCTVSGGSISSPDYPGWIRQPPGKGLEWIGSIFYSGNTYY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPHRQVFDYWGQGT LVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	218
Variable light (vl) domain ADI-71742 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLTISLQPEDFATYYCQQGWSFPYT</u> <u>FGGGTKVEIK</u>	219
vlCDR1 ADI-71742 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	220
vlCDR2 ADI-71742 hlgG4 S228P kappa	<u>AASSLQS</u>	221
vlCDR3 ADI-71742 hlgG4 S228P kappa	<u>QQGWSFPYT</u>	222
Full length light chain sequence ADI-71742 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISLQPEDFATYYCQQGWSFPYTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	223

Figure 2R: ADI-71744 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71744 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSSETLSLTCTVSGGSISSEYGWGWIRQPPGKGLEWIGSIVNSGSTYY</u> <u>NPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGPYRQVFDYWGQGLTVTVSS</u>	224
vhCDR1 ADI-71744 hlgG4 S228P kappa	<u>GSISSEYGWG</u>	225
vhCDR2 ADI-71744 hlgG4 S228P kappa	<u>SIVNSGSTYYNPSLKS</u>	226
vhCDR3 ADI-71744 hlgG4 S228P kappa	<u>ARGPYRQVFDY</u>	227
Full length heavy chain sequence ADI-71744 hlgG4 S228P kappa	QLQLQESGPGLVKPSSETLSLTCTVSGGSISSEYGWGWIRQPPGKGLEWIGSIVNSGSTYY NPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARGPYRQVFDYWGQGLTVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGKTITYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	228
Variable light (vl) domain ADI-71744 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVITITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLTISLQPEDFATYYCQQGWSFPYTFGGGTKVEIK</u>	229
vlCDR1 ADI-71744 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	230
vlCDR2 ADI-71744 hlgG4 S228P kappa	<u>AASSLQS</u>	231
vlCDR3 ADI-71744 hlgG4 S228P kappa	<u>QQGWSFPYT</u>	232
Full length light chain sequence ADI-71744 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVITITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISLQPEDFATYYCQQGWSFPYTFGGGTKVEIK RTVAAPSVPFI FPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	233

Figure 2S: ADI-71753 hlgG4 S228P kappa

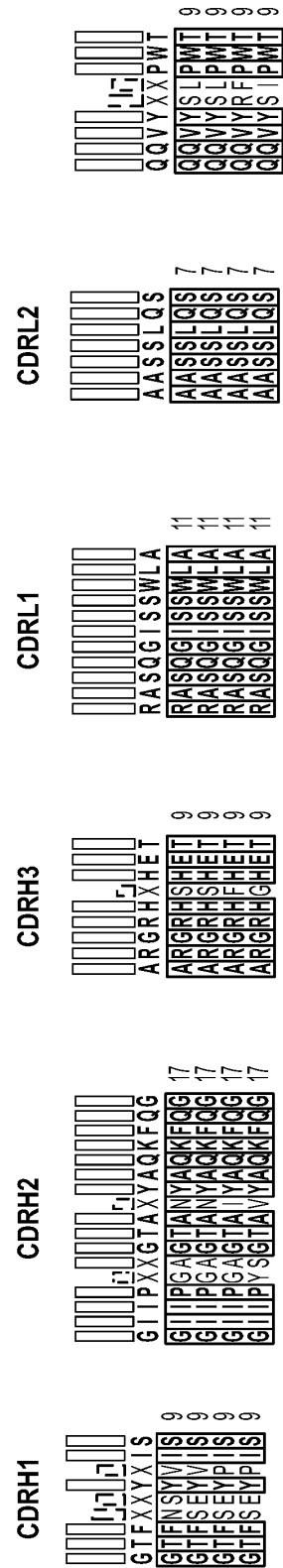
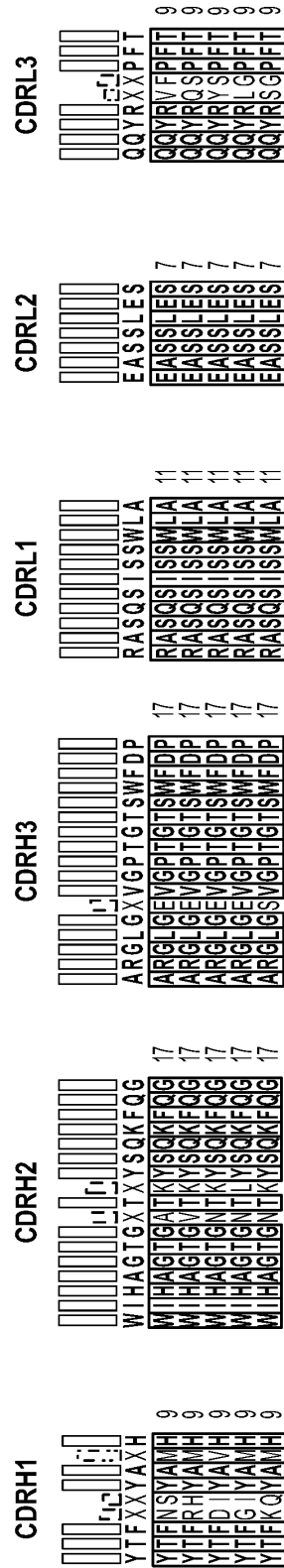
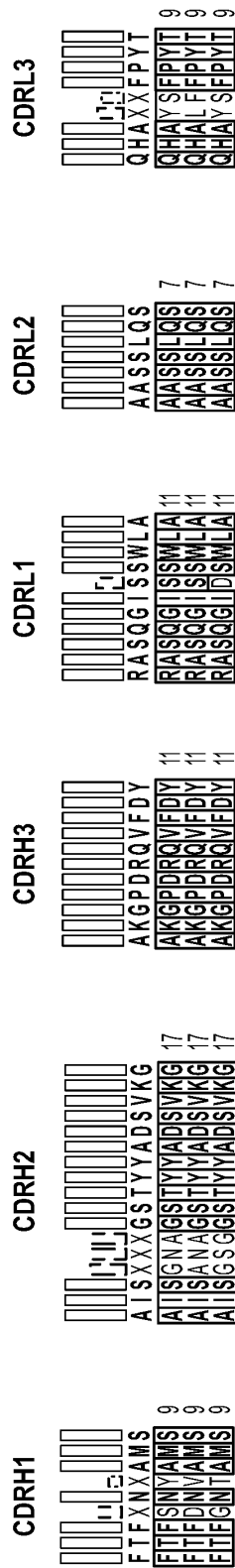
What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71753 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSETLSLTCTVSGGSIFSSDYYWSWIRQPPGKGLEWIGVIAYSGSTYY</u> <u>NPSLKS</u> RVTISVDTSKNQFSLKLSSATAADTAVYYC <u>ARGPFRQVFDY</u> WGQGLTVTVSS	234
vhCDR1 ADI-71753 hlgG4 S228P kappa	<u>GSIFSSDYYWS</u>	235
vhCDR2 ADI-71753 hlgG4 S228P kappa	<u>VIAYSGSTYYNPSLKS</u>	236
vhCDR3 ADI-71753 hlgG4 S228P kappa	<u>ARGPFRQVFDY</u>	237
Full length heavy chain sequence ADI-71753 hlgG4 S228P kappa	QLQLQESGPGLVKPSETLSLTCTVSGGSIFSSDYYWSWIRQPPGKGLEWIGVIAYSGSTYY NPSLKS RVTISVDTSKNQFSLKLSSATAADTAVYYCARGPFRQVFDYWGQGLTVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLG	238
Variable light (vl) domain ADI-71753 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> ISSLPEDFATYYC <u>QQGSSFPYT</u> FGGGTKVEIK	239
vlCDR1 ADI-71753 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	240
vlCDR2 ADI-71753 hlgG4 S228P kappa	<u>AASSLQS</u>	241
vlCDR3 ADI-71753 hlgG4 S228P kappa	<u>QQGSSFPYT</u>	242
Full length light chain sequence ADI-71753 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> ISSLPEDFATYYC <u>QQGSSFPYT</u> FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	243

Figure 2T: ADI-71755 hlgG4 S228P kappa

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain ADI-71755 hlgG4 S228P kappa	<u>QLQLQESGPGLVKPSETLSLTCTVSGGSISSPDYPWGWI</u> <u>RQPPGKGLEWIGSIFYSGNTYY</u> <u>NPSLKS</u> <u>SRVTISVDTSKNQFSLKLSSVTAADTAVYYC</u> <u>ARGPFRQVFDYWGQGLVTVSS</u>	244
vhCDR1 ADI-71755 hlgG4 S228P kappa	<u>GSISSPDYPWG</u>	245
vhCDR2 ADI-71755 hlgG4 S228P kappa	<u>SIFYSGNTYYNPSLKS</u>	246
vhCDR3 ADI-71755 hlgG4 S228P kappa	<u>ARGPFRQVFDY</u>	247
Full length heavy chain sequence ADI-71755 hlgG4 S228P kappa	QLQLQESGPGLVKPSETLSLTCTVSGGSISSPDYPWGWI RQPPGKGLEWIGSIFYSGNTYYNPSLKS SRVTISVDTSKNQFSLKLSSVTAADTAVYYC ARGPFRQVFDYWGQGLVTVSSASTKGPSVF FLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSS VTVPSSSLGTTKTYTCNVDPKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVDSQEDPEVQF NWIYVDGVEVHNAKTKPREEQFNSTYRVV SVLTFLHQDWLNGKEYKCKVSNKGLPSSIE KTIKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYK TTPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMEALHNHYTQKSLSLGL	248
Variable light (vl) domain ADI-71755 hlgG4 S228P kappa	<u>DIQMTQSPSSVSASVGDRVTITCRASQGISSWLA</u> <u>WYQQKPGKAPKLLIYAASSLQSGVPSR</u> <u>FSGSGSGTDFTLT</u> <u>ISSLPEDFATYYCQQGWSFPYT</u> <u>FGGGTKVEIK</u>	249
vlCDR1 ADI-71755 hlgG4 S228P kappa	<u>RASQGISSWLA</u>	250
vlCDR2 ADI-71755 hlgG4 S228P kappa	<u>AASSLQS</u>	251
vlCDR3 ADI-71755 hlgG4 S228P kappa	<u>QQGWSFPYT</u>	252
Full length light chain sequence ADI-71755 hlgG4 S228P kappa	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLA WYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLPEDFATYYC QQGWSFPYTFGGGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTY LSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC	253

Figure 2U: AB-837 mIgG1 D265A lambda

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain AB-837 mIgG1 D265A lambda	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGLIDPTNSD TRYSPSFQGGVTTISADKSI STAYLQWSSLKASDTAMYYCAREPSLYVSDTGYPWRGY DYPGFAYWGQGT LVT VSS	874
vhCDR1 AB-837 mIgG1 D265A lambda	GYSFTSYW	875
vhCDR2 AB-837 mIgG1 D265A lambda	IDPTNSDT	876
vhCDR3 AB-837 mIgG1 D265A lambda	AREPSLYVSDTGYPWRGYDYPGFAY	877
Full length heavy chain sequence AB-837 mIgG1 D265A lambda	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGLIDPTNSD TRYSPSFQGGVTTISADKSI STAYLQWSSLKASDTAMYYCAREPSLYVSDTGYPWRGY DYPGFAYWGQGT LVT VSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTV TWNSSGLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKK IVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTIITLTPKVT CVVVAISKDDPEVQFS WFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE KTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPEN YKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK	878
Variable light (vl) domain AB-837 mIgG1 D265A lambda	DIELTQPPSVSVSPGQTASITCSGDNLPKSVHWYQQKPGQAPV LVIYSYKSERPSG I PERFGSNGSNTATLTISGTQAEDEADYYCSAYDFTSVVFGGGTKLTVL	879
vlCDR1 AB-837 mIgG1 D265A lambda	<u>NLPKSKS</u>	880
vlCDR2 AB-837 mIgG1 D265A lambda	<u>SYKSER</u>	881
vlCDR3 AB-837 mIgG1 D265A lambda	<u>SAYDFTSVV</u>	882
Full length light chain sequence AB-837 mIgG1 D265A lambda	DIELTQPPSVSVSPGQTASITCSGDNLPKSVHWYQQKPGQAPV LVIYSYKSERPSG I PERFGSNGSNTATLTISGTQAEDEADYYCSAYDFTSVVFGGGTKLTVL GQPKSSPSVTLFPPSSSELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQG METTQPSKQSNKYMSSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRADCS	883



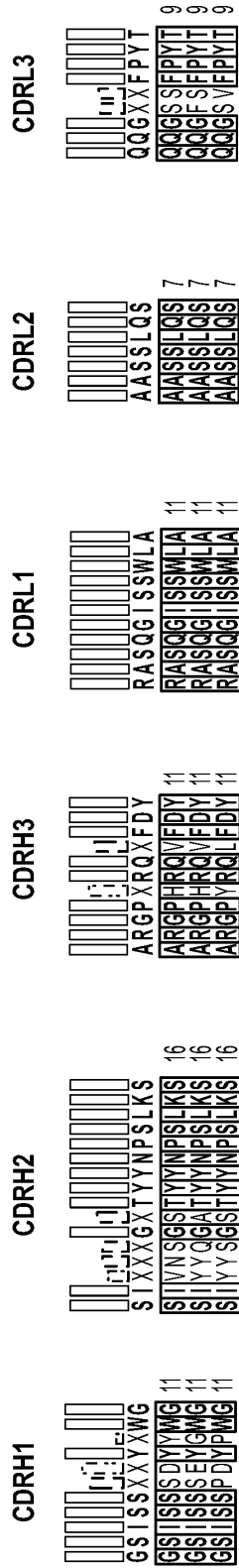


FIG. 3D

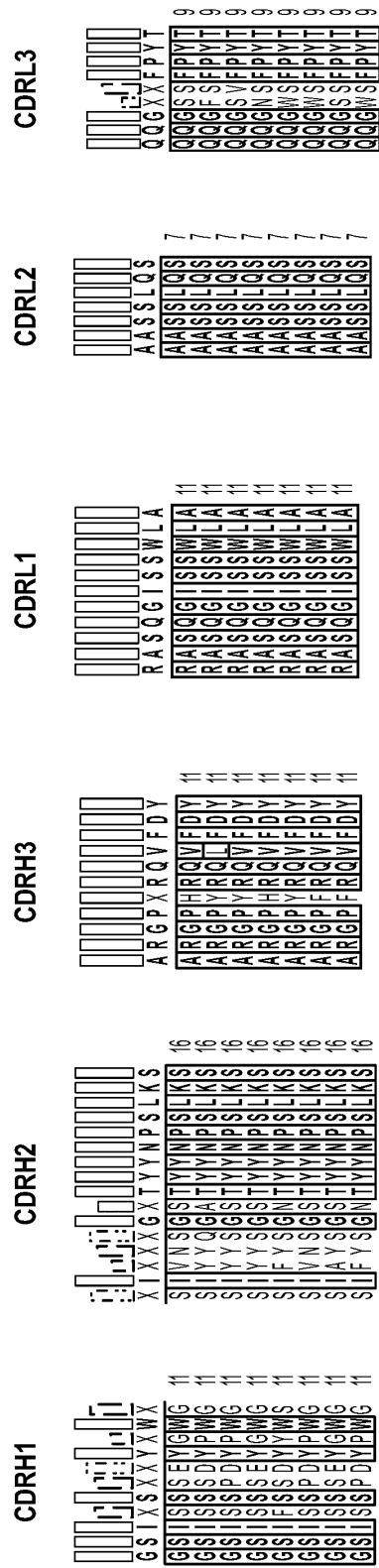
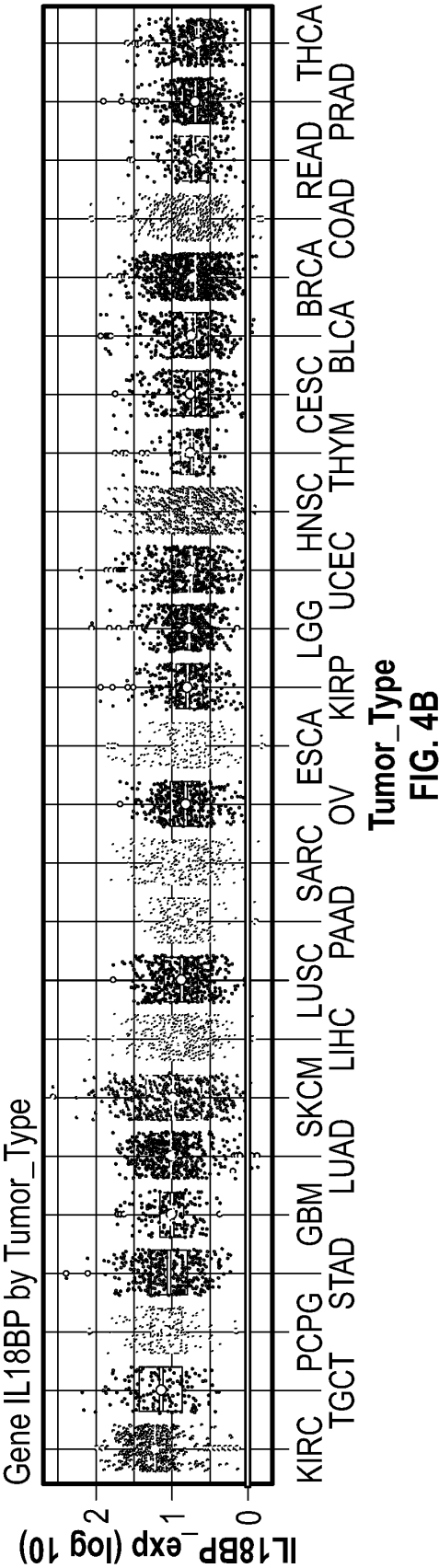
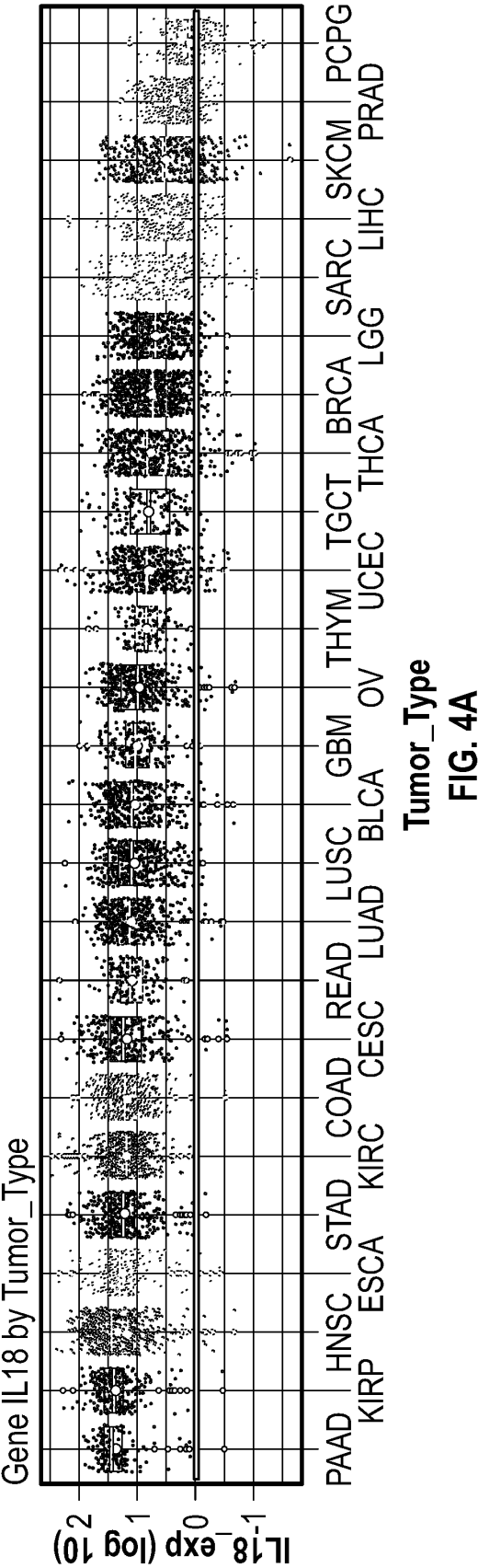


FIG. 3E



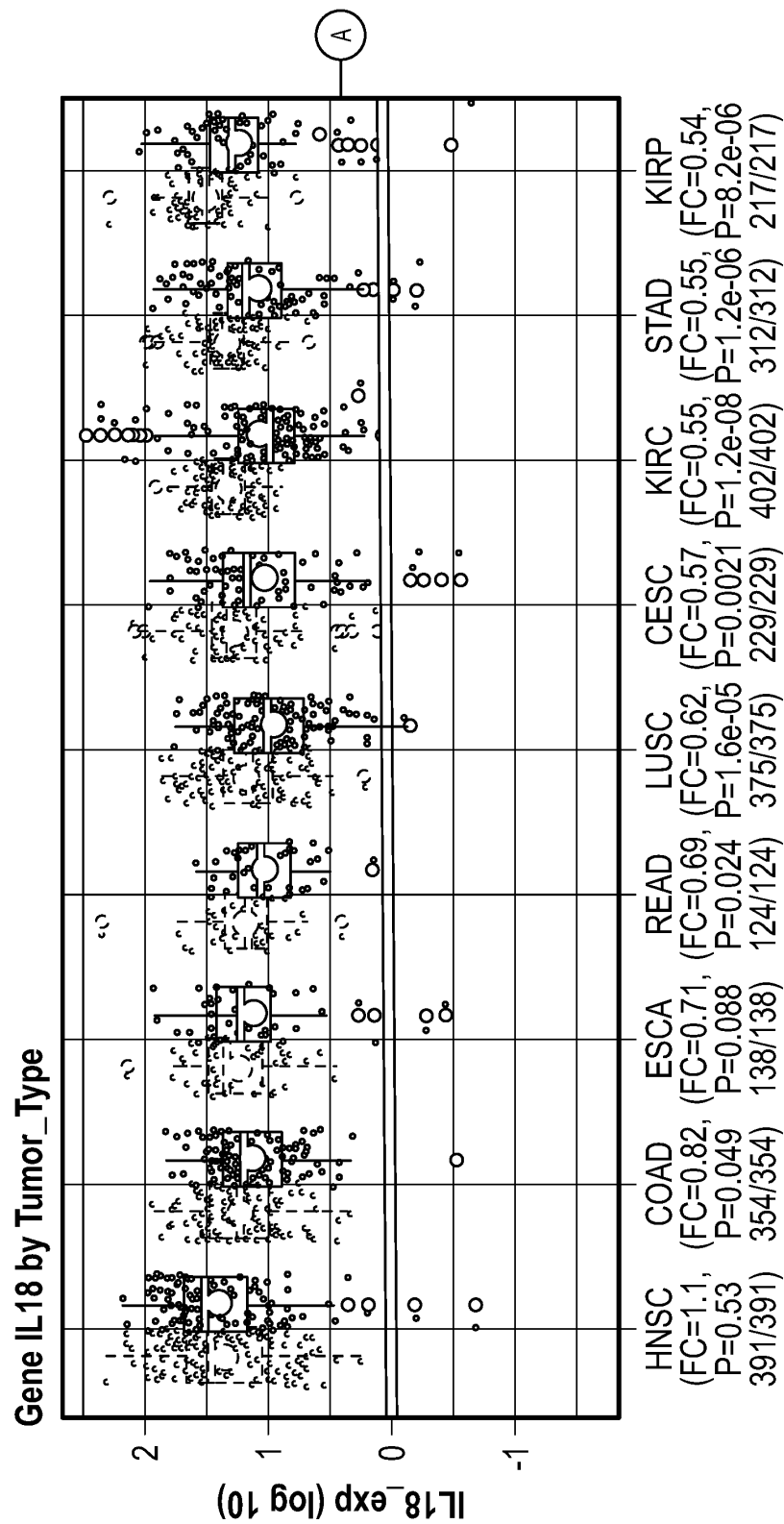


FIG. 5A

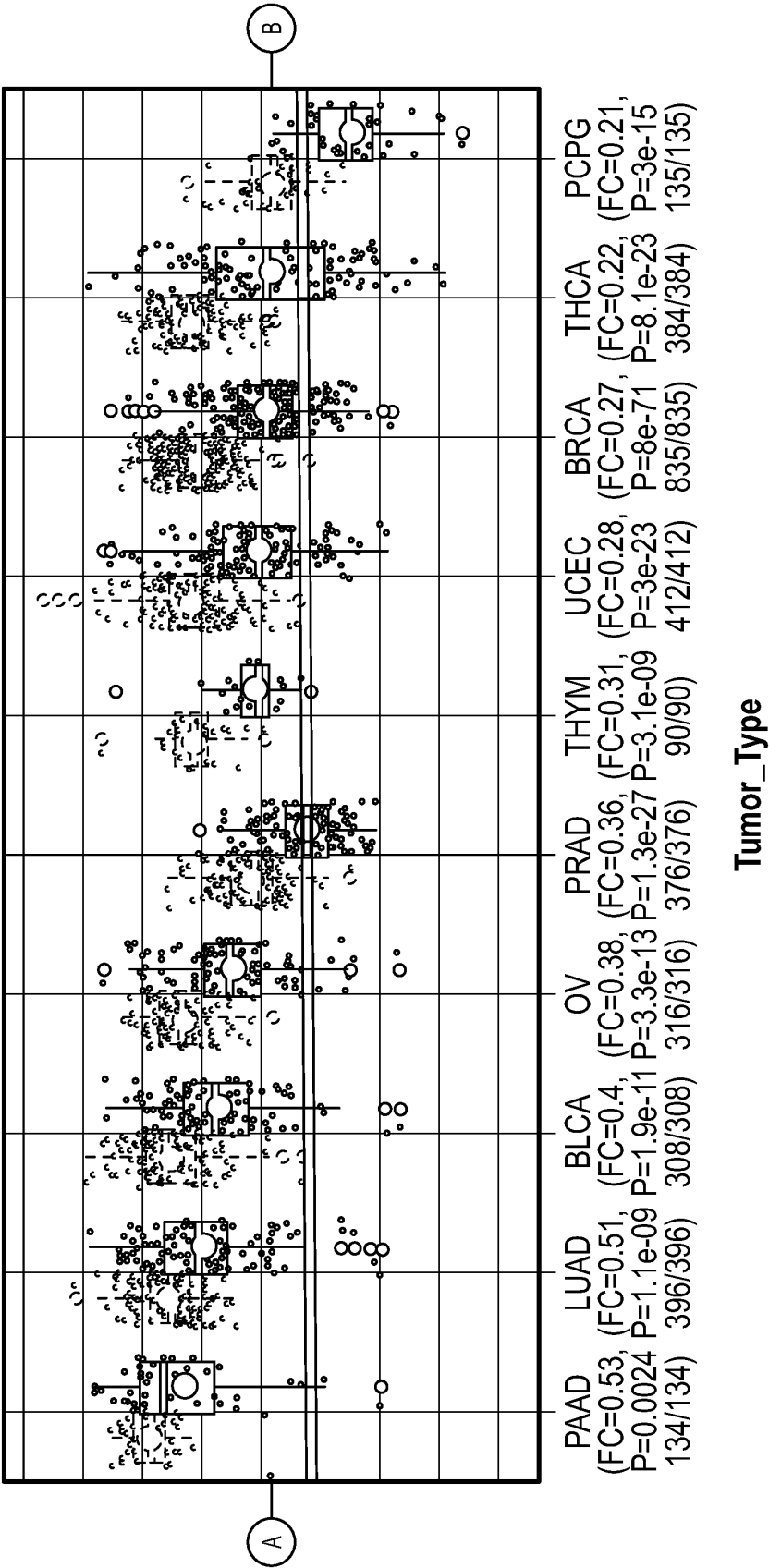


FIG. 5A (Continued)



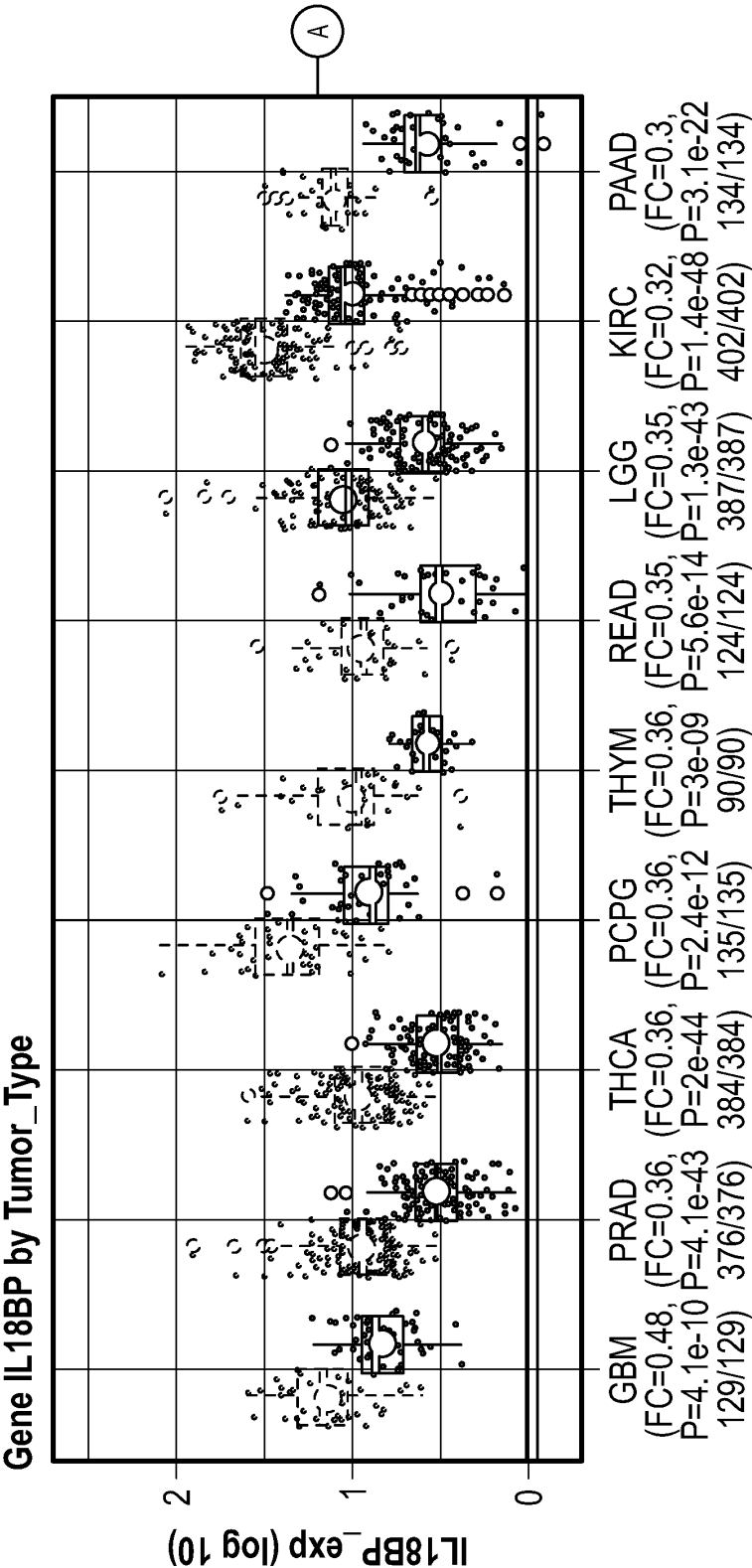


FIG. 5B

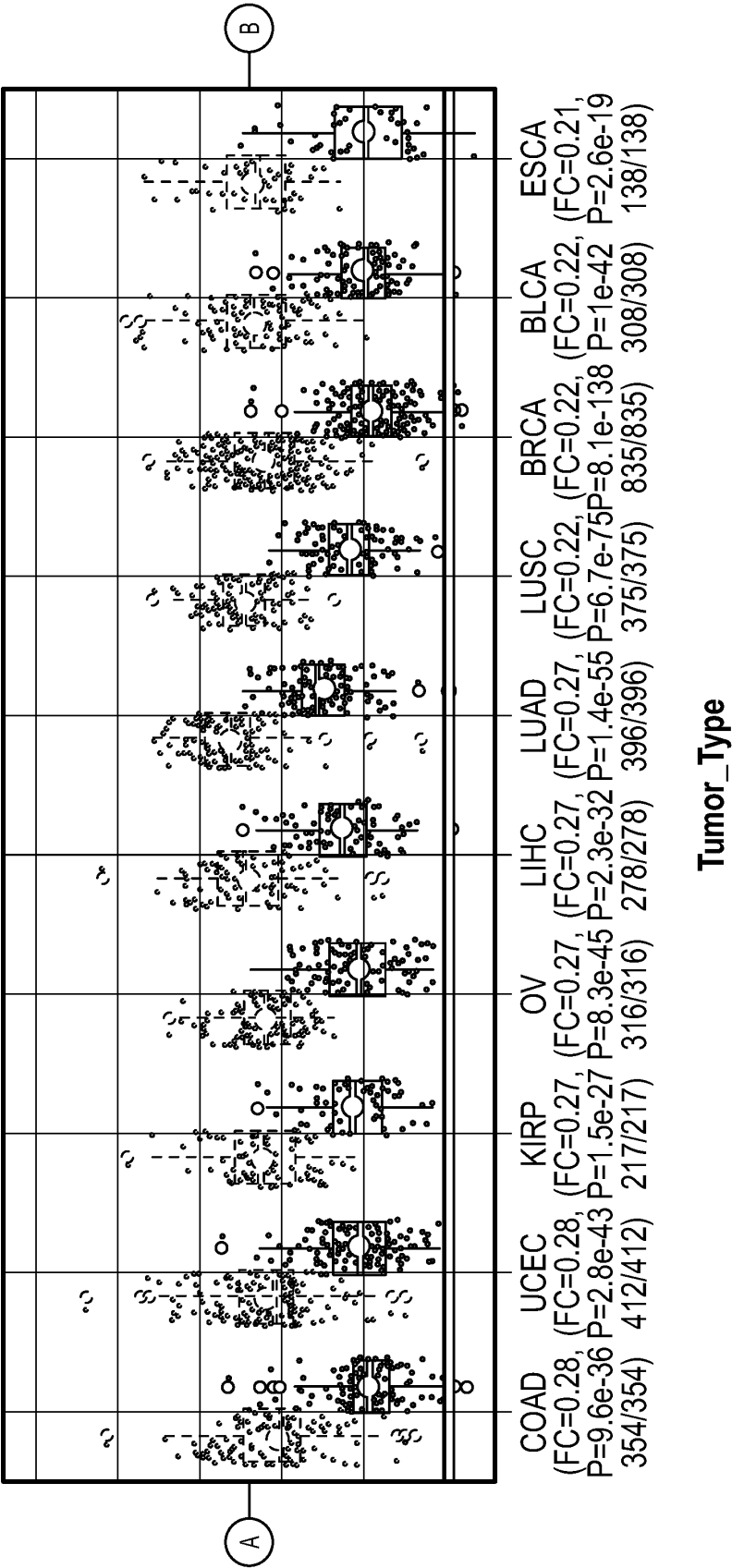


FIG. 5B (Continued)

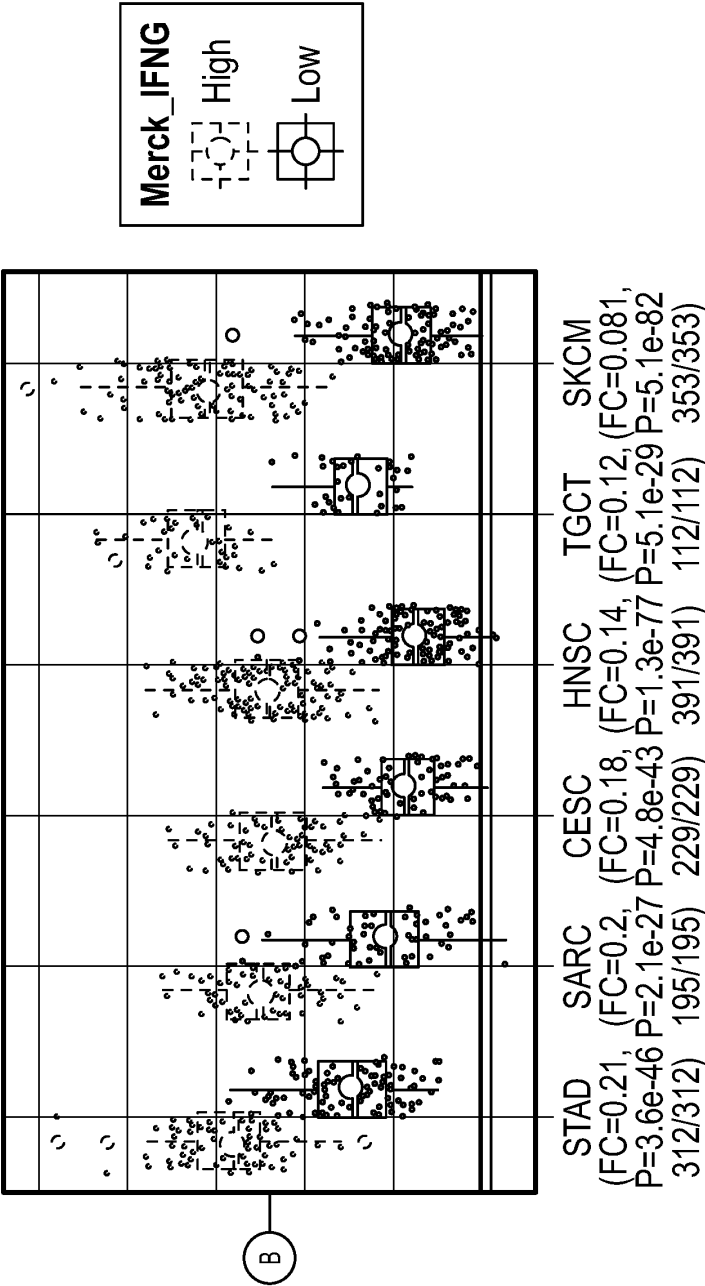


FIG. 5B (Continued)

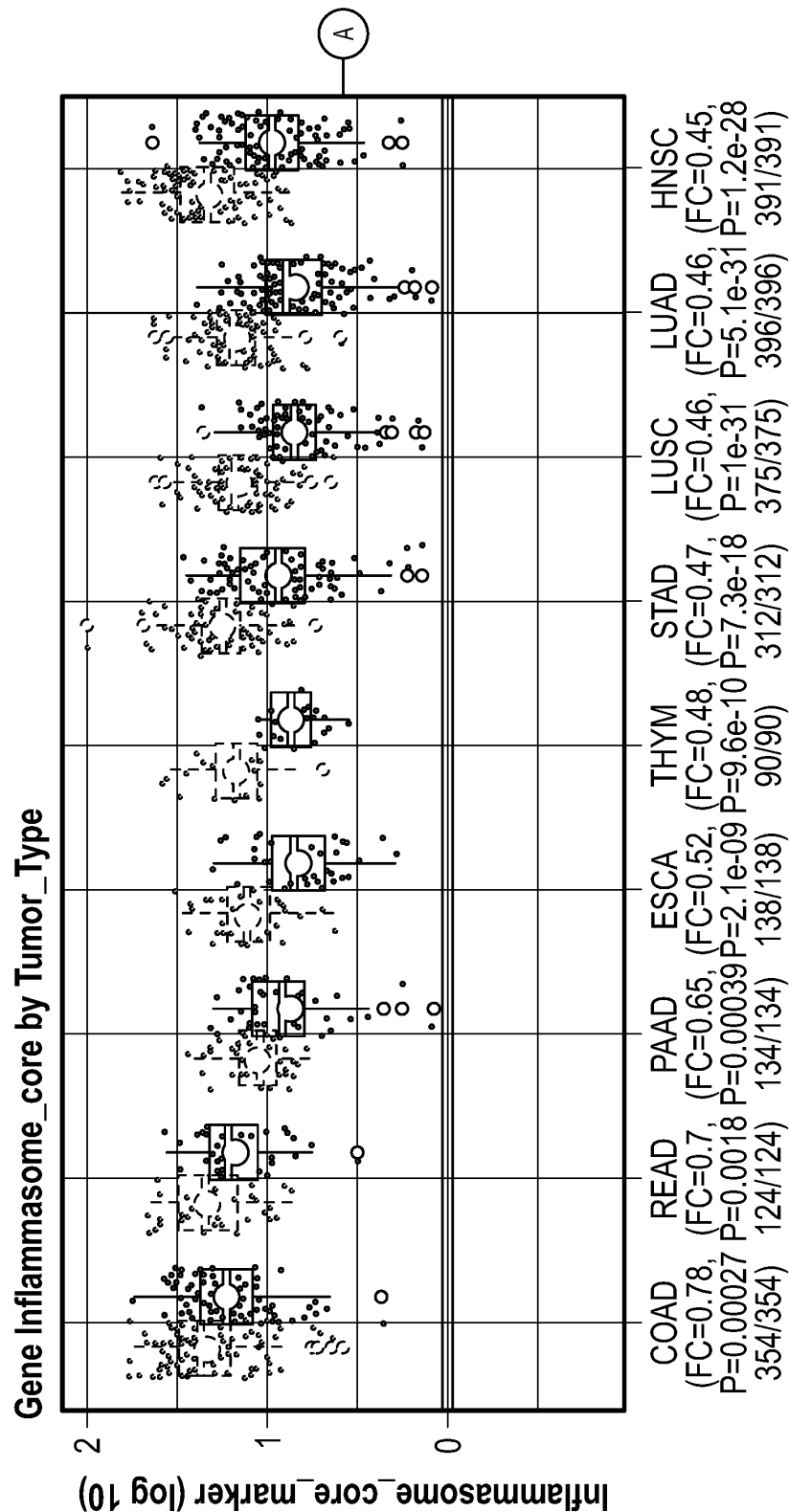


FIG. 6A



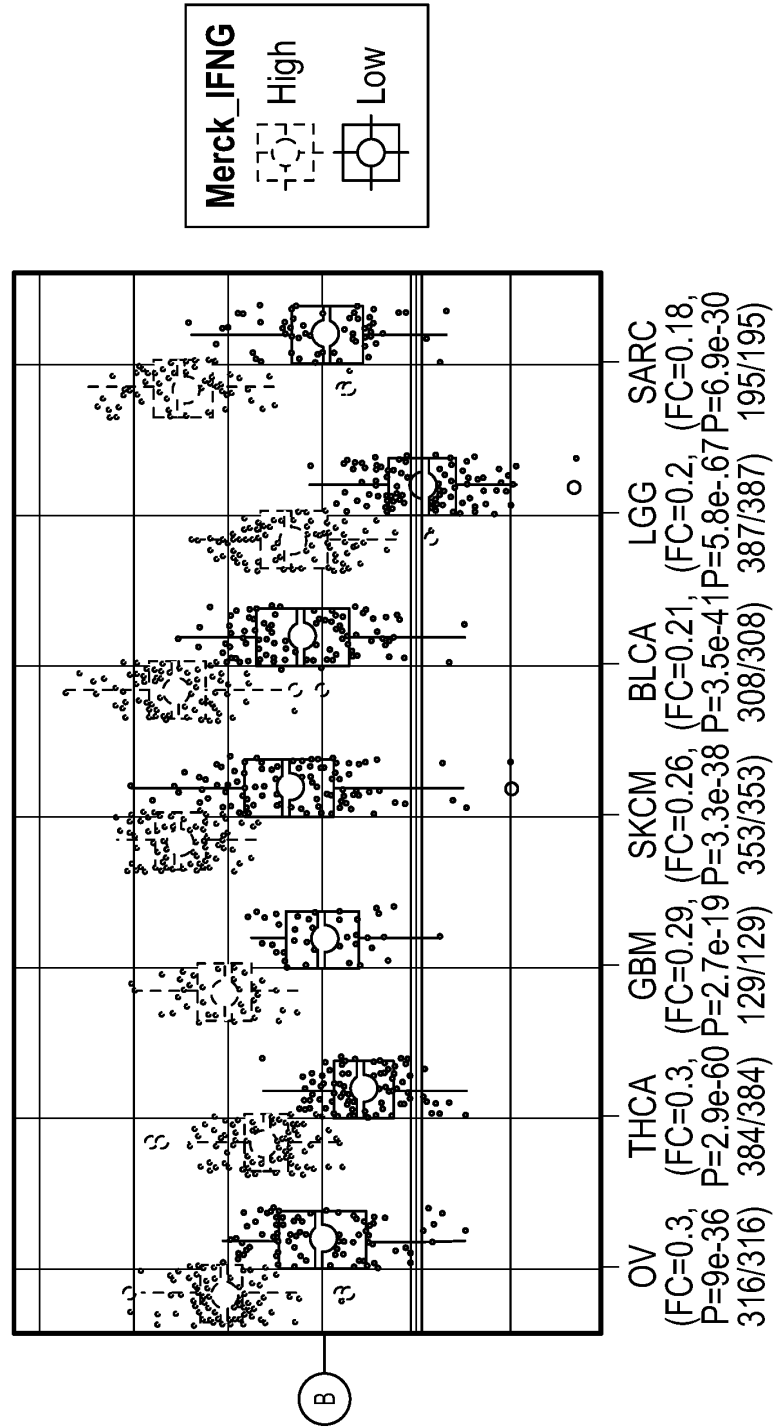


FIG.6A (Continued)

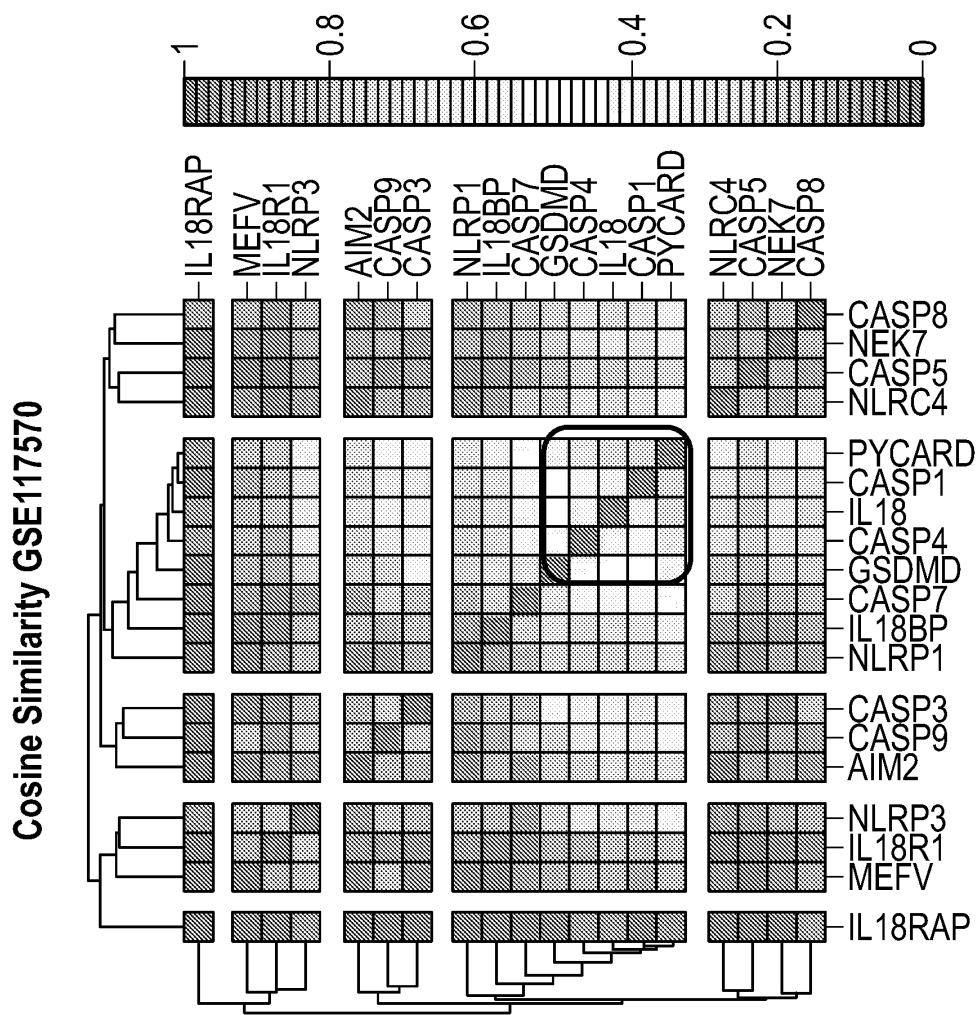


FIG. 6B

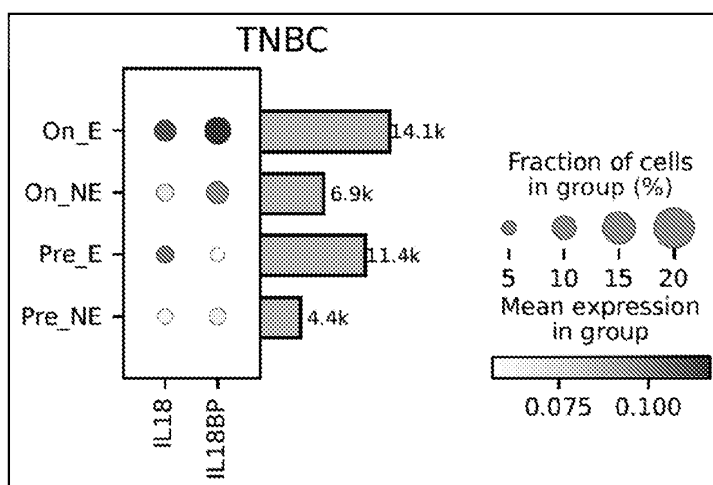
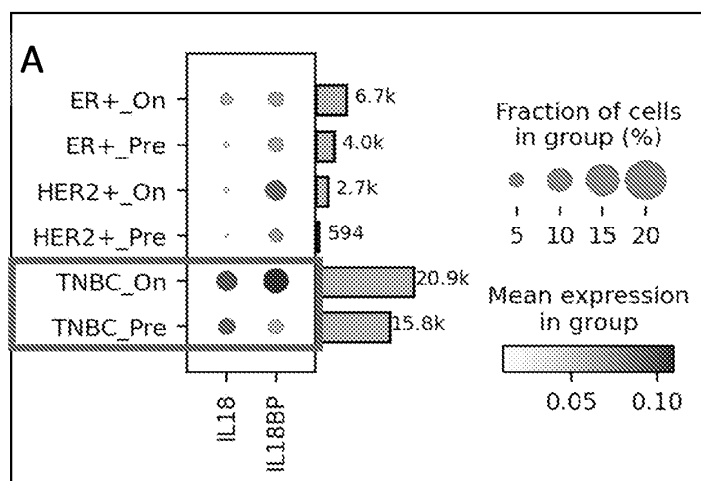
Figure 7

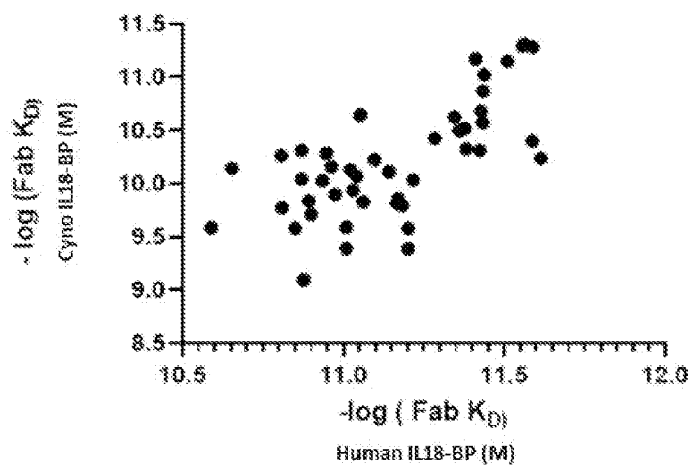
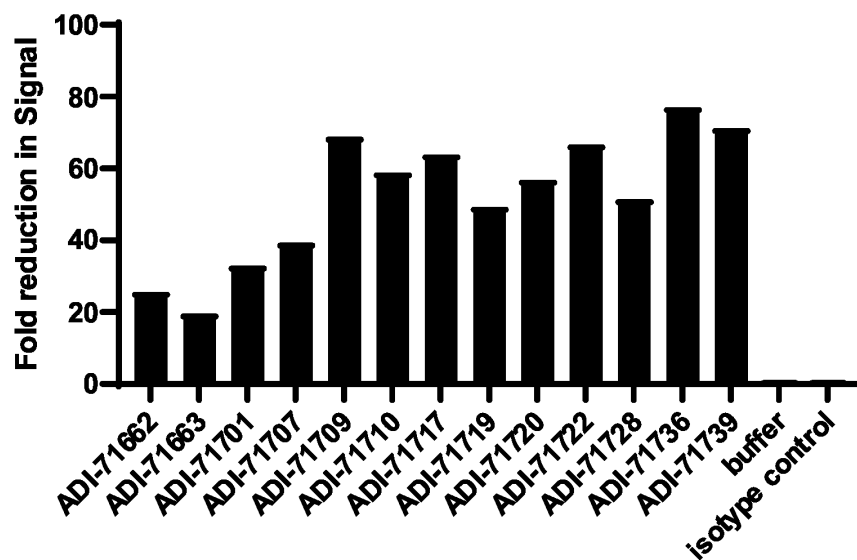
Figure 8**Figure 9**

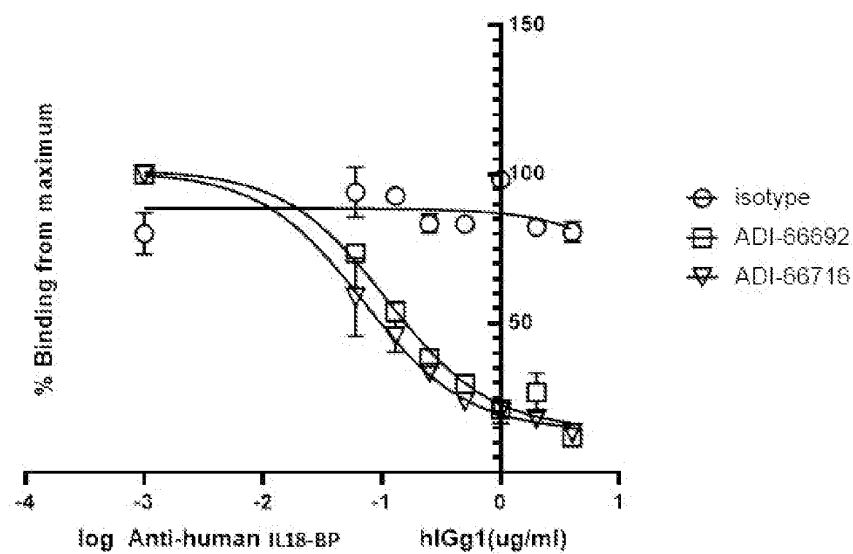
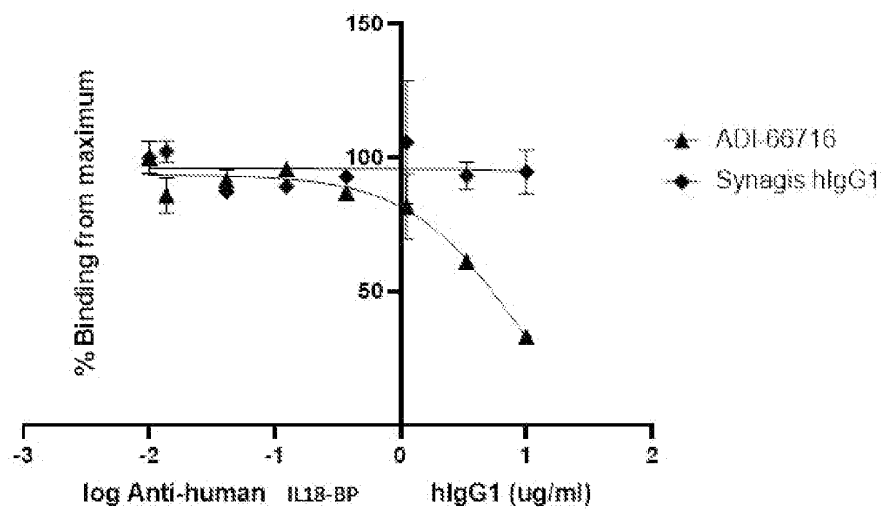
Figure 10**Figure 11**

Figure 12

	IC50 (ug/ml)	
	Human IL18- IL18BP	Cyno IL18-IL18BP
ADI-66692	0.278	
ADI-66716	0.2076	8.183

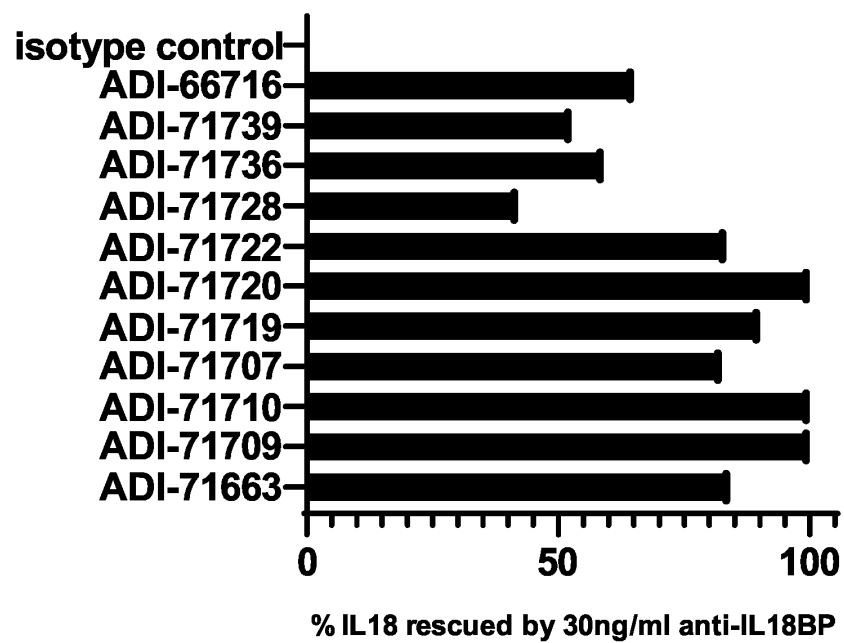
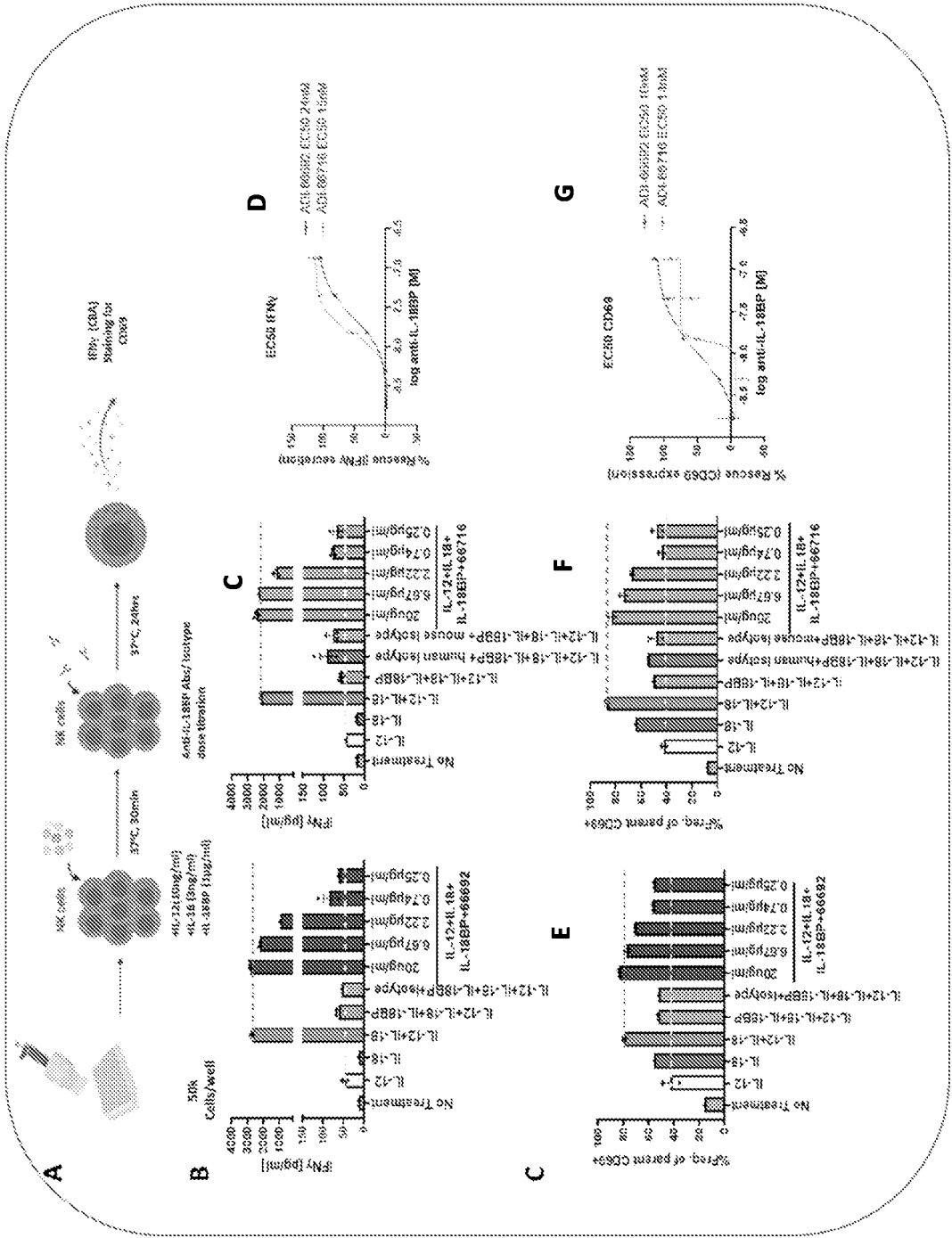
Figure 13

Figure 14A-14G



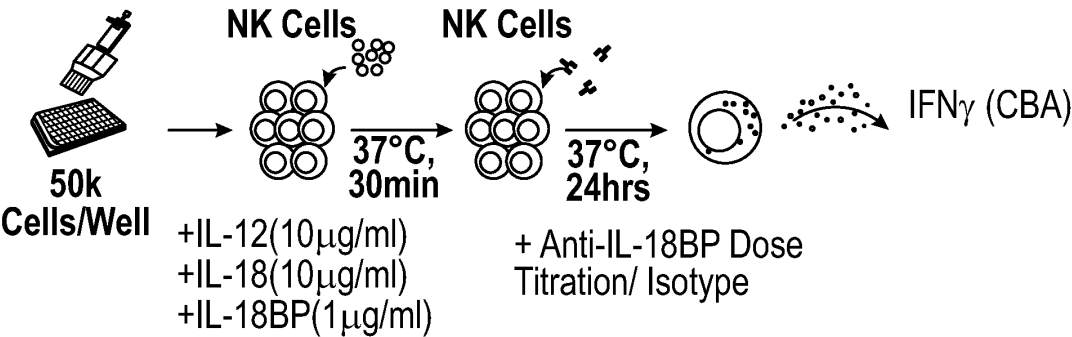


FIG. 14H

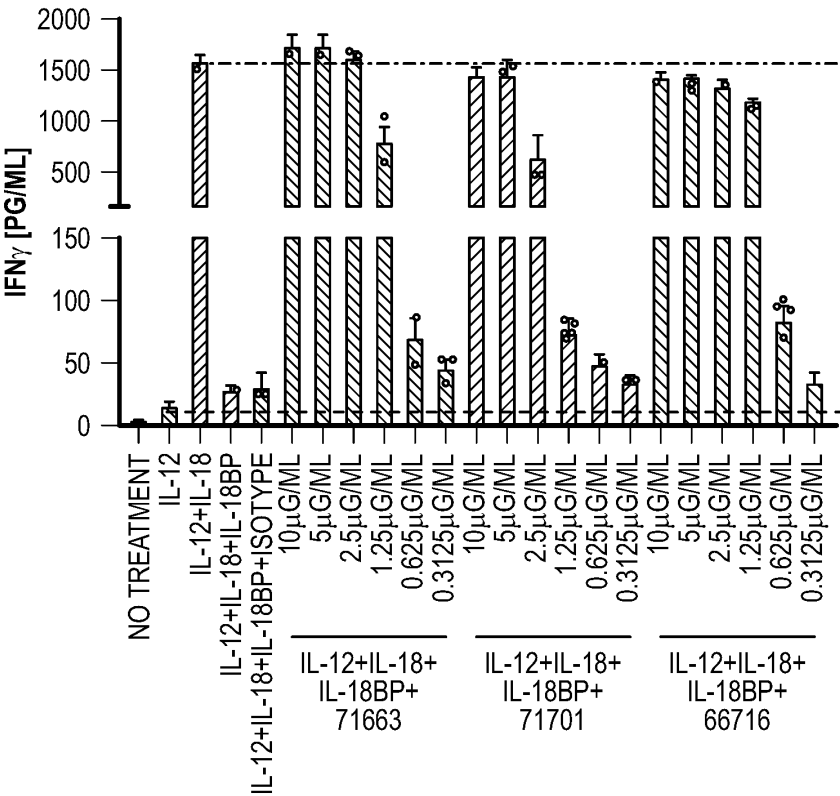


FIG. 14I



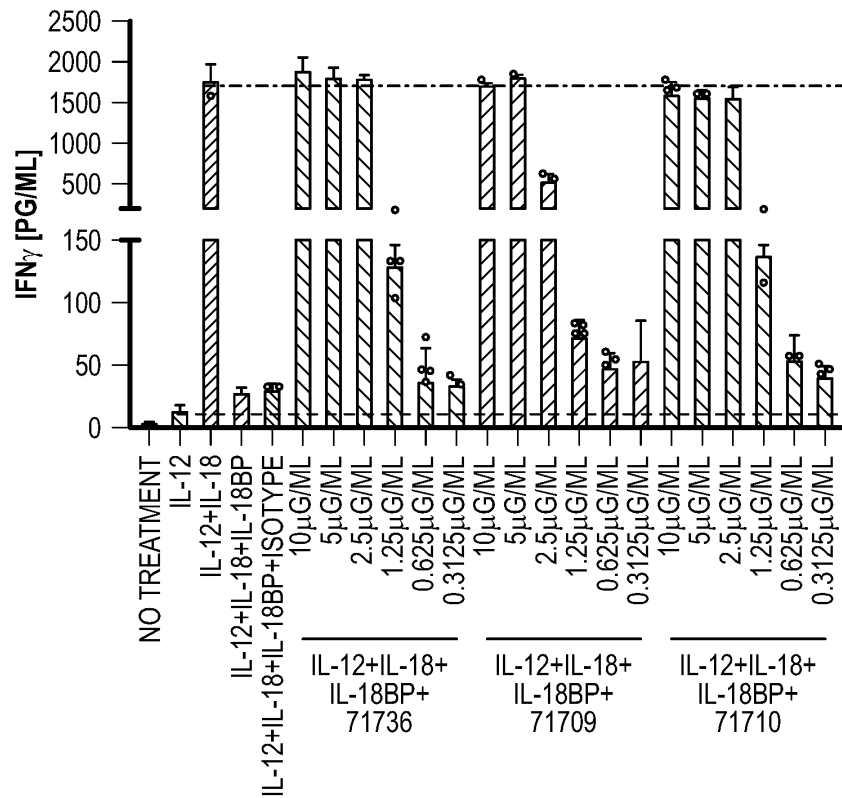


FIG. 14L

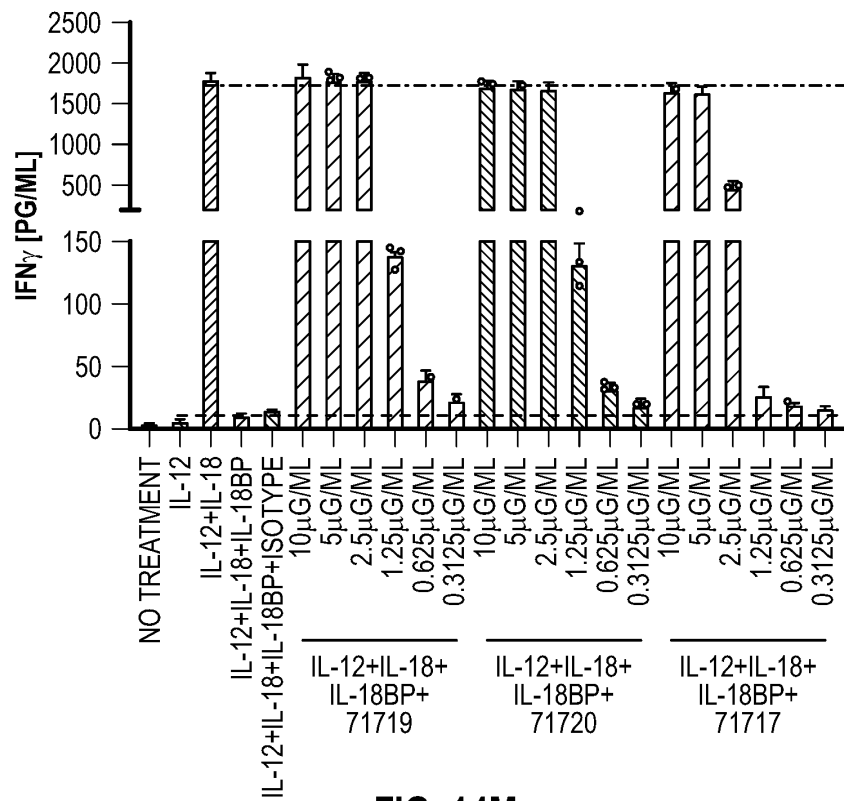


FIG. 14M

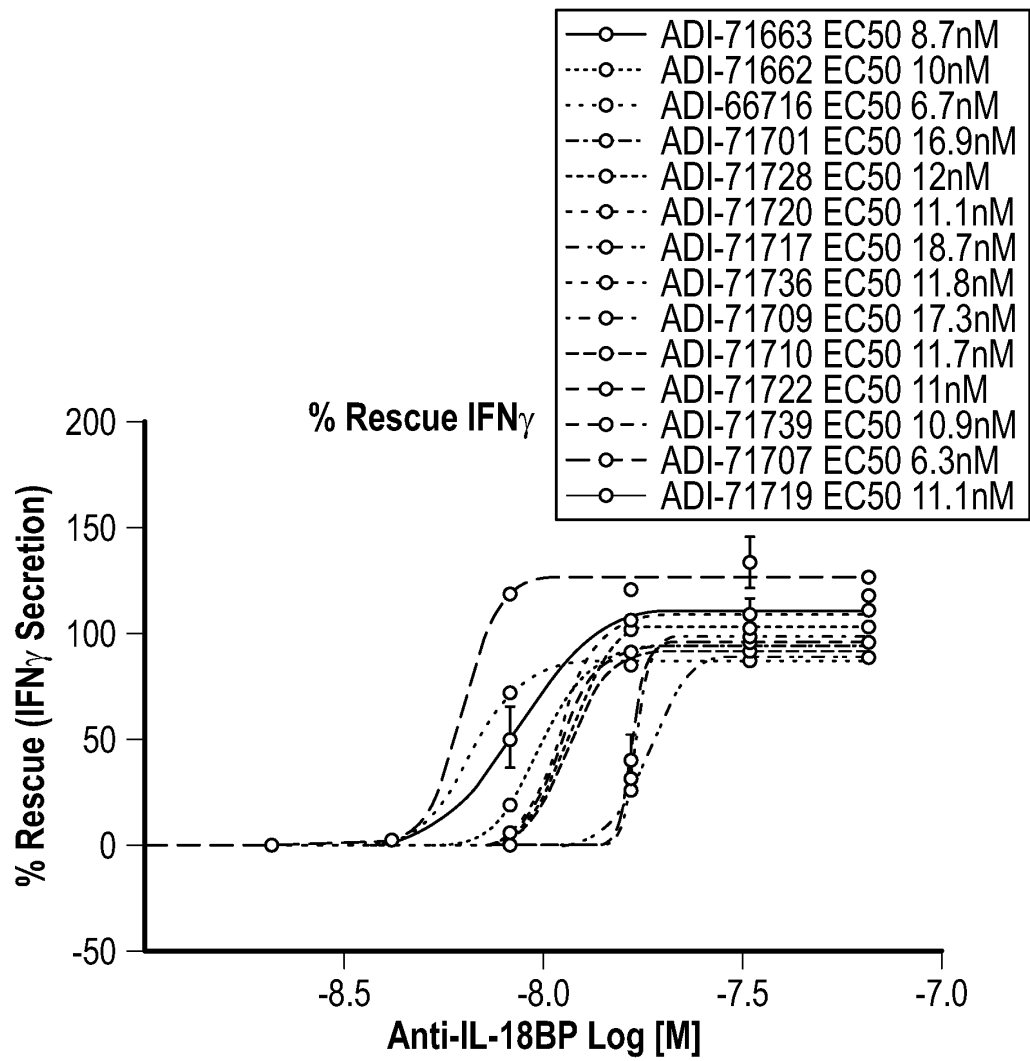


FIG. 14N

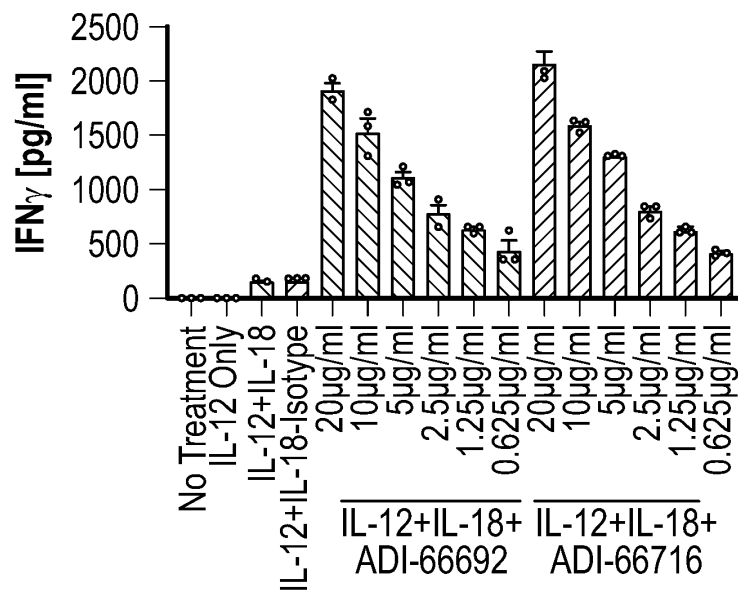
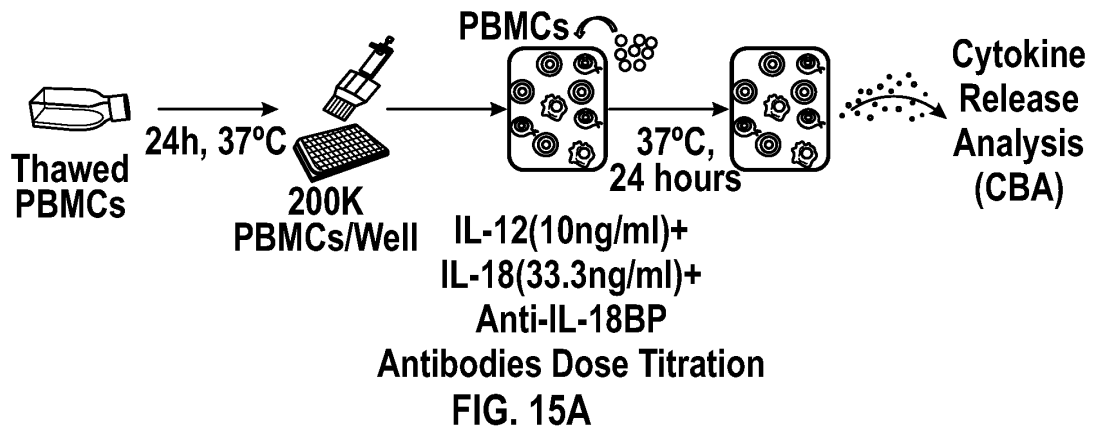


FIG. 15B

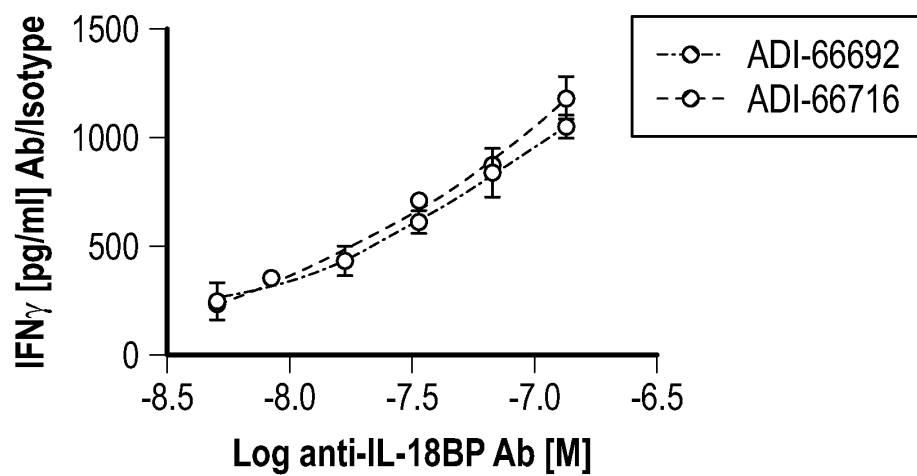


FIG. 15C

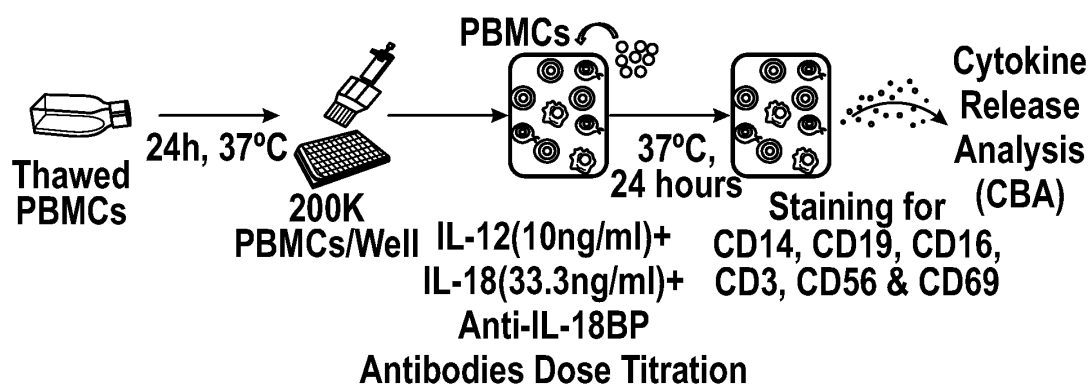


FIG. 15D

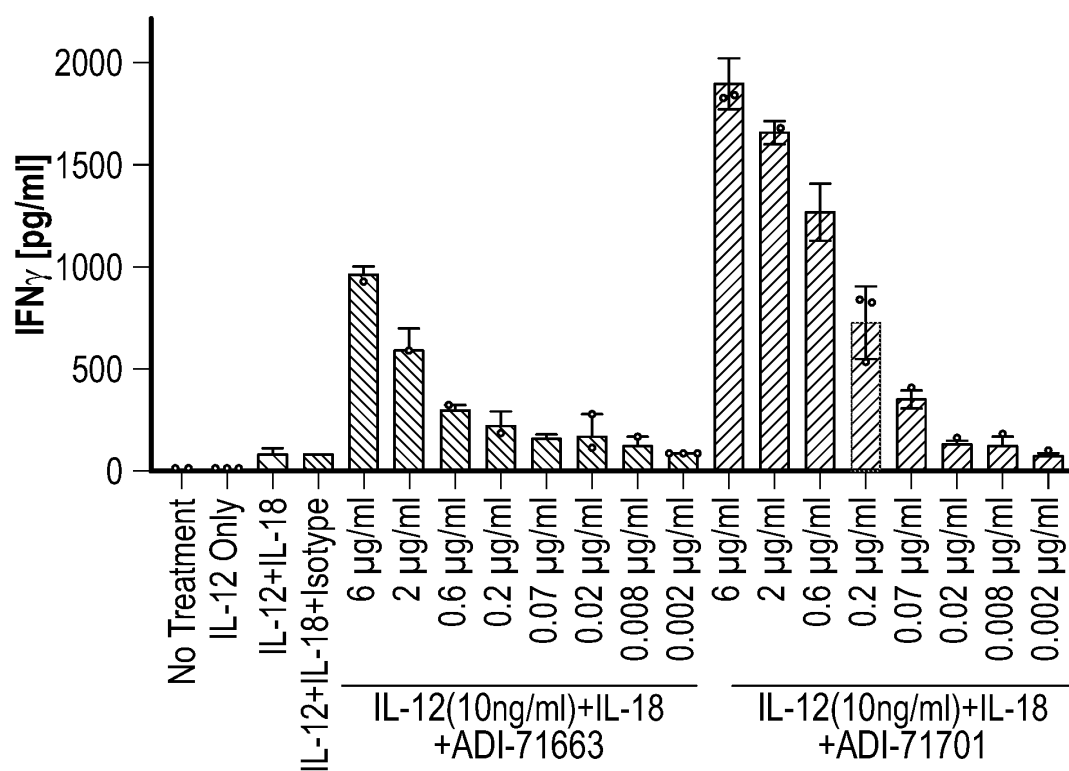
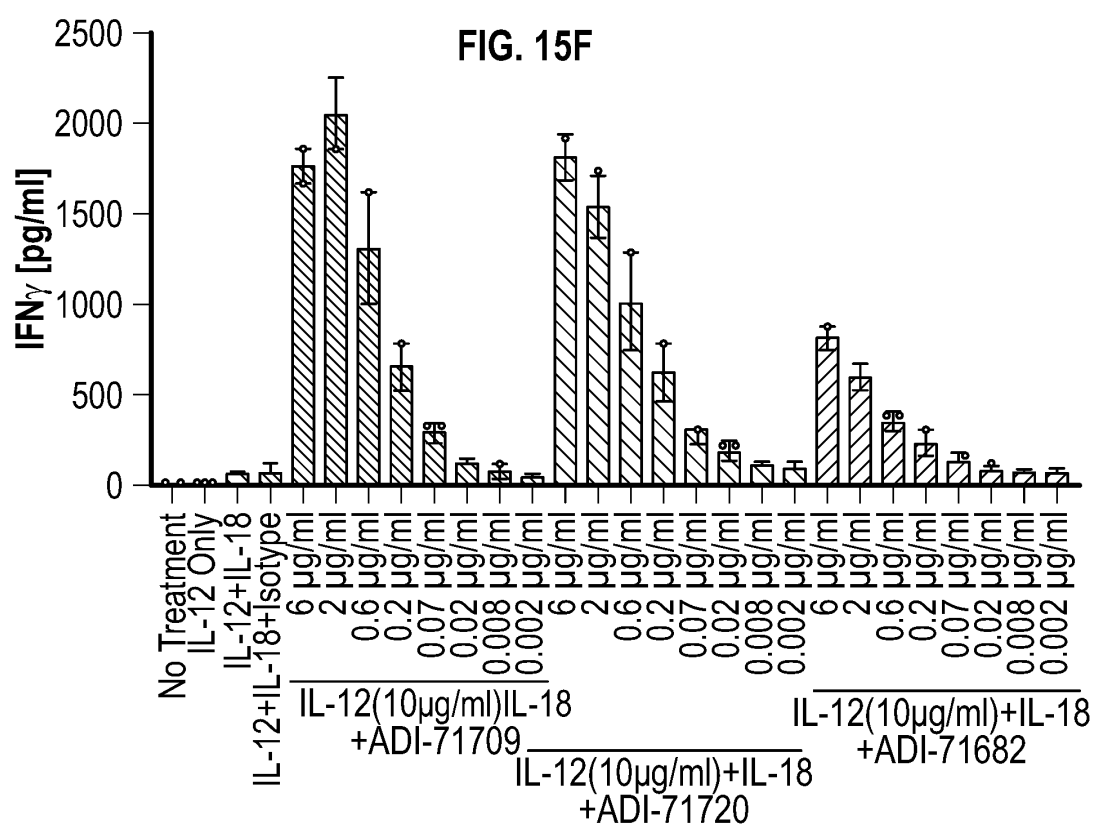
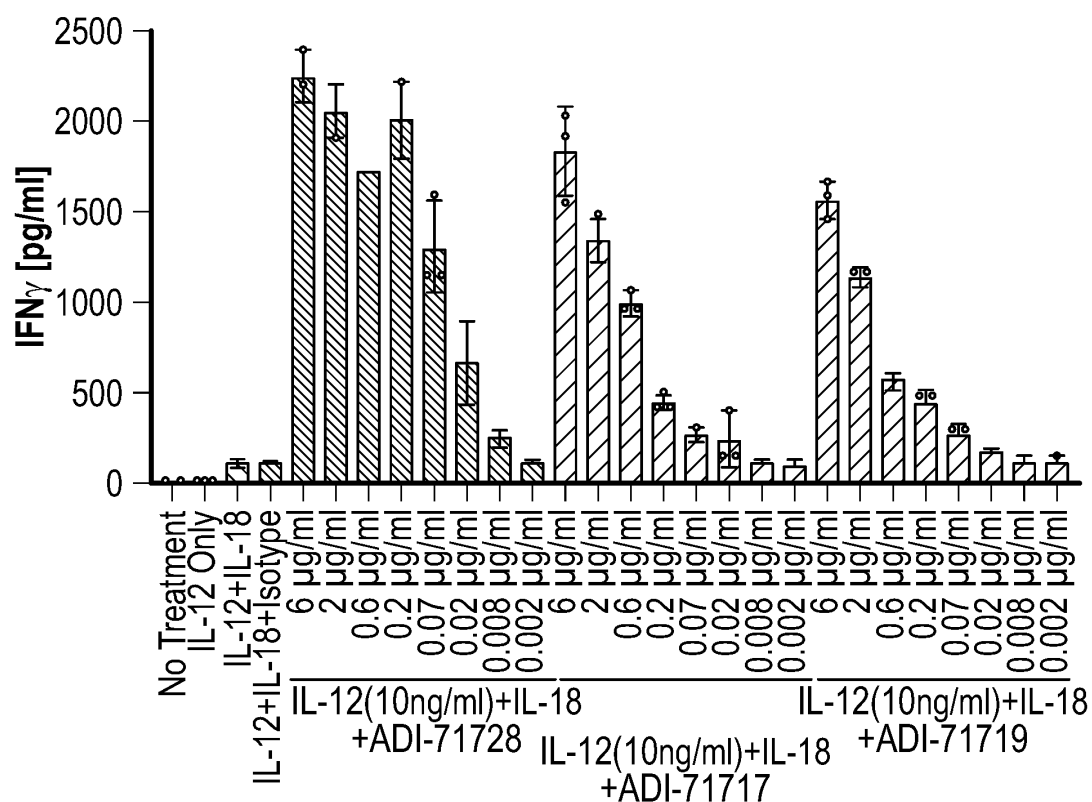


FIG. 15E



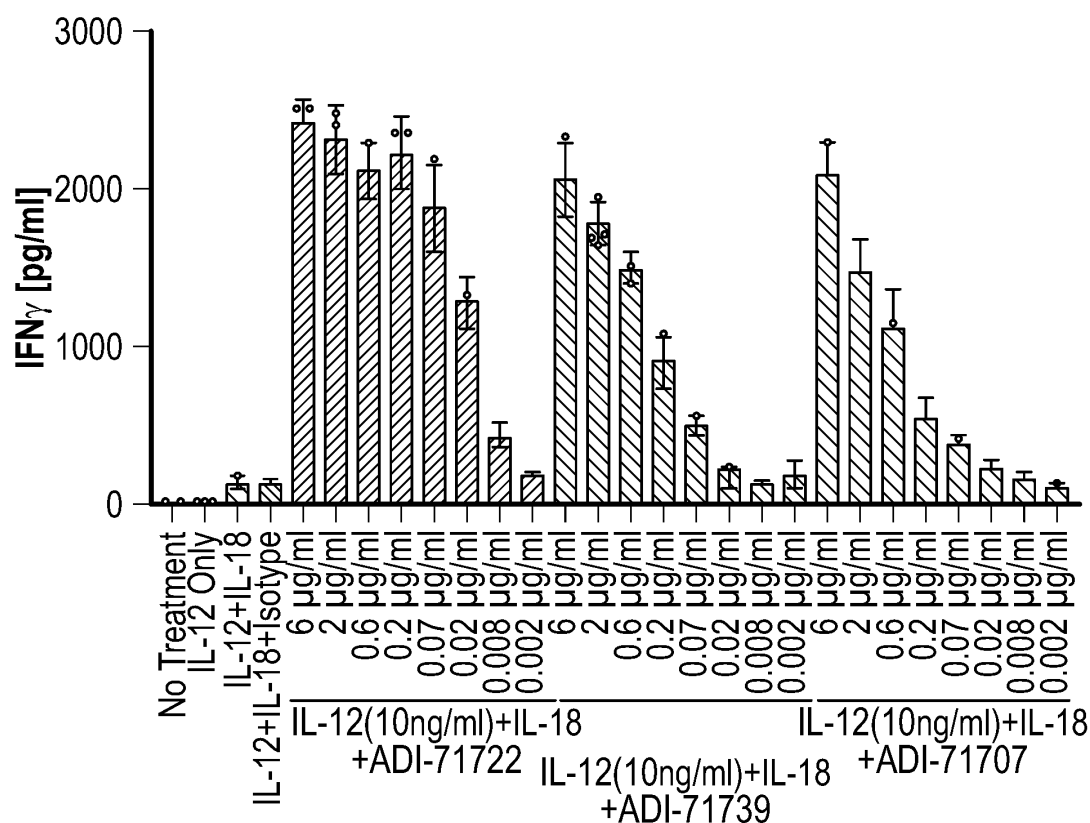


FIG. 15H

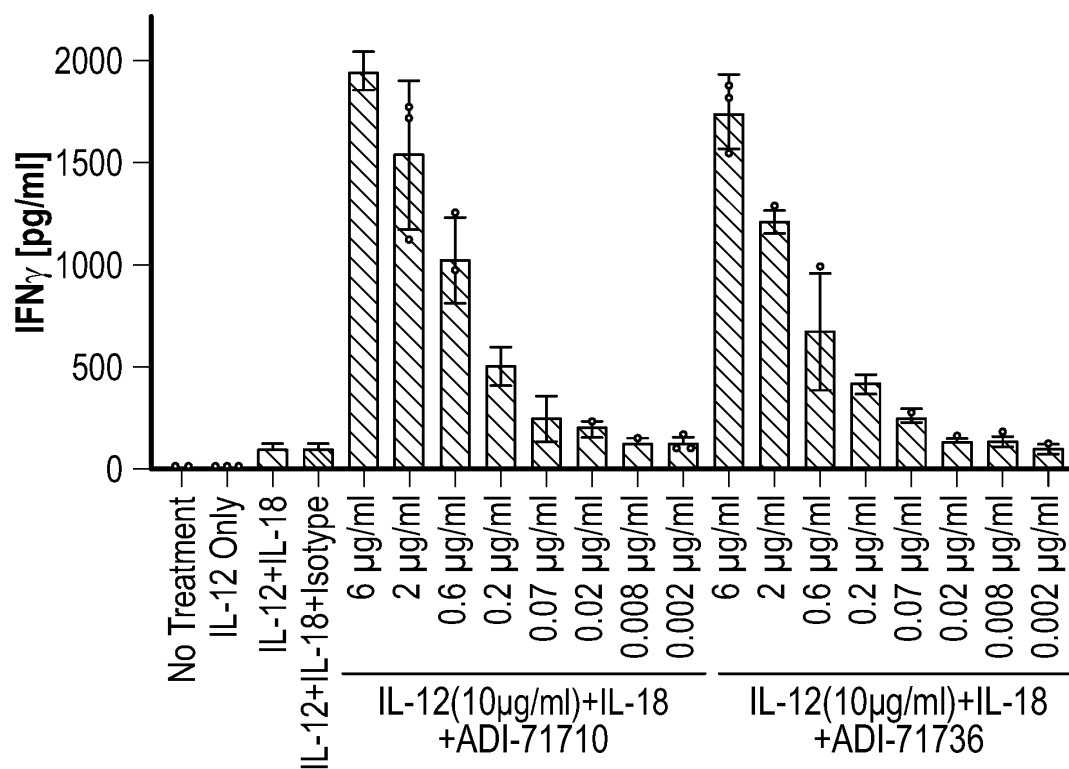


FIG. 15I

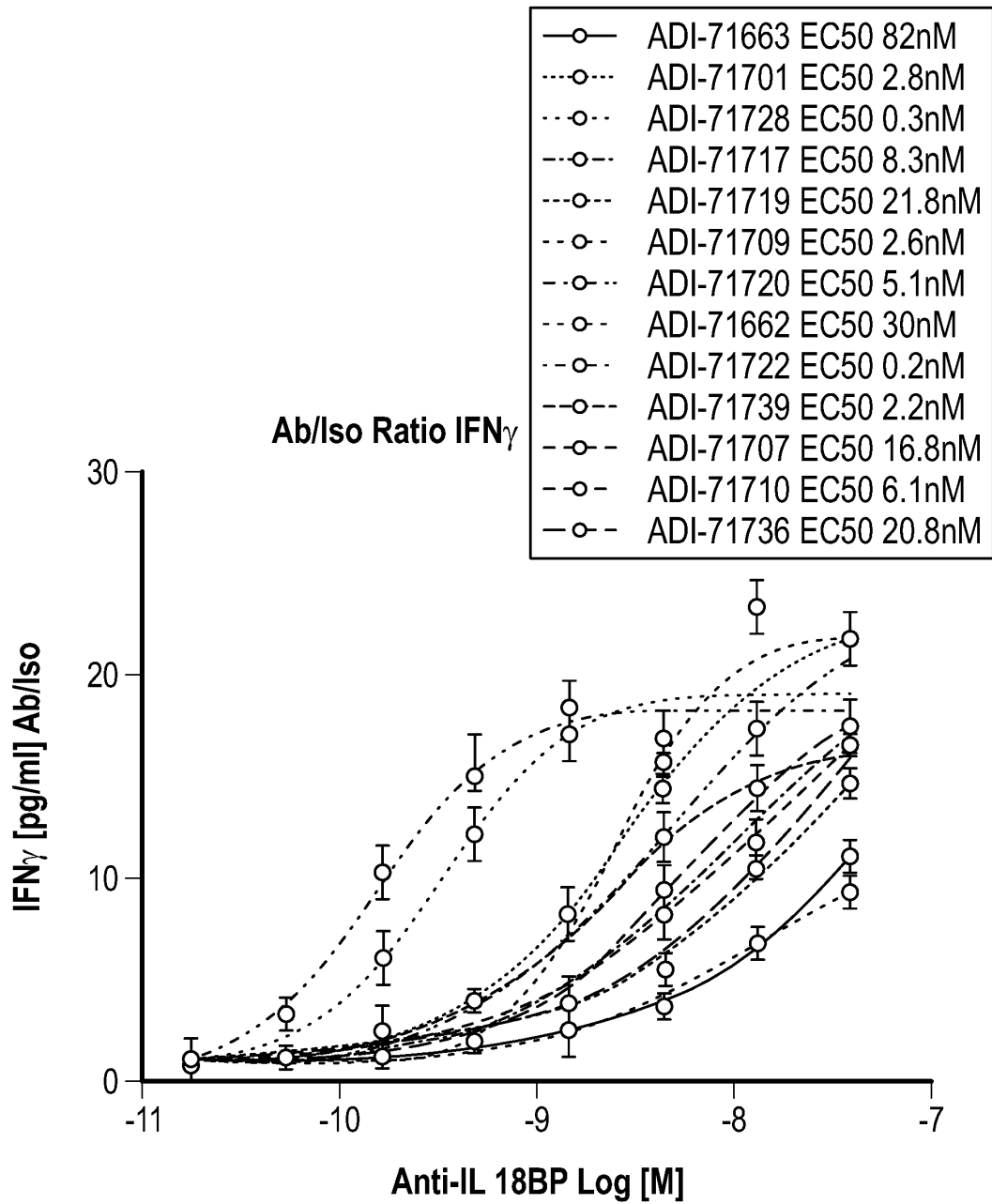


FIG. 15J

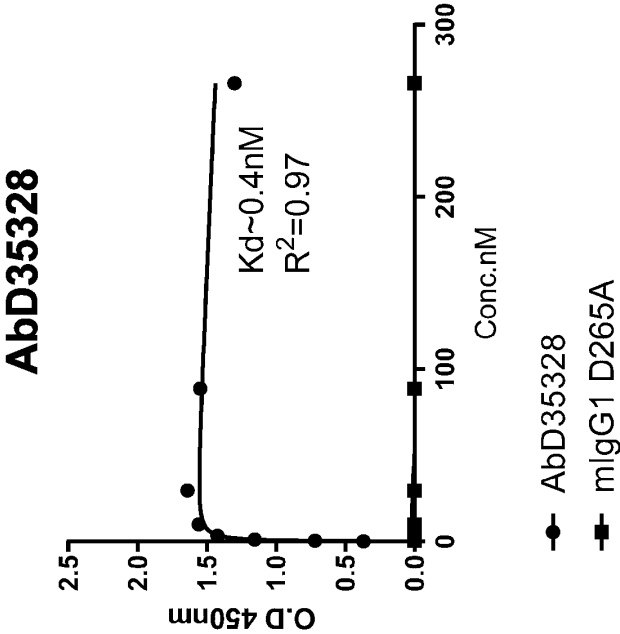


Figure 16

Figure 17

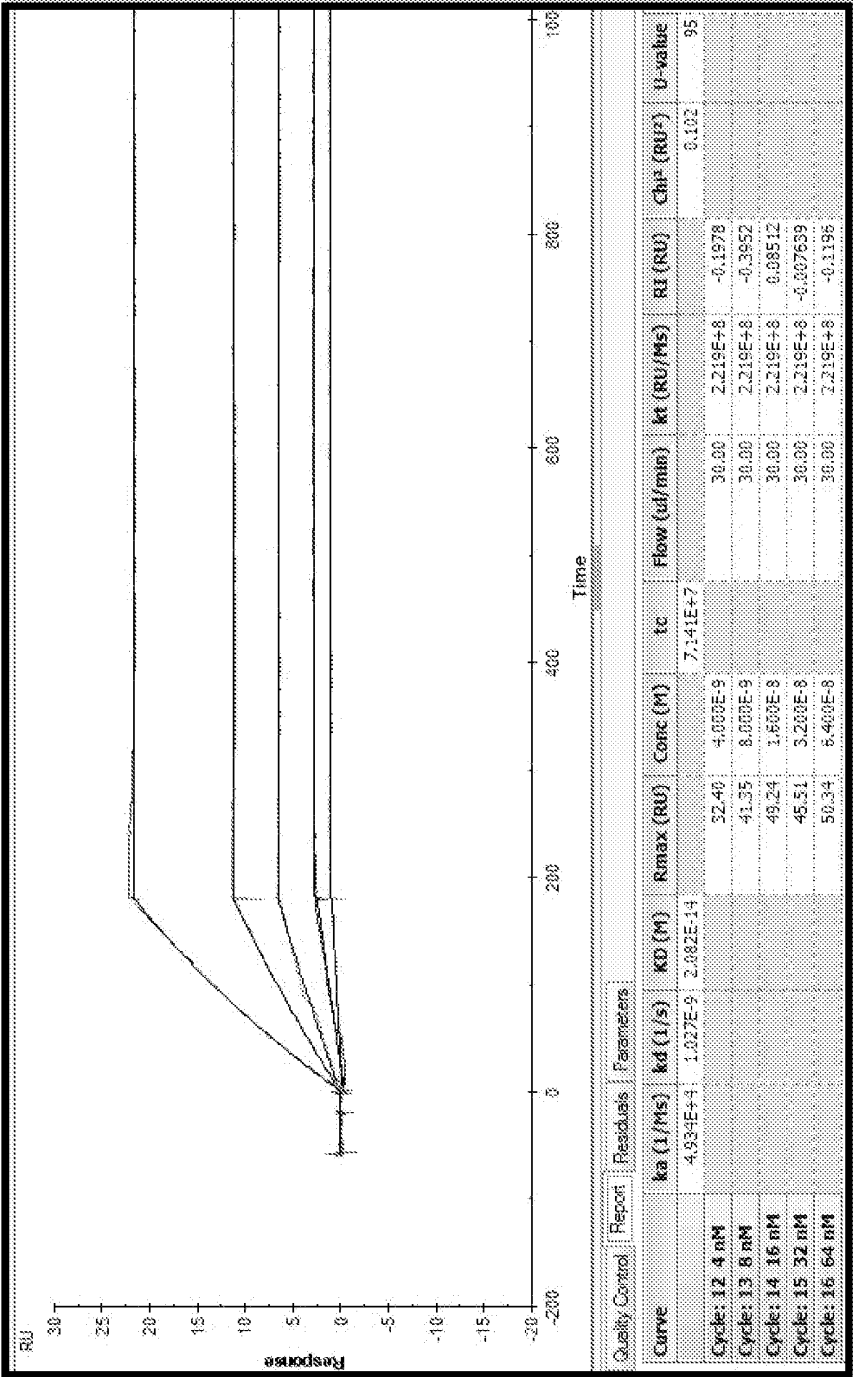


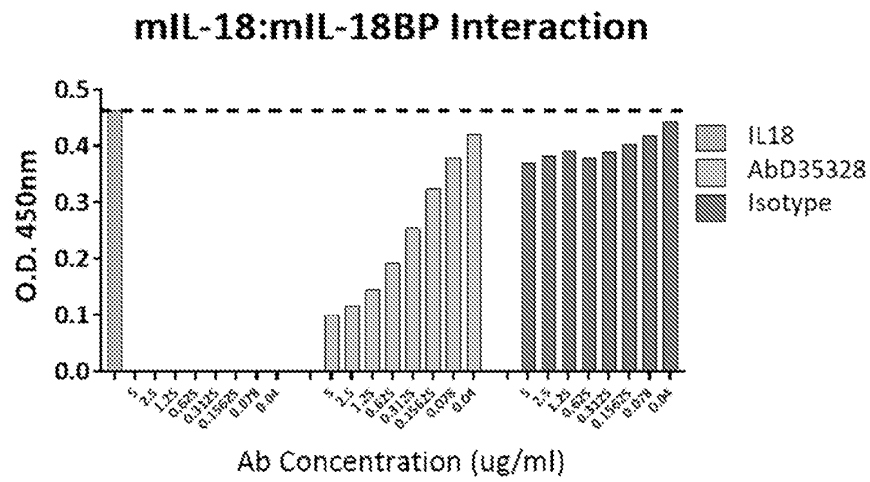
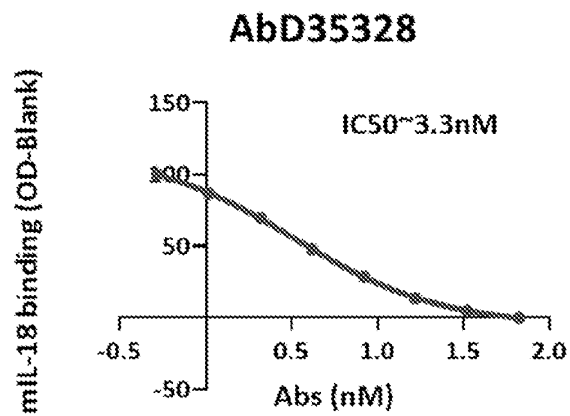
Figure 18**Figure 19**

Figure 20

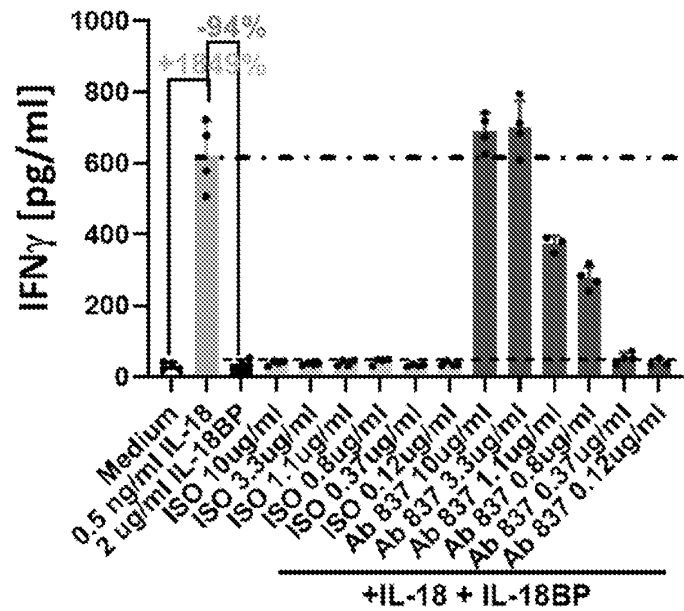


Figure 21

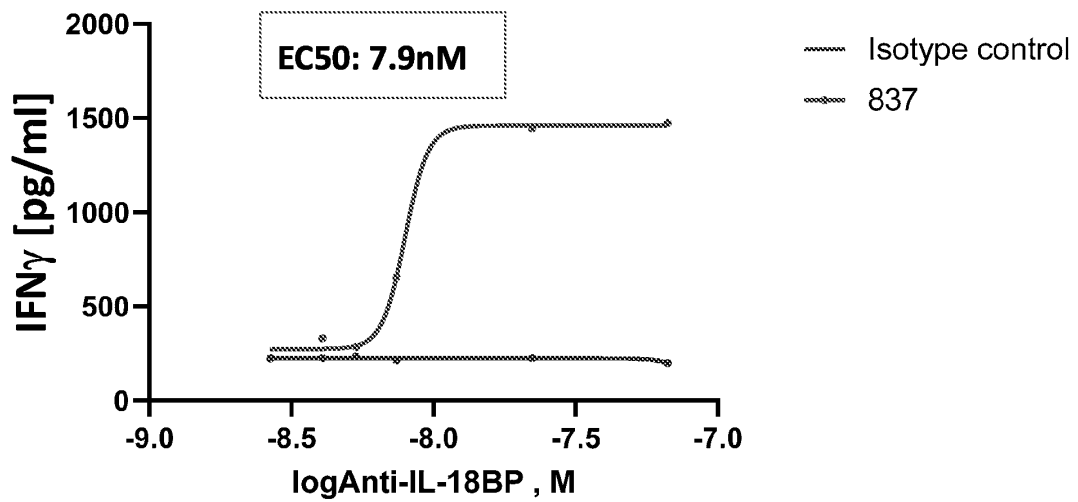


Figure 22A-22F

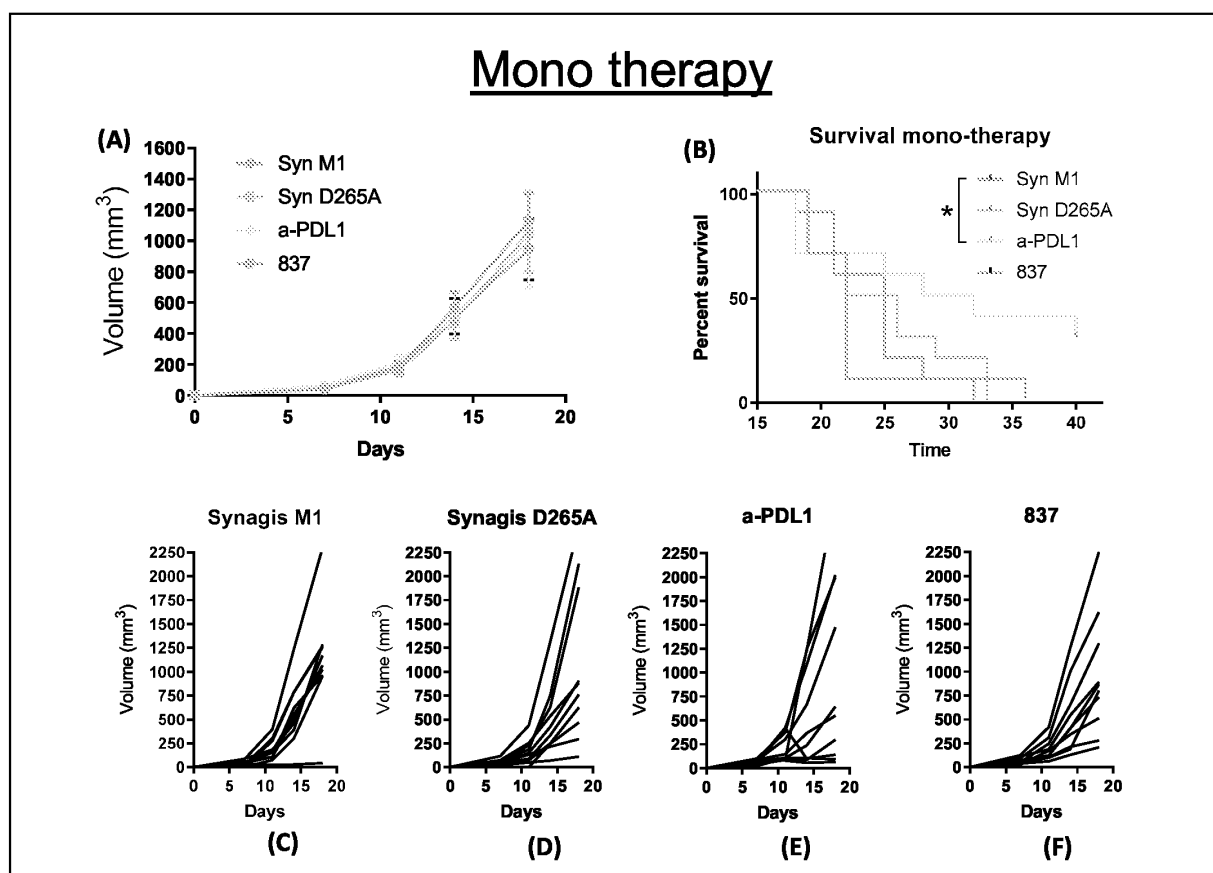
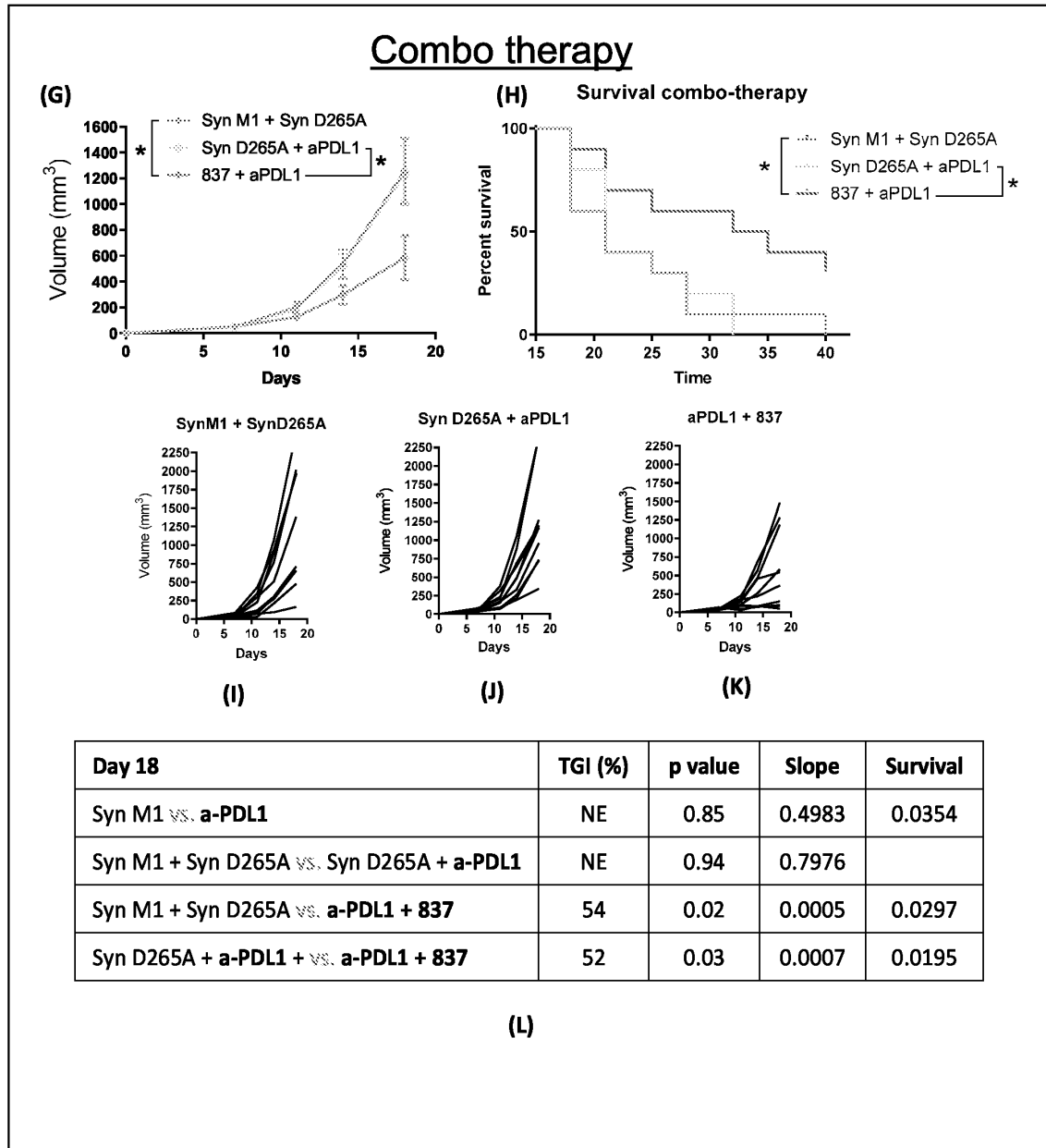


Figure 22G-22L**Figure 23A-23F****(A)**

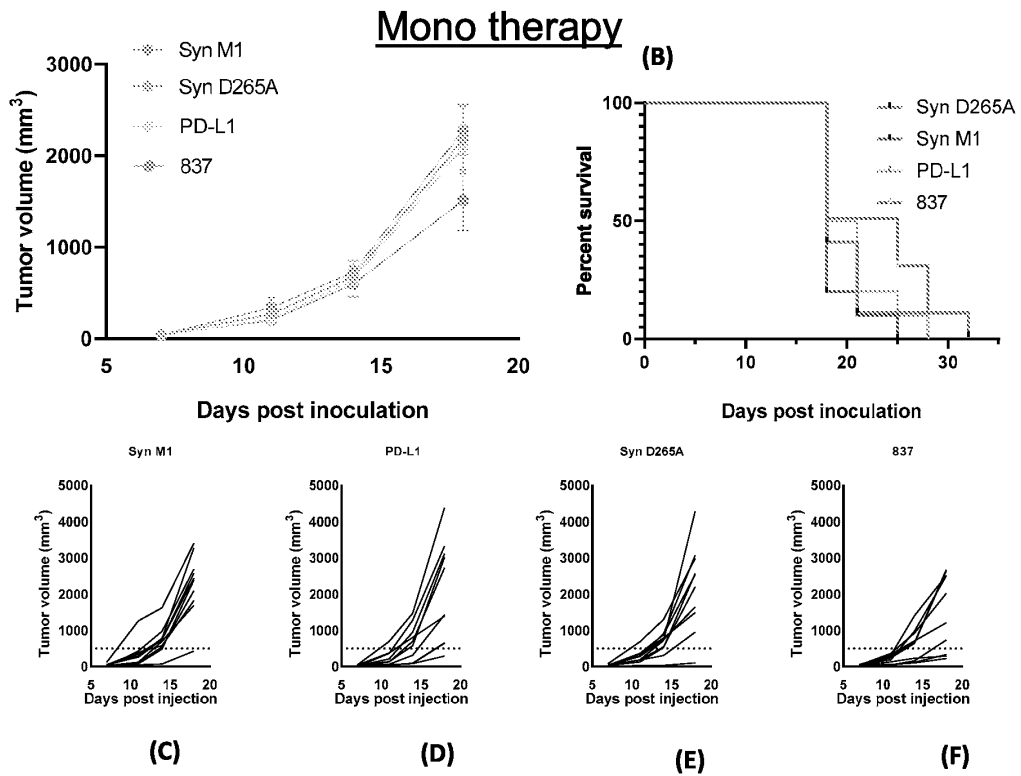
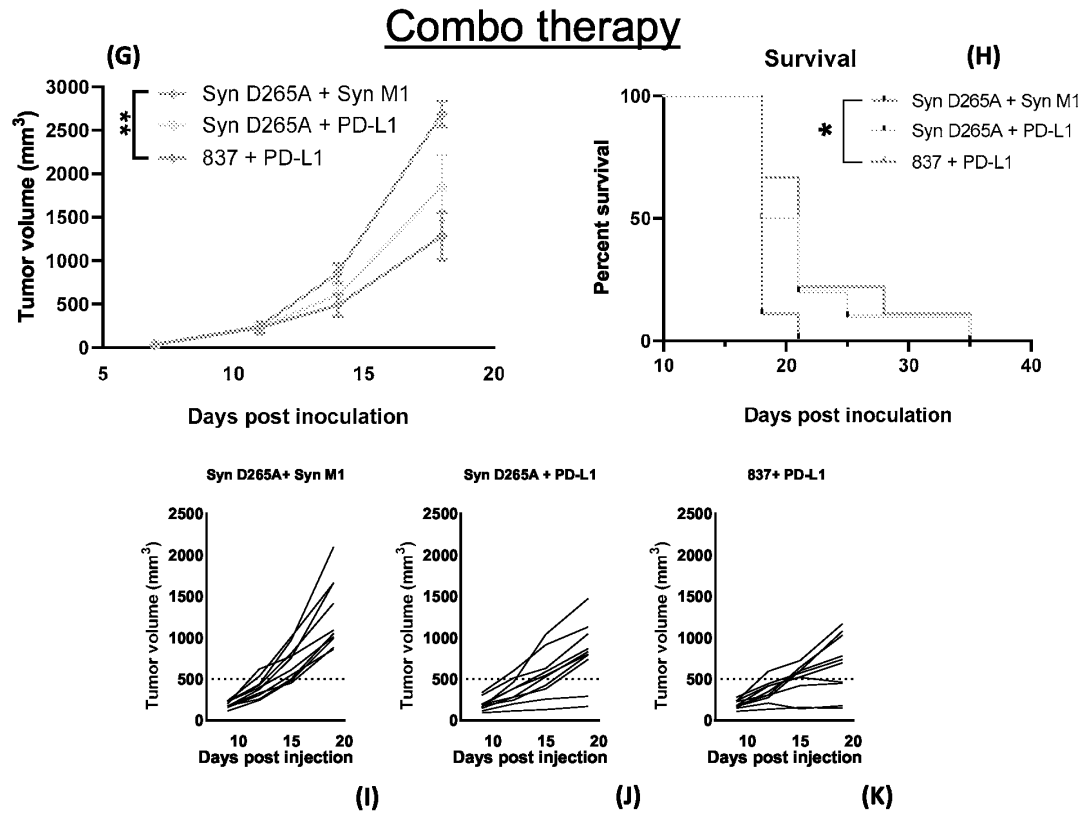
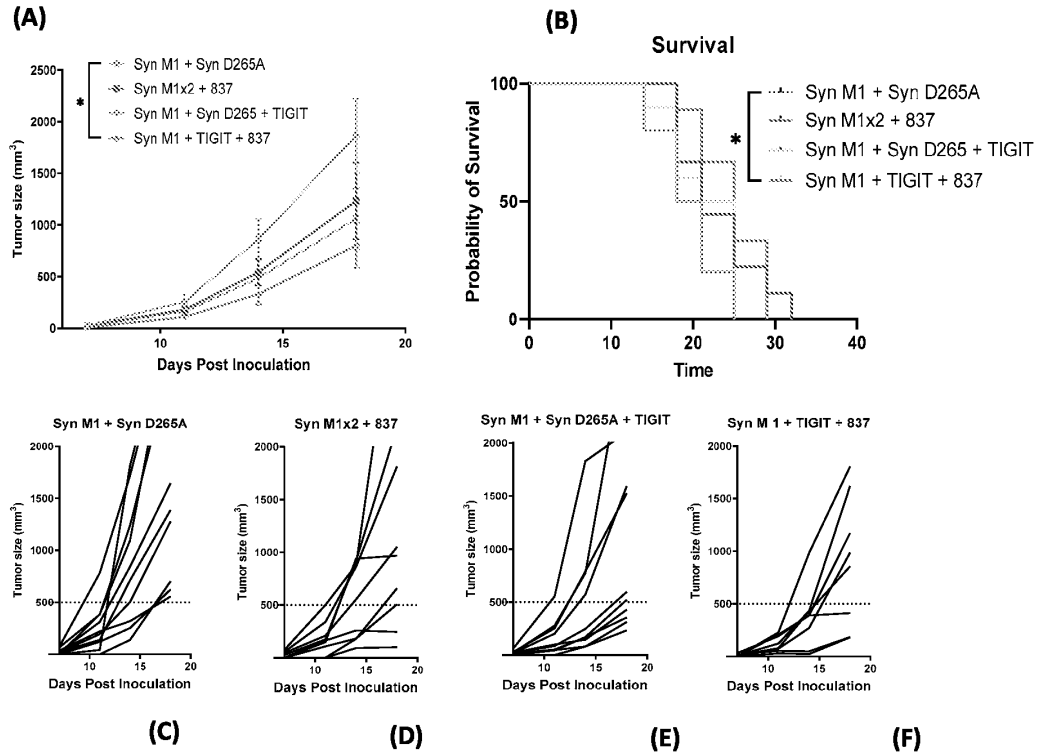


Figure 23G-23L



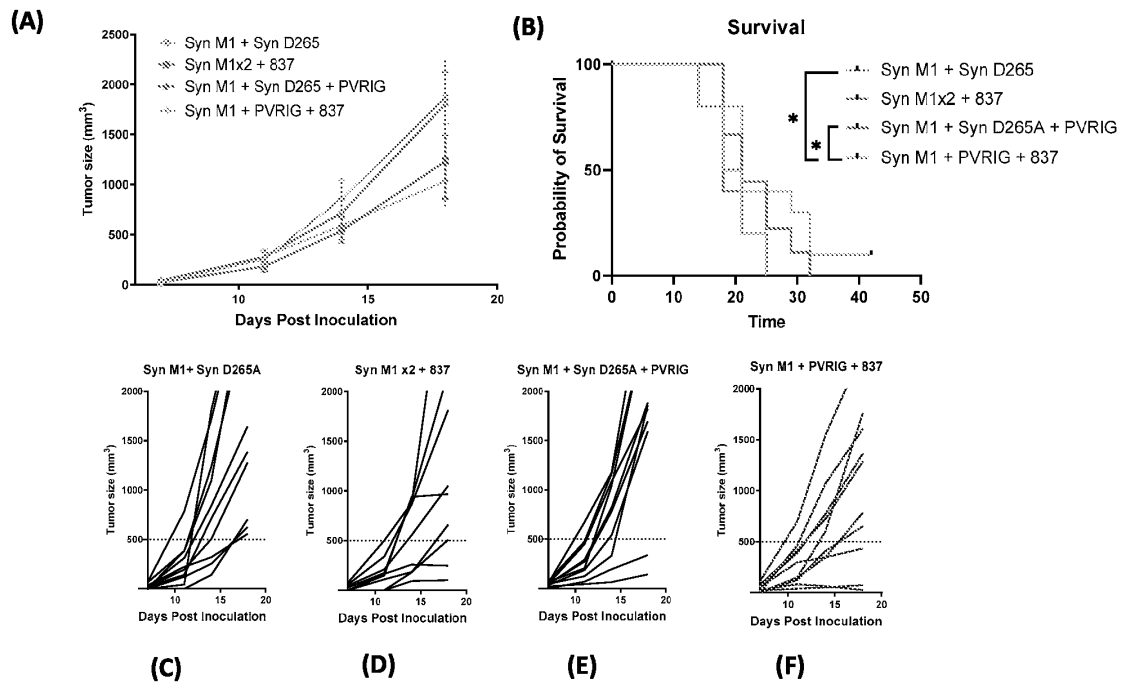
Day 18	TGI (%)	p value	Slope	Survival
Syn D265A vs. 837	31.4	0.2542	0.0927	
837 vs. PDL1	37.3	0.4471	0.1502	
Syn D265A + Syn M1 vs. Syn D265A + aPDL1	30.8	0.0708	0.0105	
Syn D265A + Syn M1 vs. 837+aPDL1	52.3	0.0023	<0.0001	0.0261
Syn D265A + aPDL1 vs. 837+aPDL1	31.1	0.3392	0.0771	

(L)

Figure 24A-24G

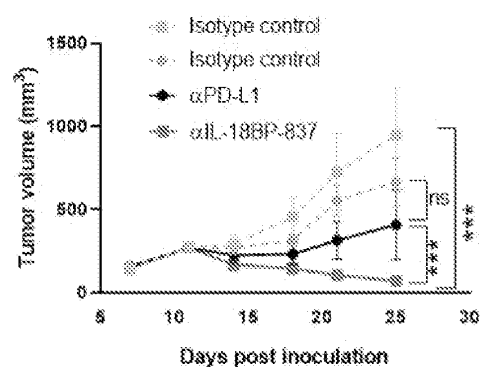
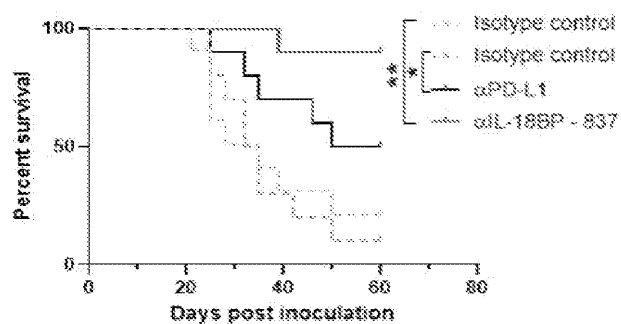
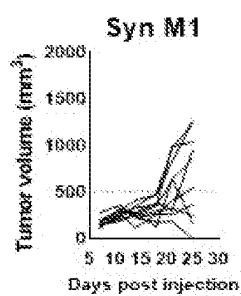
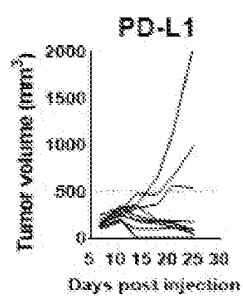
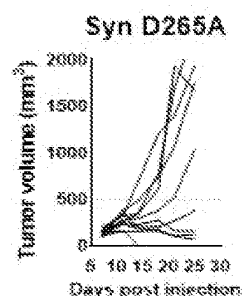
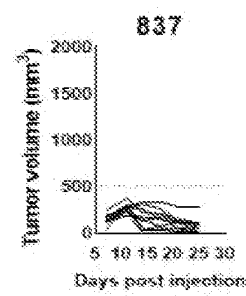
Day 18	TGI (%)	p value	Slope	Survival
Syn M1 + Syn D265A <i>vs.</i> Syn M1 x2 + 837	34	0.211	0.0594	
Syn M1 + Syn D265A <i>vs.</i> Syn M1 + Syn D265A + TIGIT	43	0.112	0.0105	
Syn M1 + Syn D265A <i>vs.</i> Syn M1 + TIGIT + 837	57	0.021	0.0005	0.0133
Syn M1 + Syn D265A + 837 <i>vs.</i> Syn M1 + TIGIT + 837	35	0.256	0.1278	
Syn M1 + Syn D265A + TIGIT <i>vs.</i> Syn M1 + TIGIT + 837	24	0.4393	0.2958	

(G)

Figure 25A-25G

Day 18	TGI (%)	p value	Slope	Survival
Syn M1 + Syn D265A $\forall$ s. Syn M1 x2 + 837	34	0.211	0.0594	
Syn M1 + Syn D265A $\forall$ s. Syn M1 x2 + PVRIG	3	0.83	0.73	
Syn M1 + Syn D265A $\forall$ s. Syn M1 + PVRIG + 837	44	0.167	0.0034	0.034
Syn M1 + Syn D265A + PVRIG $\forall$ s. Syn M1 + PVRIG + 837	42	0.193	0.0055	0.0295
Syn M1 + Syn D265A + 837 $\forall$ s. Syn M1 + PVRIG + 837	16	0.963	0.442	

(G)

Figure 26A-26G**(A)****(F)****(B)****(C)****(D)****(E)**

Day 25	TGI (%)	p value	Slope (p value)	Survival
Syn D265A vs. 837	94.2	0.0113	<0.0001	**
Syn mlgG1 vs. aPDL1	38.2	0.7252	0.7137	*
837 vs. aPDL1	81.6	0.11	<0.0001	

(G)

Figure 27A-27F

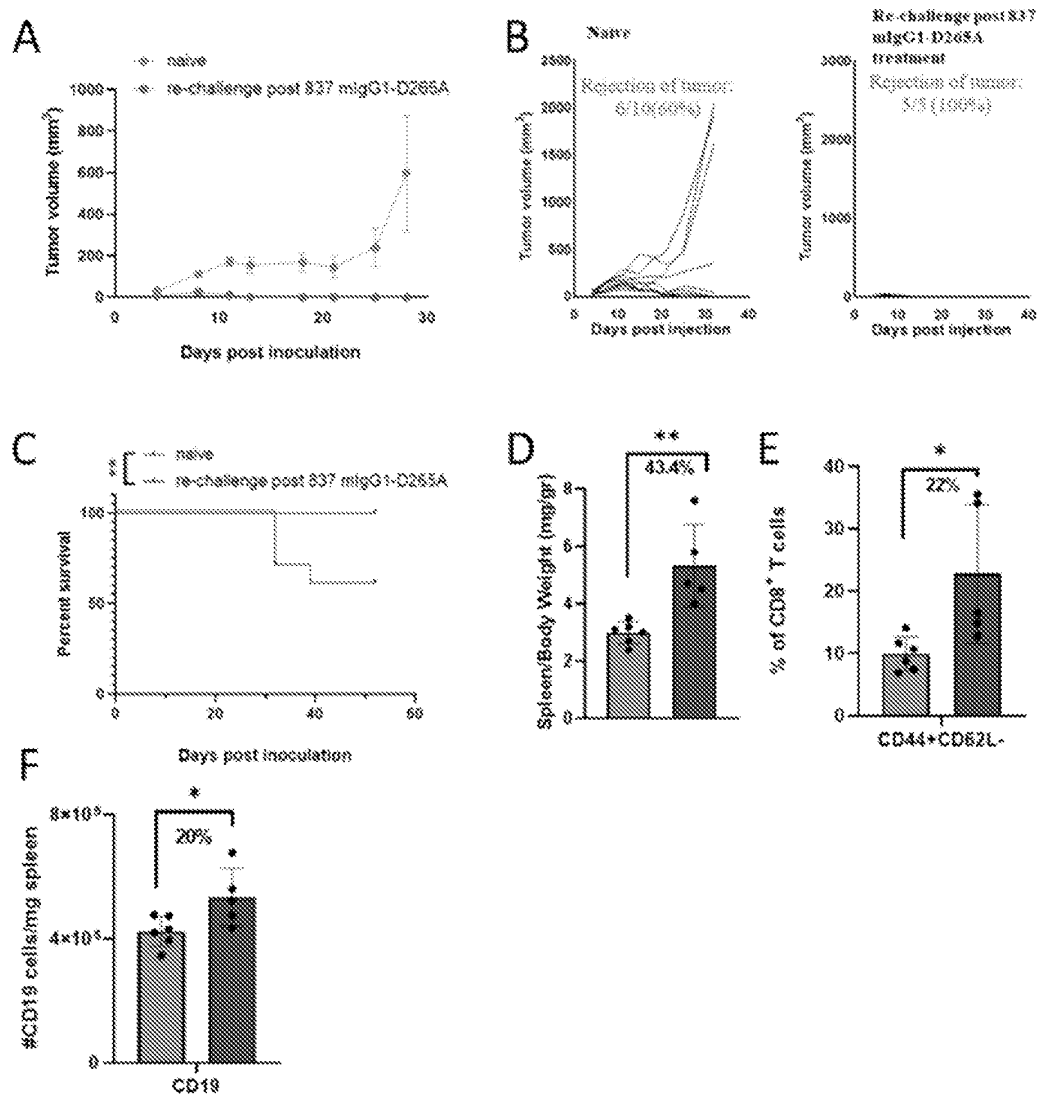


Figure 28A-28F**A. Human IL18BP Full length**

MTMRHNWTPDLSPLWVLLCAHVVTLLVRATPVSQTTTAATASVRSTKDCPSQPPVFPAAKQCPALEVT
 WPEVEVPLNGTSLSCVACSRFPNFSILYWLGNCSFIEHLPGRLEWEGSTSRERGSGTQLCKALVLEQLT
 PALHSTNFSCVLVDPEQVQVRHVLAQLWAGLRATLPPTQEALPSSHSSPQQQG (SEQ ID NO:254)

B. Human IL18BP secreted chain

TPVSTTTAATASVRSTKDCPSQPPVFPAAKQCPALEVT
 VPLNGTTLTSLCTACSRFPNFSILYWLGNCSFIEHLPGRLEWEGSTSRERGSGTQLCKALVLEQLT
 PALHSTNFSCVLVDPEQVQVRHVLAQLWAGLRATLPPTQEALPSSHSSPQQQG (SEQ ID NO:255)

C. Mouse IL18BP Full length

MTMRHCWTAGPSSWWVLLLYVHVILARATSAPQTTATVLTGSSKDCSSWSPAVPTKQYPALDVIWPEKE
 VPLNGTTLTSLCTACSRFPNFSILYWLGNCSFIEHLPGRLEWEGSTSRERGSGTQLCKALVLEQLT
 TNFSCLFVDPGQVAQYHIIAQLWDGLKTAPSPSQETLSSHSPVSRAGPGVA (SEQ ID NO:256)

D. Mouse IL18BP secreted chain

TSAPQTTATVLTGSSKDCSSWSPAVPTKQYPALDVIWPEKE
 VPLNGTTLTSLCTACSRFPNFSILYWLGNCSFIEHLPGRLEWEGSTSRERGSGTQLCKALVLEQLT
 TNFSCLFVDPGQVAQYHIIAQLWDGLKTAPSPSQETLSSHSPVSRAGPGVA (SEQ ID NO:257)

E. Human IL18

MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESDFGKLESKLSVIRNLNDQVLFIDQ
 GNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGMAVTISVKCEKISTLSCENKIISFK
 EMNPPDNIDKTKSDIIFQKRVPGHDKMFEFSSYEGYFLACEKERDLFKLILKKKEDEL
 GDRSIMFTVQNE (SEQ ID NO:258)

F. Mouse IL18

MAAMSEDCVNFKEMMFIDNTLYFIPEENGDLSDNFGRLHCTTAVIRNINDQVLFVDKR
 QPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLAVTSLVKDSKMSTLSCNKKIISFEEM
 DPPENIDDIQSDLIFFQKRVPGHDKMFEFSSYEGHFLACQKEDDAFKLILKKKDENGDK
 SVMFTTLNLHQS (SEQ ID NO:259)

Figure 29A

CHA.7.518.1.H4(S241P)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFDYNINWVRQAPGGGLEWMGVYIPYIGSGYAQKFGQGRVTMTTRDTSTVYMELSRLSEDT AVYYCAREDKTARNAMDYWGQGLTVTVSS	260
vhCDR1	GYTFDYN	261
vhCDR2	IYPYIGGS	262
vhCDR3	AREDKTARNAMDY	263
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYTFDYNINWVRQAPGGGLEWMGVYIPYIGSGYAQKFGQGRVTMTTRDTSTVYMELSRLSEDT AVYYCAREDKTARNAMDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL SSWTVTPSSSLGTTKTYTCNVVDHKPSNTKDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVWVDVSEQEDPEVQFNWVW DGVEVHNAKTKPREEQFNSTYRWVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLIG	264
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHFHWGTP YTFGGQGTKLEIK	265
vlCDR1	ENIYSN	266
vlCDR2	EAT	267
vlCDR3	QHFHWGTPYT	268
Full length light chain	DIQMTQSPSSLSASVGDRTTTCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHFHWGTP YTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSSTLTLSKADYEKHK WYACEVTHQGLSPVTKSFNRGEC	269

Figure 29B

CHA.7.538.1.2.H4(S241P)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYAFTNLYIEWVRQAPGQGLEWIGVINPGSGGIY Y AQKFQGRVTMTADTSTSTVYME	270
	LSSLRSEDTAVY Y CARSETHDTWFA Y WGQGLTVTVSS	
vhCDR1	GYAFTNLY	271
vhCDR2	INPGSGGI	272
vhCDR3	ARSETHDTWFA Y	273
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYAFTNLYIEWVRQAPGQGLEWIGVINPGSGGIY Y AQKFQGRVTMTADTSTSTVYME	274
	LSSLRSEDTAVY Y CARSETHDTWFA Y WGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS	
	GVHTFPAVLQSSGLYSLSSVTPSPSSLGTKTYTCNV D HKPSN T KVDKRVESKYGPPCP Y CPAPEFLGGPSVFLFPPKPKD T LMISR	
	TPEVTCV V VDV S QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQD W LV N GKEYCKCKVSNKGLPSSIEK T ISKA	
	KGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK T TPPVLDSDGSFFLYSRLTVDKSRWQEGNV	
	FSCVMHEALHNHYTQKSLSL S G	
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCKASQSVRIA V AWFQQKPGKAPKALIV L ASTRHTGVPSRFSGSGSGTDFLT L TISSVQPEDFATY	275
	Y C LQHWNPY T TFGGQTKLEIK	
vICDR1	QSVRIA	276
vICDR2	LAS	277
vICDR3	LQHWNPYT	278
Full length light chain	DIQMTQSPSSLSASVGDRVTITCKASQSVRIA V AWFQQKPGKAPKALIV L ASTRHTGVPSRFSGSGSGTDFLT L TISSVQPEDFATY	279
	Y C LQHWNPY T TFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV V CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD	
	STYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 30A

CPA.9.083

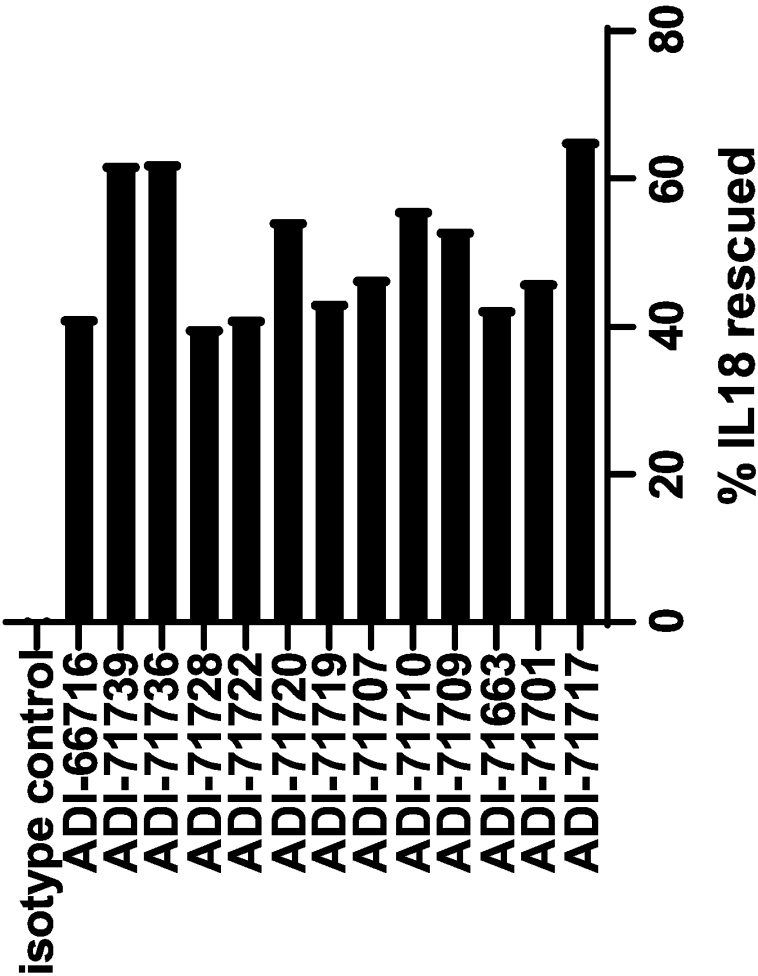
What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTVPVYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGYGMDVWGQGTTVVSS	280
vhCDR1	GFTFSSYA	281
vhCDR2	ISYDGTVPV	282
vhCDR3	ARDPLPLHYGYGMDV	283
Full length HC (IgG4(S241P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTVPVYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGYGMDVWGQGTTVVSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPTVTSWN SGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGKTYYTCNVDHKPSNTKVDKRVESKYGPCPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVAVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRWSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRL TVDKSRWQEAGNPFSCVMHEALHNHYTQKSLSLSG	284
Variable light (vl) domain	QSALTQPRASGNPGQRVITSCSGSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFC AV WDGDRRS LQ LGGGTQLAVLG	285
vlCDR1	SSNMGRRP	286
vlCDR2	SN	287
vlCDR3	AVWDGDRRS LQ	288
Full length light chain	QSALTQPRASGNPGQRVITSCSGSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFC AV WDGDRRS LQ LGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV ETTPSKQSNKYAAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	289

Figure 30B

CPA.9.086

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYAGEVKYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWVGQGTTVVSS	290
vhCDR1	GFTFSSYA	291
vhCDR2	ISYAGEVK	292
vhCDR3	ARDPLPLHYGMDV	293
Full length HC (IgG4(S241P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYAGEVKYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWVGQGTTVVSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGKTYYTCNVDHKPSNTKVDKRVESKYGPCPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVAVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRWSVLTVLHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCVMHEALHNHYTQKSLSLSG	294
Variable light (vl) domain	QSALTQPRASGNPGQRVITISCGSSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFC AVWDDIGRVL QLGGGTQLAVLG	295
vlCDR1	SSNMGRRP	296
vlCDR2	SN	297
vlCDR3	AVWDDIGRVLQ	298
Full length light chain	QSALTQPRASGNPGQRVITISCGSSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFC AVWDDIGRVL QLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKS HR SYSCQVTHEGSTVEKTVAPTECS	299

Figure 31



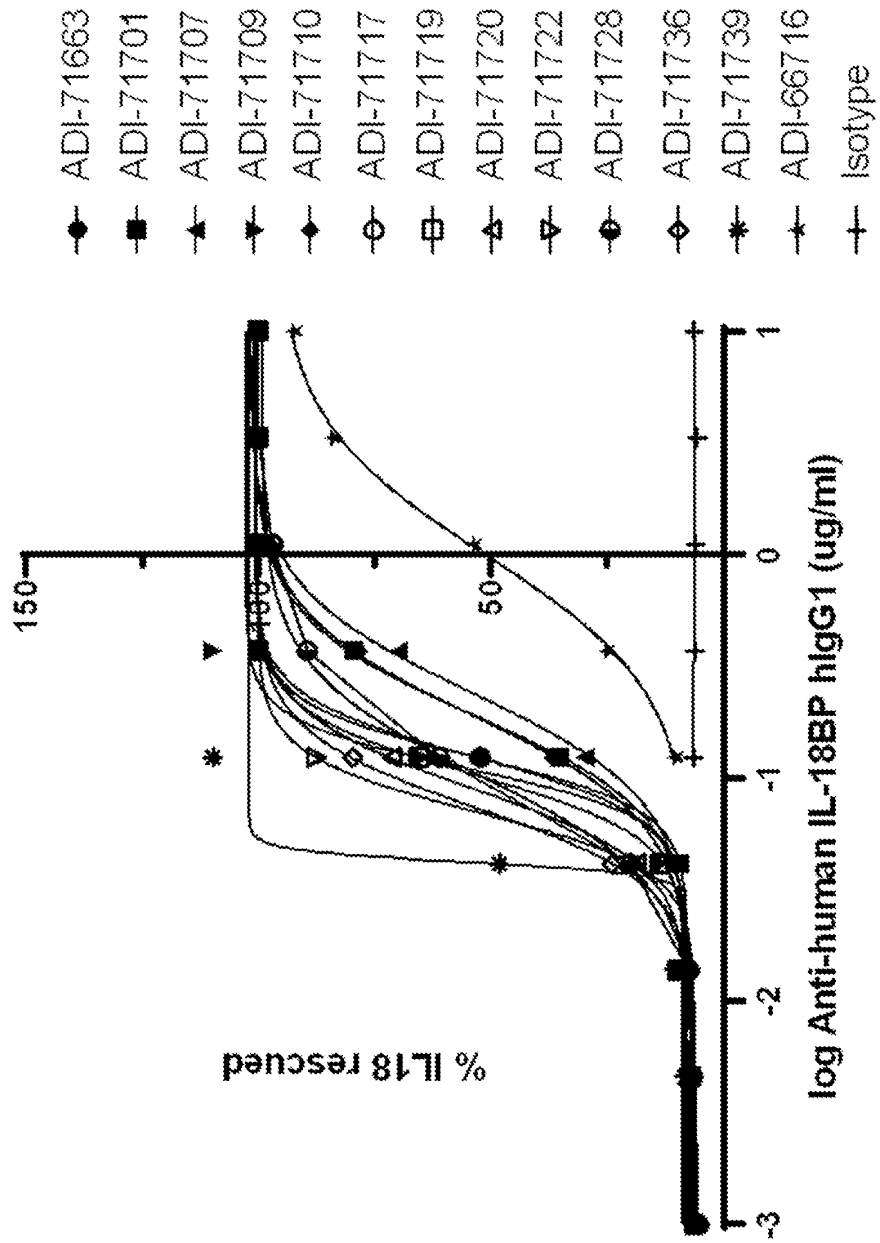


Figure 32

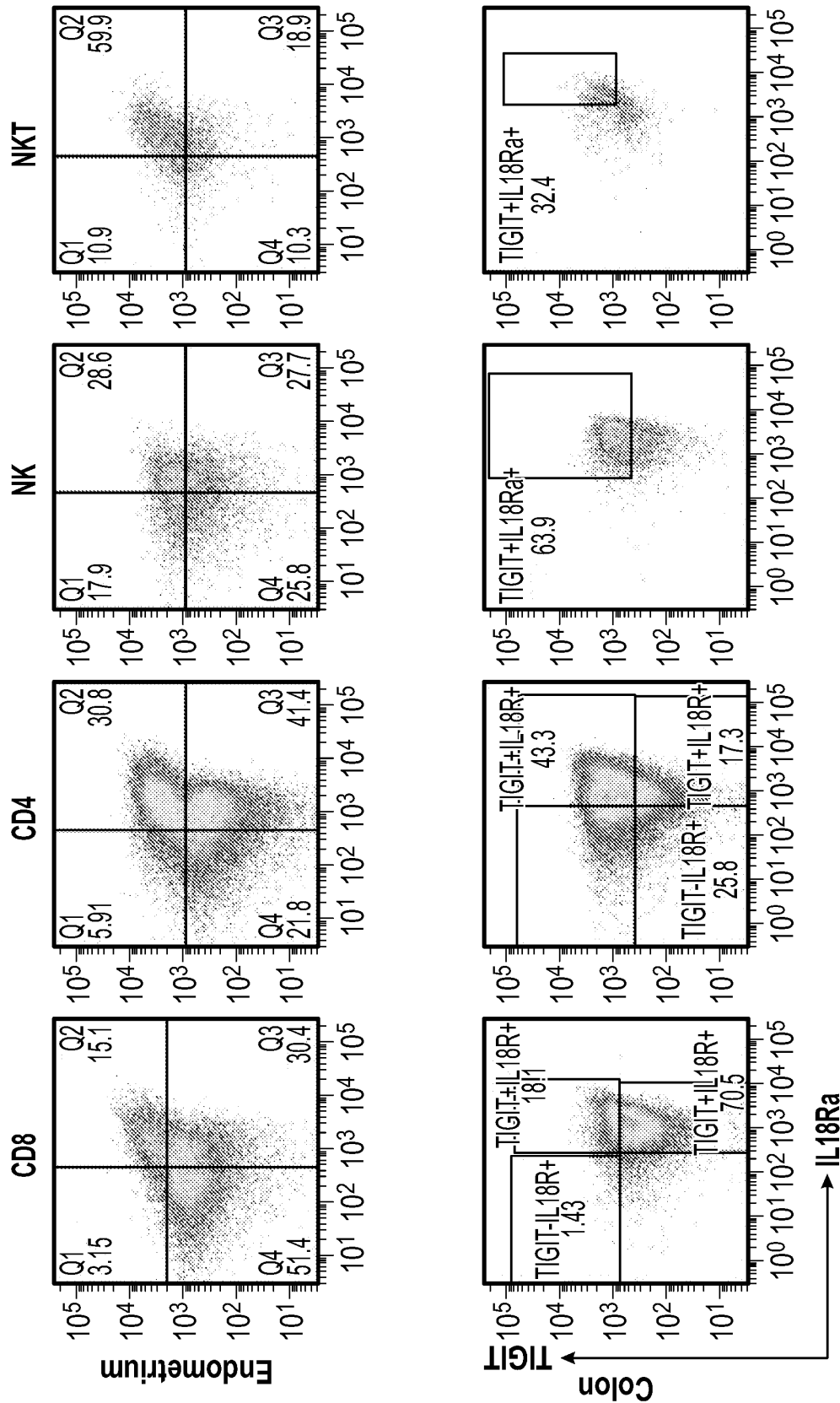


FIG. 33

Figure 34A: CPA.9.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMHWVVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKEMLVQDYVYMDVWGQGTITVTVSS	300
vhCDR1	GFTSSYG	301
vhCDR2	IRYDGSNK	302
vhCDR3	AKEMLVQDYVYMDV	303
Full length HC (IgG4(S241P); CPA.9.018.H4(S2 41P))	QVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMHWVVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKEMLVQDYVYMDVWGQGTITVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVEFSCSVMHREALHNHYTQKSLSPGK DVVMTQSPSLSPVSPGEPASISCRSSQNLHHRNGINYLNWYLQKPGQSPQQLLIYWGSNRRASGVYPDRFSGSGSGTDFTLKI SRVEAEDVGYYVYCMQGLQIPPTFGQGTIKVDIKR	304
Variable light (vl) domain	QNLHHRNGINY	305
vlCDR1	WGS	306
vlCDR2	MQGLQIPPT	307
vlCDR3		308
Full length light chain ((CPA.9.018.H4(S 241P))	DVVMTQSPSLSPVSPGEPASISCRSSQNLHHRNGINYLNWYLQKPGQSPQQLLIYWGSNRRASGVYPDRFSGSGSGTDFTLKI SRVEAEDVGYYVYCMQGLQIPPTFGQGTIKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSITYSLSSITLTLISKADYEKHKVYACEVTHQGLSPPVTKSFNRGEC	309

Figure 34B : CPA.9.027

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	310
vhCDR1	GFTSSYA	311
vhCDR2	ISYDGSNK	312
vhCDR3	ARDPLPLHYYGMDV	313
Full length HC (IgG4(S241P); CPA.9.027.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPVFPPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHFKPSNTKVDKRVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYDKSRWQEGNVFSCSVMHREALHNHYTQKS LSLSPGK	314
Variable light (vl) domain	QSALTQPRASGNPGQRVITISCSGSSNMGRRPVNWYQQIPGTAPKLLIY QNR QRPSPGV PD RFSGSQSGTSASLTI SGLQSEDEAEYFC AV WDDSLSSLQLGGGTQLAVLG	315
vlCDR1	SSNMGRRP	316
vlCDR2	SQN	317
vlCDR3	AVWDDSLSSLQ	318
Full length light chain (CPA.9.027.H4(S2 41P))	QSALTQPRASGNPGQRVITISCSGSSNMGRRPVNWYQQIPGTAPKLLIY QNR QRPSPGV PD RFSGSQSGTSASLTI SGLQSEDEAEYFC AV WDDSLSSLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKNKYAASSYLSTLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	319

Figure 34C: CPA.9.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	320
vhCDR1	GFTSSYA	321
vhCDR2	ISYDGSNK	322
vhCDR3	ARDPLPLHYYGMDV	323
Full length HC (IgG4(S241P); CPA.9.049.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPVFPPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHFKPSNTKVDKRVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYDKSRWQEGNVFSCSVMHREALHNHYTQKS LSLSPGK	324
Variable light (vl) domain	QSALTQPRASGNPGQQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSGVPDRFSGSQSGTSASLTI SGLQSEDEAEYFCAVWDDSLFSLLLGGGTQLAVLG	325
vlCDR1	SSNMGRRP	326
vlCDR2	SQN	327
vlCDR3	AVWDDSLFSLI	328
Full length light chain (CPA.9.049.H4(S2 41P))	QSALTQPRASGNPGQQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSGVPDRFSGSQSGTSASLTI SGLQSEDEAEYFCAVWDDSLFSLLLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	329

Figure 34D: CPA.9.057

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWRQPPGKGLEWIGSIYSGSTYYNPSLKSRVTISVDTS KNQFSLKLSSTAAADTA VYYCARQGAAAGNPFDIWGQGTMTVYSS	330
vhCDR1	GGSISSSSYY	331
vhCDR2	IYYSGST	332
vhCDR3	ARQGAAAGNPFDI	333
Full length HC (IgG4(S241P); CPA.9.057.H4(S2 41P))	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWRQPPGKGLEWIGSIYSGSTYYNPSLKSRVTISVDTS KNQFSLKLSSTAAADTA VYYCARQGAAAGNPFDIWGQGTMTVYSSASTKGPSVPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSTLGTKTYTCNVDPKPSNTKVDKRVEKY GPPCPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVHLQDHWLNQKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLS PGK	334
Variable light (vl) domain	QSVLTQPPSVSGTPGQRVTISCSGSSNIGSNFVYWHQQLTGTAPKLLIYRNTQRPSPGVDPDRFSGSKSGTSASLAI GGLRSEDEADYYCATWDDSLSAWYFGGGTKLTVLG	335
vlCDR1	SSNIGSNF	336
vlCDR2	RNT	337
vlCDR3	ATWDDSLSAWV	338
Full length light chain (CPA.9.057.H4(S2 41P))	QSVLTQPPSVSGTPGQRVTISCSGSSNIGSNFVYWHQQLTGTAPKLLIYRNTQRPSPGVDPDRFSGSKSGTSASLAI GGLRSEDEADYYCATWDDSLSAWYFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVT VAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS	339

Figure 34E: CPA.9.059

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNISKNTLYLQMNSLRAEDTAVYYCARGARYSYGOYPYWGQGTILVTVSS	340
vhCDR1	GFTVSSNY	341
vhCDR2	IYSGGST	342
vhCDR3	ARGARYSYGQYPY	343
Full length HC (IgG4(S241P); CPA.9.059.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNISKNTLYLQMNSLRAEDTAVYYCARGARYSYGOYPYWGQGTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTCTCNVDHDKPSNTKVDKRVESKYGPPCPPAPEFLGGPSVFLPPKPKDITLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVTHQDWWLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNNHYTQKSLSLSPGK	344
Variable light (vl) domain	DIQLTQSPSFLSASVGDRVTITCRASHDISLFSWYQQKPKGAPKLLIYAASLTQITGVPSRFGSASGTEFTLTISSLQPEDFATYYCYCLQDLSFPTWTFGGQTKVEIKR	345
vlCDR1	HDISL	346
vlCDR2	AAS	347
vlCDR3	LQLDSRPTWT	348
Full length light chain (CPA.9.059.H4(S241P))	DIQLTQSPSFLSASVGDRVTITCRASHDISLFSWYQQKPKGAPKLLIYAASLTQITGVPSRFGSASGTEFTLTISSLQPEDFATYYCYCLQDLSFPTWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	349

Figure 34F: CPA.9.083

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTTPVYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	350
vhCDR1	GFTSSYA	351
vhCDR2	ISYDGTTPV	352
vhCDR3	ARDPLPLHYYGMDV	353
Full length HC (IgG4(S241P); CPA.9.083.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTTPVYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPSVFPPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHFKPSNTKVDKRVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYVDKSRWQEGNVFSCVMHEALHNHYTQKS LSLSPGK	354
Variable light (vl) domain	QSALTQPRASGNPGQRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIY Q NRPSGV P DRFSGSQSGTSASLTI SGLQSEDEAEYFCAVWDGDRRSLQLGGGTQLAVLG	355
vlCDR1	SSNMGRRP	356
vlCDR2	SQN	357
vlCDR3	AVWDGDRRSLQ	358
Full length light chain (CPA.9.083.H4(S2 41P))	QSALTQPRASGNPGQRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIY Q NRPSGV P DRFSGSQSGTSASLTI SGLQSEDEAEYFCAVWDGDRRSLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	359

Figure 34G: CPA.9.086

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYAGEVKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	360
vhCDR1	GFTSSYA	361
vhCDR2	ISYAGEVK	362
vhCDR3	ARDPLPLHYYGMDV	363
Full length HC (IgG4(S241P); CPA.9.086.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYAGEVKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPSVFPPLPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHFKPSNTKVDKRVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYDKSRWQEGNVPFSCSVMHREALHNHYTQKS LSLSPGK	364
Variable light (vl) domain	QSALTQPRASGNPGQRTVITSCSGSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSPGV PD RFSGSGSGTSASLTISGLQSEDEAEYFCAVWDDIGRVLQLGGGTQLAVLG	365
vlCDR1	SSNMGRRP	366
vlCDR2	SN	367
vlCDR3	AVWDDIGRVLQ	368
Full length light chain (CPA.9.086.H4(S2 41P))	QSALTQPRASGNPGQRTVITSCSGSSNMGRRPVNWYQQIPGTAPKLLIY SNQ QRPSPGV PD RFSGSGSGTSASLTISGLQSEDEAEYFCAVWDDIGRVLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	369

Figure 34H: CPA.9.089

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDRTPVYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	370
vhCDR1	GFTSSYA	371
vhCDR2	ISYDRTPV	372
vhCDR3	ARDPLPLHYYGMDV	373
Full length HC (IgG4(S241P); CPA.9.089.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAISYDRTPVYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPSVFPPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTPPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYDKSRWQEGNVFSCVMHEALHNHYTQKS LSLSPGK	374
Variable light (vl) domain	QSALTQPRASGNPGQRTVITSCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVPDFRFGSGSGTSASLTISGLQSEDEAEYFCATWDDSLPRLNFGGGTKLAVLG	375
vlCDR1	SSNMGRRP	376
vlCDR2	SQN	377
vlCDR3	ATWDDSLPRLN	378
Full length light chain (CPA.9.089.H4(S2 41P))	QSALTQPRASGNPGQRTVITSCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVPDFRFGSGSGTSASLTISGLQSEDEAEYFCATWDDSLPRLNFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	379

Figure 34i: CPA.9.093

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYEGDRKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSS	380
vhCDR1	GFTSSYA	381
vhCDR2	ISYEGDRK	382
vhCDR3	ARDPLPLHYYGMDV	283
Full length HC (IgG4(S241P); CPA.9.093.H4(S2 41P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYEGDRKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTITVTVSSASTKGPSVFPPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTKYTCNVVDHFKPSNTKVDRKVE SKYGGPPCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTYDKSRWQEGNVFSCSVMHREALHNHYTQKS LSLSPGK	384
Variable light (vl) domain	QSALTQPRASGNPGQRTVITSCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSGVDPDRFSGSQSGTSASLTI SGLQSEDEAEYFCATWDDSTPHGVFGGGTKLAVLG	385
vlCDR1	SSNMGRRP	386
vlCDR2	SQN	387
vlCDR3	ATWDDSTPHGV	388
Full length light chain (CPA.9.093.H4(S2 41P))	QSALTQPRASGNPGQRTVITSCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSGVDPDRFSGSQSGTSASLTI SGLQSEDEAEYFCATWDDSTPHGVFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA VTV AWKADSSPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	389

Figure 34J: CPA.9.101

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCARGAPLFGQYPYWGQGTILVTVSS	390
vhCDR1	GFTVSSNY	391
vhCDR2	IYSGGST	392
vhCDR3	ARGAPLFGQYPY	393
Full length HC (IgG4(S241P); CPA.9.101.H4(S2 41P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCARGAPLFGQYPYWGQGTILVTVSSASTKGPSVFPLA PCSR STSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNV VDHK PSNTKVDKRVESKYG PPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVYSEDPEVQFNWYVDGVEVHNAKT KPREE QFN STYRVSVLT VL HQD WL NGKEYCKVSNKGLPSSIEK TI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYK TT PPVLDSDGSFFLYSRLTV DK SRWQEGNVFSCSVMH EAL HNHYTQKSLSLSP GK	394
Variable light (vl) domain	DIQMTQSPSSLSASVGD RV TTITCRASHAIAISLFSWYQQKPKGAPKLLIYAAS TL QTGVPSRFSGSASGTEFTLTIS LPEDFATYYCLQLDSFPTWTFGQGT K VEIKR	395
vlCDR1	HAIASL	396
vlCDR2	AAS	397
vlCDR3	LQLDSFPTWT	398
Full length light chain (CPA.9.101.H4(S2 41P))	DIQMTQSPSSLSASVGD RV TTITCRASHAIAISLFSWYQQKPKGAPKLLIYAAS TL QTGVPSRFSGSASGTEFTLTIS LPEDFATYYCLQLDSFPTWTFGQGT K VEIKRTVAAPS V FIFPPSDEQLKSGTASVVC LL NNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDS TS LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	399

Figure 34K: CPA.9.103

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNISKNTLYLQMNSLRAEDTAVYYCARGARPNGOYPYWGQGTILVTVSS	400
vhCDR1	GFTVSSNY	401
vhCDR2	IYSGGST	402
vhCDR3	ARGARPNQYYPY	403
Full length HC (IgG4(S241P); CPA.9.103.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNISKNTLYLQMNSLRAEDTAVYYCARGARPNGOYPYWGQGTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVEISKYGPCCPAPAEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVYSEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRVSVLT/LHQDWLNGKEYCKVSNKGLPSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPGK	404
Variable light (vl) domain	DIQLTQSPSFSLASVGDRTVTITCRASHGIKSLFSWYQQKPGKAPKLLIYAASITLQTGVPSRFRSGSASGTEFTLTISSLQPEDFATYYCLQLDSFPTWTFGQGTKEIKR	405
vlCDR1	HGIKSL	406
vlCDR2	AAS	407
vlCDR3	LQLDSFPTWT	408
Full length light chain (CPA.9.103.H4(S241P))	DIQLTQSPSFSLASVGDRTVTITCRASHGIKSLFSWYQQKPGKAPKLLIYAASITLQTGVPSRFRSGSASGTEFTLTISSLQPEDFATYYCLQLDSFPTWTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	409

Figure 34L: BM26 hlgG4 (BM26-H4) (WO2016/028656A1, Clone 31C6)

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTS DKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTSS	410
vhCDR1	GYTFSSYV	411
vhCDR2	IDPYNDGA	412
vhCDR3	ARGGPYGWYFDV	413
Full length HC (IgG4(S241P))	EVQLQQSGPELVKPGSSVKMSCKASGYTSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTS DKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSSASTKGPSVFPPLAPCSRSTSESTAAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESK YGPCCPCPAPEFLGGPSVFLPPKPKDILMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRBEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLS LSPGK	414
Variable light (vl) domain	DIQMTQSPASLSASVGETVTTITCRASEHIYSYLWYQQKQKQKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSLKI NSLQPEDFGTYYCQHHFGSPLTFGAGTTLELK	415
vlCDR1	EHIYSY	416
vlCDR2	NAK	417
vlCDR3	QHHFGSPLT	418
Full length light chain	DIQMTQSPASLSASVGETVTTITCRASEHIYSYLWYQQKQKQKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSLKI NSLQPEDFGTYYCQHHFGSPLTFGAGTTLELKRIVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	419

Figure 34M: BM29 IgG4 (BM29-H4) (US2016/0176963A1, Clone 22G2)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSSETLSLTCTVSGGVS SGIYY WSWIRQPPGKGLEWIGYIYSGSTNYPNPSLKSRVTISVDTS KNQFSLKLSSTVAADTA VYY CARDY YVSGNY YNVDY YFFGVDV WGQGTITVTVSS	420
vhCDR1	GGSVSSGIYY	421
vhCDR2	IYYSGST	422
vhCDR3	ARDYYVSGNYYNVDY YFFGVDV	423
Full length HC (IgG4(S241P))	QVHLQESGPGLVKPSSETLSLTCTVSGGVS SGIYY WSWIRQPPGKGLEWIGYIYSGSTNYPNPSLKSRVTISVDTS KNQFSLKLSSTVAADTA VYY CARDY YVSGNY YNVDY YFFGVDV WGQGTITVTVSSASTKGPSVPLAPCSRSTS ESTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITYTCNV VDHKPSNTK VDKRVESKYGGPPCPAPPEFLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDV SQEDPEVQFNWYVDGVEVHNA KITPREHQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVY TLPQSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTTPVLD SDGSFFLYSRLTV DKSRWQEGNV FSCSVMEALHN HYTQKSLSLSPGK	424
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRA TGIPARFSGSGGTDFLT TISS LEPEDFAVYYCQQRSNW PPLFT FGPGTKVDIK	425
vlCDR1	QSVSSY	426
vlCDR2	DAS	427
vlCDR3	QQRSNW PPLFT	428
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRA TGIPARFSGSGGTDFLT TISS LEPEDFAVYYCQQRSNW PPLFT FGPGTKVDIKRTVAAPS VFI PPSPDEQLKSGTASV CLLN NFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	429

Figure 34N: CHA.9.536.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTEYTLHWVRQAPQGLEWMGGINPNNGGTSYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCARSGYYDYSFAYWGQGTLVTVSS	430
vhCDR1	GYTFTEYTLH	431
vhCDR2	GINPNNGGTS	432
vhCDR3	SGYYDYSFAY	433
Full length HC (IgG4(S241P); CHA.9.536.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTFTEYTLHWVRQAPQGLEWMGGINPNNGGTSYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCARSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKYTCNVDHKPSNTKVDKRVESKYGPCCPAPPEFLGGPSVFLFPPKPKDITLMISRTEPVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSLRTVTDKSRWQEGNVPFSCSVMEALHNHYTQKSLSLSPGK	434
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVTITCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	435
vlCDR1	RASQDVKNAAVV	436
vlCDR2	SPSYRYT	437
vlCDR3	QQHYSTPFT	438
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRTVTITCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	439

Figure 340: CHA.9.536.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTLHWVRQAPQGQLEWIGINPNNGGTSYAQKFQGRVTMTV DTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSS	440
vhCDR1	GYTFTEYTLH	441
vhCDR2	GINPNNGGTS	442
vhCDR3	SGYYDYSEAY	443
Full length HC (IgG4(S241P) CHA.9.536.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTLHWVRQAPQGQLEWIGINPNNGGTSYAQKFQGRVTMTV DTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPP CPPCAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDGVEVHNATKPREEQFNST YRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPG K	444
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITTCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIK	445
vlCDR1	RASQDVKNAAVV	446
vlCDR2	SPSYRYT	447
vlCDR3	QQHYSTPTFT	448
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRTVITTCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	449

Figure 34P: CHA.9.536.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTLHWVRQAPQGQLEWIGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSS	450
vhCDR1	GYTFTEYTLH	451
vhCDR2	GINPNNGGTS	452
vhCDR3	SGYYDYSEAY	453
Full length HC (IgG4(S241P); CHA.9.536.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTLHWVRQAPQGQLEWIGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK	454
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTFTISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	455
vlCDR1	RASQDVKNAAVV	456
vlCDR2	SPSYRYT	457
vlCDR3	QQHYSTPFT	458
Full length light chain (CHA.9.536.4.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTFTISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	459

Figure 34Q: CHA.9.536.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVD TSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSS	460
vhCDR1	GYTFTEYTLH	461
vhCDR2	GINPNNGGTS	462
vhCDR3	SGYYDYSEAY	463
Full length HC (IgG4(S241P); CHA.9.536.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVD TSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPP CPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDGVEVHNATKPREEQFNST YRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPG K	464
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCRASQDVKNAAVVWYQQKPKGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIK	465
vlCDR1	RASQDVKNAAVV	466
vlCDR2	SPSYRYT	467
vlCDR3	QQHYSTPTFT	468
Full length light chain (CHA.9.536.5.H4(S241P))	DIQMTQSPSSLSASVGDRTTTCRASQDVKNAAVVWYQQKPKGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	469

Figure 34R: CHA.9.536.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVD TSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSS	470
vhCDR1	GYTFTEYTLH	471
vhCDR2	GINPNNGGTS	472
vhCDR3	SGYYDYSEAY	473
Full length HC (IgG4(S241P); CHA.9.536.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVD TSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPP CPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPREEQFNST YRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPG K	474
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTITCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTF TISSVQPEDFATYYCQOHYSTPFTFGQGTGLEIK	475
vlCDR1	RASQDVKNAAVV	476
vlCDR2	SPSYRYT	477
vlCDR3	QQHYSTPFT	478
Full length light chain (CHA.9.536.6.H4(S241P))	DIQMTQSPSSLSASVGDRTTITCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTF TISSVQPEDFATYYCQOHYSTPFTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	479

Figure 34s: CHA.9.536.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSS	480
vhCDR1	GYTFTEYTLH	481
vhCDR2	GINPNNGGTS	482
vhCDR3	SGYYDYSEAY	483
Full length HC (IgG4(S241P); CHA.9.536.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDGVEVHNATKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPGK	484
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITTCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTLTISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIK	485
vlCDR1	RASQDVKNAAVV	486
vlCDR2	SPSYRYT	487
vlCDR3	QQHYSTPTFT	488
Full length light chain (CHA.9.536.7.H4(S241P))	DIQMTQSPSSLSASVGDRTITTCRASQDVKNAAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTLTISSLQPEDFATYYCQOHYSTPTFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	489

Figure 34T: CHA.9.536.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSS	490
vhCDR1	GYTFTEYTLH	491
vhCDR2	GINPNNGGTS	492
vhCDR3	SGYYDYSEAY	493
Full length HC (IgG4(S241P); CHA.9.536.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSEAYWGQGTLTVTYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVVDGVEVHNATKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPGK	494
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITTCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTFTISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	495
vlCDR1	RASQDVKNAAVV	496
vlCDR2	SPSYRYT	497
vlCDR3	QQHYSTPFT	498
Full length light chain (CHA.9.536.8.H4(S241P))	DIQMTQSPSSLSASVGDRTITTCRASQDVKNAAVVWYQQKPKGAPKLLIYSPSYRYTGVPSRFSGSGTDFTFTISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	499

Figure 34U: CHA.9.560.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKFGQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGYYVGMIDYWGQGTLVTVSS	500
vhCDR1	GYTFTNYGMN	501
vhCDR2	WINTYTGEPT	502
vhCDR3	NGYYVGMIDY	053
Full length HC (IgG4(S241P); CHA.9.560.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKFGQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGYYVGMIDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPGK	504
Variable light (vl) domain	QAVVTQEPSLTVSPGGTIVTLTCRSSTGAVTTSNHANWFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	505
vlCDR1	RSSTGAVTTSNHAN	506
vlCDR2	GTNGRGS	507
vlCDR3	ALWFSNHWV	508
Full length light chain (CHA.9.560.1.H4(S241P))	QAVVTQEPSLTVSPGGTIVTLTCRSSTGAVTTSNHANWFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVEITTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	509

Figure 34V: CHA.9.560.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKQFGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGNGYYVGM DYWGQGT LVTVSS	510
vhCDR1	GYTFTNYGMN	511
vhCDR2	WINTYTGEPT	512
vhCDR3	GNGYYVGM DY	513
Full length HC (IgG4(S241P); CHA.9.560.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKQFGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGNGYYVGM DYWGQGT LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDGVEVHNATKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMH EA LHNHYTQKSLSPGK	514
Variable light (vl) domain	QAVVTQEPSLTVSPGGTIVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRGSWTPARFSGSLLGGKALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	515
vlCDR1	GSSTGAVTTSNHAN	516
vlCDR2	GTNGRGS	517
vlCDR3	ALWFSNHWV	518
Full length light chain (CHA.9.560.3.H4(S241P))	QAVVTQEPSLTVSPGGTIVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRGSWTPARFSGSLLGGKALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA V TVAWKADSSPVKAGVETITPPSKQSN N KYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	519

Figure 34W: CHA.9.560.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGYYVGM DYWGQGTLVTVSS	520
vhCDR1	GYTFTNYGMN	521
vhCDR2	WINTYTGEPT	522
vhCDR3	GN GYYVGM DY	523
Full length HC (IgG4(S241P); CHA.9.560.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTFITNYGMNWRQAPQGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGYYVGM DYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDGVEVHNATKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSPGK	524
Variable light (vl) domain	QAVVTQEPSLTVSPGGTIVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRSGVPARFSGSLLGGKALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	525
vlCDR1	GSSTGAVTTSNHAN	26
vlCDR2	GTNGRGS	527
vlCDR3	ALWFSNHWV	528
Full length light chain (CHA.9.560.4.H4(S241P))	QAVVTQEPSLTVSPGGTIVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRSGVPARFSGSLLGGKALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	529

Figure 34X: CHA.9.560.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFT LDTSTS TAYLEISSLRSEDTAVYYCSRNGNGYVGMIDYWGQGTLVTVSS	530
vhCDR1	GYTFTNYGMIN	530
vhCDR2	WINTYTGEPIT	530
vhCDR3	GNNGYVGMIDY	530
Full length HC (IgG4(S241P); CHA.9.560.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFT LDTSTS TAYLEISSLRSEDTAVYYCSRNGNGYVGMIDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPC PPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPREEQFNSTY RVVSVLTVILHODWLNQKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGK QAVVTQEPSTLVSPGGTITLTGSSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRGSWTPARFSGSLGGA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	530
Variable light (vl) domain	QAVVTQEPSTLVSPGGTITLTGSSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRGSWTPARFSGSLGGA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	530
vlCDR1	GSSTGAVTTSNHAN	530
vlCDR2	GTNGRGS	530
vlCDR3	ALWFSNHWV	530
Full length light chain (CHA.9.560.5.H4(S241P))	QAVVTQEPSTLVSPGGTITLTGSSSTGAVTTSNHANWVQQKPGQAFRGLRGTNGRGSWTPARFSGSLGGA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW KADSSPVKAGVETITTPSKQSNKKAASSYLSLTPEQWKSIRSYSCQVTHEGSTVEKTVAPTECS	530

Figure 34Y: CHA.9.560.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFT LDTSTS TAYLEISSLRSEDTAVYYCSRNGNGYVGMIDYWGQGTLVTVSS	540
vhCDR1	GYTFTNYGMIN	541
vhCDR2	WINTYTGEPIT	542
vhCDR3	GNNGYVGMIDY	543
Full length HC (IgG4(S241P); CHA.9.560.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFT LDTSTS TAYLEISSLRSEDTAVYYCSRNGNGYVGMIDYWGQGTLVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDY FPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPCC PPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGK QAVVTQEPISLTSPGGTITLTGSSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSVGPARGSGSLGGKA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	544
Variable light (vl) domain	QAVVTQEPISLTSPGGTITLTGSSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSVGPARGSGSLGGKA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	545
vlCDR1	GSSTGAVTTSNHAN	546
vlCDR2	GTNGRGS	547
vlCDR3	ALWFSNHWV	548
Full length light chain (CHA.9.560.6.H4(S241P))	QAVVTQEPISLTSPGGTITLTGSSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSVGPARGSGSLGGKA ALTI SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW KADSSPVKAGVETITTPSKQSNKKAASSYLSLTPEQWKSIRSYSCQVTHEGSTVEKTVAPTECS	549

Figure 34Z: CHA.9.560.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFTLDASTSTAYLEISSLRSEDTAVYYCSRNGNGYVVGMDYWGQGTLVTVSS	550
vhCDR1	GYTFTNYGMN	551
vhCDR2	WINTYTGEPIT	552
vhCDR3	GNGYVVGMDY	553
Full length HC (IgG4(S241P); CHA.9.560.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTFTLDASTSTAYLEISSLRSEDTAVYYCSRNGNGYVVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVILHODWLNQKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGKQAVVTQEPSTLVSPGGTIVTLTCSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSWTPARFSGSLGGKALTI	554
Variable light (vl) domain	SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	555
vlCDR1	GSSTGAVTTSNHAN	556
vlCDR2	GTNGRGS	557
vlCDR3	ALWFSNHWV	558
Full length light chain (CHA.9.560.7.H4(S241P))	QAVVTQEPSTLVSPGGTIVTLTCSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSWTPARFSGSLGGKALTI	559

Figure 34AA: CHA.9.560.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDASTSTAYLEISSLRSEDTAVYYCSRNGNGYVVGMDYWGQGTLVTVSS	560
vhCDR1	GYTFITNYGMN	561
vhCDR2	WINTYTGEPT	562
vhCDR3	GNNGYVVGMDY	563
Full length HC (IgG4(S241P); CHA.9.560.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDASTSTAYLEISSLRSEDTAVYYCSRNGNGYVVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPREEQFNSTYRVVSVLTVILHODWLNQKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGKQAVVTQEPSTLVSPGGTITLTGSSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSGVPARFSGSLGGKALTI	564
Variable light (vl) domain	SGAQPEDEAEYVCALWFSNHWVFGGGTKLTVL	565
vlCDR1	GSSTGAVTTSNHAN	566
vlCDR2	GTNGRGS	567
vlCDR3	ALWFSNHWV	568
Full length light chain (CHA.9.560.8.H4(S241P))	QAVVTQEPSTLVSPGGTITLTGSSSTGAVTTSNHANWVQKPGQAFRGLRGTNGRGSGVPARFSGSLGGKALTI	569

Figure Figure 34BB: CHA.9.546.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCARWLLSYIAMDYWGQGTLLVTSS	570
vhCDR1	GFTSSYIMS	571
vhCDR2	TISGGGTNTY	572
vhCDR3	WLLSYIAMDY	573
Full length HC (IgG4(S241P); CHA.9.546.1.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCARWLLSYIAMDYWGQGTLLVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKAQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPG K	574
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCRASQININVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFGSGGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	575
vlCDR1	RASQININWLT	576
vlCDR2	KASNLHT	577
vlCDR3	QQGQSYPT	578
Full length light chain (CHA.9.546.1.H4(S 241P))	DIQMTQSPSSLSASVGDRTTTCRASQININVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFGSGGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	579

Figure 34CC: CHA.9.547.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	580
vhCDR1	GFTSSYIMS	581
vhCDR2	TISGGGTNTY	582
vhCDR3	WLLSYYAMDY	583
Full length HC (IgG4(S241P); CHA.9.547.1.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTIKAKAQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPG K	584
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFGSGGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	585
vlCDR1	RASQININWLT	586
vlCDR2	KASNLHT	587
vlCDR3	QQGQSYPT	588
Full length light chain (CHA.9.547.1.H4(S 241P))	DIQMTQSPSSLSASVGDRTTTCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFGSGGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	589

Figure 34DD: CHA.9.547.2

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQGLVTVSS</u>	590
vhCDR1	GFTSSYIMS	591
vhCDR2	TISGGGTNTY	592
vhCDR3	WLLSYIAMDY	593
Full length HC (IgG4(S241P); CHA.9.547.2.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQGLVTVSS</u> ASTKGPSVFPLA <u>PCSRSTSE</u> TAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TYRVSVLTIVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKAQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHNAHNYTQKSLSPG K	594
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCOQGQSYPTTFGGQGTKLEIK	595
vlCDR1	RASONINWLT	596
vlCDR2	KASNLHT	597
vlCDR3	QQGQSYPT	598
Full length light chain (CHA.9.547.2.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCOQGQSYPTTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPPVTKSFNRGEC	599

Figure 34EE: CHA.9.547.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	600
vhCDR1	GFTSSYIMS	601
vhCDR2	TISGGGTNTY	602
vhCDR3	WLLSYYAMDY	603
Full length HC (IgG4(S241P); CHA.9.547.3.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTISSAKAKQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDSKRWDQEGNVFSCSVMHEALHNHYTQKSLSLSPG K	604
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININVWLTWYQQKPKGAPKLLIYKASNLHTGVPSRFGSGSGTDFTLTIS S LQPEDFATYYCQGGQSYPTFTGGQGTKLEIK	605
vlCDR1	RASQININWLT	606
vlCDR2	KASNLHT	607
vlCDR3	QQGQSYPT	608
Full length light chain (CHA.9.547.3.H4(S 241P))	DIQMTQSPSSLSASVGDRITITCRASQININVWLTWYQQKPKGAPKLLIYKASNLHTGVPSRFGSGSGTDFTLTIS S LQPEDFATYYCQGGQSYPTFTGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	609

Figure 34FF: CHA.9.547.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLR AEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	610
vhCDR1	GFTSSYIMS	611
vhCDR2	TISGGGTNTY	612
vhCDR3	WLLSYYAMDY	613
Full length HC (IgG4(S241P); CHA.9.547.4.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLR AEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLA PCRSTSEST AALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNV DHPKPSNTKVDKR VESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT VILHQQDWLNGKEYCKVSNKGLPSSIEKTI SKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTV DKSRLWQEGNVFSCSV MHEALHNHYTQKSLSLSPG K	614
Variable light (vl) domain	DIQMTQSPSSLSASVGDRIITITCRASQININVWLTWYQQKPKGAPKLLIYKASNLHTGVPSRFGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	615
vlCDR1	RASQININVWLT	616
vlCDR2	KASNLHT	617
vlCDR3	QQGQSYPT	618
Full length light chain CHA.9.547.4.H4(S 241P))	DIQMTQSPSSLSASVGDRIITITCRASQININVWLTWYQQKPKGAPKLLIYKASNLHTGVPSRFGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	619

Figure 34GG: CHA.9.547.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	620
vhCDR1	GFTSSYIMS	621
vhCDR2	TISGGGTNTY	622
vhCDR3	WLLSSYYAMDY	623
Full length HC (IgG4(S241P); CHA.9.547.6.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTISSAKAKQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSPG K	624
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	625
vlCDR1	RASONINWLT	626
vlCDR2	KASKSHT	627
vlCDR3	QQGQSYPT	628
Full length light chain (CHA.9.547.6.H4(S 241P))	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	629

Figure 34HH: CHA.9.547.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQGLVT</u> VSS	630
vhCDR1	GFTSSYIMS	631
vhCDR2	TISGGGTNTY	632
vhCDR3	WLLSYIAMDY	633
Full length HC (IgG4(S241P) for CHA.9.547.7.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQGLVT</u> VSSASTKGPSVFPLA <u>PCSRSTSE</u> TAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFN TYRVSVELTVLHQDWLNGKEYCKVKSNKGLPSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH <u>EA</u> LHNHYTQKSLSPG K	634
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	635
vlCDR1	RASONINWLT	636
vlCDR2	KASKSHT	637
vlCDR3	QQGQSYPT	638
Full length light chain for CHA.9.547.7.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRASONINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTDFTLTI SS LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	639

Figure 34II: CHA.9.547.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	640
vhCDR1	GFTSSYIMS	641
vhCDR2	TISGGGTNTY	642
vhCDR3	WLLSYYAMDY	643
Full length HC (IgG4(S241P); CHA.9.547.8.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPG K	644
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITTCRASQININVWLTWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTYTFGGQGTKLEIK	645
vlCDR1	RASQININVWLT	646
vlCDR2	KASKSHT	647
vlCDR3	QQGQSYPT	648
Full length light chain (CHA.9.547.8.H4(S 241P))	DIQMTQSPSSLSASVGDRTITTCRASQININVWLTWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTYTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	649

Figure 34J: CHA.9.547.9

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	650
vhCDR1	GFTSSYIMS	651
vhCDR2	TISGGGTNTY	652
vhCDR3	WLLSSYYAMDY	653
Full length HC (IgG4(S241P); CHA.9.547.9.H4(S 241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLA PCSR STSESTAALGCLVK DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNV DKP SN TKV DKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSD ED PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT TVL HQD W LN G KEYCK V SNKGLPSSIEK T ISKAKGQPREPQVY T LP PSQ EE M TKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYK T TPPVLDSDGSFFLYSRLTV D KSRWQEGNVFSCSV M HEALHNHYTQKSLSLSPG K	654
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITTCRASQININVWLTWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	655
vlCDR1	RASQININVWLT	656
vlCDR2	KASKSHT	657
vlCDR3	QQGQSYPT	658
Full length light chain (CHA.9.547.9.H4(S 241P))	DIQMTQSPSSLSASVGDRTITTCRASQININVWLTWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	659

Figure 34KK: CHA.9.541.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPTVYAQKFQGRVTM TRDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	660
vhCDR1	GYTITNYGMN	661
vhCDR2	WINTYTGEPT	662
vhCDR3	GNGNPLGMDY	663
Full length HC (IgG4(S241P); CHA.9.541.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPTVYAQKFQGRVTM TRDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPP CPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNST YRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPG K	664
Variable light (vl) domain	EIVLTQSPA ^L TLSPGERATLSCGNGNPLGMDY ^L WYQQKPGQAPRLLIYDTSKLASGIPARFSGSGGTDFTLTISS L EPEDFAVYYCFQGS ^L GYPLTFGQGT ^L KEIK	665
vlCDR1	GNGNPLGMDY	666
vlCDR2	DTSKLAS	667
vlCDR3	FQSGGYPLT	668
Full length light chain (CHA.9.541.1.H4(S241P))	EIVLTQSPA ^L TLSPGERATLSCGNGNPLGMDY ^L WYQQKPGQAPRLLIYDTSKLASGIPARFSGSGGTDFTLTISS L EPEDFAVYYCFQGS ^L GYPLTFGQGT ^L KEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDS ^L TYSLSS ^L TLTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	669

Figure 34LL: CHA.9.541.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	670
vhCDR1	GYTITNYGMN	671
vhCDR2	WINTYTGEPY	672
vhCDR3	GNGNPLGMDY	673
Full length HC (IgG4(S241P); CHA.9.541.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTKYTCNVVDHKPSNTKVDKRVESKYGPP CPCPAPEFLGGPSVFLFPPKPKDITLMSKTPETVCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNST YRVVSVLTIVLHODWLNQKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPG K	674
Variable light (vl) domain	EIVLTQSPAATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKSLASGIPARFSGSGGTDTYTLTISS L EPEDFAVYYCFQGSQGYPLTFGQGTKEIK	675
vlCDR1	GNGNPLGMDY	676
vlCDR2	DTSKLAS	677
vlCDR3	FQSGGYPLT	678
Full length light chain (CHA.9.541.3.H4(S241P))	EIVLTQSPAATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKSLASGIPARFSGSGGTDTYTLTISS L EPEDFAVYYCFQGSQGYPLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSITYSLSSITLTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	679

Figure 34MM: CHA.9.541.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	680
vhCDR1	GYTITNYGMN	681
vhCDR2	WINTYTGEPY	682
vhCDR3	GNGNPLGMDY	683
Full length HC (IgG4(S241P); CHA.9.541.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPITYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTKYTCNVVDHKPSNTKVDKRVESKYGPP CPCPAPEFLGGPSVFLFPPKPKDITLMSKRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNST YRVVSVLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHIALHNHYTQKSLSPG K	684
Variable light (vl) domain	EIVLTQSPAATLSLSPGERATLSCGNGNPLGMDYVYQQKPGQAPRLWYDTSKLASGVPARFSGSGSGTDYTLTIS SL EPEDFAVYYCFQGSQGYPLTFGQGTGLEIK	685
vlCDR1	GNGNPLGMDY	686
vlCDR2	DTSKLAS	687
vlCDR3	FQSGGYPLT	688
Full length light chain (CHA.9.541.4.H4(S241P))	EIVLTQSPAATLSLSPGERATLSCGNGNPLGMDYVYQQKPGQAPRLWYDTSKLASGVPARFSGSGSGTDYTLTIS SL EPEDFAVYYCFQGSQGYPLTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSITYSLSSITLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	689

Figure 34NN CHA.9.541.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPTVYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	690
vhCDR1	GYTITNYGMN	691
vhCDR2	WINTYTGEPT	692
vhCDR3	GNGNPLGMDY	693
Full length HC (IgG4(S241P); CHA.9.541.5.H4(S241P))	QVQLVQSGAEVKKPGASVKVSKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGEPTVYAQKFQGRFTMT LDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSSTSESTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPP CPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTIVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDDKSRWQEGNVFSCSVMHIALHNHYTQKSLSPG K	694
Variable light (vl) domain	EIVLTQSPA TLSPGERVTMSCGNGNPLGMDYVYQQKPGQAPRLWYDTSKLASGVPARFSGSGGTIDYTLTI SSM EPEDFAVYYCFQGSQGYPLTFGQGTKLEIK	695
vlCDR1	GNGNPLGMDY	696
vlCDR2	DTSKLAS	697
vlCDR3	FQGSQGYPLT	698
Full length light chain (CHA.9.541.5.H4(S241P))	EIVLTQSPA TLSPGERVTMSCGNGNPLGMDYVYQQKPGQAPRLWYDTSKLASGVPARFSGSGGTIDYTLTI SSM EPEDFAVYYCFQGSQGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSITYSLSSITLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	699

Figure 400: CHA.9.541.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	700
vhCDR1	GYTITNYGMN	701
vhCDR2	WINTYTGEPT	702
vhCDR3	GNGNPLGMDY	703
Full length HC (IgG4(S241P); CHA.9.541.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGK	704
Variable light (vl) domain	EIVLTQSPA TL SLSPGERATL SCGNGNPLGMDY WYQQKPGQAPRL LIYDTSKL ASGIPARFSGSGSGTDYTLTISSL L EPEDFAVYYCFQSGGYPLTFGQGTKLEIK	705
vlCDR1	GNGNPLGMDY	706
vlCDR2	DTSKLAS	707
vlCDR3	FQSGGYPLT	708
Full length light chain (CHA.9.541.6.H4(S241P))	EIVLTQSPA TL SLSPGERATL SCGNGNPLGMDY WYQQKPGQAPRL LIYDTSKL ASGIPARFSGSGSGTDYTLTISSL L EPEDFAVYYCFQSGGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	709

Figure 34PP: CHA.9.541.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	710
vhCDR1	GYTITNYGMN	711
vhCDR2	WINTYTGEPT	712
vhCDR3	GNGNPLGMDY	713
Full length HC (IgG4(S241P) CHA.9.541.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKITYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYRVVSVLTVILHODWLNQKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSPGK	714
Variable light (vl) domain	EIVLTQSPA TL SLSPGERATL SCGNGNPLGMDY WYQQKPGQAPRL WYDTSKLASGVPARFSGSGSGTDYTLTIS SL EPEDFAVYYCFQGSGLYPLTFGQGTKLEIK	715
vlCDR1	GNGNPLGMDY	716
vlCDR2	DTSKLAS	717
vlCDR3	FQGSGLYPLT	718
Full length light chain (CHA.9.541.7.H4(S241P))	EIVLTQSPA TL SLSPGERATL SCGNGNPLGMDY WYQQKPGQAPRL WYDTSKLASGVPARFSGSGSGTDYTLTIS SL EPEDFAVYYCFQGSGLYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	719

Figure 34QQ: CHA.9.541.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	720
vhCDR1	GYTITNYGMN	721
vhCDR2	WINTYTGEPT	722
vhCDR3	GNGNPLGMDY	723
Full length HC (IgG4(S241P); CHA.9.541.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPQGQLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPREEQFNSTYRVVSVLTVILHQQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSPGKEIVLTQSPA TL SLSPGERVTM SCNGNPLGMDY WYQQKPGQAPRLWIYDTSKLASGVPARFSGSGGTDTYTLTISSM EPEDFAVYYCFQGGGYPLTFGQGTKLEIK	724
Variable light (vl) domain	EPEDFAVYYCFQGGGYPLTFGQGTKLEIK	725
vlCDR1	GNGNPLGMDY	726
vlCDR2	DTSKLAS	727
vlCDR3	FQGGGYPLT	728
Full length light chain (CHA.9.541.8.H4(S241P))	EIVLTQSPA TL SLSPGERVTM SCNGNPLGMDY WYQQKPGQAPRLWIYDTSKLASGVPARFSGSGGTDTYTLTISSM EPEDFAVYYCFQGGGYPLTFGQGTKLEIKRTVAAPSVFIFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	729

Figure 34RR: CHA.9.547.10

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	730
vhCDR1	GFTSSYIMS	731
vhCDR2	TISGGGTNTY	732
vhCDR3	WLLSYYAMDY	733
Full length HC for CHA.9.547.10.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRTSESTAALGCLVK DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TYRVSVELTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHNAHNNHYTQKSLSPG K	734
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTGDTFTLTIS S LQPEDFATYYCQQGQSYPTYTFGGQGTKLEIK	735
vlCDR1	RASQININWLS	736
vlCDR2	KASKSHT	737
vlCDR3	QQGQSYPT	738
Full length light chain For CHA.9.547.10.H4(S241P))	DIQMTQSPSSLSASVGDRTTTCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTGDTFTLTIS S LQPEDFATYYCQQGQSYPTYTFGGQGTKLEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	739

Figure 345S: CHA.9.547.11

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSS	740
vhCDR1	GFTSSYIMS	741
vhCDR2	TISGGGTNTY	742
vhCDR3	WLLSYYAMDY	743
Full length HC for CHA.9.547.11.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVSTISGGGTINTYYADSVKGRFTISRDN SKN TLYLQMNSLRRAEDTAVYYCAKWLSSYYAMDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TYRVSVELTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKQGPPEPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSRLTVYDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPG K	744
Variable light (vl) domain	DIQMTQSPSSLSASVGDRIITITCRASQININVWL ^S WYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGGTDFLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	745
vlCDR1	RASQININVWLS	746
vlCDR2	KASKSHT	747
vlCDR3	QQGQSYPT	748
Full length light chain For CHA.9.547.11.H4(S241P))	DIQMTQSPSSLSASVGDRIITITCRASQININVWL ^S WYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGGTDFLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSS ^T LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	749

Figure 34TT: CHA.9.547.12

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQTLVTVSS</u>	750
vhCDR1	GFTSSYIMS	751
vhCDR2	TISGGGTNTY	752
vhCDR3	WLLSYIAMDY	753
Full length HC For CHA.9.547.12.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYIAMDYWGQTLVTVSSASTKGPSVFPLA</u> PCSRSTSESTAALGCLVK DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TYRVSVELTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKAQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPG K	754
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITTCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTGDTFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIK	755
vlCDR1	RASQININWLS	756
vlCDR2	KASKSHT	757
vlCDR3	QQGQSYPT	758
Full length light chain for CHA.9.547.12.H4(S241P))	DIQMTQSPSSLSASVGDRTITTCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGTGDTFTLTIS S LQPEDFATYYCQQGQSYPTFTGGQGTKLEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	759

Figure 34UU: CHA.9.547.13

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYYAMDYWGQTLVTVSS</u>	760
vhCDR1	GFTSSYIMS	761
vhCDR2	TISGGGTNTY	762
vhCDR3	WLLSYYAMDY	763
Full length HC for CHA.9.547.13.H4(S241P)	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVA <u>TISGGGTNTYYADSVKGRFTISRDN</u> SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYYAMDYWGQTLVTVSS</u> ASTKGPSVFPLA <u>PCSRSTSE</u> TAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFN TYRVSVLTIVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSRLTVDKSRWQEGNVFSCSVMHNAHNNHYTQKSLSPG K	764
Variable light (vl) domain	DIQMTQSPSSLSASVGDRIITITCRASQININVWLSWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFLTIS S LQPEDFATYYCOQGQSYPTFTGGQGTKLEIK	765
vlCDR1	RASQININWLS	766
vlCDR2	KASKSHT	767
vlCDR3	QQGQSYPT	768
Full length light chain for CHA.9.547.13.H4(S241P)	DIQMTQSPSSLSASVGDRIITITCRASQININVWLSWYQQKPKGAPKLLIYKASKSHTGVPSRFSGSGSGTDFLTIS S LQPEDFATYYCOQGQSYPTFTGGQGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	769

Figure 34VV: CHA.9.543

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASMKISCKASGYSTFGYTMNWRQSHGKNLEWLGLIPYNGGTSYNQNFKGKATLTVDTSSTAYMELLSTVSD SAVYYCARGVRFALDYWGQGTSVSVSS	770
vhCDR1	GVSFTGYTMN	771
vhCDR2	LIFPYNGGTS	772
vhCDR3	GVRFALDY	773
Full length HC for CHA.9.543.H4(S24 1P))	Mouse hybridoma, sequence not available	774
Variable light (vl) domain	DVVMQTQTPLSLPVSFGDQVSISSQSLANSYGNTYLSWYLHKPGQSPQLLYEISNRFSGVPDRFSGSGGTDFTLNISTIKPEDLGMYYC LQGTQHPWTTFGGGKLEIK	775
viCDR1	RSSQSLANSYGNTYLS	776
viCDR2	EISNRFS	777
viCDR3	LQGTQHPWT	778
Full length light chain for CHA.9.543.H4(S24 1P))	Mouse hybridoma, sequence not available	779

Figure 34WW: BM26 mouse IgG1 (BM26-M1) (WO2016/028656A1, Clone 31C6)

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTS DKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTSS	780
vhCDR1	GYTFSSVV	781
vhCDR2	IDPYNDGA	782
vhCDR3	ARGGPYGWYFDV	783
Full length HC	EVQLQQSGPELVKPGSSVKMSCKASGYTSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTS DKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTSSAKITPPSVVPLAPGSAQINSMVTL GCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTPSSWTPSETVTCNVVVAHPASSTKVDDKKIVPR DCGCKPCICTVPEVSSVFIPPKPKDVLTTITLTPKVTCTVVDISKDDPEVQFSWFDVDDVEVHTAQTPREEQFNST FRSYSELPIMHQDWLNGKEFKCRVNSAAPAPIEKTIKTKGRPKAPQVYTIIPPKQMAKDKVSLTCMITDFFP EDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYVSKLVNQQSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG K	784
Variable light (vl) domain	DIQMTQSPASLSASVGETVTTTCRASEHIYSYLSWYQQKQKQKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSLKI NSLQPEDFGTYYCQHHFGSPLTFGAGTTLELK	785
vlCDR1	EHIYSY	786
vlCDR2	NAK	787
vlCDR3	QHHFGSPLT	788
Full length light chain	DIQMTQSPASLSASVGETVTTTCRASEHIYSYLSWYQQKQKQKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSLKI NSLQPEDFGTYYCQHHFGSPLTFGAGTTLELKRAADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKI DGSERQNGVLNSWTDQDSKSDSTYSMSSTLTLTKEDEYERHNSYTCEATHKLTSTSPIVKSFNRNEC	789

Figure 34XX: BM29 mouse IgG1 (BM29-M1) (US2016/0176963A1, Clone 22G2)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGIYYSGSTNYPNPSLKSRVTISVDTS KNQFSCLKLSSVTAADTA VYYCARDYYVSGNYYNVDYYFFGVDVWGQGTITVTSS	790
vhCDR1	GGSVSSGIYY	791
vhCDR2	IYYSGST	792
vhCDR3	ARDYYVSGNYYNVDYYFFGVDV	793
Full length HC	QVHLQESGPGLVKPSSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGIYYSGSTNYPNPSLKSRVTISVDTS KNQFSCLKLSSVTAADTA VYYCARDYYVSGNYYNVDYYFFGVDVWGQGTITVTSSAKTTPPSVYPLAPGSAAQ TNSMVTLGCLVKGYPPEPVITVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTPSSTWPSSETVTCNVAHPASSTK VDKKIVPRDCGCKPCICTVPEVSSVFFPPPKPKDVLITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTP REEQFNSTFRSVSELPMHQDWLNGKEFKCRVNSAAPAPIEKTIKTKGRPKAPQVYITPPPKQMAKDKVSLT CMITDFFPEDITVVEWQWNGQPAENYKNTQPMIDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHTE KSLSHSPGK	794
Variable light (vl) domain	EIVLTQSPA TLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLLIYDASNRA TGIPARFSGSGGTDFLTIS LEPEDFAVYYCQQRSNWPPLFTFGPGTKVDIK	795
vlCDR1	QSVSSY	796
vlCDR2	DAS	797
vlCDR3	QQRSNWPPLFT	798
Full length light chain	EIVLTQSPA TLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLLIYDASNRA TGIPARFSGSGGTDFLTIS LEPEDFAVYYCQQRSNWPPLFTFGPGTKVDIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKI DGSERQNGVLNSWTDQDSKDSYMSSTLTITKDEYERHNSYTCEATHKTTSTSPIVKSFNRNEC	799

Figure 34YY

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:10 from US2017281764)	DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMHWWVRQAPEKGLEWVAFISSGSS SIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCARMRLDYYAMDYWGQG GTSVTVSS	800
vHCDR1 (SEQ ID NO:11 from US2017281764)	NFGMH	801
vHCDR2 (SEQ ID NO:12 from US2017281764)	FISSGSSSIYYADTVKG	8-2
vHCDR3 (SEQ ID NO:13 from US2017281764)	MRLDYYAMDY	803
Light chain (SEQ ID NO:14 from US2017281764)	DVQITQSPSYLAASPGETITINCRASKSISKYLAWYQEKPGKTNKLLIYSGSTLQSGIPS RFSGSGGTDFTLTISSLEPEDFAMYYCQQHNEYPWTFGGGKLEIK	804
vLCDR1 (SEQ ID NO:15 from US2017281764)	RASKSISKYLA	805
vLCDR2 (SEQ ID NO:16 from US2017281764)	SGSTLQS	806
vLCDR3 (SEQ ID NO:17 from US2017281764)	QQHNEYPWT	807

Figure 34ZZ

From US20170281764 (JN Bioscieces)

What	sequence	SEQ ID NO:
Heavy chain		
(SEQ ID NO:18 from	EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKNLEWIGINPNNG	808
US2017281764)	GTSYNQKFKGRATLTVDKSSSTAYMELRSLTSDDSA VYYCARPGWYNYAMDYWG	
vHCDR1	QGTSTVTVSS	809
(SEQ ID NO:19 from	EYTMH	
US2017281764)		
vHCDR2	GINPNNGGTSYNQKFKG	810
(SEQ ID NO:20 from		
US2017281764)		
vHCDR3	PGWYNYAMDY	811
(SEQ ID NO:21 from		
US2017281764)		
Light chain		
(SEQ ID NO:22 from	DIVMTQSHKEMSTSVGDRVNITCKASQGVSTAVAWYQQKPGQSPKLLIYSASYRYT	812
US2017281764)	GVPDRFTGSGSGTDFITISSVQAEDLAVYHCQQHYPWPWTFGGGTKLEIK	
vLCDR1	KASQGVSTAVA	813
(SEQ ID NO:23 from		
US2017281764)		
vLCDR2	SASYRYT	814
(SEQ ID NO:24 from		
US2017281764)		
vLCDR3	QQHYITPWT	815
(SEQ ID NO:25 from		
US2017281764)		

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Figure 34AAA

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:26 from US2017281764)	EVQLVESGGGLVKPGGSLKLSCAASGFAFSDYDMSWVRQTPEKRLEWVA YISDGGY NTYYPDITVKGGRFTISRDNAKNTLYLQMSSLSKSEDTAIYYCARQILLRYYFDYWGQGT TLTVSS	816
vhCDR1 (SEQ ID NO:27 from US2017281764)	DYDMS	817
vhCDR2 (SEQ ID NO:28 from US2017281764)	YISDGGYNTYYPDITVKG	818
vhCDR3 (SEQ ID NO:29 from US2017281764)	QILLRYYFDY	819
Light chain (SEQ ID NO:30 from US2017281764)	DIVMSQSPSSLA VSVGEKVTMTCKSSQSLLYSSNQKNYLA WYQQKPGQSPKLLIYW ASTRESGVPDRFTGSGSGTDFLTITSSVKAEDLA VYYCQQYHSYPWTFGGGTKLEIK	820
vLCDR1 (SEQ ID NO:31 from US2017281764)	KSSQSLLYSSNQKNYLA	821
vLCDR2 (SEQ ID NO:32 from US2017281764)	WASTRES	822
vLCDR3 (SEQ ID NO:33 from US2017281764)	QQYHSYPWT	823

Figure 348BB

From US20170281764 (JN Biosciences)

What sequence

Heavy chain
(SEQ ID NO:35 from
US2017281764)

SEQ ID NO:

824

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAFISSGSSS
IYYADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRLDYYAMDYWGQ
GTMVTVSS

Light chain
(SEQ ID NO:37 from
US2017281764)

825

DIQMTQSPSSLSASVGDRVTITCRASKSISKYLAWYQQKPGKAPKLLIYSGSTLQSGV
PSRFSGSGSGTDFLTITSSLPEDFATYYCQQHNEYWPWTFGGGTKVEIK

From US20170281764 (JN Biosciences)

What sequence

Heavy chain
(SEQ ID NO:34 from
US2017281764)

SEQ ID NO:

826

MDSRLNLVFLVLILKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWV
RQAPGKGLEWVAFISSGSSSIYYADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY
YCARMRLDYYAMDYWGQGTMTVTVSS

Light chain
(SEQ ID NO:36 from
US2017281764)

827

MRFQVQVLGLLLLWISGAQCIDIQMTQSPSSLSASVGDRVTITCRASKSISKYLAWYQ
QKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTDFLTITSSLPEDFATYYCQQHNEY
WTFGGGTKVEIK

Figure 34CCC

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG; see also, WO2016011264)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:15 from WO2015009856)	EVQLVESGGGLTQPGKSLKLSCEASGFTSSFTMHWVRQSPGKGLEWVAFIRSGSIVF YADAVRGRFTISRDNAKNLLFLQMNDLKSEDTAMYYCARRPLGHNTFDSWGQGTLLVT VSS	828
vhCDR1 (SEQ ID NO:4 from WO2015009856)	GFTFSFTMH	829
vhCDR2 (SEQ ID NO:5 from WO2015009856)	FIRSGSIVFYADAVRG	830
vhCDR3 (SEQ ID NO:6 from WO2015009856)	RPLGHNTFDS	831
Light chain (SEQ ID NO:13 from WO2015009856)	DIVMTQSPSSLA VSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASI RFTGVPRDFTGSGSGTDYTLTITSVQAEDMGQYFCQQGINNPLTFGDGTKLEIKR	832
vLCDR1 (SEQ ID NO:1 from WO2015009856)	KSSQSLYYSGVKENLLA	833
vLCDR2 (SEQ ID NO:2 from WO2015009856)	ASIRFT	834
vLCDR3 (SEQ ID NO:3 from WO2015009856)	QQGINNPLT	835

Figure 34DDD

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG; see also, WO2016011264)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:16 from WO2015009856)	EVQLQQSGPELVKPGTSMKISKASGYSTGHLMNWVKQSHGKNLEWIGLIIPYNGGTS YNQKFKGKATLTVDKSSSTAYMELLSLTSDDSA VYFCSRGLRGFYAMDYWGQGTSVT VSS	836
vhCDR1 (SEQ ID NO:10 from WO2015009856)	GYSFTGHLMN	837
vhCDR2 (SEQ ID NO:11 from WO2015009856)	LIIPYNGGTSYNQKFKG	838
vhCDR3 (SEQ ID NO:12 from WO2015009856)	GLRGFYAMDY	839
Light chain (SEQ ID NO:14 from WO2015009856)	DVVLTTQPLSLSVSGDQVSISCRSSQSLVNSYGNTFLSWYLHKPGQSPQLLIFGISNRFS GVPDFRFGSGSGTDFTLKISTIKPEDLGMYYCLQGTHTQPTTFGPGTKLEVK	840
vLCDR1 (SEQ ID NO:7 from WO2015009856)	RSSQSLVNSYGNTFLS	841
vLCDR2 (SEQ ID NO:8 from WO2015009856)	GISNRFS	842
vLCDR3 (SEQ ID NO:9 from WO2015009856)	LQGTHTQPPT	843

Figure 34EEE

From US 9713641 (Table 5, reproduced herein; SEQ ID NOs: are from US 9713641)

Sequences and germlines (GL) of TIGIT ABPs													
Ab	VH	GL	CDR- H1 ¹		SIYSGA	TFYNPSL	K	CDR- H3 ³	VH Protein (SEQ ID NOS 573-577)	VL GL	RASQSV	CDR- L2 ⁵	CDR- L3 ⁶
			(SEQ ID NOS 558-562)	(SEQ ID NOS 563-567)				(SEQ ID NOS 578-582)			(SEQ ID NOS 583-587)	(SEQ ID NOS 588-592)	(SEQ ID NOS 593-597)
MAB1-IgG4	VH4-39	WG	GSITSSSY	SIYSGA	ARDANY	TFYNPSL	DP	ARDANY	QLQESGPGGLVKPSETLSLTCTVSGGSISSY YWGWIQPPGKGLWIGSIYSGATFYNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYCA RDANYGSAWAFDPWGQGLTVTVSS (SEQ ID NO)	VK3-11	SSYLA	DASNRAT	QQHFNLP T
MAB2-IgG4	VH4-39	WG	GSISSTSHY	SIYSGS	ARDANY	TFYNPSL	DP	ARDANY	QLQESGPGGLVKPSETLSLTCTVSGGSISS KYWGWIQPPGKGLWIGSIYSGSTFYN PSLKSRTISVDTSKNQFSLKLSVTAADTAV YYCARDANYGSAWAFDPWGQGLTVTVSS (SEQ ID NO)	VK3-11	SSYLA	DASNRAT	QQHFNLP T
MAB3-IgG4	VH4-39	WG	GSISSTSHY	SIYSGSTF	ARDANY	YNPJLS	DP	ARDANY	QLQESGPGGLVKPSETLSLTCTVSGGSISS SHYWGWIQPPGKGLWIGSIYSGSTFYN PSLKSRTISVDTSKNQFSLKLSVTAADTAV YYCARDANYGSAWAFDPWGQGLTVTVSS (SEQ ID NO)	VK3-11	SSYLA	DASNRAT	QQHFNLP T
MAB4-IgG4	VH4-39	WG	GSISSTSHY	SIYSGSTF	ARDANY	YNPJLS	DP	ARDANY	QLQESGPGGLVKPSETLSLTCTVSGGSISS SHYWGWIQPPGKGLWIGSIYSGSTFYN PSLKSRTISVDTSKNQFSLKLSVTAADTAV YYCARDANYGSAWAFDPWGQGLTVTVSS (SEQ ID NO)	VK3-11	SSYLA	DASNRAT	QQHFNLP T
MAB5-IgG4	VH4-39	WG	GSISSTSHY	SIYSGS	ARDANY	TFYNPSL	KG	ARDANY	QLQESGPGGLVKPSETLSLTCTVSGGSISS SHYWGWIQPPGKGLWIGSIYSGSTFYN PSLKSRTISVDTSKNQFSLKLSVTAADTAV YYCARDANYGSAWAFDPWGQGLTVTVSS (SEQ ID NO)	VK3-11	SSYLA	DASNRAT	QQHFNLP T

¹ Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems.² According to the Kabat numbering system.³ According to the IMGT numbering system.⁴ According to the Kabat and Chothia numbering systems.⁵ According to the Kabat and Chothia numbering systems.⁶ According to the Kabat, Chothia, and IMGT numbering systems.

From US 9713641 (Table 5, reproduced herein; SEQ ID NOs: are from US 9713641)

⁷ Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems. According to the Kabat numbering system.

⁸ According to the Kabat numbering system.

⁹ According to the IMGT numbering system.

¹⁰ According to the Kabat and Chothia numbering systems.

¹¹ According to the Kabat numbering system.

¹² According to the Kabat, Chothia, and IMGT numbering systems.

Figure 34GGG

From US 9713641 (Table 5, reproduced herein; SEQ ID NOs: are from US 9713641)

Sequences and germ lines (GL) of TIGIT ABPs											
Ab	CDR- H1 ¹³ (SEQ ID NOS 638- 642)	CDR- H2 ¹⁴ (SEQ ID NOS 643- 647)	CDR- H3 ¹⁵ (SEQ ID NOS 648- 652)	CDR- L1 ¹⁶ (SEQ ID NOS 658- 662)	CDR- L2 ¹⁷ (SEQ ID NOS 663- 667)	CDR- L3 ¹⁸ (SEQ ID NOS 668- 672)	VL Protein (SEQ ID NOS 673-677)				
MAB1 1-1gG4	GH3E3GLY WG	SYMSGSY YNPSLKS	ARDGVLA LNKRSFDI	RASQSV SSSYLA	GASSRAT	QQHTVRP PLT	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA YGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQHTVRPPL TFGGGTKEIK (SEQ ID NO)				
MAB1 2-1gG4	GH3E3GLY WG	SYMSGSY YNPSLKS	ARDGVLA LNKRSFDI	RASQSV SSSYLA	GASSRAT	QQHTVRP PLT	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA YGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQHTVRPPL TFGGGTKEIK (SEQ ID NO)				
MAB1 3-1gG4	YTFGNYY MH	INPSLGLT SYAQKQ G	ARGGRIT WIGAFDI	RASQSV SNLA	GASTRAT	QQYVWW PPLT	EIVMTQSPATISVSPGERATLSCRASQSVSSSYLA YGASTRATGIPARFSGSGGTFTLTISLQSEDFAVYYCQYVWWPP LTFGGGTKEIK (SEQ ID NO)				
MAB1 4-1gG4	YTFPAY MH	INPSLGLT SYAQKQ G	ARGGRIT WIGAFDI	RASQSV SNLA	GASTRAT	QQYVWW PPLT	EIVMTQSPATISVSPGERATLSCRASQSVSSSYLA YGASTRATGIPARFSGSGGTFTLTISLQSEDFAVYYCQYVWWPP LTFGGGTKEIK (SEQ ID NO)				
MAB1 5-1gG4	YTFREY MH	INPSLGLT TSYARKF QG	ARGGRIT WIGAFDI	RASQSV SNLA	GASTRAT	QQYVWW PPLT	EIVMTQSPATISVSPGERATLSCRASQSVSSSYLA YGASTRATGIPARFSGSGGTFTLTISLQSEDFAVYYCQYVWWPP LTFGGGTKEIK (SEQ ID NO)				

¹³ Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems.¹⁴ According to the Kabat numbering system.¹⁵ According to the IMGT numbering system.¹⁶ According to the Kabat and Chothia numbering systems.¹⁷ According to the Kabat and Chothia numbering systems.¹⁸ According to the Kabat, Chothia, and IMGT numbering systems.

Figure 34HHH

From US 9713641 (Table 5, reproduced herein; SEQ ID NOs: are from US 9713641)

Sequences and germlines (GL) of TIGIT ABPs									
Ab	CDR- H1 ¹⁹ (SEQ ID NOS)	CDR- H2 ²⁰ (SEQ ID NOS)	CDR- H3 ²¹ (SEQ ID NOS)	CDR- L2 ²² (SEQ ID NOS)	CDR- L3 ²³ (SEQ ID NOS)	CDR- L4 ²⁴ (SEQ ID NOS)	CDR- L5 ²⁵ (SEQ ID NOS)	CDR- L6 ²⁶ (SEQ ID NOS)	CDR- L7 ²⁷ (SEQ ID NOS)
MAB 16- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 696-701)	VH 702- GL 707	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)
MAB 17- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 702-707)	VH 708- GL 713	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)
MAB 18- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 708-713)	VH 714- GL 719	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)
MAB 19- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 714-719)	VH 720- GL 725	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)
MAB 20- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 720-725)	VH 726- GL 731	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)
MAB 21- IgG4	VH 678- GL 683	YTFREY MH	INPSIGL TSYARKF QG	ARGGR TTWIG ALDI	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	VH Protein (SEQ ID NOS 726-731)	VH 732- GL 737	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)	QVQLVQSGAEVKPKPGASVKVCKASGYTFREYMH WVRAQPGGGLWMGIIINPSIGLTSYARKFQGRVT MTRDTSTSTVYMELSLRSEDATVYVCARGGRITWI GALDIWGQGTMTVTVSS (SEQ ID NO)

¹⁹ Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems.

²⁰ According to the Kabat numbering system.

²¹ According to the IMGT numbering system.

²² According to the Kabat and Chothia numbering systems.

²³ According to the Kabat and Chothia numbering systems.

²⁴ According to the Kabat, Chothia, and IMGT numbering systems.

Figure 34III

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:7 from WO2016028656)	EVQLQESGPGLVKPSQSLSTCSVTGSSIASDYWGWRKFPGNKMEWMGFITYSGSTSY NPSLKSRIISITRDTSKNQFFLQLHSVTDDTATYSCARMPSFITLASLSTWEGYDFWGP GTMVTVSS	884
vhCDR1 (SEQ ID NO:1 from WO2016028656)	SDYWG	885
vhCDR2 (SEQ ID NO:2 from WO2016028656)	FITYSGSTSYNPSLKS	886
vhCDR3 (SEQ ID NO:3 from WO2016028656)	MPSFITLASLSTWEGYFDF	887
Light chain (SEQ ID NO:8 from WO2016028656)	DIQMTQSPSLLSASVGDRVTLNCKASQSIHKNLAWYQQKLGAPKFLIYYANSLQTGPS RFSGSGSGTDFTLTISGLQPEDVATYFCQQYYSGWTFGGGKVELK	888
vLCDR1 (SEQ ID NO:4 from WO2016028656)	KASQSIHKNLA	889
vLCDR2 (SEQ ID NO:5 from WO2016028656)	YANSLQT	890
vLCDR3 (SEQ ID NO:6 from WO2016028656)	QQYYSGWT	891

Figure 34KKK

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:11 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT MVTVSS	900
vhCDR1 (from WO2016028656)	SDYWG	901
vhCDR2 (from WO2016028656)	FITYSGSTSYNP SLKS	902
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	903
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:12 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYN PSLKSRTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	904
vhCDR1 (from WO2016028656)	SDYWG	905
vhCDR2 (from WO2016028656)	FITYSGSTSYNP SLKS	906
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	907

Figure 34LLL

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:13 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	908
vhCDR1 (from WO2016028656)	SDYWG	909
vhCDR2 (from WO2016028656)	FITYSGSTSYNP SLKS	910
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	911
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:14 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT MVTVSS	912
vhCDR1 (from WO2016028656)	SDYWG	913
vhCDR2 from WO2016028656)	GFITYSGSTSYNP SLKS	914
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	915

Figure 34MMMM

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	sequence		
Heavy chain (SEQ ID NO:15 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGGGT MVTVSS	916	
vhCDR1 (from WO2016028656)	SDYWG	917	
vhCDR2 (from WO2016028656)	FITYSGSTSYNP SLKS	918	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	919	
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	sequence		
Heavy chain (SEQ ID NO:16 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYN PSLKSRTISVDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGGG TMVTVSS	920	
vhCDR1 (from WO2016028656)	SDYWG	921	
vhCDR2 (from WO2016028656)	FITYSGSTSYNP SLKS	922	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	923	

Figure 34NNN

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	sequence		
Heavy chain (SEQ ID NO:17 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDWGGQ GTMVTVSS	924	
vhCDR1 (from WO2016028656)	SDYWG	925	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	926	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	927	
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	sequence		
Heavy chain (SEQ ID NO:18 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQPPGKGLEWIGFI TYSGSTSYNPSLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFI TLASLSTWEGYFDWGGQTMVTVSS	928	
vhCDR1 (from WO2016028656)	SDYWG	929	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	930	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	931	

Figure 34000

From WO2016028656 (Table 4, reproduced herein)		WO 2023/178192	142/299	PCT/US2023/064460
What	sequence	SEQ ID NO:		
Heavy chain (SEQ ID NO:19 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQQPGKGLEWIGFI TYSGSTSYNPSLKSRLTISRDTSKNQFSKLSSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMTVTSS	932		
vhCDR1 (from WO2016028656)	SDYWG	933		
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	934		
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	935		
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:		
What	sequence			
Heavy chain (SEQ ID NO:20 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGSSISDYGWIRQPPGKGLEWMGFI TYSGSTSYNPSLKSRLTISRDTSKNQFSKLSSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMTVTSS	936		
vhCDR1 (from WO2016028656)	SDYWG	937		
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	938		
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	939		

Figure 34PPP

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	sequence		
Heavy chain (SEQ ID NO:21 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLHSVTAADTA VYYCARMPSFITLASLSTWEGYFDWFQGQ GTMVTVSS	940	
vhCDR1 (from WO2016028656)	SDYWG	941	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	942	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	943	
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	Sequence		
Heavy chain (SEQ ID NO:22 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQPPGKGLEWIGFITYSGSTSYN PSLKSRITISRDTSKNQFSLKLHSVTAADTA VYYCARMPSFITLASLSTWEGYFDWFQGQ TMVTVSS	944	
vhCDR1 (from WO2016028656)	SDYWG	945	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	946	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	947	

Figure 34QQQ

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	Sequence		
Heavy chain (SEQ ID NO:37 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSSAS	948	
vhCDR1 (from WO2016028656)	SDYWG	949	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	950	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	951	
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	Sequence		
Heavy chain (SEQ ID NO:38 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	952	
vhCDR1 (from WO2016028656)	SDYWG	953	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	954	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	955	

Figure 34RRR

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:39 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWI RKPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTVTAADTA VYYCARMPSFITLASLSTWEGYDFWGQG TMVTVSS	956
vhCDR1 (from WO2016028656)	SDYWG	957
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	958
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	959
From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:40 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWI RKPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTVTAADTA VYYCARMPSFITLASLSTWEGYDFWGQG TMVTVSS	960
vhCDR1 (from WO2016028656)	SDYWG	961
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	962
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	963

Figure 34SSS

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:41 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPPGKGMWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSVTAADTAVYYCARMPSFITLASLSTWEGYFDWGGQ GTMVTVSS	964
vhCDR1 (from WO2016028656)	SDYWG	965
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	966
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	967
From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:42 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPPGKGMWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSVTAADTAVYYCARMPSFITLASLSTWEGYFDWGGQ GTMVTVSS	968
vhCDR1 (from WO2016028656)	SDYWG	969
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	970
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	971

Figure 34TTT

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:43 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQFPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTVADDTAVYYCARMPSFITLASLSTWEGYDFDFWGQG TMVTVSS	972
vhCDR1 (from WO2016028656)	SDYWG	973
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	974
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	975
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:44 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQFPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSTVADDTAVYYCARMPSFITLASLSTWEGYDFDFWGQ GTMVTVSS	976
vhCDR1 (from WO2016028656)	SDYWG	977
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	978
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	979

Figure 34UUU

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	Sequence		
Heavy chain (SEQ ID NO:45 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCSVTGSSIASDYWGWIQQPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYDFDFWGQG TMVTVSS	980	
vhCDR1 (from WO2016028656)	SDYWG	981	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	982	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	983	
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:	
What	Sequence		
Heavy chain (SEQ ID NO:46 from WO2016028656)	EVQLQQSGAGLLKPSETLSLTCSVTGSSIASDYWGWIQQPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYDFDFWGQ GTMVTVSS	984	
vhCDR1 (from WO2016028656)	SDYWG	985	
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	986	
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	987	

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Figure 34VVV

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:47 from WO2016028656)	EVQLQESGPGLVKPPGTLSTCSVTGSSIASDYWGWVRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDWFGQ GTMVTVSS	988
vhCDR1 (from WO2016028656)	SDYWG	989
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	990
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	991

Figure 34WWW

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2016028656)	EVQLQESGPGLVKPPSETLSLTCAVSGSSISSDYWGWRQPPGKGLEWIGFITYSGSTSYN SLKSRITISRDTSKNQFSLKLHSTAAADTAVYYCARMPSFITLASLSTWEGYFDWFGQT MVTVSS	992
vhCDR1 (SEQ ID NO: from WO2016028656)	SDYWG	993
vhCDR2 (SEQ ID NO: from WO2016028656)	FITYSGSTSYNPSLKS	994
vhCDR3 (SEQ ID NO: from WO2016028656)	MPSFITLASLSTWEGYFDF	995

Figure 34XXX

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:24 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGSSISSDYWGWRQPPGKGLEWMGFITYSGSTSYN PSLKSRITISRDTSKNQFSLKLHVSVTAADTAVYYCARMPSFITLASLSTWEGYFDWGGQ TMVTVSS	996
vhCDR1 (from WO2016028656)	SDYWG	997
vhCDR2 (WO2016028656)	FITYSGSTSYNPSLKS	998
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDF	999

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:25 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP SRFSGSGGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	1000
vLCDR1 (from WO2016028656)	KASQSIHKNLAW	1001
vLCDR2 (from WO2016028656)	YANSLQT	1002
vLCDR3 (from WO2016028656)	QQYYSGWT	1003

Figure 34YY

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:26 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGVP RFSGSGGTDFLTISSLQPEDFATYYCCQQYYSGWTFGGGTKVEIK	1004
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1005
vICDR2 (from WO2016028656)	YANSLQT	1006
vICDR3 (from WO2016028656)	QQYYSGWT	1007

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:27 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGIP RFSGSGGTDFLTISSLQPEDFATYYCCQQYYSGWTFGGGTKVEIK	1008
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1009
vICDR2 (from WO2016028656)	YANSLQT	1010
vICDR3 (from WO2016028656)	QQYYSGWT	1011

Figure 34ZZZ

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:28 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKLLIYYANSLQGTGVP SRFSGSGGTDFLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	1012
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1013
vICDR2 (from WO2016028656)	YANSLQT	1014
vICDR3 (from WO2016028656)	QQYYSGWT	1015

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:29 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQGTGVP RFSGSGGTDFLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	1016
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1017
vICDR2 (from WO2016028656)	YANSLQT	1018
vICDR3 (from WO2016028656)	QQYYSGWT	1019

Figure 34AAAA

From WO2016028656 (Table 4, reproduced herein)

What	sequences	SEQ ID NO:
Light chain (SEQ ID NO:30 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQTGIPS RFSGSGGTDFLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	1020
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1021
vICDR2 (from WO2016028656)	YANSLQT	1022
vICDR3 (from WO2016028656)	QQYYSGWT	1023

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:48 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP SRFSGSGGTDFLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	1024
vICDR1 (from WO2016028656)	KASQSIHKNLAW	1025
vICDR2 (WO2016028656)	YANSLQT	1026
vICDR3 (WO2016028656)	QQYYSGWT	1027

Figure 34BBBB

From WO2016028656 (Table 4, reproduced herein)		What		sequence		SEQ ID NO:	
Light chain		(SEQ ID NO:49 from		DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGVP		1028	
WO2016028656)				RFGSGSGTDFLTISLQPEDFATYYCCQQYYSGWTFGGGTKVEIK			
vICDR1		KASQSIHKNLAW				1029	
(from WO2016028656)							
vICDR2		YANSLQT				1030	
(WO2016028656)							
vICDR3		QQYYSGWT				1031	
(WO2016028656)							
From WO2016028656 (Table 4, reproduced herein)		What		sequence		SEQ ID NO:	
Light chain		(SEQ ID NO:50 from		DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQGTGVP		1032	
WO2016028656)				SRFSGSGGTDFLTISLQPEDFATYFCQQYYSGWTFGGGTKVEIK			
vICDR1		KASQSIHKNLAW				1033	
(from WO2016028656)							
vICDR2		YANSLQT				1034	
(WO2016028656)							
vICDR3		QQYYSGWT				1035	
(WO2016028656)							

Figure 34CCCC

From WO2016028656 (Table 4, reproduced herein)		What		sequence		SEQ ID NO:	
Light chain		(SEQ ID NO:51 from		DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGVP		1036	
WO2016028656)				RFGSGSGTDFTLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK			
vICDR1		(from WO2016028656)		KASQSIHKNLAW		1037	
vICDR2		(WO2016028656)		YANSLQT		1038	
vICDR3		(WO2016028656)		QQYYSGWT		1039	
From WO2016028656 (Table 4, reproduced herein)		What		sequence		SEQ ID NO:	
Light chain		(SEQ ID NO:52 from		DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQGTGIPS		1040	
WO2016028656)				RFGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK			
vICDR1		(from WO2016028656)		KASQSIHKNLAW		1041	
vICDR2		(WO2016028656)		YANSLQT		1042	
vICDR3		(WO2016028656)		QQYYSGWT		1043	

Figure 34DDDD

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSTCTVTGYSITSDYAWNWI RQFPGNKLEWMGYISNSGSAS YNPSLKSRSITRDTSKNQFFLQLNSVTTEDATYYCAT LIYYDYGGAMNFWGQGTSVT VSS	1044
vhCDR1 (from WO2016028656)	GYSITSDYAWN	1045
vhCDR2 (WO2016028656)	YISNSGSASYNPSLKS	1046
vhCDR3 (WO2016028656)	LIYYDYGGAMNF	1047

Figure 34EEEE

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:62 from WO2016028656)	DIVMTQSHKFMSTSVGDRVSITCKASQGVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPPDRFTG SGSGTDFITFTISSVQSEDLAVYYCQHYYSTPWTFGGGTKLEIK	1047
vICDR1 (from WO2016028656)	KASQGVSTTV A	1049
vICDR2 (WO2016028656)	SASYRYT	1050
vICDR3 (WO2016028656)	QHYYSTPWT	1051
vICDR2 variant (WO2016028656)	YASNLQT	1052
vICDR2 variant (WO2016028656)	YASSLQT	1053
vICDR2 variant (WO2016028656)	YASTLQT	1054
vICDR2 variant (WO2016028656)	YATTLQT	1055
vICDR2 variant (WO2016028656)	YASYLQT	1056
vICDR2 variant (WO2016028656)	YANQLQT	1057
vICDR2 variant (WO2016028656)	YAGSLQT	1058
vICDR2 variant (WO2016028656)	YASQLQT	1059
vICDR2 variant (WO2016028656)	YADSLQT	1060

Figure 34FFFF

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:62 from WO2016028656)	DIVMTQSHKFMSTSVGDRVSITCKASQGVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPPDRFTG SGSGTDFITFTISSVQSEDLAVYYCQHYYSTPWTFGGGKLEIK	1061
vICDR1 (from WO2016028656)	KASQGVSTTV A	1062
vICDR2 (WO2016028656)	SASYRYT	1063
vICDR3 (WO2016028656)	QHYYSTPWT	1064
vICDR3 variant (WO2016028656)	QYYYS GFT	1065
vICDR3 variant (WO2016028656)	QYYYS GYT	1066
vICDR3 variant (WO2016028656)	QYYYS GIT	1067
vICDR3 variant (WO2016028656)	QYYYS GVT	1068
vICDR3 variant (WO2016028656)	QYYYS GLT	1069

Figure 34GGGG

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSTCTVTGYSTSDYAWNWRQFPGNKLEWMGYISNSGSAS YNPSLKSRSITRDTSKNQFFLQLNSVTTEDATYYCATLIYYDYGGMNFWGQGTSVT VSS	1070
vhCDR1 (from WO2016028656)	GYSITSDYAWN	1071
vhCDR2 (WO2016028656)	YISNSGSASYNPSLKS	1072
vhCDR3 (WO2016028656)	LIYYDYGGMNF	1073
vHCDR3 variant (WO2016028656)	MPSFITLASLSTFEGYFDF	1074
vHCDR3 variant (WO2016028656)	MPSFITLASLSTYEGYFDF	1075
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	1076
vHCDR3 variant (WO2016028656)	MPSFITLASLSTVEGYFDF	1077
vHCDR3 variant (WO2016028656)	MPSFITLASLSTLEGYFDF	1078

Figure 34HHHH

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO: 94 from WO2016028656)	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNNDGAKYNEK FKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTTVSS	1079
vhCDR1 (from WO2016028656)	SYVMH	1080
vhCDR2 (WO2016028656)	YIDPYNNDGAKYNEKFK	1081
vhCDR3 (WO2016028656)	GPYGWYFDV	1082
vhCDR2 variant (WO2016028656)	YIDPYNrGAKYNEKFG	1083
vhCDR2 variant (WO2016028656)	YIDPYNIGAKYNEKFG	1084
vhCDR2 variant (WO2016028656)	YIDPYNkGAKYNEKFG	1085
vhCDR2 variant (WO2016028656)	YIDPYNfGAKYNEKFG	1086
vhCDR2 variant (WO2016028656)	YIDPYNsGAKYNEKFG	1087
vhCDR2 variant (WO2016028656)	YIDPYNvGAKYNEKFG	1088
vhCDR2 variant (WO2016028656)	YIDPYNdGAKYNEKFG	1089
vhCDR2 variant (WO2016028656)	YIDPYNdGAKYNEKFKG	1090
vhCDR2 variant (WO2016028656)	YIDPYNdGAKYNEKFKG	1091
vhCDR2 variant (WO2016028656)	YIDPYNdGAKYNEKFKG	1092
vhCDR2 variant (WO2016028656)	YIDPYNDeAKYNEKFKG	1093
vhCDR2 variant (WO2016028656)	YIDPYNdIAKYNEKFKG	1094
vhCDR2 variant (WO2016028656)	YIDPYNdKAKYNEKFKG	1095
vhCDR2 variant (WO2016028656)	YIDPYNdSgAKYNEKFKG	1096
vhCDR2 variant (WO2016028656)	YIDPYNdYAKYNEKFKG	1097
vhCDR2 variant (WO2016028656)	YIDPYNdVAKYNEKFKG	1098

Figure 34III

From WO2016028656 (Table 4, reproduced herein)			SEQ ID NO:
What	sequence		
Light chain			
(SEQ ID NO:94 from WO2016028656)	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQKSPQLLVYNAKTLAEGVPSRFGSG		1099
vICDR1	SGTQFSLKINSIQPEDFGTYTCQHFGSPLTFGAGTTLELK		
(from WO2016028656)	RASEHIYSYLS		1100
vICDR2	NAKTLAE		1101
(WO2016028656)			
vICDR3	QHHFGSPLT		1102
(WO2016028656)			
vLCDR2 variant (WO2016028656)	AAKTLAE		1103
vLCDR2 variant (WO2016028656)	YAKTLAE		1104
vLCDR2 variant (WO2016028656)	WAKTLAE		1105
vLCDR2 variant (WO2016028656)	SAKTLAE		1106
vLCDR2 variant (WO2016028656)	TAKTLAE		1107
vLCDR2 variant (WO2016028656)	IAKTLAE		1108
vLCDR2 variant (WO2016028656)	VAKTLAE		1109
vLCDR2 variant (WO2016028656)	NNKTLAE		1110
vLCDR2 variant (WO2016028656)	NIKTLAE		1111
vLCDR2 variant (WO2016028656)	NLLTLAE		1112
vLCDR2 variant (WO2016028656)	NTKTLAE		1113
vLCDR2 variant (WO2016028656)	NVKTLAE		1114

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Figure 34JJJJ

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:124 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQRLIEWIGYIDPYNDGAKYS QKFQGRVTLTRDTSASTAYMELSSLRSEDTAVYYCARGGPGYGWYFDVVGQGTTVTSS	1115
vhCDR1 (from WO2016028656)	SYVMHW	1116
vhCDR2 (from WO2016028656)	YIDPYNDGAKYSQKFQ	1117
vhCDR3 (from WO2016028656)	GGPYGWYFDV	1118
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:125 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQRLIEWIGYIDPYNDGAKYS QKFQGRVTLTSDKSASTAYMELSSLRSEDTAVYYCARGGPGYGWYFDVVGQGTTVTSS	1119
vhCDR1 (from WO2016028656)	SYVMH	1120
vhCDR2 (from WO2016028656)	YIDPYNDGAKYSQKFQ	1121
vhCDR3 (from WO2016028656)	GGPYGWYFDV	1122

Figure 34KKKK

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:126 from WO2016028656)	EVQLVQSGAEVKKPGASVKVCKASGYTFSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTRDTSTSTVYMELSSLRSEDTAVYYCARGGPGYGWYFDVWGQGTTTIVTVSS	1123
vhCDR1 (from WO2016028656)	SYVMH	1124
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQ	1125
vhCDR3 (SEQ ID NO:13 from WO2016028656)	GGPYGWYFDV	1126
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:127 from WO2016028656)	EVQLVQSGAEVKKPGASVKVCKASGYTFSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSTSTVYMELSSLRSEDTAVYYCARGGPGYGWYFDVWGQGTTTIVTVSS	1127
vhCDR1 (from WO2016028656)	SYVMH	1128
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	1129
vhCDR3 (from WO2016028656)	GGPYGWYFDV	1130

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Figure 34LLLL

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:128 from WO2016028656)	EVQLVQSGAEVKKPGSSVKVSKASGYTFSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVTLTSDKSTSTAYMELSSLRSEDTAVYYCARGGPGYGWYFDVWVGQGTITVTVSS	1131
vhCDR1 (from WO2016028656)	SYVMH	1132
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	1133
vhCDR3 (from WO2016028656)	GGPYGWYFDV	1134
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:129 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSKASGYTFSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSTSTAYMELSLRSDDTVYYCARGGPGYGWYFDVWVGQGTITVTVSS	1135
vhCDR1 (from WO2016028656)	SYVMH	1136
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	1137
vhCDR3 (from WO2016028656)	GGPYGWYFDV	1138

Figure 34MMMM

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From WO2016028656 (Table 4, reproduced herein)	What sequence	SEQ ID NO:			
Light chain (SEQ ID NO:130 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKAPKLLIYNAKTLAEGVPSRFSGSGCTDFTLTISSLQPEDFATYYCQHHFGSPLTFGQGTRLEIK	1139			
vICDR1 (from WO2016028656)	RASEHIYSYLS	1140			
vICDR2 (from WO2016028656)	NAKTLAE	1141			
vICDR3 (from WO2016028656)	QHHFGSPLT	1142			
From WO2016028656 (Table 4, reproduced herein)	What sequence	SEQ ID NO:			
Light chain (SEQ ID NO:131 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKAPKLLIYNAKTLAE GVPSRFSGSGSGTQFTLTISSLQPEDFATYYCQHHFGSPLTFGQGTRLEIK	1143			
vICDR1 (from WO2016028656)	RASEHIYSYLS	1144			
vICDR2 (from WO2016028656)	NAKTLAE	1145			
vICDR3 (from WO2016028656)	QHHFGSPLT	1146			

Figure 34NNNNN

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From WO2016028656 (Table 4, reproduced herein)	What sequence	SEQ ID NO:			
Light chain (SEQ ID NO:132 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPKGVPKLLIYNAKTLAEGVPSRFSG SGSGTDFLTITSSLPEDVATYYCQHHFGSPLTFGQGTREIK	1147			
vICDR1 (from WO2016028656)	RASEHIYSYLS	1148			
vICDR2 (from WO2016028656)	NAKTLAE	1149			
vICDR3 (from WO2016028656)	QHHFGSPLT	1150			
From WO2016028656 (Table 4, reproduced herein)	What sequence	SEQ ID NO:			
Light chain (SEQ ID NO:133 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPKGVPKLLIYNAKTLAEGVPSRFSG SGSGTQFTLTITSSLPEDVATYYCQHHFGSPLTFGQGTREIK	1151			
vICDR1 (from WO2016028656)	RASEHIYSYLS	1152			
vICDR2 (from WO2016028656)	NAKTLAE	1153			
vICDR3 (from WO2016028656)	QHHFGSPLT	1154			

Figure 340000

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain	EVQLVQSGAEVKKPGASVKVCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYA	1155
(SEQ ID NO:129 from	QKFQGRVTLTSDKSISTAYMELSRLSDDTVVYYCARGGPGYGWYFDVWGQGTTVTVSS	
WO2016028656)		
vhCDR2 variant	YIDPYNDGAKYAQKFQG	1156
(from WO2016028656)		
vhCDR2 variant	YIDPYNDGAKYSQKFQG	1157
(from WO2016028656)		

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain	EVQLVQSGAEVKKPGASVKVCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQ	1158
(SEQ ID NO:129 from WO2016028656)	KFQGRVTLTSDKSISTAYMELSRLSDDTVVYYCARGGPGYGWYFDVWGQGTTVTVSS	
vhCDR3 variant (from WO2016028656)	GGPYGAYFDV	1159
vhCDR3 variant (from WO2016028656)	GGPYGDYFDV	1160
vhCDR3 variant (from WO2016028656)	GGPYGEYFDV	1161
vhCDR3 variant (from WO2016028656)	GGPYGFYFDV	1162
vhCDR3 variant (from WO2016028656)	GGPYGGYFDV	1163
vhCDR3 variant (from WO2016028656)	GGPYGIYFDV	1164
vhCDR3 variant (from WO2016028656)	GGPYGKYFDV	1165
vhCDR3 variant (from WO2016028656)	GGPYGNYFDV	1166
vhCDR3 variant (from WO2016028656)	GGPYGQYFDV	1167
vhCDR3 variant (from WO2016028656)	GGPYGRYFDV	1168
vhCDR3 variant (from WO2016028656)	GGPYGSYFDV	1169
vhCDR3 variant (from WO2016028656)	GGPYGTYFDV	1170
vhCDR3 variant (from WO2016028656)	GGPYGVYFDV	1171
vhCDR3 variant (from WO2016028656)	GGPYGYFDV	1172

Figure 34PPPP

From WO2016028656 (Table 4, reproduced herein)		
What	sequence	SEQ ID NO:
VH 18G10	QVQLMESGPGLVQPSQTLSTCTVSGFPLTSYTVHWVRQPPGKGLEWIGAIWSSGSTDYNSA	1173
(SEQ ID NO:136 from WO2016028656)	LKSRLLNINRDSSKSQVFLKMNSLQTEDTAIFYCTKSGWAFFDYWGQGVMVTVSS	
VL 18G10	DIQMTQSPFLLSASVGDRVTLNCLASQNIYKSLAWYQLKLGAPKLLIYNANSLQAGIPSRFSG	1174
(SEQ ID NO:137 from WO2016028656)	SGSGTDFALTISGLQPEDVATYFCQQYSGGYTFGAGTKLELK	
From WO2016028656 (Table 4, reproduced herein)		
What	sequence	SEQ ID NO:
VH 11A11	EVQLVESGGDLVQPGRSLKISCVASGFTFSDYYMAWVRLAPQKGLEWVASISYEGSRTHYGD	1175
(SEQ ID NO:138 from WO2016028656)	SVRGRFIISRDNPKNILYLQMNSLGSDDATYFCARHTGTLDWLVYWGQGTLLVIVSS	
VL 11A11	NIVMAQSPKSMSSISAGDRVMTMNCCKASQNVDDNNIAWYQQKPGQSPKLLIFYASNRYSGVPDR	1176
(SEQ ID NO:139 from WO2016028656)	FTGGGYGTDFTLTIKSVQAEDAAFYQCRIYNFTFGSGTKLEIK	

Figure 340000

CHA.9.547.18

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLE WVATISGGSGKQYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKWLLSYIAMDYWGQGTLVTVSS	1177
vhCDR1	GFTFSSYI	1178
vhCDR2	ISGGSGKQ	1179
vhCDR3	AKWLLSYIAMDY	1180
Variable light (vl) domain	DIQMTQSPSSLASVGDRTITCRASQSMAIWLSWYQQKPGKAPKLL IYKASKSHITGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQGQSYP YTFGQGTLKLEIK	1181
vlCDR1	QSMAIW	1182
vlCDR2	KAS	1183
vlCDR3	QQGQSYPT	1184

Human IgG1 constant region

AASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPR
ASNTKVDKKVEPKSCDKTHITCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1185)

Human IgG1 D265A constant region

AASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPR
ASNTKVDKKVEPKSCDKTHITCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1186)

Human IgG1 N297A constant region

AASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPR
ASNTKVDKKVEPKSCDKTHITCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1187)

Human IgG2 constant region

AASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVVDHKPR
ASNTKVDKVERKCCVECPCPAPPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
STYRVVSVLTVLHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
VEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1188)

Human IgG3 constant region

AASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYTCNVNHHKPR
ASNTKVDKRVELKTPGLDTHITCPRCEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPELLGGPSVFLFPPKPK
DITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTFRVSVLTVLHQDWLNGKEYCKVSNKALPAPIE
KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPMLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNRTQKSLSLSPGK (SEQ ID NO:1189)

Figure 35B

Human IgG4 constant region (Wild Type)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVVDHKP
SNTKVDKRVESKYGPPCPSPCAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNNYKTTTPPVVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1189)

Human IgG4 constant region (S241P hinge mutant)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVVDHKP
SNTKVDKRVESKYGPPCP[CPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNNYKTTTPPVVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1190)

Human kappa light chain
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEHKHKVYAC
EVTHQGLSSLSPVTKSFNRGEC (SEQ ID NO:1191)

Human lambda light chain
GOPKAAPSVITLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITPSKQSNKMYAASSYLSLTPEQWKSHRSYSC
QVTHEGSTVEKTVAPTECS (SEQ ID NO:1192)

Figure 36A

CHA.7.518.1.H4(S241P)		What	sequence	SEQ ID NO:
Variable heavy (vh) domain			QVQLVQSGAEVKKPGASVKVSCKASGYTFDTYNINWVRQAPGQGLEWMGYIYPYIGSGYAQKFQGRVTMTRDTSTSTVYVMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS	1193
vhCDR1			GYTFDTYN	1194
vhCDR2			IYPYIGGS	1195
vhCDR3			AREDKTARNAMDY	1196
Full length HC			QVQLVQSGAEVKKPGASVKVSCKASGYTFDTYNINWVRQAPGQGLEWMGYIYPYIGSGYAQKFQGRVTMTRDTSTSTVYVMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKITYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTJVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKQPREPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPGK	1197
Variable light (vl) domain			DIQMTQSPSSLSASVGDRTVITTCRVSENIYSNLAWYQQKPKAPKLLIYEATNLAEGVPSRFSGSGTDFTLTISSLQPEDFATYYCQHFHWGTPYTFGGQTKLEIK	1198
vlCDR1			ENIYSN	1199
vlCDR2			EAT	1200
vlCDR3			QHFHWGTPYT	1201
Full length light chain			DIQMTQSPSSLSASVGDRTVITTCRVSENIYSNLAWYQQKPKAPKLLIYEATNLAEGVPSRFSGSGTDFTLTISSLQPEDFATYYCQHFHWGTPYTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1202

Figure 36B
CHA.7.538.1.2.H4(S241P)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYAFNLYIEWVRQAPGGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY MELSLRSEDTAVYYCARSETHDTWFAYWGQGTLLVTSS	1203
vhCDR1	GYAFNLYL	1204
vhCDR2	INPGSGGI	1205
vhCDR3	ARSETHDTWFAY	1206
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYAFNLYIEWVRQAPGGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY MELSLRSEDTAVYYCARSETHDTWFAYWGQGTLLVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKNG LPSSIEKTIKAKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRIT VDKSRWQEGNVFSCSVMHIALHNHYTQKSLSLSPGK	1207
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIVLASTRHTGVPSPRFGSGSGTDFLTITSSVQPEDF ATYYCLQHWNPYPYTFGGQGTKLEIK	1208
vlCDR1	QSVRIA	1209
vlCDR2	LAS	1210
vlCDR3	LQHWNPYPY	1211
Full length light chain	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIVLASTRHTGVPSPRFGSGSGTDFLTITSSVQPEDF ATYYCLQHWNPYPYTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKSTYSLSSITLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1212

Figure 36C

CHA.7.502		
What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLVESGGDLVQPGGSRKLSCTASGFTSNFGMHVWRQAPKEGLEWVAYISSGS <u>STIYADTVKGRFTISRDN</u> PENTLF LQMTSLRSED TAMYYC <u>TRLDY</u> TNSYSMDHWG QGTSVTYSS	1213
vhCDR1	GFTFSNFG	1214
vhCDR2	ISSGSSTI	1215
vhCDR3	TRLDYYTNSYSMDH	1216
Variable light (vl) domain	QIVLTQSPALMSASPGEKVTLTCSASSLPYVYWYQQKPGSSPKPWYI <u>LT</u> SNLASGVP ARFGSGRSGTSYSLTSSVEAEDAATYYCQQWSSNPFTFGSGTKLEIK	1217
vlCDR1	SSLPY	1218
vlCDR2	LTS	1219
vlCDR3	QQWSSNPFT	1220

Figure 36D

CHA.7.503			SEQ ID NO:
What	sequence		
Variable heavy (vh) domain	QVQLQQSGAELAKPGASVKMSCKASGYTFTSNWMHWVKQRPGQGLEWIGYINP <u>SNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTSADSAVYVCALMISAWLPYWG</u> QGTLLTVSA	1221	
vhCDR1	GYTFTSNW	1222	
vhCDR2	INPSNGYT	1223	
vhCDR3	ALMISAWLPY	1224	
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRASQSVSASSSYVHWYQQKPGQPPKLLIKYASSLE SGVPARFSGSGGTDFTLNIHPVEEEDTATYYCHLTWEIPYTFGGGTKLEIK	1225	
vlCDR1	QSVSASSSY	1226	
vlCDR2	YAS	1227	
vlCDR3	LHTWEIPYT	1228	

Figure 36E

CHA.7.506		
What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELTRPGASVNLSCKASGYTFTSYWMQWVKQRPQGQGLEWIGAIYPG <u>DGDIRFNQKFKGKATLTADESS</u> TAYMQLSSLASEDSAVVYCATYYRYDDYWGQGT TLTVSS	1229
vhCDR1	GYTFTSYW	1230
vhCDR2	IYPGDGDT	1231
vhCDR3	ATYYRYDDY	1232
Variable light (vl) domain	QIVLTQSPAIMASAPGEKVTMTCSASSSVSYMHWWYQQKSGTSPKRWIYDTSKLASG VPTRFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPYTFGGGTKLEIK	1233
vlCDR1	SSVS	1234
vlCDR2	DTS	1235
vlCDR3	QQWSSNPYT	1236

Figure 36F

CHA.7.508	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLQSGPD ¹ LVKPGASMKISKASGYTFIDYNIHWVKQSQGKSLDWIGYIY PYNGGT ² GYNQKFKNKATLTVDSSSTAYMEVRS ³ LT ⁴ FEDSAVFCAREADYYG NRGQEDYWGQGT ⁵ LVTVSA	1237
vhCDR1	GYTFIDYN	1238
vhCDR2	IYPYNGGT	1239
vhCDR3	AREADYYGNRGQFDY	1240
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASEN ¹ IFSN ² LAWYQQKQKSPQLLWGEA NLADGVPSRFSGSGGTQYSLKINSLSQSEDFGNYYCQHFWGTPYTFGGGTTL EIK	1241
vlCDR1	ENIFSN	1242
vlCDR2	GEA	1243
vlCDR3	QHF ¹ WGTPYT	1244

Figure 36G

CHA.7.510	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	QVTLKESGPGILQPSQTLSLTCSFSGFSINTSGTGVGWIRQPSGKGLEWLTHI <u>WWNDNKFYNTFLKSR</u> LTISKETSNNQVFLKIASVDTADAATYYCARMAYGN <u>LW</u> FVNWGQGTAVST	1245
vhCDR1	GFSLNTSGTG	1246
vhCDR2	IWWNDNK	1247
vhCDR3	ARMAYGNLWFVN	1248
Variable light (vl) domain	DIVLTQSPASLAVSLGQRASISCRASRSVTISGYSYMYWYQQKPGQPPRLIFY <u>LASN</u> LAGVPARFSGSGGTDFTLNIHPVEEEDAAIYYC <u>QHSREL</u> PYTFGGGT KLEIK	1249
vlCDR1	RSVTISGYSY	1250
vlCDR2	LAS	1251
vlCDR3	QHSRELPLYT	1252

Figure 36H

CHA.7.512					
What	sequence		SEQ ID NO:		
Variable heavy (vh) domain	QIQLVQSGPELKPRETVKISKASGYTFTDYSMHVWKQAPGKGLKWMGW <u>INTETGEPTYADDFKGRFAFSLEASASSAYLQINILKDEDTATYFCARSRGGYY</u> <u>EDYYALDYWGQGTSTVSS</u>		1253		
vhCDR1	GYTFTDYS		1254		
vhCDR2	INTETGEP		1255		
vhCDR3	ARSRGGYEDYYALDY		1256		
Variable light (vl) domain	DIQMTQSPASLSASVGESVTITCRASGNIHY ¹ LAWYQQKQKSPQLLVYNAK NLADGVPSRFSGSGGTQFSLKINSIQPEDFGSY ² Y ³ CQ ⁴ HF ⁵ WIS ⁶ PPT ⁷ FGG ⁸ G ⁹ T ¹⁰ K ¹¹ L ¹² E ¹³ IK		1257		
vlCDR1	GNIHY ¹		1258		
vlCDR2	NAK		1259		
vlCDR3	QHF ⁵ WIS ⁶ PPT ⁷		1260		

Figure 36I

CHA.7.514	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLRQSGADLVKPGASVKLSCTASGFNIKDTYIDWVKORPEQGLDWIGRID <u>PANGNTKYDPKFKQGKATITDTSSNTAYLQSLNLTSED</u> TAVYYCARYG <u>SY</u> PF <u>DY</u> WGRGTTLAVSS	1261
vhCDR1	GFNIKDTY	1262
vhCDR2	IDPANGNT	1263
vhCDR3	ARYGSYPYFDY	1264
Variable light (vl) domain	SIVMTQTPKFLISAGDRVTITCKASQSV <u>RNDVAWYQQKPGQSPKLL</u> MY <u>AS</u> <u>NRYTGPDRFTGS</u> GYGTDFTFTITVQAEDLAWFCQ <u>QDYSSPPT</u> FGGGTKL EIK	1265
vlCDR1	QSVRND	1266
vlCDR2	YAS	1267
vlCDR3	QQDYSSPPT	1268

Figure 36J

CHA.7.516					
What	sequence		SEQ ID NO:		
Variable heavy (vh) domain	QVQLQQSGPELVRPGSVKISKVSGYTFDYYMHVWKQSHAKSLEWIGIIS PYSGNTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDSAIYVCAREGDLP MFAYWGQGGLTVTSA		1269		
vhCDR1	GYTFTDYV		1270		
vhCDR2	ISPYSGNT		1271		
vhCDR3	AREGDLPMIFAY		1272		
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVYIYWYQQNPQSSPRLLIYDTSILA SGVPFRFSGSGGTSYSLTISRMEAEDAATYCCQQWTSYPLTFGSGTKLELK		1273		
vlCDR1	SSVSY		1274		
vlCDR2	DTS		1275		
vlCDR3	QQWTSYPLT		1276		

Figure 36K

CHA.7.518	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLQSQGP EL VKPGASVKISCKASGYTFTDYNINWVKQSHGKSLEWIGYIY PYIGGSGYNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVYYCAREDKTARN <u>AMDYWGQGTPVTVSS</u>	1277
vhCDR1	GYTFTDYN	1278
vhCDR2	IYPYIGGS	1279
vhCDR3	AREDKTARNAMIDY	1280
Variable light (vl) domain	DIQMTQSPASLSVSGETVTIICRVSENIYSNLAWYQQKQKSPQLLVYEATN LAEGVPSRFSGSGGTQYSLKINSLSQSEDFGSYYCQHFWGTPYTFGGGTKLEI K	1281
vlCDR1	ENIYSN	1282
vlCDR2	EAT	1283
vlCDR3	QHFWGTPYT	1284

Figure 36L

CHA.7.520_1	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWNWRQFPGNKLEWMGY <u>ISYSGSTSYNPSLKSRI</u> STRDTSKNQFFLQLNSVTTEDTATYYCARHYRPPYA <u>MDYWGQGTSVTVSS</u>	1285
vhCDR1	GYSITSDYA	1286
vhCDR2	ISYSGST	1287
vhCDR3	ARHYRPPYAMDY	1288
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSP <u>KLLVYFAS</u> TRESGVPDFRIGSGSGTDFTLTITISVQAEDLADYFCQQQHYPFTF GSGTKLEIK	1289
vlCDR1	QSLNSSNQKNY	1290
vlCDR2	FAS	1291
vlCDR3	QQHYSTPFT	1292

Figure 36M

CHA.7.520_2	What	sequence	SEQ ID NO:
Variable heavy (vh) domain		QVQLKQSGPGLVQPQSLSITCTVSGFSLTSFGVHWVRQSPGKGLEWLGVI <u>WSGGTTVYDAAFISRLSISKDNSKSQVFFKMNSLQTNDTAIYCAR</u> <u>KRGNFY</u> <u>VMDYWGQGTSTVTVSS</u>	1293
vhCDR1		GFSLTSFG	1294
vhCDR2		IWSGGTT	1295
vhCDR3		ARKRGNFYVMIDY	1296
Variable light (vl) domain		DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSP <u>KLLVYFAS</u> TRESGVPDFRIGSGSGTDFTLTITISVQAEDLADYFCQQQHYPFTF SGGTKLEIK	1297
vlCDR1		QSLNSSNQKNY	1298
vlCDR2		FAS	1299
vlCDR3		QQHYSTPFT	1300

Figure 36N

CHA.7.522					
What	sequence	SEQ ID NO:			
Variable heavy (vh) domain	QVQLQQPGSELVRPGTSVKLSCKASGYTFTSYWVHWVQRHGGQGLEWIG NWPGSGSTNYDEKFKSGTTLTVDTSSTAYMHLSSLTSEDSAVYYCTRGVLR FPLDYWGQGTTLTVSS	1301			
vhCDR1	GYTFTSYW	1302			
vhCDR2	VYPGSGST	1303			
vhCDR3	TRGVLRFPPLDY	1304			
Variable light (vl) domain	DIVMTQAAPSPVPTPGESVSISCRSSKSLHSHNGNTLYWFLQRPQGSPHLLI YRMSNLASGVPDRFSGSGGTFTLRISRVEAEDVGVYYCMQHLEYPLTFGA GTKLELK	1305			
vlCDR1	KSLHSHNGNTY	1306			
vlCDR2	RMS	1307			
vlCDR3	MQHLEYPLT	1308			

Figure 360

CHA.7.524	What	sequence	SEQ ID NO:
Variable heavy (vh) domain		QVQLQQSGPEVWRPGSVVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGII SIYSGNTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYQCAREGDLPL MFAYWGQGTLVTVSA	1309
vhCDR1		GYKFPDYV	1310
vhCDR2		ISIYSGNT	1311
vhCDR3		AREGDLPMIFAY	1312
Variable light (vl) domain		QIVLTQSPAIMASAPGEKVTMTNCNASSSVSYMYWYQQKPISSPRLLIYDTSNL ASGVPRFRFSGSGTSYSLTIGRMEAEDAATYYCQQWSSYPLTFGAGTKVEV K	1313
vlCDR1		SSVSY	1314
vlCDR2		DTS	1315
vlCDR3		QQWSSYPLT	1316

Figure 36P

CHA.7.526					
What	sequence	SEQ ID NO:			
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLTAYNINWVRQPPGKGLEWLGMI WGDGNTDYN S PLKRLTISKDNSKQVFLKMDSLQTD T DDTARYYCARDLKVR RDSPTMDYWGQGTSTVSS	1317			
vhCDR1	GFSLTAYN	1318			
vhCDR2	IWGDGNT	1319			
vhCDR3	ARDLKVRRDSPYTM DY	1320			
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSP KLLIYWAS N RESGVPDRFTGSGSGTDFTLTIS S VQAEDLAVYYCHQYLSSTF GGGTKLEIK	1321			
vlCDR1	QSVLYSSNQKNY	1322			
vlCDR2	WAS	1323			
vlCDR3	HQYLSST	1324			

Figure 36Q

CHA.7.527	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLTCTVTGYSLTSDYAWNWIQFPGNKLEWMGYITYSGGT ¹³²⁵ TYNPSLKSRISITRDTSKNQFFLQLTSVTTEDTATYCA ¹³²⁶ RRGSGTTV ¹³²⁷ VGDWYFDV ¹³²⁸ WGAGTTTVSS	
vhCDR1	GYSLTSDYA	1326
vhCDR2	ITYSGGT	1327
vhCDR3	ARRGSGTTVGDWYFDV	1328
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKYYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTPTISSVTAEDLAVYYCQQFYTPYTFGGTKLEMK	1329
vlCDR1	QSLLYSFNQKY	1330
vlCDR2	WAS	1331
vlCDR3	QQFYTPYT	1332

Figure 36R

CHA.7.528	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQVQQSGPELVKPGASVKISKASGYTFTKSNMHWVKQSHGKSLEWIGYI YPYNGGTGYNQNFKSKATLTVDISSSTAYMELRSLTLEDSAVYLCAREADYYG <u>NRGQFDYWGGQTLVTYSA</u>	1334
vhCDR1	GYTFTKSN	1335
vhCDR2	IYPYNGGT	1336
vhCDR3	AREADYYGNRGQFDY	1337
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASDNI FSN ILAWYHQKQKSPHLLWYGAT NLADGVPSRFSGSGGTQYSLKINSIQSEDFGDYYCQHFWGTPYTFGGGTKL EIK	1338
vlCDR1	DNIFSN	1339
vlCDR2	GAT	1340
vlCDR3	QHFWGTPYT	

Figure 36S

CHA.7.530	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	QVQLQQSGAELMRPGTSVKVSCKASGYAFTNHLIEWIKRPGQGQGLEWIGV NPGSDSTDYNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSLYYNS WFVYWGQGGLTVTSA	1341
vhCDR1	GYAFTNHL	1342
vhCDR2	INPGSDST	1343
vhCDR3	ARSLYYNSWFFVY	1344
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKRGKSPQLLVYNAKT LVEGVPSRFSGSGGTQFSLKINSIQPEDFGSYQCQHHYGTPYTFGGGGTKLEI K	1345
vlCDR1	ENIYSY	1346
vlCDR2	NAK	1347
vlCDR3	QHHYGTPYT	1348

Figure 36T

CHA.7.534	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLQSGAEIVKPGASVRLSCTASGFSIRDITYIHVVKQRPEQQGLDWIGKID <u>PANGKSEYDPKFQGRATMTTDTSSNTAYLQLSLTSED</u> <u>AVVYCTRYGYYPYE</u> <u>DVWGAGTTTVFS</u>	1349
vhCDR1	GFSIRDY	1350
vhCDR2	IDPANGKS	1351
vhCDR3	TRYGYYPYFDV	1352
Variable light (vl) domain	SIVMTQTPKELLVSAGDRVAITCKASQSVRHDVWWYQQKPGQSPKLLIYYAS SRYTGVPPDRFTGSGYGTDFTFTISTVQAEALALYFC <u>LQDFSSPWTFGGG</u> TKLE IK	1353
vlCDR1	QSVRHD	1354
vlCDR2	YAS	1355
vlCDR3	LQDFSSPWT	1356

Figure 36U

CHA.7.535	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKTSGYTFTKNTIMHWVRQSHGKSLEWIGGI <u>NPNSGGASFNQKFMGKATLTVDKSSSTAYMELRSLTSEDSAVVYC</u> <u>ARDGYD</u> <u>GDWFFDVWGAGTTTVSS</u>	1357
vhCDR1	GYTFTKNT	1358
vhCDR2	INPNSGGA	1359
vhCDR3	ARDGYDGDWFFDV	1360
Variable light (vl) domain	DIQMNQSPFSLASLGDTVTITCHASQNIYVWILSWYQQKPGNIPKLLIYKAS DLHTGVPSRFGSGSGTDFTLNISSLQPEDIAITYCQQGQSYPRITFGGGTKLEI K	1361
vlCDR1	QNIYVW	1362
vlCDR2	KAS	1363
vlCDR3	QQGQSYPRIT	1364

Figure 36V

CHA.7.537	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLIGHGVNWIQQPPGKGLEWLGVIWGDGNTDYNALKSRSLISKDNSKQVFLKMNSLQTDDTARYFCVNSAMDYWGQGTAVTVSS	1365
vhCDR1	GFSLIGHG	1366
vhCDR2	IWGDGNT	1367
vhCDR3	AVNSAMDY	1368
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTINCTASENVASFVSWYQQKPEQSPKLLIYGT SNRYTGVPRFTGGSGATDFTLTSSVQAEDLGDYHCGQSYNYPFTFGSGTKL EIE	1369
vlCDR1	ENVASF	1370
vlCDR2	GTS	1371
vlCDR3	GQSYNYPFT	1372

Figure 36W

CHA.7.538_1		SEQ ID
What	sequence	NO:
Variable heavy (vh) domain	QVQLQQSGAELVRPGASVKVSCKTSGYAFTNLYIEWVKQRPQGQGLEWIGV NPGSGGIYYNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCARSETHDT WFAYWGQGGLTVTSA	1373
vhCDR1	GYAFTNLY	1374
vhCDR2	INPGSGGI	1375
vhCDR3	ARSETHDTWFAY	1376
Variable light (vl) domain	DIVMTQSQKFISTVSGDRVSITCKASQSVRIA V AWFQQKPGQSPKALIV LAST RHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNPYPYTFGGGTKLE IKR	1377
vlCDR1	QSVRIA	1378
vlCDR2	LAS	1379
vlCDR3	LQHWNPYPY	1380

Figure 36X

CHA.7.538_2		
What	sequence	
Variable heavy (vh) domain	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIG DIYPGGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYCASPYGSGS <u>SYGFAFWGQGTLTVSA</u>	SEQ ID NO: 1381
vhCDR1	GYTFTNYW	1382
vhCDR2	IYPGGGYT	1383
vhCDR3	ASPYGSSYGFAF	1384
Variable light (vl) domain	DIVMTQSQKFISTVSGDRVSITCKASQSVRIA V AWFQQKPGQSPKALIVLAST RHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNYPYTFGGGTKLE IKR	1385
vlCDR1	QSVRIA	1386
vlCDR2	LAS	1387
vlCDR3	LQHWNYPYT	1388

Figure 36Y

CHA.7.543	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLSGYGIKWVRQPPGKGLEWLGTIWGDGSTDYNSALKSRSLISKDNSQVFLKMTSLQTDDTARYYCASDSLGITFGYWGQGTLITVSA	1389
vhCDR1	GFSLSGYG	1390
vhCDR2	IWGDGST	1391
vhCDR3	ASDSLGITFGY	1392
Variable light (vl) domain	DIQMTQTSSLSASLGDRVTISCRASQDINYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGGTDSLTSINLEQEDIAITYFCQQGNTLPLTFGAGTKLELK	1393
vlCDR1	QDISNY	1394
vlCDR2	YTS	1395
vlCDR3	QQGNTLPLT	1396

Figure 36Z

CHA.7.544	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLTSYAITWVRQPPGKGLEWLGVIV PGGGTNYNSALKSRLSISKDNSKSHLFKMNLSLQTDDETARYYCVRSYDGYLD WYFDVWGTGTTVTYSS	1397
vhCDR1	GFSLTSA	1398
vhCDR2	IWPGGGT	1399
vhCDR3	VRSYDGYLDWYFDV	1400
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLSCKASENVGTVYSWYQQKPDQSPKLLIYG SNRYTGVPRFTGSGSATDFTLISSVQAEDLSDYHCGQSYSPYTFGGGTKL EII	1401
vlCDR1	ENVGT	1402
vlCDR2	GAS	1403
vlCDR3	GQSYSPYT	1404

Figure 36AA

CHA.7.545 What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMG WINTYSGVSTFPDDFKGRFAFSLETSASTAYLQINNLIKNEDSATYFCARLGM <u>GSTTGAGYFDVWGTGTTTVSS</u>	1405
vhCDR1	GYTFTTYG	1406
vhCDR2	INTYSGVS	1407
vhCDR3	ARLGMGSTTGAGYFDV	1408
Variable light (vl) domain	DIVLTQSPAIMASAPGEKVTMTCSASSVSSWYLHWYQQKSGASPKLWIYG <u>TSNLASGVPARFSGSGTSLTSSVEAEDAATYCCQQYRSDPYTFGSGTKL</u> EIK	1409
vlCDR1	SSVSSWY	1410
vlCDR2	GTS	1411
vlCDR3	QQYRSDPYT	1412

Figure 36AB

CHA.7.546					
What	sequence	SEQ ID NO:			
Variable heavy (vh) domain	QIQLVQSGPELKPGETVKISKASGYTFTTYGMSWVKQAPGKGLKWMGW INTYSGVSTYADDDFEGRFASFLETSVSTAYLQINNLIKNNEDTATYFCARLGRGST TGAGYLDVWGTGTTVTSS	1413			
vhCDR1	GYTFTTYG	1414			
vhCDR2	INTYSGVS	1415			
vhCDR3	ARLGRGTTGAGYLDV	1416			
Variable light (vl) domain	DIVLTQSPAIMASAPGEKVSMTCSASSVSSWYLHWYQQKSGASPKLWIYG TSNLASGVPARFSGSGTSYSLTSSVEAEDAATYCCQQYHSDPYTFGSGTK LEIK	1417			
vlCDR1	SSVSSWY	1418			
vlCDR2	GTS	1419			
vlCDR3	QQYHSDPYT	1420			

Figure 36AC

CHA.7.547					
What	sequence	SEQ ID NO:			
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMG WINTYSGVSTFPDDFKGRFAFSLETSASTAYLQINNLIKNEDSATYFCARLGM GSTTGAGYFDVWGTTGTTTVSS	1421			
vhCDR1	GYTFTTYG	1422			
vhCDR2	INTYSGVS	1423			
vhCDR3	ARLGMGSTTGAGYFDV	1424			
Variable light (vl) domain	ENVLTQSPAIMASLGEKVTLSCRASSVNYMYWYQQKSDASPKLWYYTSN LAPGVPARFSGSGSGNSYLTSSVEGEDAATYYCQQFTSSPWTFGGGTKLEI K	1425			
vlCDR1	SSVNY	1426			
vlCDR2	YTS	1427			
vlCDR3	QQFTSPWWT	1428			

Figure 36AD

CHA.7.548	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	EVQLQSGPELVKPGASVKISCKASGYTFDYSMNWVKQSHGKSLEWIGDI TPNNGSPNYNQKFKDKATLTVDKSSSTVYMEIRSLTSEDSAVVY <u>CASLFEDY</u> WGHGTTLTVSS	1429
vhCDR1	GYTFDYS	1430
vhCDR2	ITPNNGSP	1431
vhCDR3	ASLFEDY	1432
Variable light (vl) domain	DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPK LLIYGASTRDSGVPDRFTGSGSGTDFLTITISVQAEDLAVVY <u>CQNDHTYPYTF</u> GGGTKLEIK	1433
vlCDR1	QSLNSGNQKNY	1434
vlCDR2	GAS	1435
vlCDR3	CQNDHTYPYT	1436

Figure 36AE

CHA.7.549					
What	sequence	SEQ ID NO:			
Variable heavy (vh) domain	QVQLQQPGTELVPKGSVKLSCKASGFTFTTHWMHWRQRPQGQGLEWIG NIYPSNGGSNYNEKFKTKATLTVDRSSSTAYMHLSSLTSEDSAVYYCARRVN <u>WDGYFDYWGQGTTLT</u> VSS	1437			
vhCDR1	GFTFTTHW	1438			
vhCDR2	IYPSNGGS	1439			
vhCDR3	ARRVNWDGYFDY	1440			
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAVWYQQKPGQSPKLLIYS <u>ASYRYS</u> GVDPDRFTGSGGTDFTLTISNVQSEDLADYFCQQYNSYPLTFFGGGTK LEIK	1441			
vlCDR1	QNVGTN	1442			
vlCDR2	SAS	1443			
vlCDR3	QQYNSYPLT	1444			

Figure 36AF

CHA.7.550	sequence	SEQ ID NO:
What		
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWJHWVKQRPQGQGLEWIGNI NPSNGGTINYNKFKSKAALTVDKSSSTAYMQLSLTSEDSAVVYCARRGLPYF FDYWGQGTTLTVSS	1445
vhCDR1	GYTFTSYW	1446
vhCDR2	INPSNGGT	1447
vhCDR3	ARRGLPYFFDY	1448
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCCKGQNVGYNVAWVYQKPGQSPKALVY SASDRHSGVPDRFAGSGGTDFTLTISNVQSEDLAEYFCQQYNSYPLIFGAG TKLELK	1449
vlCDR1	QNVGYN	1450
vlCDR2	SAS	1451
vlCDR3	QQYNSYPLT	1452

Figure 36AG

CHA.7.518.4		SEQ ID
What	sequence	NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFDYNINWVRQAPGQGLEWMG YIPYIGSGYAKFQGRVTMTTRDTSSTVYMELSSLRSEDTAVYYCAREDKT ARNAMDYWGQGTLVTVSS	1453
vhCDR1	GYTFDYN	1454
vhCDR2	IYPYIGGS	1455
vhCDR3	AREDKTARNAMIDY	1456
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRVSENIYDVLAWYQQKPGKAPKLLIYEATN LAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHFWGTPYTFGGQGTKLEI K	1457
vlCDR1	ENIYDV	1458
vlCDR2	EAT	1459
vlCDR3	QHFWGTPYT	1460

Figure 37A From WO 2017/041004		
What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:5 from WO 2017/041004)	EVQLQQSGAELVRSGASVKMSCKVNNDYFTFTNYNMHWLRQTPGQQGLEWIGYIYPCNGDITYNQKF KGKATLTADTSSSTAYMQIISLTSEDP AVYFCARQGIHYIYIDVWVGAGTTTVTVSSG	1461
vhCDR1 (SEQ ID NO:6 from WO 2017/041004)	DYFTFTNYNMH	1462
vhCDR2 (SEQ ID NO:7 from WO 2017/041004)	YIYPGNGDITYNQ	1463
vhCDR3 (SEQ ID NO:8 from WO 2017/041004)	QGIHYIYIDV	1464
Light chain (SEQ ID NO:3 from WO 2017/041004)	DIEMTQSPATLSVTPGDRVSLSCRASQSIRDYLHWYQQKSHESPRLLIKYVVSQISGISIPSRFSGSGSEF TILSINSVEPEDVGYYCQNGHSLPLTFGSGTKLEIKRTV	1465
vICDR1 (SEQ ID NO:9 from WO 2017/041004)	RASQSIRDYLVH	1466
vICDR2 (SEQ ID NO:10 from WO 2017/041004)	YVVSQIS	1467
vICDR3 (SEQ ID NO:11 from WO 2017/041004)	QNGHSLPLT	1468

Figure 37B

From WO 2017/041004

What

Heavy chain

(SEQ ID NO:32 from WO
2017/041004)

vhCDR1

(SEQ ID NO:34 from WO
2017/041004)

vhCDR2

(SEQ ID NO:35 from WO
2017/041004)

vhCDR3

(SEQ ID NO:36 from WO
2017/041004)

Light chain

(SEQ ID NO:33 from WO
2017/041004)

viCDR1

(SEQ ID NO:37 from WO
2017/041004)

viCDR2

(SEQ ID NO:38 from WO
2017/041004)

viCDR3

(SEQ ID NO:39 from WO
2017/041004)

WO 2023/178192

206/299

PCT/US2023/064460

sequence SEQ ID NO:

QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHWVKQRPQGQGLEWIGYINPSTIGYTEYNQKFK 1469
DKATLTADKSSSTAYMQRLSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA

SDWMH 1470

YINPSTGYTEYNQKFKD 1471

GSSGSWFAY 1472

DIVLTQSPASLAIVSLGQRATISCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASNLESGVPAFSGS 1473
GSGTDFTLNIHPVEEDTATYYCQHSWEIPYTFGGGTKLEIK

RASQSVSTSSYSYMH 1474

YASNLES 1475

QHSWEIPYT 1476

Figure 37C

From WO 2017/041004

What

Heavy chain

(SEQ ID NO:32 from WO
2017/041004)

vhCDR1

(SEQ ID NO:34 from WO
2017/041004)

vhCDR2

(SEQ ID NO:35 from WO
2017/041004)

vhCDR3

(SEQ ID NO:36 from WO
2017/041004)

Light chain

(SEQ ID NO:40 from WO
2017/041004)

vlCDR1

(SEQ ID NO:41 from WO
2017/041004)

vlCDR2

(SEQ ID NO:42 from WO
2017/041004)

vlCDR3

(SEQ ID NO:43 from WO
2017/041004)

WO 2023/178192

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PCT/US2023/064460

sequence SEQ ID NO:

QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHVVKQRPQGQGLEWIGYINPSTIGYTEYNQKFK 1477
DKATLTADKSSSTAYMQRLSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA

SDWMH 1478

YINPSTGYTEYNQKFKD 1479

GSSGSWFAY 1480

DVVMVTQTPLTSLVTIGQPAISCKSSQSLNNSDGKTYLNWLLQRPQGQSPKRLIYLVSKLDSGYPDRTFG 1481
SGSGTDFTLKISRVEAEDLGYYCWCWGTHFPRTFGGKLEIK

KSSQSLNNSDGKTYLN 1482

LVSKLDS 1483

WQGTHFPRT 1484

Figure 37D

From WO 2018/017864 (334M5 antibody)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:30 from WO 2018/017864)	EVQLQQSVAEIVRPGETSVTISCKASGYTFTNYWLGWVYKQRPQGHGLEWIGDIFPGGDYPNYNEKFKG KATLTADTSSSTAYMQLSLTSEDSSVYFCIRGYFDVWVGAGITTVTVSS	1485
vhCDR1 (SEQ ID NO:31 from WO 2018/017864)	TNYWLG	1486
vhCDR2 (SEQ ID NO:32 from WO 2018/017864)	DIFPGGDYPNYNEKFKG	1487
vhCDR3 (SEQ ID NO:33 from WO 2018/017864)	TRGYFDV	1488
Light chain (SEQ ID NO:25 from WO 2018/017864)	DIQMTQSPFSSLVSAGEKVTMSCKSSQSLNSENQKNYLAWFQQKPGQPPKMLIYGASTR ESGVPDRFTGSGGTDFTLTISVQAEDLA VYYCQNDHSHYPFTFCGSGTKLEIKR	1489
viCDR1 (SEQ ID NO:26 from WO 2018/017864)	KSSQSLNSENQKNYLA	1490
viCDR2 (SEQ ID NO:27 from WO 2018/017864)	GASTRES	1491
viCDR3 (SEQ ID NO:28 from WO 2018/017864)	QNDHSYP	1492

Figure 38A

From WO 2017/041004

What	sequence	SEQ ID NO:
Heavy chain		
(SEQ ID NO:5 from WO 2017/041004)	EVQLQQSGAELVRSGASVKMSCKVNDYFTFTNYNMHWLRQTPGQGLEWIGVYYPG	1493
vhCDR1	NGDTNYNQKFKGKATLTADTSSTAYMQIISLTSEDPAVYFCARQGIHYYIDVWVG	
(SEQ ID NO:6 from WO 2017/041004)	AGTTVTVSSG	1494
vhCDR2	DYFTFTNYNMH	
(SEQ ID NO:7 from WO 2017/041004)	YYPGNGDTNYNQ	1495
vhCDR3	QGIHYYIDV	1496
(SEQ ID NO:8 from WO 2017/041004)		
Light chain		
(SEQ ID NO:3 from WO 2017/041004)	DIEMTQSPATLSVTPGDRVSLSCRASQSIRDYLVHWYQQKSHESPRLLIKYVVSQISGIP	1497
vLCDR1	SRFSGSGSGSEFTLSINSEPEDVGVVYQCQNGHSLPLTFGSGTKLEIKRTV	
(SEQ ID NO:9 from WO 2017/041004)	RASQSIRDYLH	1498
vLCDR2	YVSQSI	1499
(SEQ ID NO:10 from WO 2017/041004)	QNGHSLPLT	1500
vLCDR3		
(SEQ ID NO:11 from WO 2017/041004)		

Figure 38B
From WO 2017/041004

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHWVKQRPQGQGLEWIGYINPSTGYTE YNQKFQDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYWGQGTLLVTVSA	1501
vhCDR1 (SEQ ID NO:34 from WO 2017/041004)	SDWMH	1502
vhCDR2 (SEQ ID NO:35 from WO 2017/041004)	YINPSTGYTEYNQKFKD	1503
vhCDR3 (SEQ ID NO:36 from WO 2017/041004)	GSSGSWFAY	1504
Light chain (SEQ ID NO:33 from WO 2017/041004)	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASNLESGVP ARFSGSGGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK	1505
vlCDR1 (SEQ ID NO:37 from WO 2017/041004)	RASQSVSTSSYSYMH	1506
vlCDR2 (SEQ ID NO:38 from WO 2017/041004)	YASNLES	1507
vlCDR3 (SEQ ID NO:39 from WO 2017/041004)	QHSWEIPYT	1508

Figure 38C
From WO 2017/041004

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHWVKQRPGQGLEWIGYINPSTGYTE YNQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA	1509
vhCDR1 (SEQ ID NO:34 from WO 2017/041004)	SDWMH	1510
vhCDR2 (SEQ ID NO:35 from WO 2017/041004)	YINPSTGYTEYNQKFKD	1511
vhCDR3 (SEQ ID NO:36 from WO 2017/041004)	GSSGSWFAY	1512
Light chain (SEQ ID NO:40 from WO 2017/041004)	DVVMTQTPLTSLSVTIGQPASISCKSSQSLLNSDGKTYLNNWLLQRPQGQSPKRLIYLVSKLD SGV PDRFTGSGSGTDFTLKISRVEAEDLGVYYCWWQGTGTHFPRTFGGGTKLEIK	1513
vlCDR1 (SEQ ID NO:41 from WO 2017/041004)	KSSQSLLNSDGKTYLN	1515
vlCDR2 (SEQ ID NO:42 from WO 2017/041004)	LVSKLDS	1516
vlCDR3 (SEQ ID NO:43 from WO 2017/041004)	WQGTGTHFPRT	1517

Figure 38D

From WO 2018/017864 (334M5 antibody)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:30 from WO 2018/017864)	EVQLQQSV AELVRPGTSVTISCKASGYTFTNYWLGWVKQRPGHGLEWIGDIFPGGDYPNY NEKFKGKATLTADTSSSTAYMQLSSLTSEDSSVYFCTRGYFDVWVGAGTTVTIVSS	1518
vhCDR1 (SEQ ID NO:31 from WO 2018/017864)	TNYWLG	1519
vhCDR2 (SEQ ID NO:32 from WO 2018/017864)	DIFPGGDYPNYNEKFKG	1520
vhCDR3 (SEQ ID NO:33 from WO 2018/017864)	TRGYFDV	1521
Light chain (SEQ ID NO:25 from WO 2018/017864)	DIQMTQSPSSLSV SAGEKVTMSCKSSQSLNSENQKNYLA W FQQKPGQPPKMLIYGASTR ESGV PDRFTGSGSGTDFTLTISVQAEDLA VYYCQNDHSHYPFTFGSGTKLEIKR	1522
vlCDR1 (SEQ ID NO:26 from WO 2018/017864)	KSSQSLNSENQKNYLA	1523
vlCDR2 (SEQ ID NO:27 from WO 2018/017864)	GASTRES	1524
vlCDR3 (SEQ ID NO:28 from WO 2018/017864)	QNDHSYP	1525

Figure 38E

TABLE 11									
Summary of Antibody Binding and Blocking Antibody Details (mouse)									
Antibody	293T-mouse		Mouse		mouse		human		
	CD112R	gMFI (fold increase over isotype)	CD112R	Binding ELISA EC50 (ng/ml)	CD112R blocking ELISA max inhibition (%)	CD112R blocking ELISA max inhibition (%)	CD112/CD112R blocking ELISA max inhibition (%)	CD112/CD112R blocking ELISA max inhibition (%)	CD112/CD112R blocking ELISA max inhibition (%)
Antibody A	104.6		34.5		93.3		90.6		
Antibody B	133.3		27.4		92.5		88.9		
Antibody C	88.1		41.0		90.1		97.8		
Antibody 32	14.9		269.5		0.0		75.1		
Antibody 33	73.3		38.3		28.3		78.8		
Antibody 34	72.2		24.2		20.3		80.0		
Antibody 35	55.6		21.5		24.2		81.7		
Antibody 36	76.3		25.1		41.6		86.2		
Antibody 46	74.8		180.6		88.0		97.6		
Antibody 58	79.4		411.7		85.7		97.3		

Figure 38F

Table of Sequences			
SEQ ID NO	Clone No	Description	Sequence
1	1	VH CDR1	RTFERYTMR
2	2	VH CDR2	AIYVNGKNTTYNDGVN
3	3	VH CDR3	AKDYSSNDWIDYMDV
4	2	VL CDR1	QASQDISRYLN
5	2	VL CDR2	DASHLAT
6	3	VL CDR3	QQFDLFPET
7	2	VH FR1	EVQLVESGGGLVHPGDSLRISCAASG
8	2	VH FR2	WYQAFKDELNVY
9	2	VH FR3	RPTISRDNSKNTLYLQMNISLRADTAVYYC
10	2	VH FR4	WGQFTVTVSS
11	2	VH DNA	GAGGTCGAGCTGCTGAGTCTGGGGA GGCTCTCTCAAGCTTGGGGTCTCTG AGACTCTCTCTGCTGGGCTCTGAGTCT ACCTTCAGTGAATATACCTTGAAGTCT GTTCGGCAGGCTCTCAGGGAAGGGCTG GACTGCTCTCTGAGCTCTTGTAGGTACT GGTACAGGACATATCTACCTCAGACTCT GAGAAAGGCTGGGTCTACCTCTCTCAGA GACAACTCTAAGAAACCTCTCTCTCTG CTAATGAGTACCTGAGAGCTGGAGAC ACGGCTCTCTCTCTCTCTCTCTCTCTCT TACAGCTCTCTCTCTCTCTCTCTCTCTCT GCAATGAGCTCTCTCTCTCTCTCTCTCTCT ACTGTCAGCTCTCTCTCTCTCTCTCTCTCT
12	2	VH Protein	EVQLVESGGGLVHPGDSLRISCAASG TPREYTHRWVQAPKDELNVYAIYVNG GDSYVADSVSRFTISRDNSKNTLYLQ MNSLRADTAVYYCAKDYSSNDWIDY MDVNDQGTITVTVSS
13	2	VL FR1	DIQMTQSPSSLSASVGDRVTITC
14	2	VL FR2	WYQQKPKAPKLLIY
15	2	VL FR3	QPERFPGSGSGTDEFTFTISSLQPEDL ATYYC
16	2	VL FR4	FGGGTVEIK
17	2	VL DNA	GACATCCAGATGACCTAGTCTCATCTC TCTCTCTCTCTCTCTCTCTCTCTCTCT GTCTACCTCTCTCTCTCTCTCTCTCTCT GACATGAGGACTATTTAATTTGGTAT CAGCAGAAATCAGGGAAGCTCTCTCT CTCTCTCTCTCTCTCTCTCTCTCTCTCT GCAACAGGCTCTCTCTCTCTCTCTCTCT GCAAGTGGATCTCTCTCTCTCTCTCTCT TTCACCTCAGAGCTCTCTCTCTCTCTCT GATATTCAGCATCTCTCTCTCTCTCTCT TTCGATCTCTCTCTCTCTCTCTCTCTCT GGAGGACCTAGGTTGAGATCAA

Figure 38G

Table of Sequences			
SEQ ID NO	Clone No.	De- scrip- tion	Sequence
18	3	VL Protein	DSQNTGSPSSLSAEVQDENTVTCQSQ DAHYVANNVQKSPQAKLLITDQKL APQVPSQSSQSDNTFTTSLQQR DAATYVGGPVALPPTDQSTVTEK
19-100: Not used			
101	5	WH CDR1	STPSHYMSI
102	5	WH CDR3	ASQDREFTYVLRKQ
103	5	WH CDR3	AKDYSSQWVYKQV
104	5	VL CDR1	QKQGLIENVLI
105	5	VL CDR2	QAKELAT
106	5	VL CDR3	QKPLLPFT
107	5	WH FR1	WQGLSSQSSLSQFQKSLKCAAGI
108	5	WH FR2	WYQKQFQKLENY
109	5	WH FR3	FTTSSRLDHSNTVLYQKSLKADSTV YK
110	5	WH FR4	WQSTTFTVSE
111	5	WH DRB	QKSTTCAGACCTGTTGGNTVTCQQLK QKTTGGATKQKQTHKSSQSSQCCVY DAAGTCVYTHKSSQSSQSSQSSQSSQ KQCTTSSQSSQSSQSSQSSQSSQSSQ STGCTVAGCTVQSSQSSQSSQSSQSSQ KQSTQKQCTYKQKNTVTCQSSQSSQ QSSQSSQSSQSSQSSQSSQSSQSSQ STSSQSSQSSQSSQSSQSSQSSQSSQ GAKNTVTCAGSSQSSQSSQSSQSSQ CAATVTCAGSSQSSQSSQSSQSSQSSQ KQSSQSSQSSQSSQSSQSSQSSQSSQ TAKCTCCSSQSSQSSQSSQSSQSSQ QKSTSSQSSQSSQSSQSSQSSQSSQ KQCTVAGCTVTC
112	5	WH Protein	EVQILRSQKLYQKMSRLVYASGP TFEYVANNVQKSPQAKLLITDQKL KSTFTSSQSSQSSQSSQSSQSSQSSQ QKSLRLDHSNTVLYQKSLKADSTV QKSTTFTVSE
113	5	VL FR1	DSQNTGSPSSLSAEVQDENTVTCQSQ
114	5	VL FR2	WYQKQFQKLENY
115	5	VL FR3	QVPSQSSQSDNTFTTSLQQR KFTVQ
116	5	VL FR4	QKQSTVTEK
117	5	VL DRB	QKSTTCAGACCTGTTGGNTVTCQQLK QKTTGGATKQKQTHKSSQSSQCCVY DAAGTCVYTHKSSQSSQSSQSSQSSQ KQCTTSSQSSQSSQSSQSSQSSQSSQ STGCTVAGCTVQSSQSSQSSQSSQSSQ KQSTQKQCTYKQKNTVTCQSSQSSQ QSSQSSQSSQSSQSSQSSQSSQSSQ STSSQSSQSSQSSQSSQSSQSSQSSQ GAKNTVTCAGSSQSSQSSQSSQSSQ CAATVTCAGSSQSSQSSQSSQSSQSSQ KQSSQSSQSSQSSQSSQSSQSSQSSQ TAKCTCCSSQSSQSSQSSQSSQSSQ QKSTSSQSSQSSQSSQSSQSSQSSQ KQCTVAGCTVTC

[illegible]

Figure 38I

Table of Sequences			
SEQ ID NO	Clone No	Description	Sequence
318	58	VL Protein	DTGHTGSPNLLASVGGPTTITQKSG LIRNLLSYGGSTWAPLLISTASFL EGVPERFSSGGSTDFLTLSLQPD DPAVYTGGLVGFILTRGGTVIRK
319-320		Not used	
321	58	VH CDR1	FFGGVYKNS
322	58	VH CDR2	FTGGFFTRSTFTYATVNA
323	58	VH CDR3	SGSPARTYGMST
324	58	VL CDR1	RLSGQSTSEVNF
325	58	VL CDR2	APGSLGQ
326	58	VL CDR3	QGGSTPLT
327	58	VH FR1	SPQLVERNNKLPQPRSLQCTAGG
328	58	VH FR2	WPRGAPCHNLENG
329	58	VH FR3	SPFISDGGSDIATLQMSLATGTAU YTC
330	58	VH FR4	WGGSTTVTVSS
331	58	VH DNA	GAGGTTCACGCTGCTGAGGTTTACGCGA GGGTTGATACAGCTAGCGCGGTGCTG AATGTCCTGCTGACGCTGCTGCTGCTG AATTTGCTGCTGCTGCTGCTGCTGCTG TCTGCTGCTGCTGCTGCTGCTGCTG GAGTGGCTAGCTTTCTGCTGCTGCTG TTTTGGCTGCTGCTGCTGCTGCTGCTG GGGTCTGCTGCTGCTGCTGCTGCTGCTG TCAAGGCTGCTGCTGCTGCTGCTGCTG TATTTGCTGCTGCTGCTGCTGCTGCTG GAGGCTGCTGCTGCTGCTGCTGCTGCTG ATGGAATGCTGCTGCTGCTGCTGCTGCTG GTCACGCTGCTGCTGCTGCTGCTGCTG
332	58	VH Protein	SPQLVERNNKLPQPRSLQCTAGG SPQYKNSPRGAPCHNLENG FGGSTFTYATGNNFTLGGGSKYTA TLQMSLATGTAUVTGSGSPRTTYG DPAVYTGGLVGFILTRGGTVIRK
333	58	VL FR1	DTGHTGSPNLLASVGGPTTITTC
334	58	VL FR2	NTGHTGSPNLLASVGGPTTITTC
335	58	VL FR3	GVTPSPSPSGSTGSTGTLTISLQPRD ATVTC
336	58	VL FR4	FGGGSTVIRK
337	58	VL DNA	GAGATCAGATGACCTGCTGCTGCTGCTG TCTCTGCTGCTGCTGCTGCTGCTGCTG GTTATGCTGCTGCTGCTGCTGCTGCTG AGCTTATGCTGCTGCTGCTGCTGCTGCTG CAGCATGCTGCTGCTGCTGCTGCTGCTG TCTCTGCTGCTGCTGCTGCTGCTGCTG CAGATGCTGCTGCTGCTGCTGCTGCTG GGCATGCTGCTGCTGCTGCTGCTGCTG GTCACGCTGCTGCTGCTGCTGCTGCTG GATGCTGCTGCTGCTGCTGCTGCTGCTG

Figure 38J

Table of Sequences			
SEQ ID No.	Clone No.	Seq- Name	Sequence
			AATTCACCTCCCTTCACTTTTCACGAG CCGACACAGGTTGAGTAAA
318	88	VL Protein	DTYMTDSEELASVDSSTITCEASQ SIESYLNWYQLPGEAFKLLIYAASL QSEYPSSEPSGSSSTFTLISLAPSE DFTYTCQGGSTFQTEGGSTVHK
319-400: Not used			
401	10	VH CDR1	PTPMNYAH
402	10	VH CDR3	GIENHSEHISADGDS
403	10	VH CDR3	AKGPTTYQSYFEL
404	10	VL CDR1	RLQGVSTYLA
405	10	VL CDR3	DASHRAE
406	10	VL CDR3	QGVSESTST
407	10	VH FR1	EVQLVESGGGVQPQSFSLPSGASDF
408	10	VH FR2	WYQAGPGQSLKLY
409	10	VH FR3	PTTISHHSHSLSLQLQSHSLASSTAY SYC
410	10	VH FR4	NSHSESLTYSS
411	10	VH DNA	GAATTCACCTCCCTTCACTTTTCACGAG GCTTCTGTAACCTTCGCGAGTCTCTG AGATTCCTCTGTCACGCTCTCTGATC ACCTTCAATGCTATGCTCTGCACTGG GTCTGCAAGCTTCGAGGAGAGGCTG GATTCGCTTCAAGATATGATTCAGAT AGTGCCTATATGATATGCGGACTCT GCGAGGCGCTTCCTATCTCTGAGG GACAGGCGCTACGACTCCCTCTATCTG GAAATGACGCTTTCAGCTGAGGAG AGGCGCGCTGCTCTCTGCGAGGAGG CCGCTCTCTTACCGAGACTATCTGAG CCGTGGCGAGAGGAGCTTGGTGGC GTCTCTCA
412	10	VH Protein	EVQLVESGGGVQPQSFSLPSGASDF TTDQYATWVQLNPRIKLLDVSGLSK SOLSGVADSVNHSFTIQRDGRHLYL QNHSLRSDILTYCARGPTTGGTFO LAGRSTLTUSE
413	10	VL FR1	EVQLVESGATLSLPSGASATLQ
414	10	VL FR2	WYQAGPGQSLKLY
415	10	VL FR3	SIPMPSSESGSTFTLISLSESEDF AYYVC
416	10	VL FR4	PSGHTFVSK
417	10	VL DNA	GAATTCGATTCGCTCTGCTCCAGGGAAGA ACCCTGCTTCTGCTCCAGGGAAGA GCGACCTCTCTGCTAGGCTCAGTGAG AGCTTACGAGGATTTAGCTCTGCTGAC CAGTCAAGCTTGGCTGAGTCTGAGG CTCTCTCTCTATGAGAGCTCTGAGGAG GCGCTGCGCTCTGAGGAGCTCTGAGT GCGAGTGGCTCTGAGGAGCTCTGAGT CTCTCTCTCTGAGGCTCTGAGTCTGAG GATTTGCGCTTCTTATGCTCTGAGGAG

Table of Sequences				
Seq ID	Clone No	Description	Sequence	
818	18	VL Protein	GTCTGGTCTCTGCGCTCCTATCACTTTT CCGCTGAGGAGCAAGGCTTCAGATCAAA XXVYVQSPATLSLSPFNRRATLSLSPAG SSVSYIASTQANPAQAPFLITSLSPSS ATGTPAAAGSGGGGTGTFITSLSPSS DEAVYVYQQVSPFSPFTTGGGTNYKST	
819-900: Not used				
891	39	VH CDR1	STPSGRLNS	
892	39	VH CDR2	ALESSSSSTTYKASVSS	
893	39	VH CDR3	ASDQYTDNSGSGQSYEDL	
894	39	VL CDR1	SAGSGTERTSLA	
895	39	VL CDR2	NHHHST	
896	39	VL CDR3	QQVSLAPP	
897	39	VH FR1	EVGLLESQWELQPGWELSLSPSSAG	
898	39	VH FR2	NLRQAPGGLSHVSS	
899	39	VH FR3	EPTLSPDHSITSLQLQSSSLASSTV TTC	
910	39	VH FR4	NQGRTLVTVSS	
911	39	VH DNA	GCGTGGTGGCGTTTCTTGGTCTGGTGGT GCGTGGTGGTGGTGGTGGTGGTGGTGGT AGACTCTCTTGTGCAAGCTCTGGATTC AGCTTTAGCGAGACATTAATGAGATTC GTGCGCGTGGTGGTGGTGGTGGTGGTGGT GCGTGGTCTGGTGGTCTGGTGGTGGTGGT GCGATGGAGACATCTAGCGAGATTC GTGAGAGCGCGCTTCACTATCTCTGGA GACAAATTCAGAGACACCGCTGATCTG CAAAGTAAATCTTGGATGGATCTGGAT AGCGGCTGTTTCTTCTTGGTGGTGGTGGT GGTACTATGAGAGATCTGGTGGTGGTGGT GCGGATTCGTACTTTCATTTATGGGGG AGAGGTACCTTGGTGGTGGTGGTGGTGGT	
912	39	VH Protein	EVTLLSHSHLVQSPHSLSPSLSPAG STPSGRLNSSTQANPAQAPFLITSLSPSS AGSTVYVQSPVQSPFTSPSSSPSTVYL QHSLRAEDTAVYTCARDAYVDNSG SHSTVPLSHSTVTVSS	
913	39	VL FR1	STVLTQSPATLSLSPFNRRATLSLSPAG	
914	39	VL FR2	WYQRRPGQAPRLITY	
915	39	VL FR3	GYPNRPFGGGSTGPTATLSPVQSP AVTTC	
916	39	VL FR4	SHHSHSVYSS	
917	39	VL DNA	GAAATGTTTCTTTCAGCAAGCTCTTTCAGT AGCTGCTTTTCTCTCTCTGAGGAGAGA GCGTGGTGGTGGTGGTGGTGGTGGTGGT AGCTTATAGATTTATTTAGCTTATAGT CACAGAGAAGCTTGGTCAAGCTCTCTAGG TGCCTATCTATATGAGCTCTTTCAGAGG GGCACCTGATATTTAGCTCTGGTGGTGGT GGCATGGTGGTCTGGAGCAGACTTCAGT TCTACCACTAGAGCTTAGAGCTCTAGAG	

[illegible]

Table of Sequences				
Seq ID	Gene	Da- kDa	Seq- size	Sequence
880				CTCACCATGAGAGCTCTGCAGCTTAA AGTTTTCAGACTTACTACTGAGAGAA GATATTCACACTCTCTTGCATTTTGGC TAGAGGACCAAGATTAGAGTAA
818	18	VL Protein		DIGNTQFSESLKSLKSVGRVITDRLSQ GKSTVLMVYQTFPPAKILLIHRSLI QSTPTSPFLSSGGSTPTFLIHLQPE HFAITYYQGGPYTNTFCKGHTVEIK
819-709: Not used				
701	38	VH CDR1		STPSSAAIS
702	38	VH CDR2		HYTFYCIAMYSQNRQC
703	38	VH CDR3		LSDTDRGYTHHFWCP
704	38	VL CDR1		RSASQISFTYL
705	38	VL CDR2		ASASLQG
706	38	VL CDR3		QKQDILTY
707	38	VH FR1		QKQLVQGGSLVKKPCSHVFLCKASG
708	38	VH FR2		NVRKAPQGLEKNG
709	38	VH FR3		KVTLTADSTSTAYNHLKSLSSDSTAY TTC
710	38	VH FR4		NKQHYLLTNGS
711	38	VH DNA		CAGGAGCAGCTGGTGGAGTTTGGGCTT GAGTCTGAGAAAGCTTGATCTCTGGCTC AAGHTCTCTGCAAGCTCTCTGGAGCT ACCTTGGCTGGCTGGCTGCTGAGCTTG GTCTGAGTGGCTCTGAGCTGAGCTT GAGTCTGAGAAAGCTCTCTCTCTCTCT GTAGGCTTGGCAAACTGGCAGCAGAG TTCCTGGGAGAGTTCAGATTCAGCTG GAGGATCTGAGGAGCTGAGCTGAGCT GAGCTTGGAGCTTGGCTCTGAGCT AGGCTGCTGTACTACTGGGAGAGAG AGGAGAGAGGAGCTAGCTGAGAGCTT TGTCTTGGCTCTGGAGCTGGAGCT TGGCTGAGCTCTCTCTCA
712	85	VH Protein		QKQLVQGGSLVKKPCSHVFLCKASG TTPKAAISNVRKAPQGLEKNNHIIPI VQIANTYAGSCGVITLADASTSTAYN HLKSLSSDSTAYTCASTGAGSTTNS NPLTPGQGLYTNGS
713	38	VL FR1		DIGNTQFSESLKSLKSVGRVITDRLSQ
714	38	VL FR2		NVQKPPKSKILLIF
715	38	VL FR3		GVPSFSGGAGCTSTPTLTIAGLPKNS ASVTC
716	38	VL FR4		FGGHTVEIK
717	38	VL DNA		AGCATCCAGATGAGCCAGCTCTGCTCC TTCCTGCTGCTCTCTAGAGAGAGAG GGTACCTCTACTCTCTGGAGAGTAC AGCATTAHAKTATTAATTTATAT TAGCAGAAATCTGGAGAGCTCTGAG CTCTGAGCTATCTGAGCTGAGCTT CAAGTGGCTCTCTGAGCTCTGAGCT

[illegible]

Figure 380

Table of Sequences			
SEQ ID NO	Accession	Name	Sequence
			TTGGGTTCTGATCGGGGCTCGGGGTC CTGACAGGTTTACATGGAATGGA TGA GGCAGAGGTTTACACTGAAATCAGC MMHTTGAAGTTTACAGATGTTGCGCTT TATTACTGCTTGCAGGCTCTCGAGCC CTACTTTTGGGAGAGGATCGGTT GAGATCGA
818	42	VL Protein	GIVHTGPRGLPTTGFAGLGKSSQ ELLKENGNYLYLGLYFQDEPLLY LASHKASQVFNSSSSSSSTPTLIS RURSDVGVYTCYGLAAPTGGSTT EIK
819-900 not used			
891	55	VH CDR1	PTPRDYKMG
892	49	VH CDR2	PIGKATGCTTSTYASVKG
893	55	VH CDR3	AKGPPRYTGMKV
894	49	VL CDR1	RAEQEISSEVLN
895	38	VL CDR2	AAASLQS
896	49	VL CDR3	QGSSTPLT
897	55	VH FR1	EVQLVDSGGG.VQPRASLQCTAGD
898	55	VH FR2	KPRQAPQSGLNVC
899	59	VH FR3	HTTSDGGGSIATLQAGSLYDQAV YYC
910	49	VH FR4	KQAGTSTVYK
911	59	VH CDR	QAGTTCAGCTGCTGAPCTTQVEXR QGGTGGGACAGCGAGGGGCTCTCTG NKAFTCTCTCTGAGCTTCTGGAFTC ACCTTGGCTGATTATGCTATGAGCTGG TTCCTCCAAHTTCAAGGAAAGAGCTG QAGTGGGTAAGTTTCTTGGAGCTGA GCTGATGTTGAGGAGAGAGGATGAGC GGTCTGTGAAGCGAGATTACCGATC TGAAGAGAGCTTTTAAAGCTATCTCT TATCTGCAATGAGCGGCTGAAAGCT GAGGAGCGGGGCTGCTCTGCTGCTG NAGAGATCAGAGCTCTAGCATACGGA ATGAGATATAGGGCTAGGAGCAACT GTAACTCTCTCTCA
912	49	VH Protein	EVQLVDSGGG.VQPRASLQCTAGD KPRQAPQSGLNVCGLDQVPTGK NKGSTTETATVPRFTLSSAGKSLA VLQNNGLKSHDTAVYTCSPGPESTTS KPTWAGGISTVYVSS
913	49	VL FR1	EVHTFGLSPRLASSTGQVYITC
914	55	VL FR2	KIQGAPGAPGKAIY
915	49	VL FR3	GVTVRFQGGCTGFTLTSSLGPEQV ATVTC
916	55	VL FR4	EQGGTSTEEK
917	49	VL CDR	QAGTTCAGAGTACGATCTGCRGCT TCTCTGCTGATCTTGTAGAGAGAGG GTCACCTGACTTGCCTGGGAGGTTAG AGCATAGCGAGTATTAGATTGCTAT

P

Table of Sequences			
SEQ ID NO	Clone No	Se- quence	Se- quence
			CACGAGGAAACAGGAGAAAGTCTCTTAG CCGCTGATCTATGCTTCTATCGAGTTTG CAGAGTGGCGGCTCTGATCTTAAAGGTTGAGT GAGCAGTGATCTTGGGAGGAGATTTCTCT CTGACGATCTACGAGTCTGCAACCTGAA GATTTCTGACTTACTACTCTGACGAA AGATTTCGCGGCGCTGACCTTTTCTGAG CGGACTGAGGTTGAGTCTGAA
918	88	VL Protein	EIGHTGTFSSLESAFYKNSVTITCRAGQ EIEGYLNNYQKKPKGAPFLINAGSEL ASGVTFSPFGGSGGCTPLTISLGLP DPATYYCQGGSTPLTFGGSTKVLK
919-1000 not used			
1001	82	VH CDR1	CTFFSTYALS
1002	82	VH CDR2	GIITFTGNTNNAGSPQG
1003	82	VH CDR3	NPHTGPGVYTHNFFSTF
1004	82	VL CDR1	PAHQSIISGVIN
1005	82	VL CDR2	AAHLGL
1006	82	VL CDR3	QGSILLET
1007	82	VH FR1	QVQLVQSGAEVKKPGSSVKYSDFRQAGG
1008	82	VH FR2	EVKQSGDQLQENNE
1009	82	VH FR3	RVTISAEDETSTAHNLGLSLRSTFAY YTH
1010	82	VH FR4	WQQGTSLTTHS
1011	82	VH DNA	CAGGTGCACTGCGTGCAGCTCTGGGCT GAGTGTGAAGAAAGCTTGCTCTGTGAGG AGGGTCTCTCGCAAGGCTTTTGGAGCC GCGTTTCAGCACTATGCTATCGAGCTG GTGCGACAGCTCTTGGACAGGAGCTT GAGTGGTGGGAGGGGCTCATCTCTATC TCGGCTACGCGGAGCTACGACAGCAGAG TTCCGCGGAGAGCTCGCGGTACAGG GACGATCTCGGAGACCACTCTTATG GAGCTGAGCAGCTTGGAGCTTGGAGAC AGCGGCTTTTACTACTGCTGCTGAGAGC ACCTGGACCGGAGTACAGCAGCACTTC NGTTTGTACCTCTGGGAGCAGGCTTACA TGGTGTACCTCTCTTGA
1012	82	VH Protein	QVQLVQSGAEVKKPGSSVKYSDFRQAGG TFEETALHNVKSGDQLQENNEGLIPI SGTHNVAQVAGGVTTTAADETSTAHN ELGLSLRSTFAYYYRAGTSGGCTTHSP WQFGGSLTTHSS
1013	82	VL FR1	DIGHTGAPALSAFYKNSVTITC
1014	82	VL FR2	NYQGGTGVKAPKLAY
1015	82	VL FR3	GVTEHSPGAGAGSTPLTISLGLP ATGVV
1016	82	VL FR4	SGGNSVYKIK
1017	82	VL DNA	BACATCCAGATGACCGAGCTTTCATCC TCGCTGCTGCTGATCTGTGTAAGAGCAG GTTGCATCTACTTGGCGGCTACTCTG

Figure 38Q

Table of Sequences			
SEQ ID NO	Clone No	Re-sequencing	Sequence
			AGCTTTACGAGCTATTTAAATTCGTAT CACGAGAACTAGGAAAGTCCCTAG CTCTCGTCTATATCTACCTCCGCTTC CAAAGTGGGTTCCATCAGGTTCTGAT GCGAGTGGATCTGGACAGATTTCAT CTGACCATGACAGTTTCAACTTGA GATTTCGCAATTACTACCTGACCA AGGACATCTCTACACTTTTGGGGA GGGACCAAGTTGAGATCTGA
1018	11	VL Protein	EIGHTSEVENSLASVDRPTTTRAGQ STGSLRMYQDFSSDFLLITAGSL QGGVRRPSSSSSTFTLTSLQSPF DERTTCCQSDILYTGAGTKRLK
1019-2000 not used			
1081	33	VH CDR1	SPFQNTKIL
2082	33	VH CDR2	SLISFGLAHYAGSPQG
1083	33	VH CDR3	LRDTGRSVTHHNPDP
2084	33	VL CDR1	EMQSEISYLN
2085	33	VL CDR2	AASTLQS
2086	33	VL CDR3	QQQDILYT
2087	33	VH FR1	QVQLVQSGQPKGPPKASQVPSGASQ
2088	33	VH FR2	KRLQAPGQLEKNG
2089	33	VH FR3	EYTIADSTSTANKELESLSSTFAY YYC
2010	33	VH FR4	SGQSFIVTGS
2011	33	VH CDR1	CAGGTCCAGCTGTPPSTTDEEAT QAGGTGKLLAGCTTGGTTCYTGST AAGHTFSTTHCAAGGTTCYTGAGG ACTTTCGAAACTATGCTATCAGCTGG GTTCACAGCTCTCTGACAGAGCTT GATGCTGAGGAGGCTATGCTCTTTC CCGCTKTCCKLACTAGGTCGSLAG EYTCAGGCAAGATCAATTTACCTGG GACCAAGCTACAGCAAGCTACAGG GACTGAGAGCTGAGCTTGAAGG AGGGCGGTGTCCTACTGCTGCTGAGC AGGGGACGAGATAGCTGAGGCTTC TGGTTCAGCTCTGAGCAGGGTACA TGGGTCACTCTCTGCA
2012	33	VH Pair 5-11	QVQLTQSGSEVERKPPSSVKKPSKAPGQ EFGHTASLVWGAPQQLGKNGILPI FLIAHTAGPFGKFTLTADSTSTAYH SLAVLASSTAYVTAAGTQSGVTAAG SYDFFLQGTSTTYS
2013	33	VL FR1	EIGHTSEVENSLASVDRPTTTC
2014	33	VL FR2	STQKESGKSLILY
2015	33	VL FR3	SUPSSSSSSGCTSTFTLTSLQSPDF AYYH
2016	33	VL FR4	SKKSTKRLK
2017	33	VL CDR3	GACATCCAGATGACCCAGTCTCCATCC TCCCTGCTGCTCTCTTACGAGACAGA

Table of Sequences			
Seq ID	Class No	De- cript- Name	Sequence
			GTCAACCTACACTTTCGCCGGCAGATGAG AGCATATGACAGACTTTTAAATTCAGTAT CAGCGAGAAATACGAGAACTCTTAAG CTCTTATATTATCTCTCTATTAAGTTTC CGAATAGCGGCTCCATCTACAGATTTCAT GCGATCTGAGTCTGGGACGAAATTCAT CGCATCTGATAGGATCTGCAATCTGAAA GATTTTGCAGATTACTACTGTTACGAA AGGACATCTCTTACTGCTTTTACGAGAA GGGACCGAGCTTGGAGTAAA
2008	37	VL Protein	GLYNTGPEELLSAEVYSGVTTITERASQ STSYSLNHYTQPPYAFPLLYAAGSL QGVTPSPFSGSGSSTFFLTLSGLGPE DFATVTCQGSGLYLTFGGNTVNRK
2008-2009			not used
2001	38	VH CDR1	GTFSAAIS
2002	38	VH CDR2	GVPTGCHANTAGCPLG
2003	38	VH CDR3	AGDTGAGYTHRWKWF
2004	38	VL CDR1	NSVQNIHNLIN
2005	38	VL CDR2	AAASLQS
2006	38	VL CDR3	QGVSLKLT
2007	38	VH FR1	QVQLVQSGAEVKKGQSELVKVYQKAAAG
2008	38	VH FR2	WRGASPGQGLANNE
2009	38	VH FR3	RUTTTAAGSTSTATHELGLSGLSHITAY YYC
2010	38	VH FR4	REGSLTIVTES
2011	38	VH CDR	CAHSTGCAKCTGHTGHTGCTTAAKCT GGTGTGAGAGAGCTTGKNTCTTGKNG AGHSTCTCTCKKAAAGKCTTGKGGC AGTTTCAAGAGCTGCTATATCTGAG GTGAGCAAGHCTCTTKACAAAGATC AGTGGHTGAGAGAGCTCTTCTCTATC TGNGTCAAGCAAACTAGCTACAGAG TTCAGSSGCAAGATACAGATATCTGG GATGATCTCAAGAGCAAGCTTACAGC AGCTGTAGAGCTTGAATCTTGAGGC ACAGAGCTGTATCTATCTGCAAGAGC AGGAGAGGAGATACAGAGAGCTTTC TGTTTGGGCTTGAGGCAAGCTTCA TTHATCACTCTCTCTCA
2012	38	VH Protein	QVQLVQSGAEVKKGQSELVKVYQKAAAG TFSAAKNTVLSAGFCAAGGAGSLFPI GDAHTAGAGKATTTAGAGTATATAT ELSPDSSTHTATYCAAGATATRAY HPSRSGSLTAVES
2013	38	VL FR1	DIHNTGQPSHLSAEVYSGVTTTC
2014	38	VL FR2	WVQPPYAFPLLY
2015	38	VL FR3	GVHPHPSHSGSTDPHTLSGLGPEDF ATYK
2016	38	VL FR4	FGNTVNRK

Figure 38S

Table of Sequences			
SEQ ID NO	Clone No	De- scrip- tion	Sequence
3017	34	VL DNA	GACATCCAGATGACCCAGTCTTCATCC TCCCTGCTCTCATCTCTGTAGGAGACAGA GTCACCATCACTTCCCGGCKAAGTCAG AGCATTAACAGCTATTTTAAATTGGTAT CAGCAGAAACCCAGGAAAGCCCTTAG CTCTGATCTATGCTGCTCCAGTTTG CAAAGTGGGGTCCATCAAGGTTGAGT GGCAGTGGATCTGGGACAGATTTCAGT CTCACCATCAGCAGTCTGCAAGCTGAA GATTTTGCAGCTTACTACTGTCAGCAA AGCGACATCTCTACACTTTTGKCGA GGGACCAAGCTTGACATCAA
3018	34	VL Protein	DIQNTQSPSSLEASVGGSPYTIICRASQ EISEYLNWYQQKPKAPKLLIVAAEEL QSGVPERFSSSGSDFTLTITISLQPE DPATYYCQSDILYTFGGCTKVEIK
3019-4000 not used			
4001	36	VH CDR1	GTPATYAIQ
4002	36	VH CDR2	GIFPLGGTANYAQEPQO
4003	36	VH CDR3	AKDVGSGTYRNHFWDG
4004	36	VL CDR1	RAQQTISSTLN
4005	36	VL CDR2	AAEELQE
4006	36	VL CDR3	QQSEILYT
4007	36	VH FR1	QVQLVQSGAEVHPGDSFKYCKRAEG
4008	36	VH FR2	WYRGAPGQGLENNG
4009	36	VH FR3	RVTITADESTSTAYNELSGLSKETAY YFC
4010	36	VH FR4	WQQGTLVTVEE
4011	36	VH DNA	CAGGTGCAGCTGGTGCAGTCTGGGCT GAGGTGAGAAAGCTTGGTCTCTGGTG AAGGTCTCTGCAAGGCTTCTGAGGAC ACCCTGCAACCTATGCTATCAGCTGG

Figure 38T

Table of Sequences			
SEQ ID NO	Clone No	Description	Sequence
			GTGCGACAGGTCCTCGACAGGGCTT GAGTGGATGCGAGGGATCTTDCCTCTC TCCGGTACAGCAAACTACGCACAGAG TTCCAGGKAGAGTCACGATTACGGCG GACGAATCCACGAGCAGAGCTTACATG GAGCTGACCAAGCTGAGATCTGAGGAC ACGGCGGTGTACTACTGCGGCGAGAGAC ACGGACCGGGATACACCAAGCACTTC TGGTTTGAACCTCTGGGACAGGGTACG TTGGTCACCGTCTCTCTCA
4012	36	VH Protein	QVQAVCGAENVKPGSSVIVSCKASGG TFATTALISWVBCAPGGGLENNGGIFPL SCTANYACKFQCRVTTTADERTSTAYM ELSSLESEDVAVYYCARDTCRCYTRHF WFDPMGQGTILVTVSS
4013	36	VL FR1	DIQMTQSPFSLASVQDSVTITC
4014	36	VL FR2	WYQQKPGKAPKLLIY
4015	36	VL FR3	GVPSEFSGSGSDTDFTLTISSELQPEDF ATYYC
4016	36	VL FR4	PGGGTKVEIK
4017	36	VL DNA	GACATCCAGATGACCCAGTCTCCATCC TCCCTGTCTGCATCTGTAGGAGACAGA GTCACCATCACTTGCCCGGCAAGTCAG AGCATTAACAGCTATTTAAATTGATAT CAGCAGAAACCAAGGGAAGTCCCTAAG CTCTTGATCTATGCTGCATCCAGTTTG CAAAGTGGGGTCCCATCAAGGTTCAAT GGCAGTGGATCTGGGACAGATTTCAT CTCACCATCAGCAGTCTGCCAAGCTCAA GATTTTGCAACTTACTACTGKAGCAA AGCGACATCTCTACACTTTTGCGGA GGGACCAAGTTGAGATCAAA
4018	36	VL Protein	DIQMTQSPFSLASVQDSVTITCRASQ SLSYLNWYQQKPGKAPKLLIYAASL QGVPSSEFSGSGSDTDFTLTISSELQPE DFATYYCQGSVILYTPGGGTKVEIK

Figure 38U

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.001	GGTFSSYA		IPIFGTA		AREEVSSPYGMDV		TGAVTSGHY		DTG		LLSYSGASWV	
CPA.7.002	GGTFSSA		IPIYGIT		ARDDTARRVGVPPYYVA MDV		QGIGNY		SAS		QQLKDYPIIT	
CPA.7.003	GFSLSHFS		FDPEEGGT		ATGIWYSSGWPVDY		QSLDSSGYN		LGS		MQALQTPIT	
CPA.7.004	GYLTLELS		FPEDGET		ATVSRVRGVINYYVMDV		QSLYRNGN		LGS		MQALQTPPT	
CPA.7.005	GGTFSSA		IPIYGIT		ARDDTARRVGVPPYYVA MDV		QSVDS		DAS		QQYKDWPFPT	
CPA.7.006	GGTFGYA		ITPISATI		ARGFEYSDGLLDD		QSLFYSDDGNTY		RLS		MQHMEFPLT	
CPA.7.007	GGSISSSY		IYSGST		ARGAWELRLGDWFDP		SSNIGAGYD		GNN		QSYDSSLIYVW	
CPA.7.008	SGSISSTNW		IYHSGST		ARVGPAAIY		SNNVGYEG		RNN		SAWDSSLNAVW	
CPA.7.009	GYLTLELS		FPEDGET		ATAKPGIAGQNYYYVMDV		QSLYRNGN		LGS		MQALQTPPT	
CPA.7.010	GTFSSYA		ISYDGSNK		ASSPIGYSGYWGGMMDV		SGIDVRTNK		FQSDSDK		LIWHTSGWV	
CPA.7.011	GYLTLELS		FPEDGET		ATGPAAAGVGYVMDV		QSLYRNGYN		LGS		MQALQTPPT	
CPA.7.012	GTFSSYA		ISYDGSNK		ARDVMVMVCSSTSCYFGM DV		QDIRDY		DAS		QQFENLPIT	
CPA.7.013	GYLTLELS		FPEDGET		ATGGYSSGFNYVMDV		QSLYRNGN		LGS		MQALQTPPT	
CPA.7.014	GYLTLELS		FPEDGET		ATGVTTYVYVMDV		QSLYSNGN		LGS		MQALQTPPT	
CPA.7.015	GTFSSYG		IRYDGSNK		ARDLDFWWDGMDV		QSVSSMY		GAS		QQVVSPPMYT	

Figure 38V

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.016	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYVYYVAMDV		QSVSSY		DAS		QQYDDWPQT	
CPA.7.017	GGTFNNYG		IIPFGIT		ARDRMAADGMAVFDY		SSNIGRHF		KND		SSWDAALNGVW	
CPA.7.018	GVTLELS		FDPEDGET		ATEVPMVRGARRYYVMDV		QTLLYINENNY		LGS		MQGLQTPPT	
CPA.7.019	GGISNSNYY		IYSGST		ARGAWELSLGDWFDPP		SSNIGAGYD		GNIN		QSYDSSLVYVW	
CPA.7.020	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYVYYVAMDV		QNVYGE		DTF		QQRDWPIT	
CPA.7.021	GFTFGTSS		ISFDGTEI		AKGSGNIYFYSGMDV		QSISGW		ETS		QQWYSYPLT	
CPA.7.022	GVTLELS		FDPEDGET		ATGVPAAGVYVYYVMDV		QSLLYSNGYNY		LGS		MQALQSPVT	
CPA.7.023	GVTLELS		FDPEDGET		ATDSRDGPAARGGYVYYVMDV		QSLLYINGYNY		LGS		MQALQTPPT	
CPA.7.024	GGTFSSYA		IPIFGTA		ARDAYYYDSSGYNPDAFDI		QSLHLSNGYNY		LGS		MQGLQTPRT	
CPA.7.025	GFSLTSGGMS		IDWNDDK		ARIRGMTWGFDS		QSVSSSY		GAS		QQYGTTTFA	
CPA.7.026	GVTFTAYY		INPNSGGT		ARDGAFYGYSENYYNAGWFDPP		QSLLSGNGYNY		LGS		MQALKSPLT	
CPA.7.027	GVTFTNYY		INPSSGGIT		ARAGLYNWNYPSPGMDV		SSDVGGYNY		EVS		SSYAGSNNLV	
CPA.7.028	GGSISSSYV		IYVSGT		ARGAWELRLGDWFDPP		SSNIGAGYD		GYS		QSYDSSLVYVW	
CPA.7.029	GFTFDDYA		ISWNSSGI		AKDVNRILVAGMVDY		QSLHLSNGYNY		LGS		MQGLQTPIT	
CPA.7.030	RFTFEDYA		ISWKSGGI		VKDPTLVATDRAFNI		QSLHLSNGYNY		LGS		MQYLQTPDT	

Figure 38W

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.031	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QSLDSDDGNIH		TLS		MQRKEPLT	
CPA.7.032	GFTSSYG		ISYDGSNK		AKEDRLRFLFWLFGMDV		HDIYTY		DAS		QQYDNHPPEVT	
CPA.7.033	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QDIDDD		EAS		LQHDNLPLT	
CPA.7.034	GVTLELS		FDPEDGET		ATEDPGPVAGPYYYGMDV		QSLLYNGYHY		LGS		MQALQTPPT	
CPA.7.035	GYMFTNYP		INAGTGNT		AREGMFYGYGLESYYKGGWFDP		QSLLRNGYNY		LAS		MQALQTPLT	
CPA.7.036	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QSLDSDDGNTY		TLS		MQRLQFPLT	
CPA.7.037	TYFTITY		YPSGGNT		VRDQNYYSAMDV		QDIRNY		DAS		QQFENLPIT	
CPA.7.038	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		RDISDS		DAS		HQYDNLPLT	
CPA.7.039	GFNFRGYA		ISGSGT		AQSYAQIGYGGHIDH		SGIDVATYM		YKSDSK		LIWHGSHYV	
CPA.7.040	GVTLELS		FDPEDGET		ATGVPAAIGVYYYYYMDV		QSLLYRNGYNY		WGS		MQAVQNPT	
CPA.7.041	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QNIDSS		YAS		HQSSSLPLT	
CPA.7.042	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QSVYNNY		DAS		QQYNSWPPYT	
CPA.7.043	GGTFSSYA		IPIFGTA		ARDAYYDSSGYNNPDAFDI		QSLLYSNGYNY		LGS		MQARQTPYT	
CPA.7.044	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		ESVTF		DAS		HQHTNWPLT	
CPA.7.045	GVTLELS		FDPEDGET		ATEVGYSGGSCYSYYGMDV		QSLLYRNGHNF		LGS		MQALQTPPT	
CPA.7.046	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		QTMNNY		DAS		QQYGDWLPIT	

Figure 3dX

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.047	GYTLTELS		FDPEDGET		ATAFPEATISYYYYMDV		QSLLYRNGYNY		WGS		MQAVQNPPT	
CPA.7.049	GGTFSSA		IPIYGIT		ARDDTARRVRGVPYYYYYAMDV		RSLLDSDDGNTNTH		SLS		MQRKEFPLT	
CPA.7.050	GGTFSSYA		IPIFGTA		ARGPWYYDSSGYSYAYYMDV		QSLLHSDGYNY		LGS		MQALHTPGVT	

Figure 39A

Pembrolizumab (Anti-PD1 hIgG4)		SEQ ID NO:
What	sequence	
Variable heavy (vh) domain	EVQLVLSGGGFVQPGGSLKLSCAASGFTFESSYAMSWVRQNPERRLVWVAITIGGGRNTIYYPD ^{SV} KGRFTISR DNAKN ^{TL} YLQMSSLRSEDTAMYYCTIQGYDGYTWFA ^{YW} GGQ ^{TL} VTVSS	
vhCDR1	GFTFESSYA	
vhCDR2	ITGGGRNT	
vhCDR3	TRQGYDGYTWFA ^Y	
Full length HC	EVQLVLSGGGFVQPGGSLKLSCAASGFTFESSYAMSWVRQNPERRLVWVAITIGGGRNTIYYPD ^{SV} KGRFTISR DNAKN ^{TL} YLQMSSLRSEDTAMYYCTIQGYDGYTWFA ^{YW} GGQ ^{TL} VTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTKITYTCNV ^D DHKPSNTKVD KRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVSVLT ^{VL} HLQDWLNGKEYKCKVSNKGLPSSIEKTI ^{SK} AKGQPREPQVY ^{TL} PPSQEEMT KNQV ^{SL} TCLVKGFYPSDIAVEWESNGQPENNYK ^{TT} TPPVLDSDGSF ^{FL} YSRL ^{IT} VDKSRWQEGN ^{VF} SCSV ^M HE ALHNHYTQKSLSLSPCK	
Variable light (vl) domain	DIVLTQSP ^{TS} SLA ^V SLGQRATISCRASE ^{SV} DN ^{SG} ISF ^{FM} NW ^{FQ} KPGQPPKLLIYAASNP ^{GS} GV ^{PAR} FSGSGSGT DFS ^{LN} IHPMEEDDTAM ^{YFC} QQSKEV ^{PW} TFGG ^{TE} LEIK ^{RI} VAAPSVFIFPPSDEQLKSGTASV ^V CLLNNF ^{YPR}	
vlCDR1	ESVDNSGISF	
vlCDR2	AAS	
vlCDR3	QQSKEVPW ^T	
Full length light chain	DIVLTQSP ^{TS} SLA ^V SLGQRATISCRASE ^{SV} DN ^{SG} ISF ^{FM} NW ^{FQ} KPGQPPKLLIYAASNP ^{GS} GV ^{PAR} FSGSGSGT DFS ^{LN} IHPMEEDDTAM ^{YFC} QQSKEV ^{PW} TFGG ^{TE} LEIK ^{RI} VAAPSVFIFPPSDEQLKSGTASV ^V CLLNNF ^{YPR} EAKVQW ^{KV} DNALQSGNSQESVTEQDSK ^D ST ^{YS} LSST ^{LT} LSKADYEKHK ^{VY} ACEV TH HQGLSSP ^V TKSF ^{NR} GE C	

Figure 39B

Nivolumab (Anti-PD1 hIgG4)		SEQ ID NO:
What	sequence	
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTI SRDNSKNTITLFLQMNSLRAEDTAVYYCAINDDYWGQGLTVTVSS	
vhCDR1	GITFSNSG	
vhCDR2	IWYDGSKR	
vhCDR3	ATNDDY	
Full length HC	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTI SRDNSKNTITLFLQMNSLRAEDTAVYYCAINDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGCTKTYTCNVVDHFKPSTKVDKRVES KYGPPCPCPAPEFLGGPSVFLPPKPKDITLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVQLHQDWLNGKEYCKCKVSNKGLPSSIEKTIKAKGQPREPQVYVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRAATGIPARFSGSGGTDFTLTI SSLEPEDFAVYYCQOSSNWPRITFGQGTKEIKR	
vlCDR1	QSVSSY	
vlCDR2	DAS	
vlCDR3	QOSSNWPRIT	
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRAATGIPARFSGSGGTDFTLTI SSLEPEDFAVYYCQOSSNWPRITFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC	

Figure 40A

From W02017100541 (Medimmune, LLC; also US20170306025; Durvalumab)		
What	sequence	SEQ ID NO:
Heavy chain		
(SEQ ID NO:2 from W02017100541)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVAVNIKQDGEKYYV	
vhCDR1	DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLVTVSS	
(SEQ ID NO:3 from W02017100541)		
vhCDR2		
(SEQ ID NO:4 from W02017100541)		
vhCDR3		
(SEQ ID NO:5 from W02017100541)		
Light chain		
(SEQ ID NO:1 from W02017100541)		
vLCDR1		
(SEQ ID NO:6 from W02017100541)		
vLCDR2		
(SEQ ID NO:7 from W02017100541)		
vLCDR3		
(SEQ ID NO:8 from W02017100541)		

Figure 40B

From US20170281764 (JN Biosciences)	SEQ ID NO:
What	sequence
Heavy chain (SEQ ID NO:34 from US2017281764)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADS VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGGTLVTVSAAATKGPS VFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVTP SSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKD/TLMSR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLTQDDWLNKG EYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG DIQMTQSPSSLSASVGDRTVITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYLFTPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYKHKVYVACE VTHQGLSSPVTKSFNRGEC
Light chain (SEQ ID NO:36 from US2017281764)	

Figure 40C

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVT VSA	
vhCDR1 (SEQ ID NO:17 from WO2015009856)	GFTFSDSWIH	
vhCDR2 (SEQ ID NO:18 from WO2015009856)	A WISPYGGSTYYADSVKG	
vhCDR3 (SEQ ID NO:19 from WO2015009856)	RHWPGGFDY	
Light chain (SEQ ID NO:24 from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCCQQYLHPATFGQGTKVEIKR	
vLCDR1 (SEQ ID NO:20 from WO2015009856)	RASQDVSTAVA	
vLCDR2 (SEQ ID NO:21 from WO2015009856)	SASFLYS	
vLCDR3 (SEQ ID NO:22 from WO2015009856)	QQYLYHPAT	

Figure 40D

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)		
What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO: 40 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVVRQAPGKGLEWV A WISPYGG STYY ADSVKGRFTISADTSKNTA YLQMNSLRAEDTA VYYCARRHWPGGFQDYWGQG TLVTVSSASTK (SEQ ID N0:40), or	
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTA VA WYQQKPGKAPKLLIYSASF YSG VPSRFSGSGGTDFTLTISSLQPEDF ATYYCQQL YHPATFGQGTKVEIKR (SEQ ID N0:24).	
From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO: 41 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVVRQAPGKGLEWVAWISPYGG STYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTA VYYCARRHWPGGFQDYWGQG TLVTVSS	
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTA VA WYQQKPGKAPKLLIYSASF YSGVPS RFGSGSGGTDFTLTISSLQPEDFATYYCQQLYHPATFGQGTKVEIKR	

Figure 40E

From US20160222117 (GENENTECH, INC.) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:20 from US20160222117)	EVQLVESCGGLVQPGGSLRLSCAASGFTSDSWIHVVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGGTLVT VSA	
Heavy chain (SEQ ID NO:23 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTSDSWIHVVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGGTLVT VSA	
Heavy chain (SEQ ID NO:24 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTSGSWIHVVRQAPGKGLEWVAWILPYGGSS YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGGTLVT VSA	
From US20160222117 (GENENTECH, INC.) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:21 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYLHPATFGGQGTKVEIKR	
Light chain (SEQ ID NO:26 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYNNVPWTFGGQGTKVEIKR	
Light chain (SEQ ID NO:27 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYAPPWTFGGQGTKVEIKR	

Figure 40F

From US20160222117 (GENENTECH, INC.) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:28 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYYTVPRTFGQGTKVEIKR	
Light chain (SEQ ID NO:29 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQVINTFLAWYQQKPGKAPKLLIYSASTLASGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYYTVPRTFGQGTKVEIKR	
Light chain (SEQ ID NO:30 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQQGYGVPRTFGQGTKVEIKR	
Light chain (SEQ ID NO:31 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYLFPTPTFGQGTKVEIKR	
Light chain (SEQ ID NO:32 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYFITPTTFTFGQGTKVEIKR	
Light chain (SEQ ID NO:33 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYYTPTPTFGQGTKVEIKR	
Light chain (SEQ ID NO:34 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQFFYPTPTFGQGTKVEIKR	

Figure 40G

From US201602222117 (GENENTECH, INC.)	SEQ ID NO:
What	sequence
Light chain (SEQ ID NO:35 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQSLFPTPTFGQGQTKVEIKR
Light chain (SEQ ID NO:36 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQSLYTPPTFGQGQTKVEIKR
Light chain (SEQ ID NO:37 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQSWYHPPTFGQGQTKVEIKR
Light chain (SEQ ID NO:38 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYFYPTPTFGQGQTKVEIKR
Light chain (SEQ ID NO:39 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQYWYTPYTFGQGQTKVEIKR
Light chain (SEQ ID NO:40 from US201602222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA WYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCCQSYFPTPTFGQGQTKVEIKR

Figure 40H

From WO2013079174 (Merck; Avelumab or A09-246- 2)	SEQ ID NO:
What	sequence
Heavy chain (SEQ ID NO:32 from WO2013079174)	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYIMMWVRQAPCKGLEWVSSINPSGGITFYADT VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLVTVSSASTKG PSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALH NHYTQKSLSLSPGK
Light chain (SEQ ID NO: from WO2013079174)	QSALTQPA SVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNR FSGKSGNTASLTISGLQAEDEADYYCSYTSSSTRVFGTGTKVTVLGQPKANPTVTLFPPSSEE LQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAASSYLSLTPEQW KSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 40I

From US8217149 (Hoffman La Roche; Atezolizumab)	SEQ ID NO:
What sequence	
Heavy chain (VH) (SEQ ID NO:20 from US8217149)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGQTLVTVSA
Light chain (VL) (SEQ ID NO:21 from US8217149)	DIQMTQSPSSASVGDRVTTITCRASQDVSTAVAWYQQKPGKAPKWKYSASFLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYC QQYL YH PATFGQGGTKVEIKR
Atezolizumab (alternate sequence))	SEQ ID NO:
What sequence	
Heavy chain (from IMGT database or DrugBank database)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGQTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH NHYTQKSLSLSPGK
Light chain (from IMGT database or DrugBank database)	DIQMTQSPSSASVGDRVTTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQYL YHPATFGQGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKV YACEVTHQGLSPVTKSFNRGEC

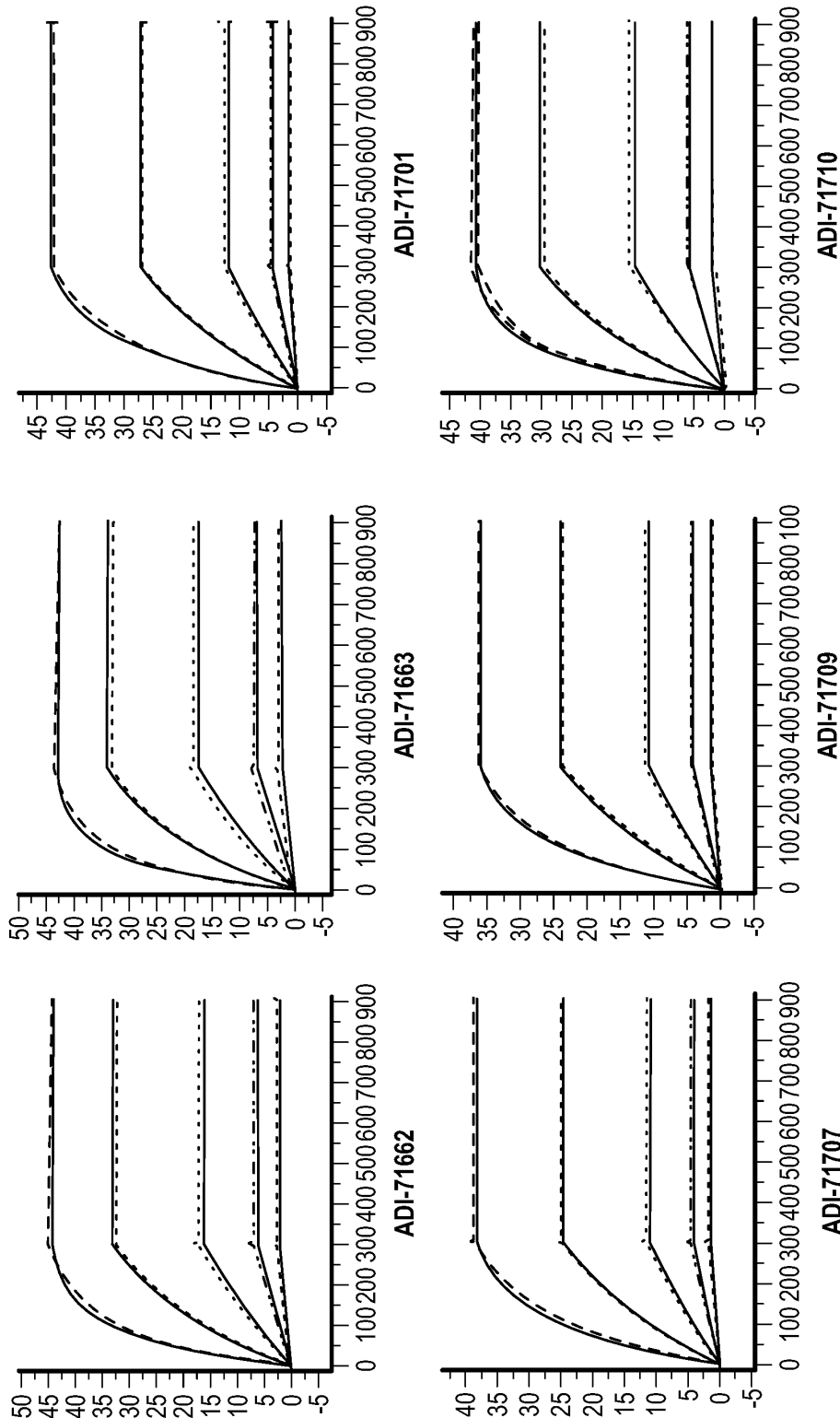


FIG. 41A

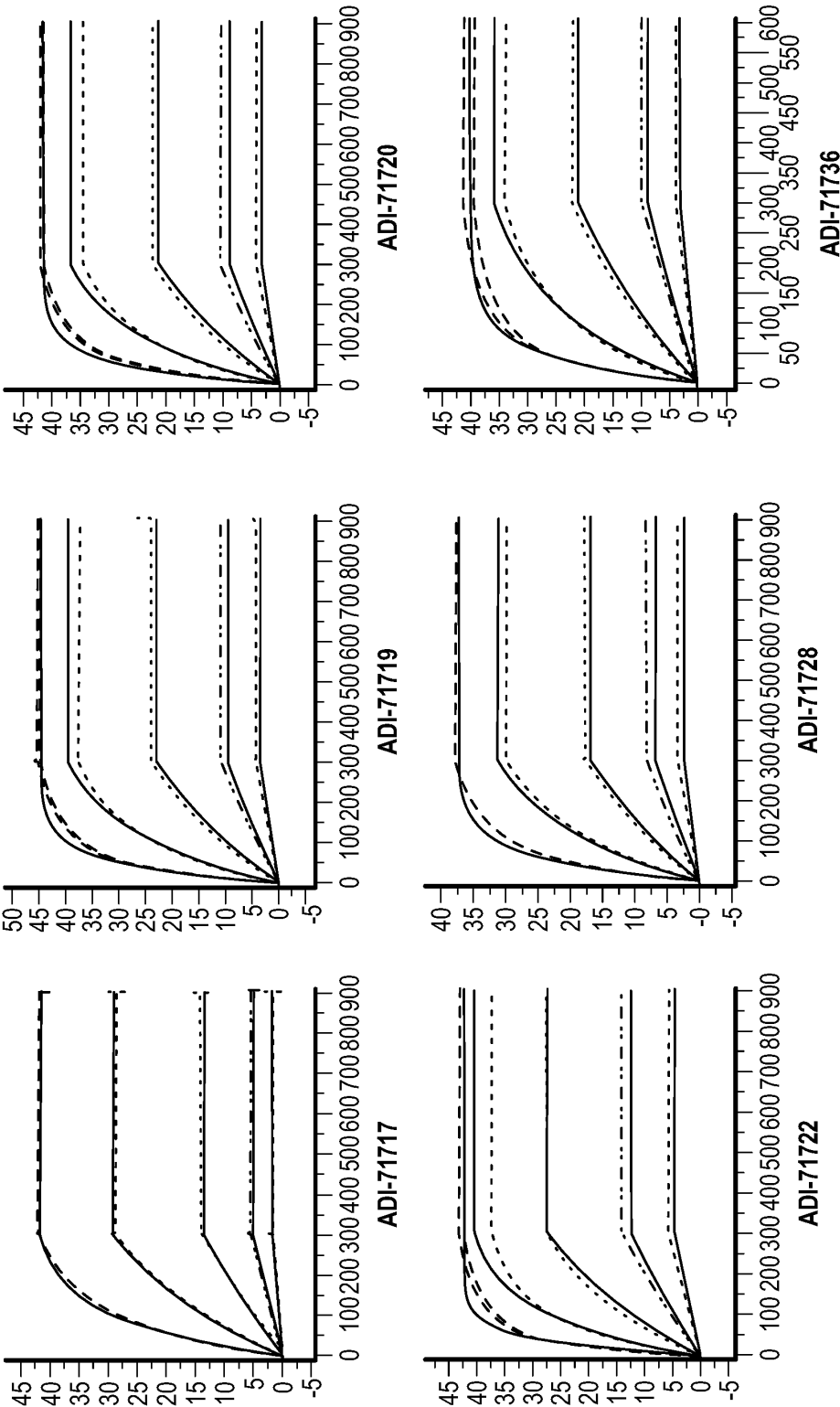
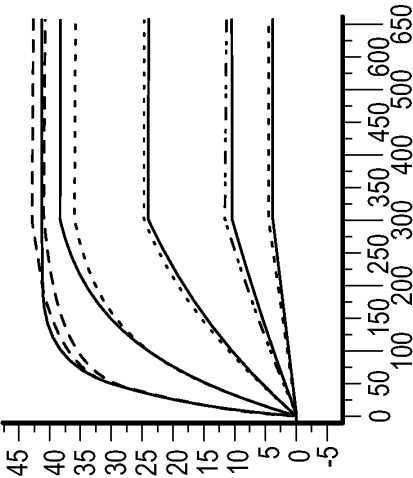
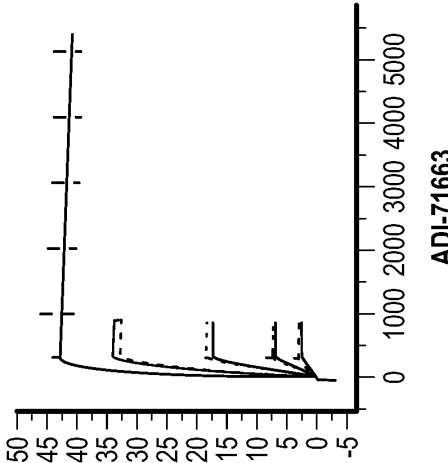


FIG. 41A (Continued)



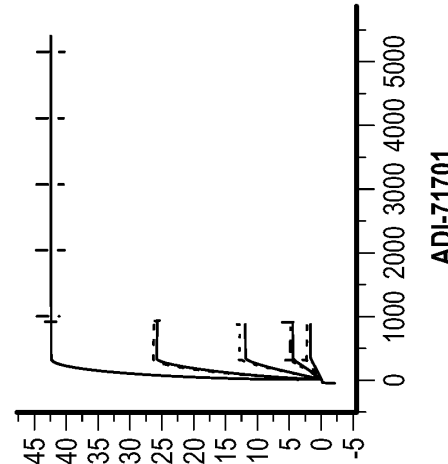
ADI-71739

FIG. 41A (Continued)

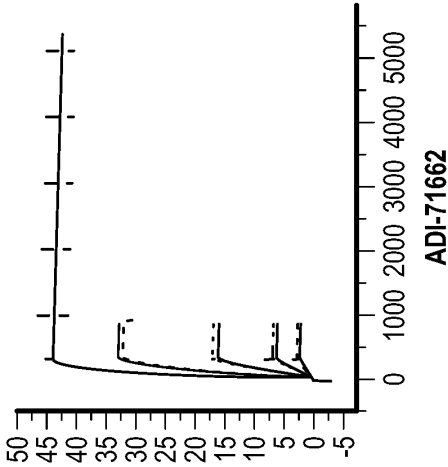


ADI-71663

FIG. 41B



ADI-71701



ADI-71662

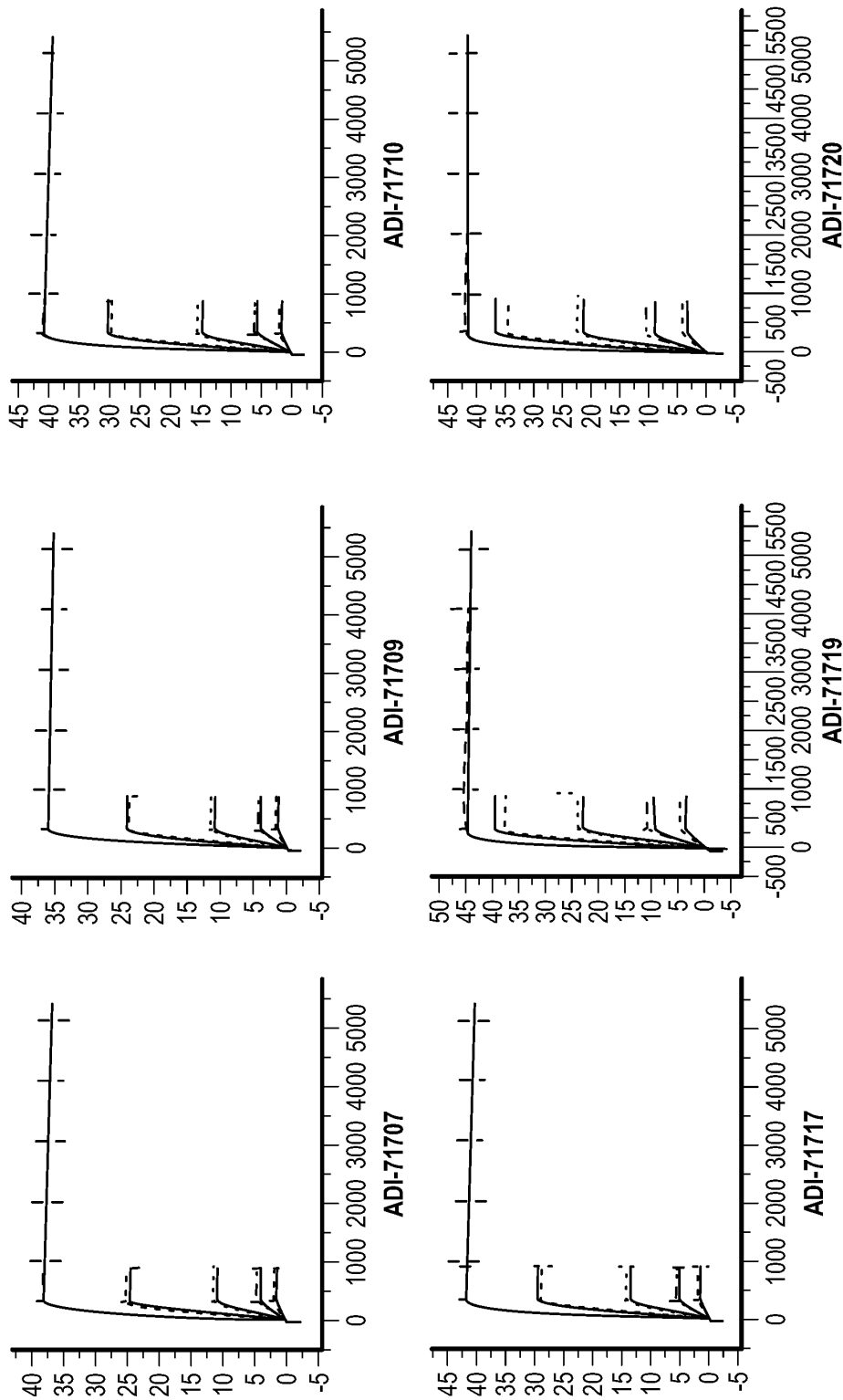


FIG. 41B (Continued)

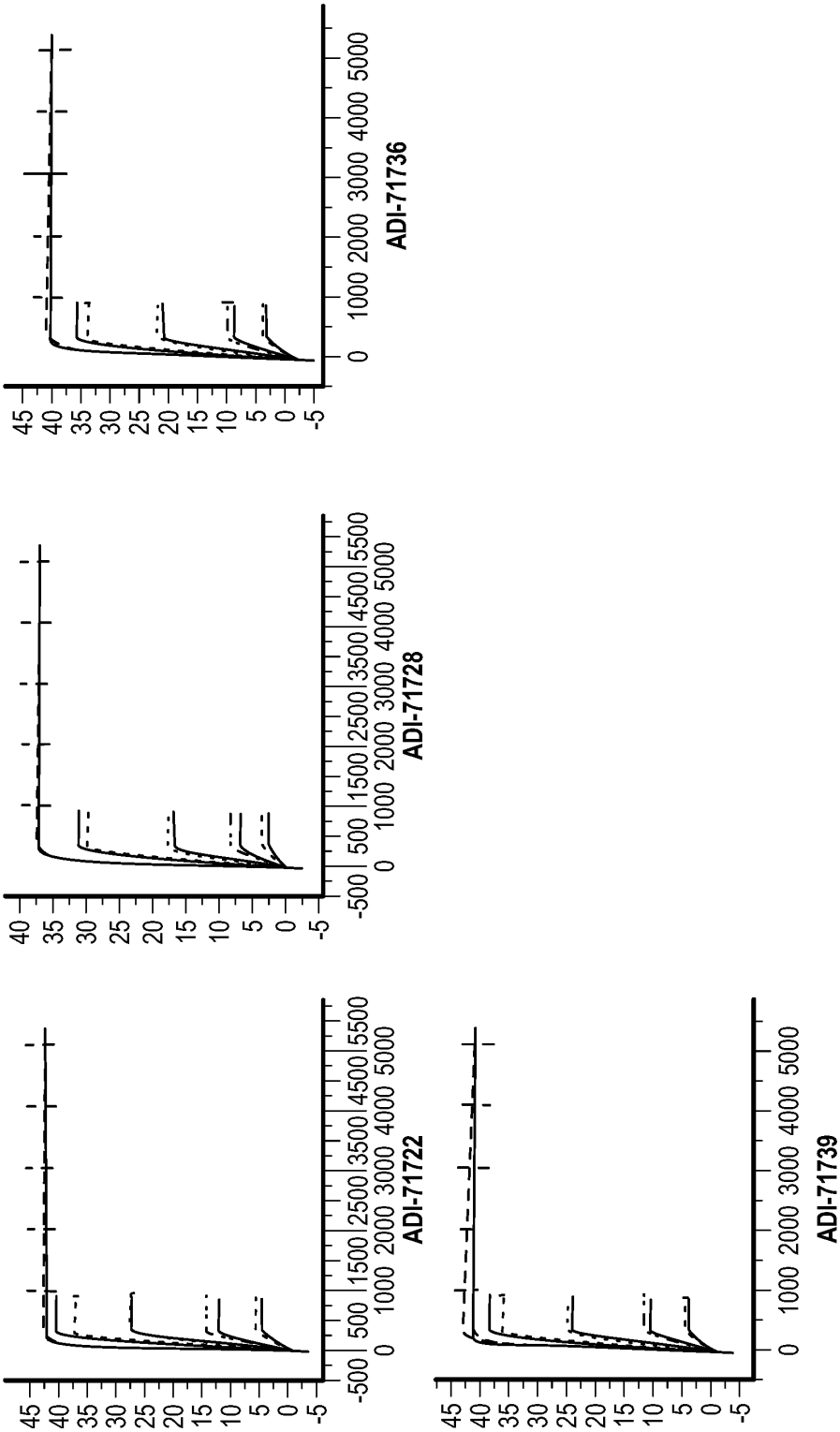


FIG. 41B (Continued)

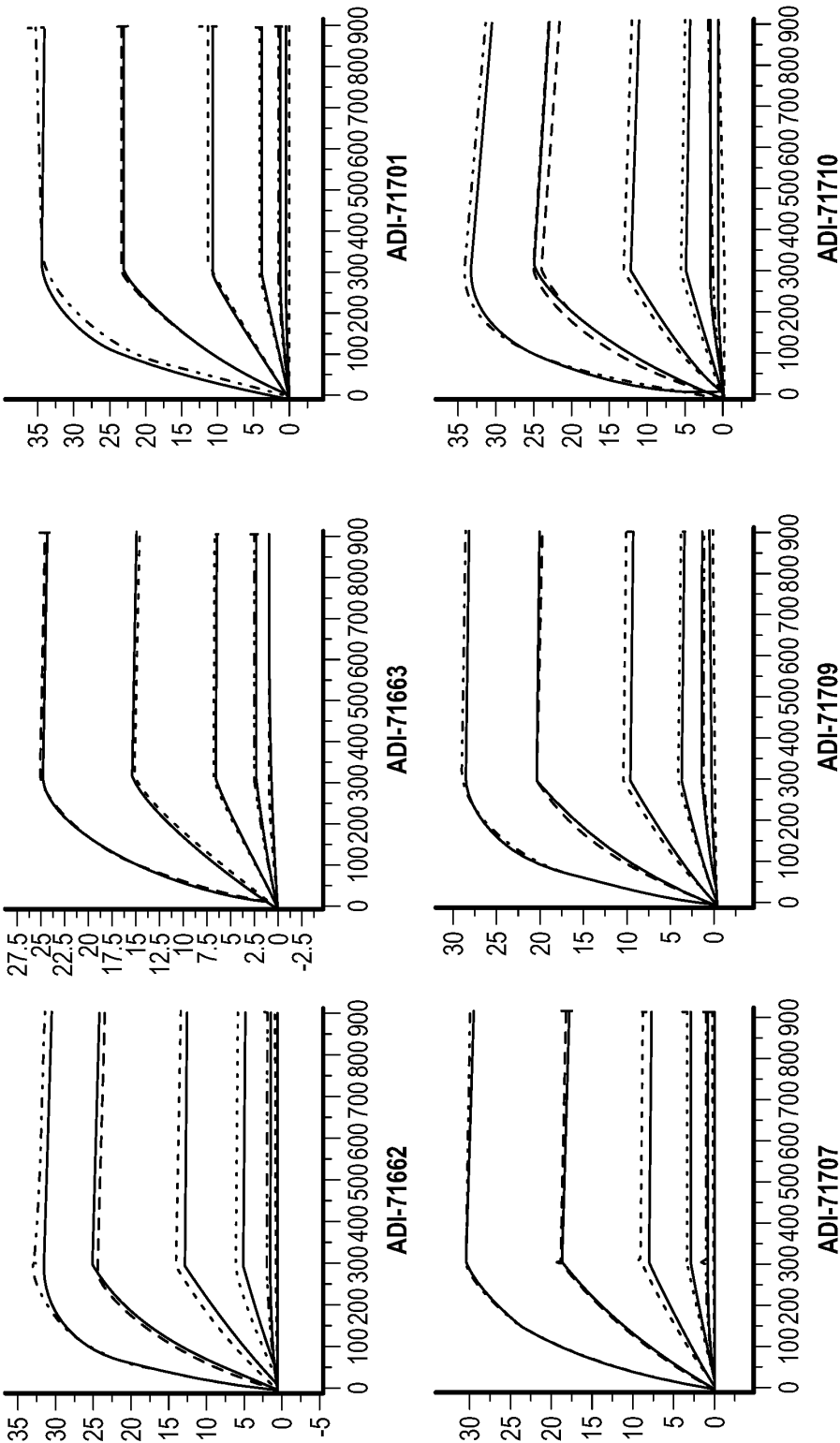


FIG. 41C

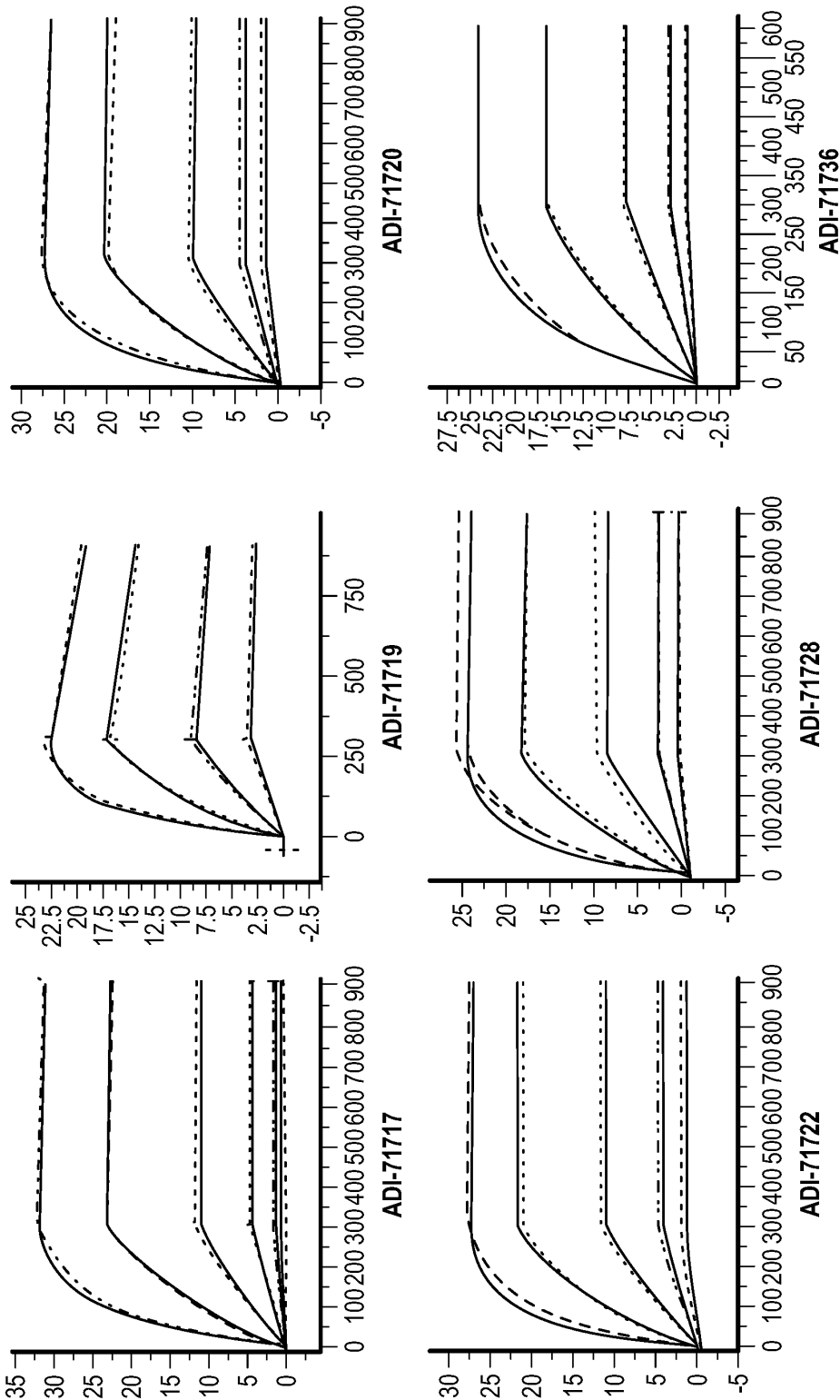


FIG. 41C (Continued)

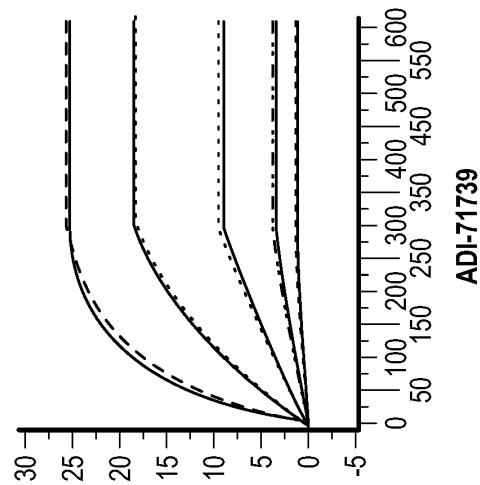


FIG. 41C (Continued)

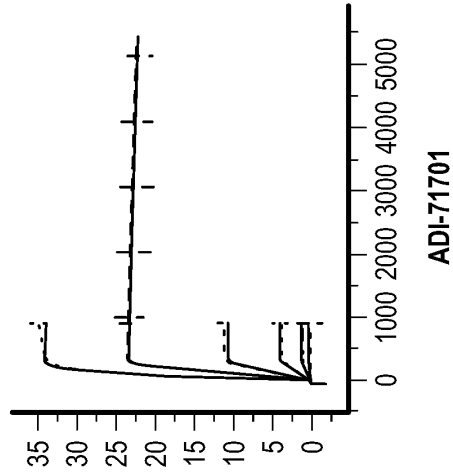
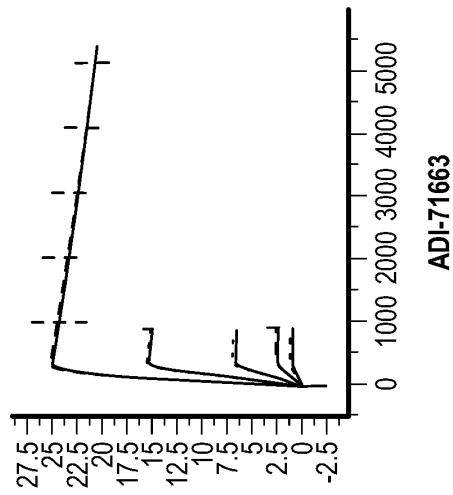
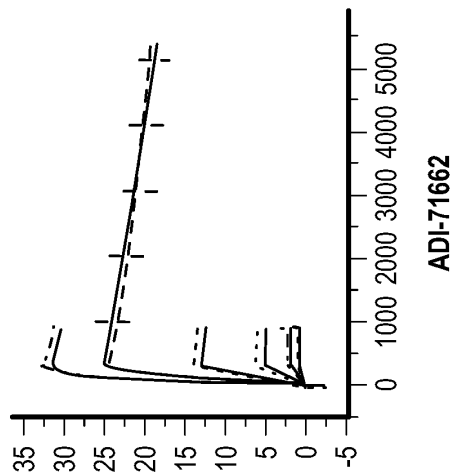


FIG. 41D

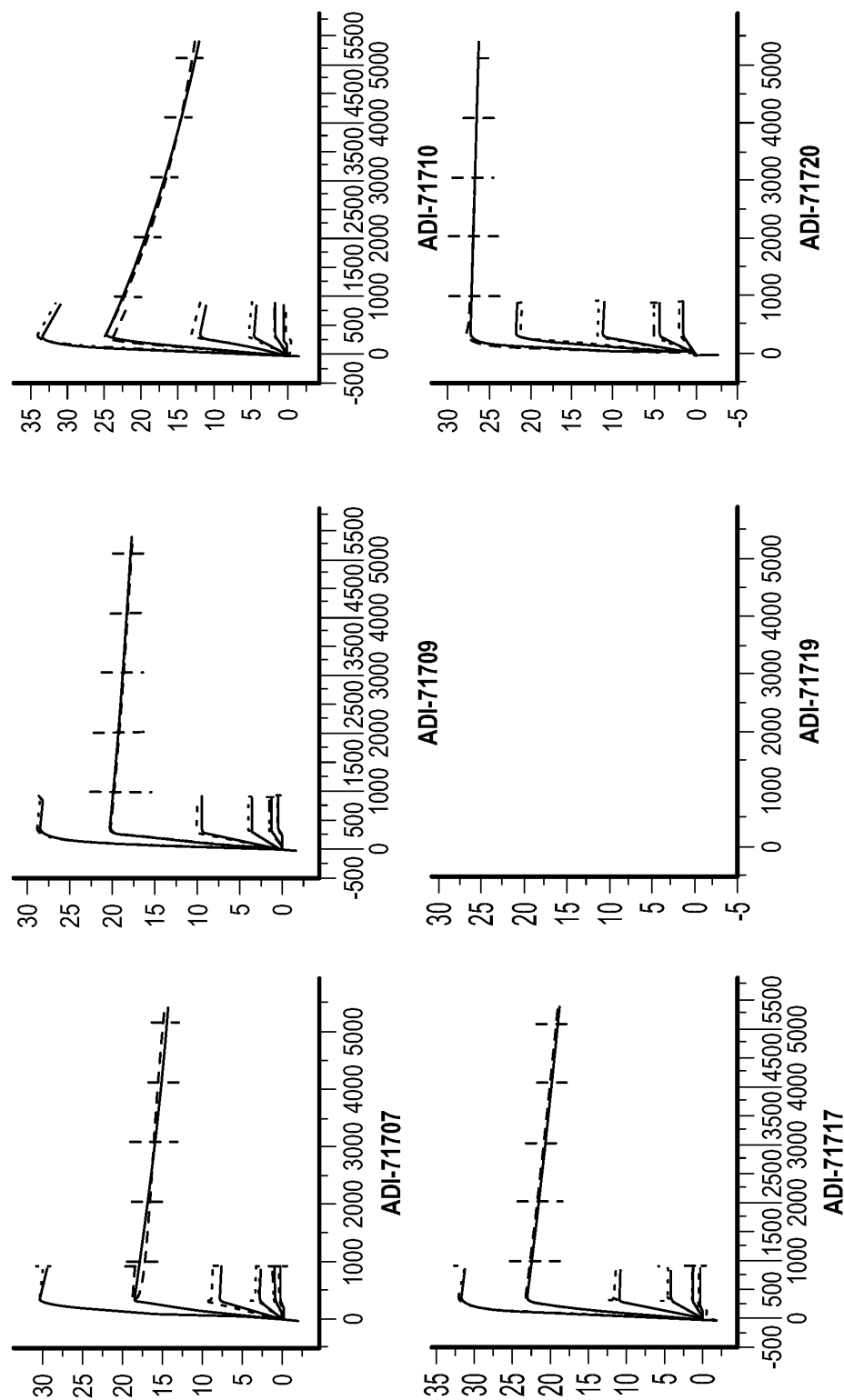


FIG. 41D (Continued)

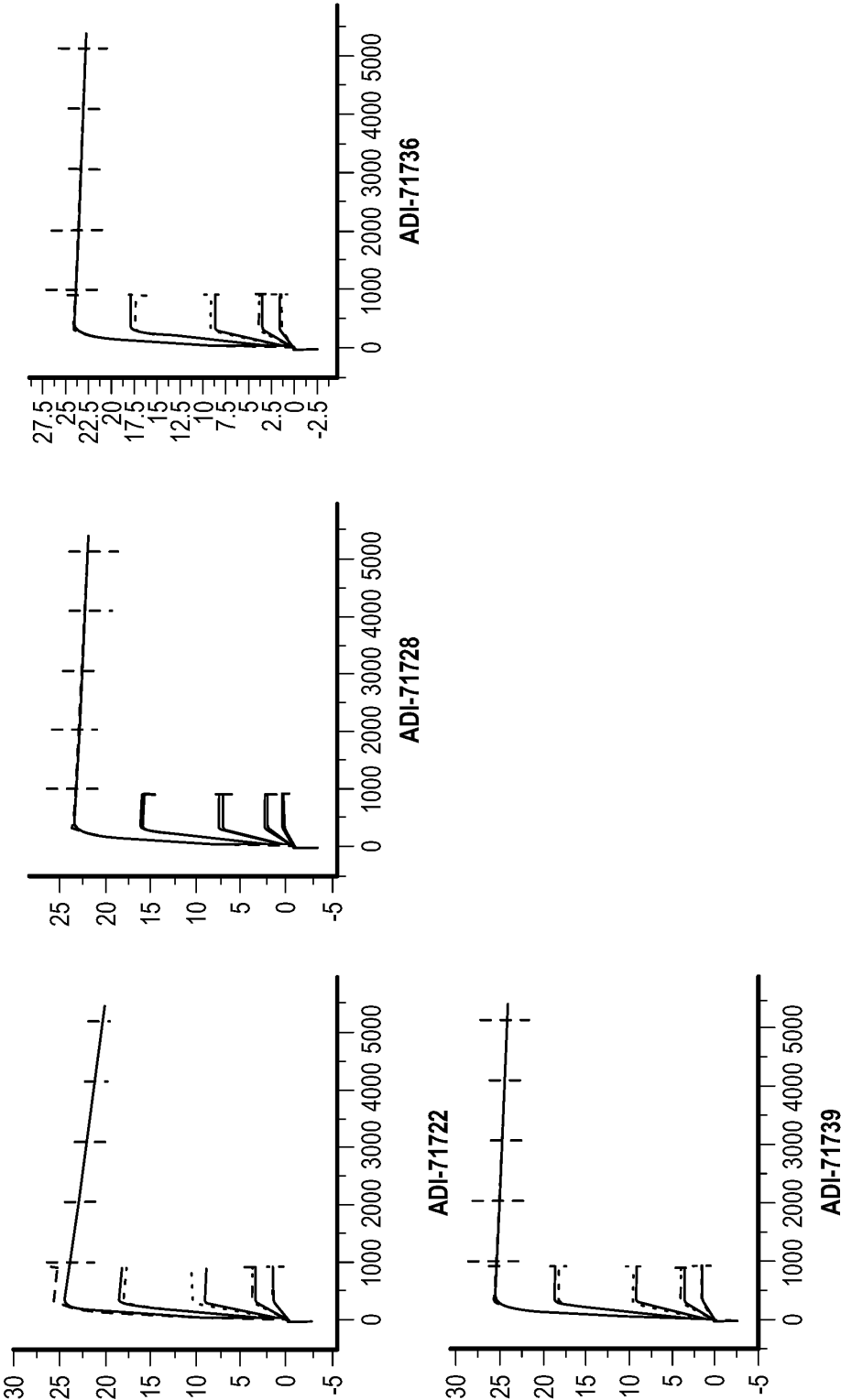


FIG. 41D (Continued)

Figure 42

	Human IL18BP				Cyno IL18BP			
	Fab K _D (M)	kon (1/Ms)	koff (1/s)		Fab K _D (M)	kon (1/Ms)	koff (1/s)	
ADI-71662	6.07E-12	1.65E+06	1.00E-05*		9.19E-11	6.44E+05	5.91E-05	
ADI-71663	5.20E-12	1.92E+06	1.00E-05*		3.74E-11	1.03E+06	3.86E-05	
ADI-71701	8.86E-12	1.13E+06	1.00E-05*		2.27E-11	4.40E+05	1.00E-05*	
ADI-71707	8.68E-12	1.15E+06	1.00E-05*		1.48E-10	3.37E+05	4.99E-05	
ADI-71709	7.98E-12	1.25E+06	1.00E-05*		5.94E-11	4.78E+05	2.84E-05	
ADI-71710	6.28E-12	1.59E+06	1.00E-05*		2.64E-10	5.35E+05	1.41E-04	
ADI-71717	7.21E-12	1.39E+06	1.00E-05*		7.69E-11	5.09E+05	3.91E-05	
ADI-71719	3.77E-12	2.65E+06	1.00E-05*		4.88E-11	5.23E+06	2.55E-04	
ADI-71720	3.73E-12	2.68E+06	1.00E-05*		2.09E-11	1.62E+06	3.40E-05	
ADI-71722	2.58E-12	3.87E+06	1.00E-05*		5.19E-12	1.93E+06	1.00E-05*	
ADI-71728	4.51E-12	2.21E+06	1.00E-05*		2.38E-11	1.65E+06	3.94E-05	
ADI-71736	3.65E-12	2.74E+06	1.00E-05*		9.51E-12	1.37E+06	1.30E-05	
ADI-71739	3.09E-12	3.24E+06	1.00E-05*		7.10E-12	1.55E+06	1.10E-05	

* Reached koff limit for 85-minute dissociation

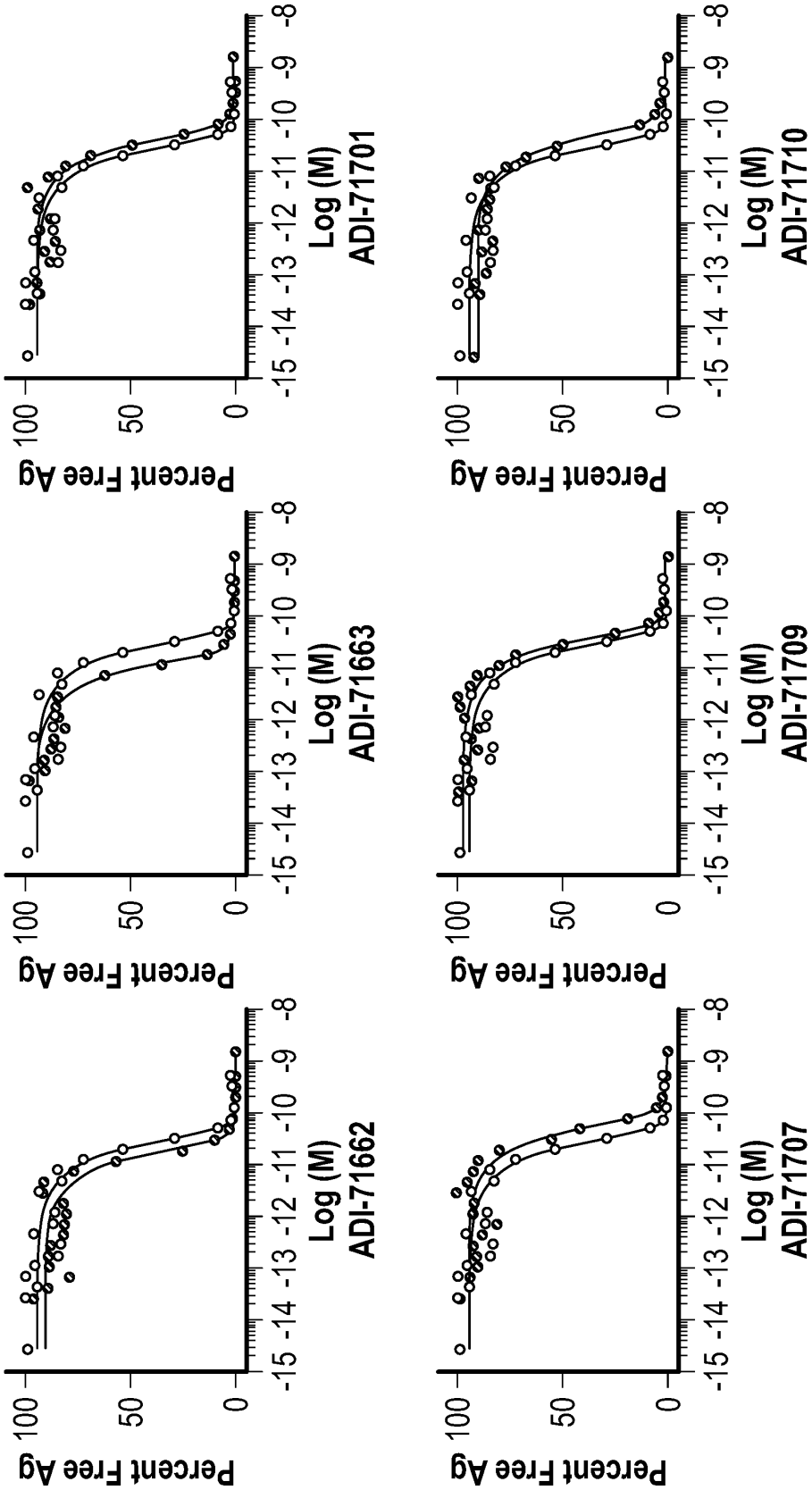


FIG. 43A

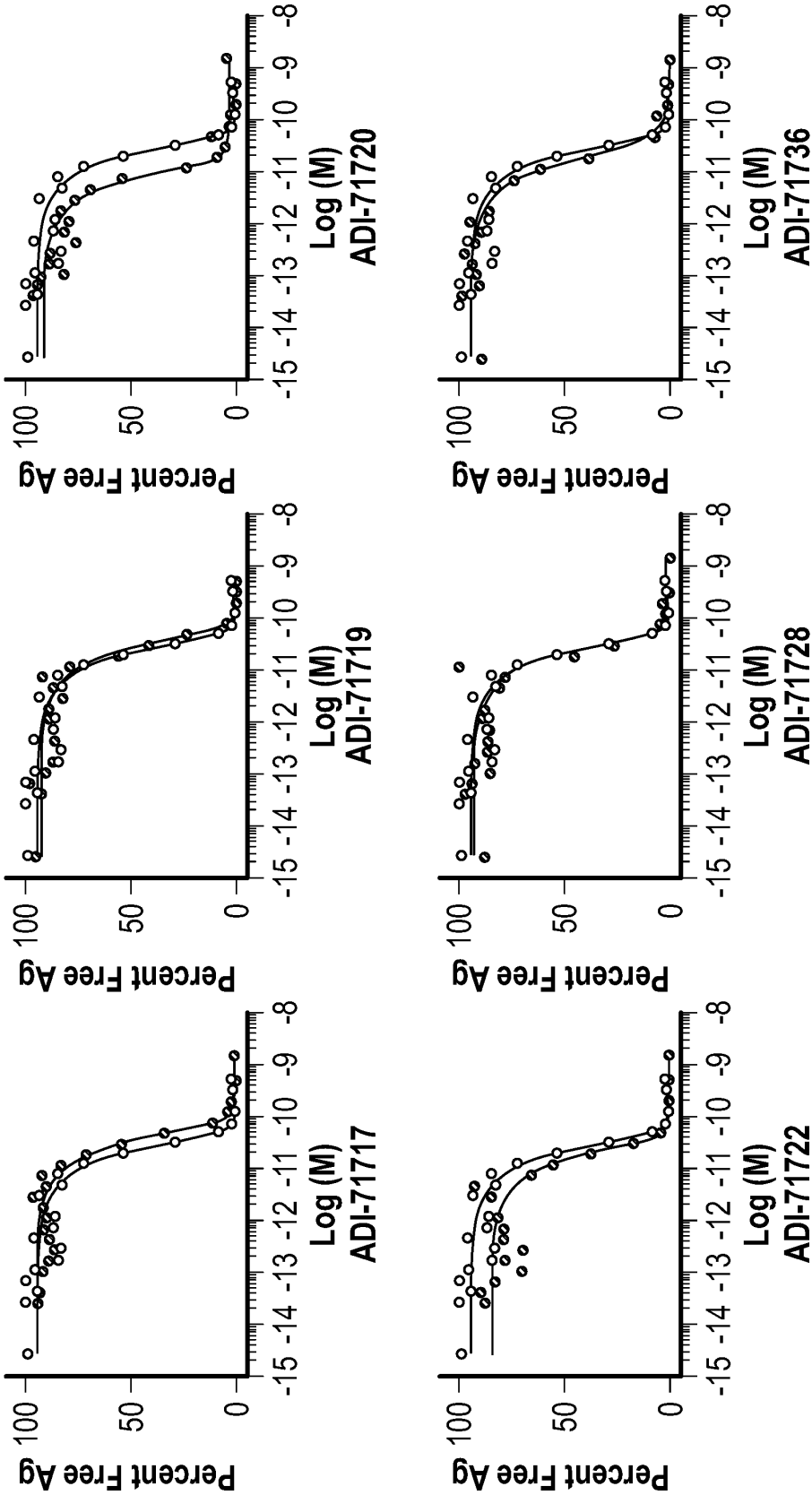


FIG. 43A (Continued)

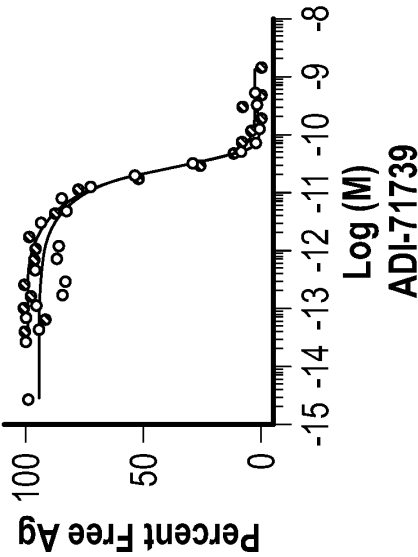


FIG. 43A (Continued)

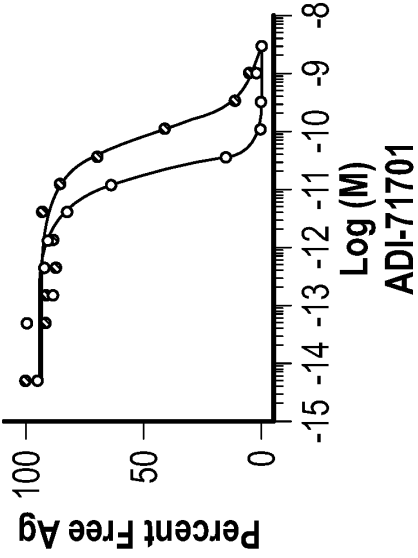
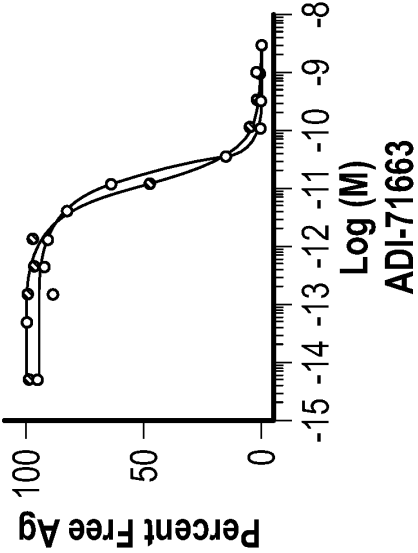
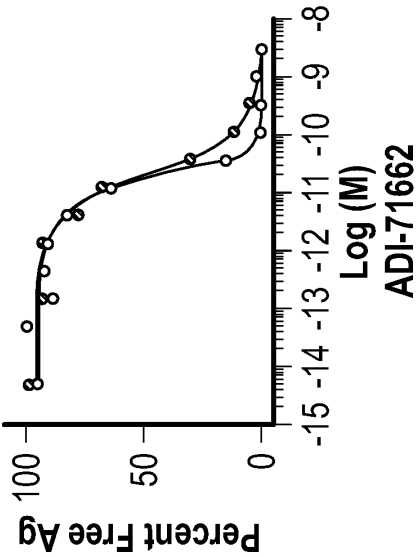


FIG. 43B

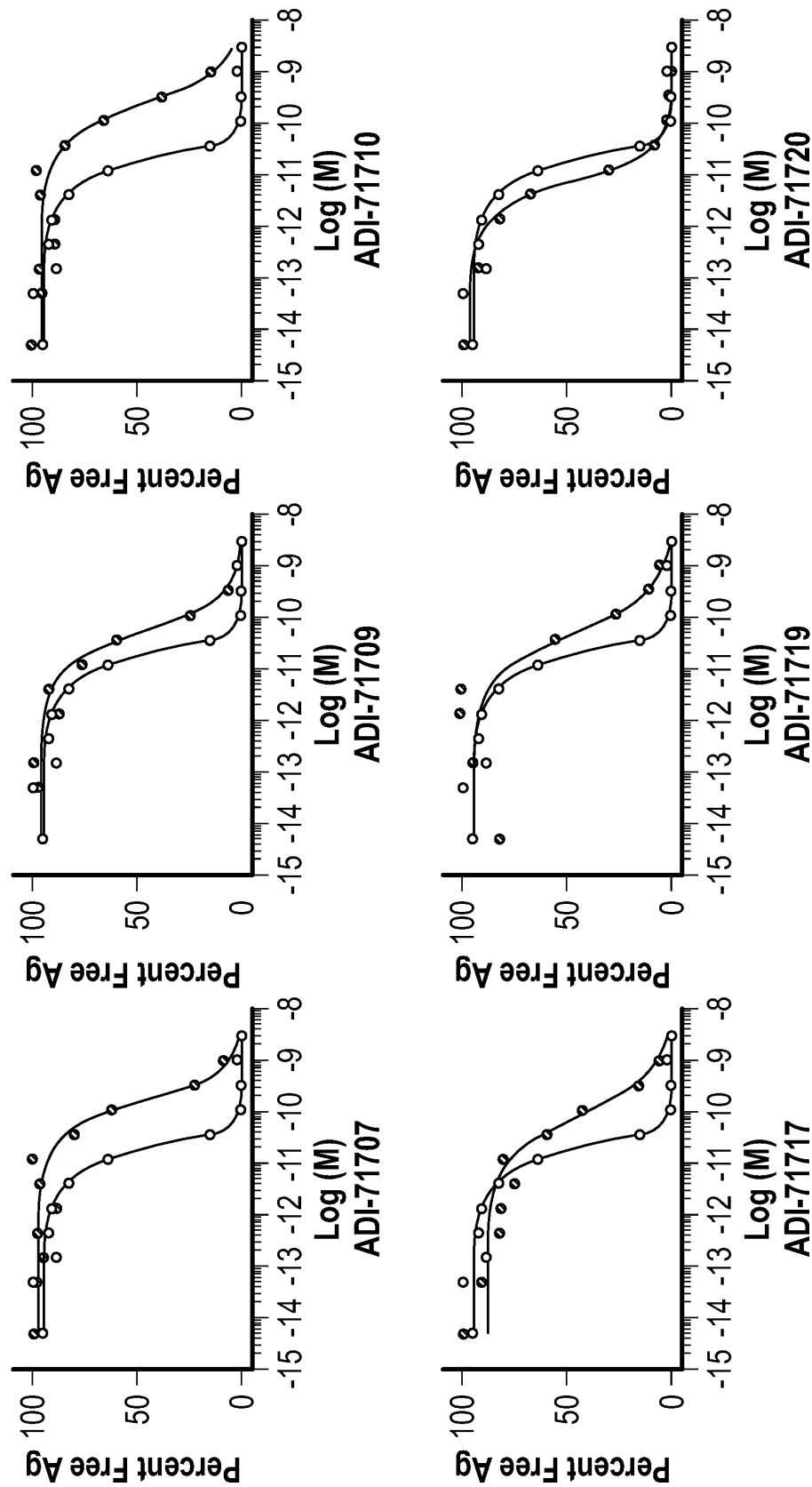


FIG. 43B (Continued)

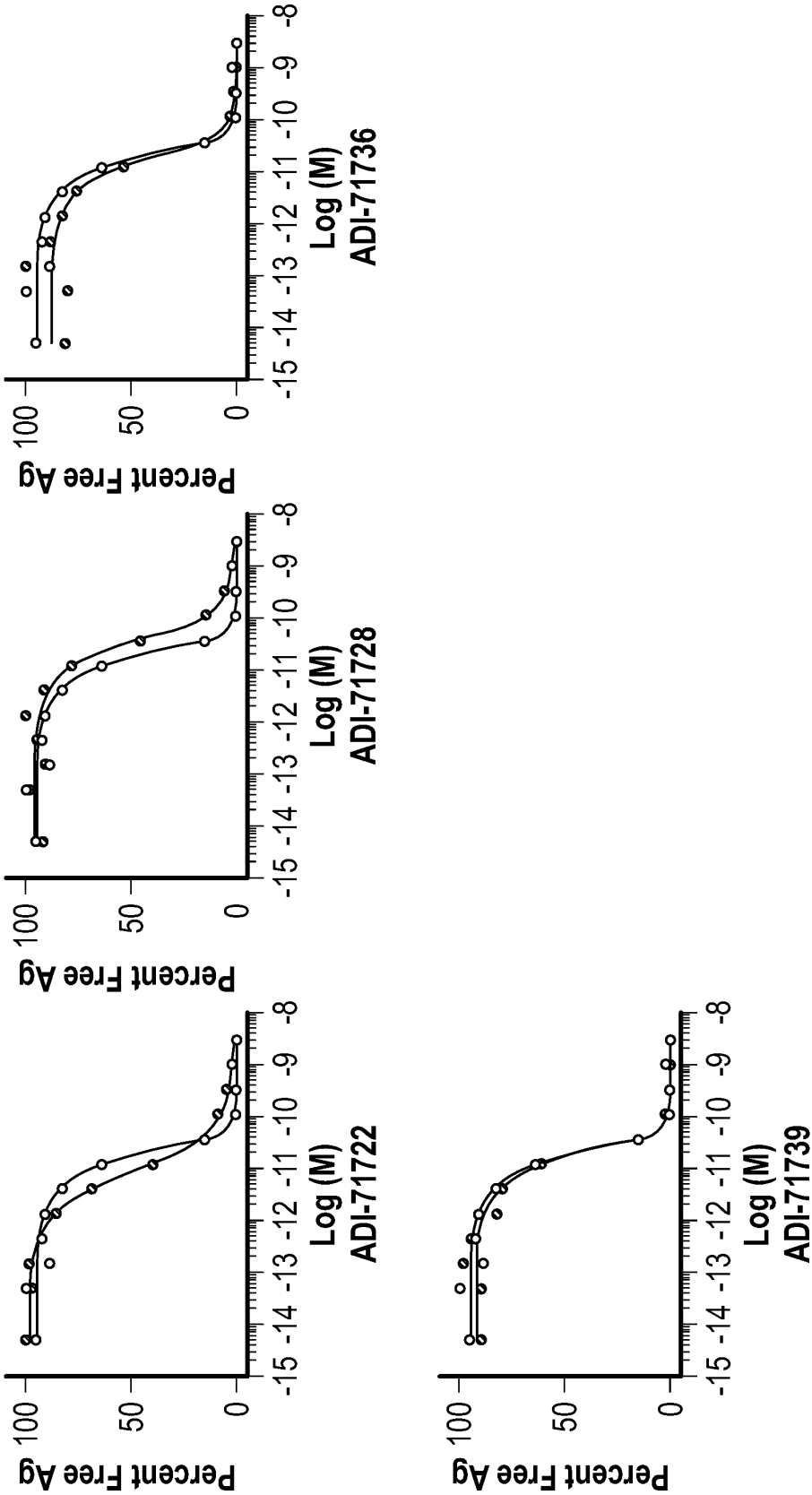


FIG. 43B (Continued)

Figure 44

	Fab K_D (M) human IL18BP	Fab K_D (M) cyto IL18BP
ADI-71662	3.10E-13	1.20E-11
ADI-71663	2.80E-13	3.60E-12
ADI-71701	1.20E-12	3.90E-11
ADI-71707	2.10E-12	5.40E-11
ADI-71709	1.30E-12	2.80E-11
ADI-71710	2.80E-12	1.40E-10
ADI-71717	1.50E-12	8.80E-11
ADI-71719	1.80E-12	4.20E-11
ADI-71720	2.90E-13	2.80E-12
ADI-71722	5.00E-13	6.80E-12
ADI-71728	3.60E-13	1.10E-11
ADI-71736	3.30E-12	3.40E-12
ADI-71739	1.00E-12	2.30E-12

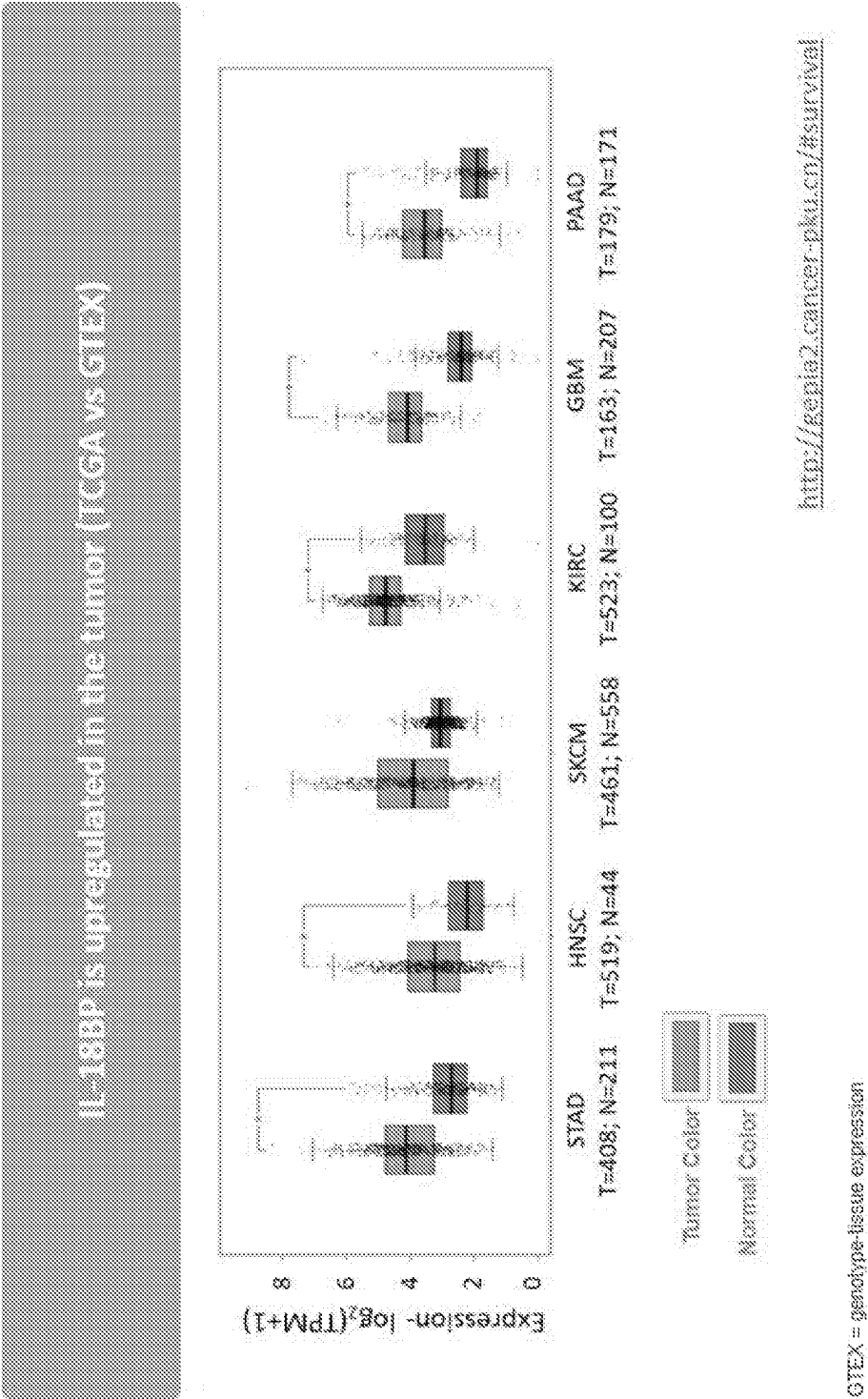
Figure 45

Human IL18-IL18BP K _D (M)	Cyno IL18-IL18BP K _D (M)
5.60E-13	1.20E-12

Figure 46

Property	Characteristics
Specificity	Human αIL-18BP species cross-reactivity with cynomolgus monkey
Isotype	Fully human IgG4 stabilized hinge S228P
Activity	Blocker antibody, enhances T/ NK cell activation works as single agent and in combination with anti-PD1 in <i>in vitro</i>
Affinity	Human: Below 1pM

Figure 47



scRNA data from CRC patients - Myeloid populations

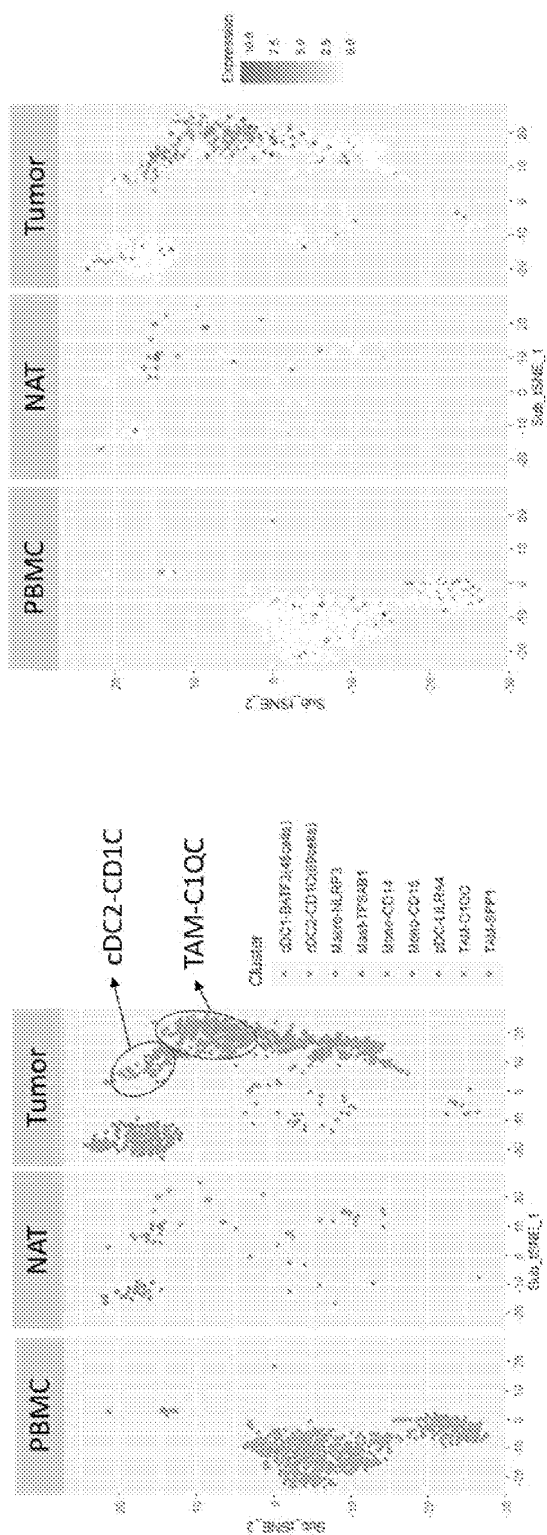


Figure 49A-49B

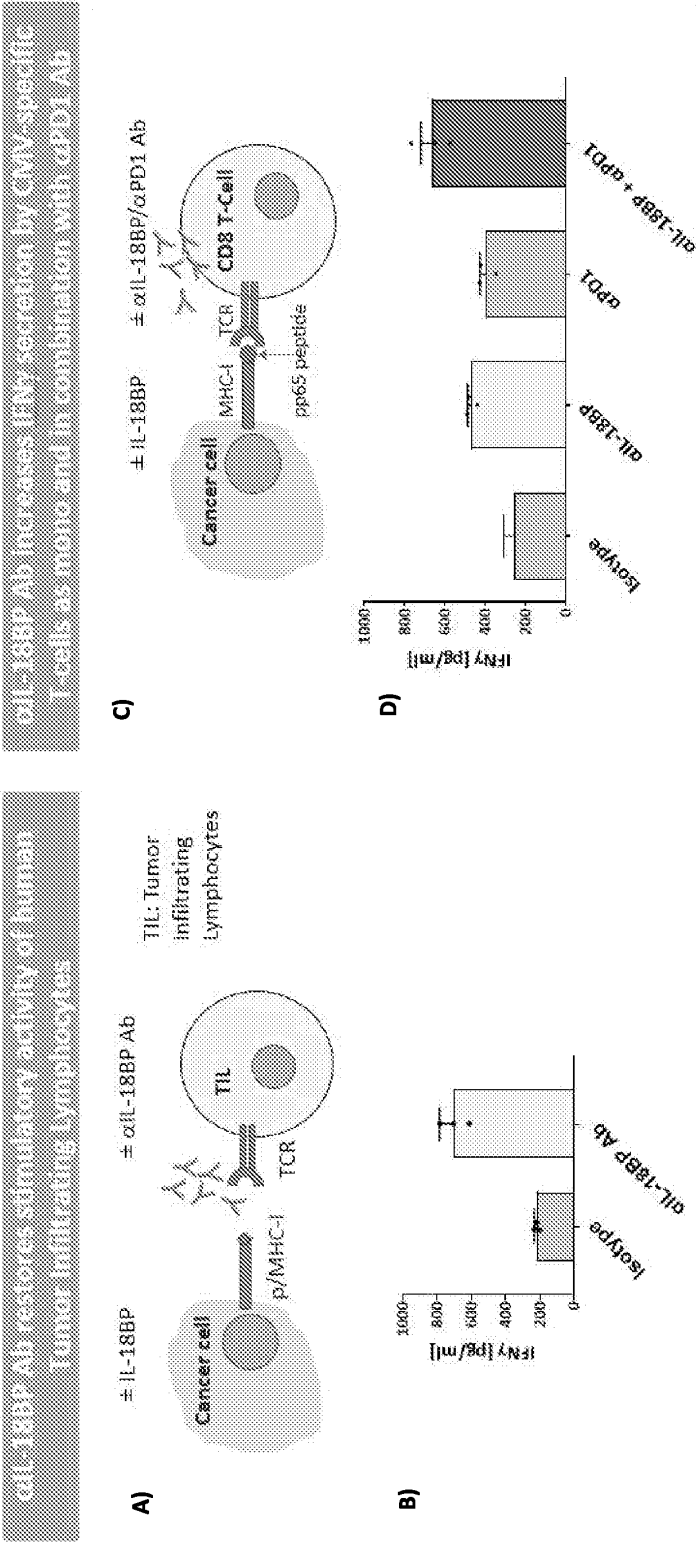


Figure 50A-50B

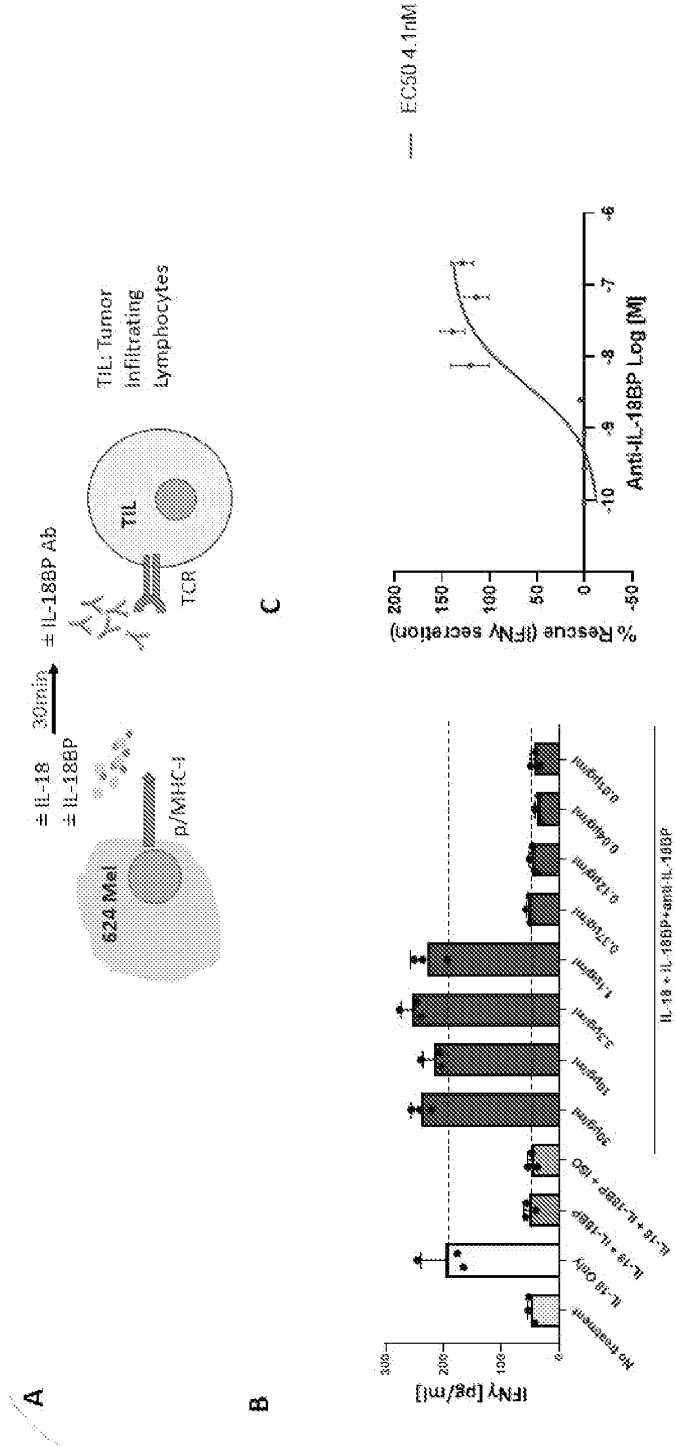
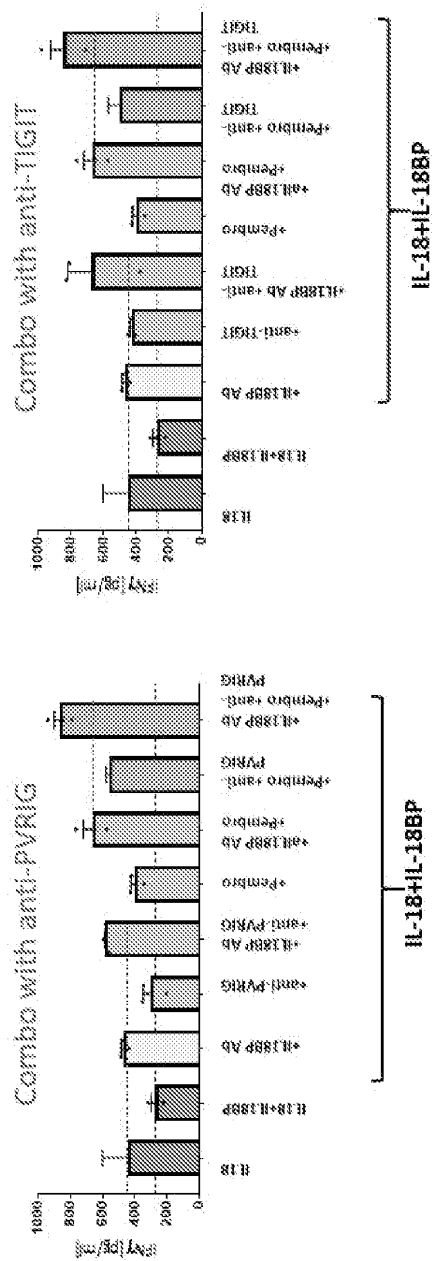
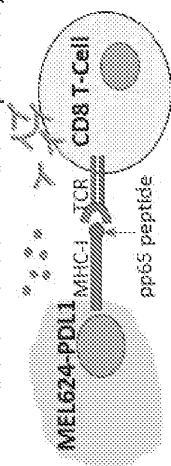


Figure 51A-51B

Anti-IL18BP antibody increased IFN γ secretion by CMV-specific T-cells as mono and in combination with anti-pVRIG/anti-TIGIT/Pembrolizumab

 $\pm$ IL-18+IL-18BP $\pm$ Ab-722/Pembro./anti-PVRIG/anti-TIGIT

Potential combination of IL-18BP, PD-1 and DNAM-1 axis blockade

Figure 52

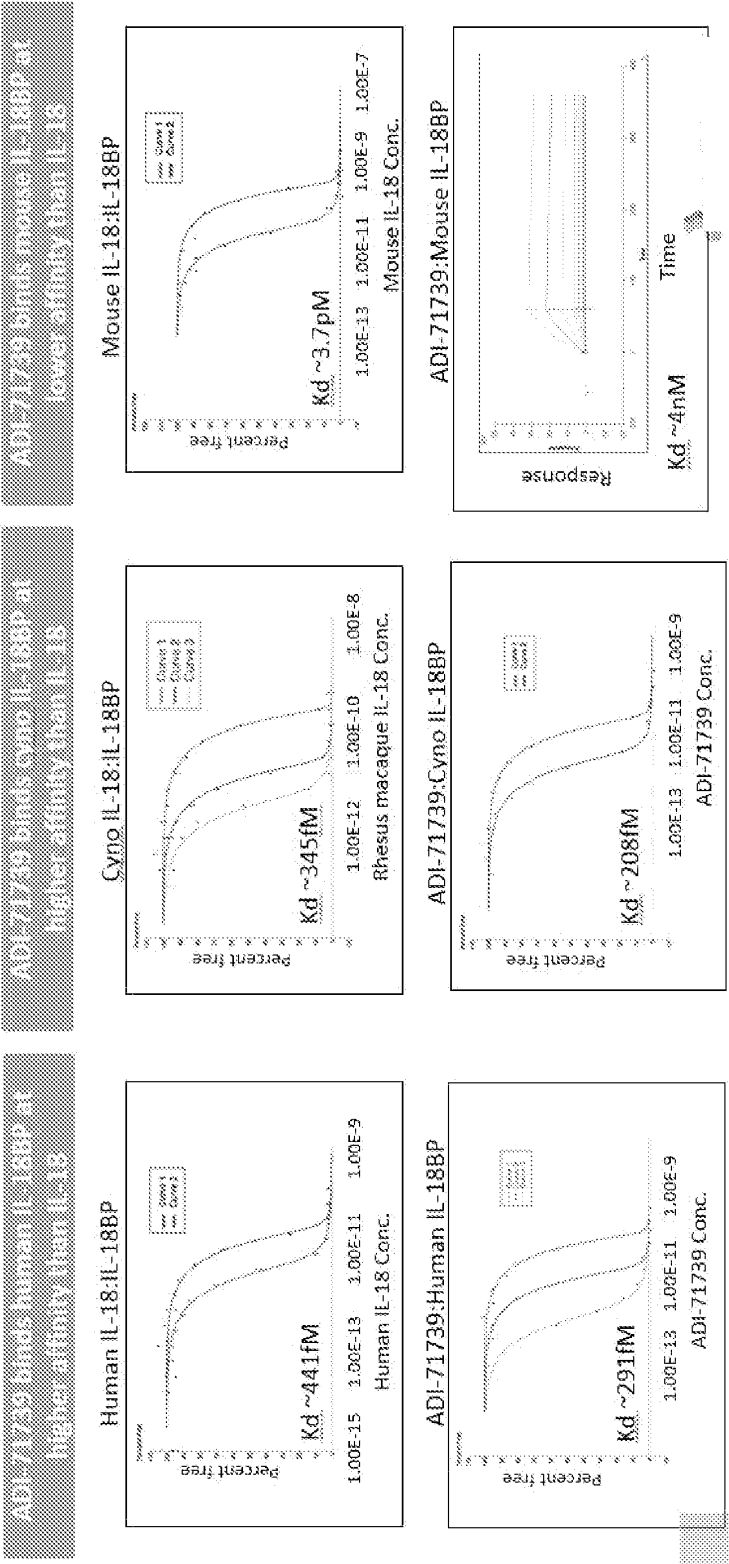


Figure 53

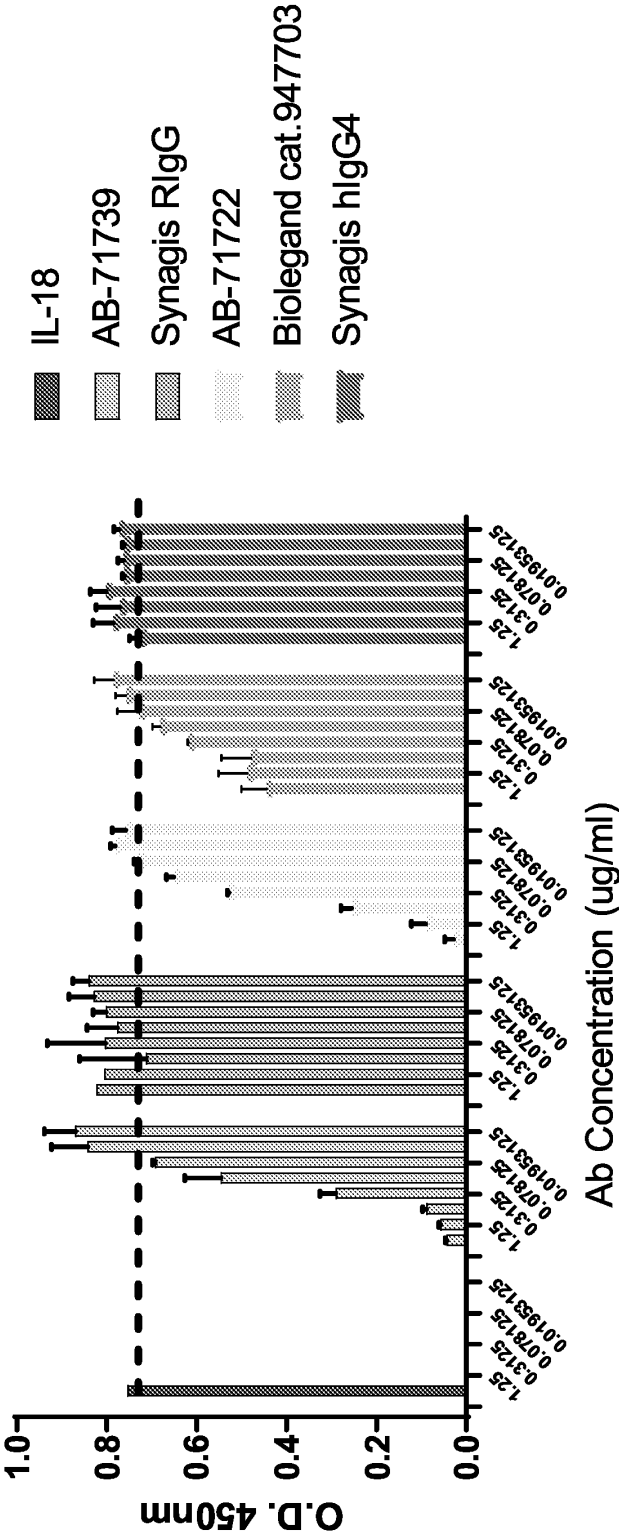


Figure 54

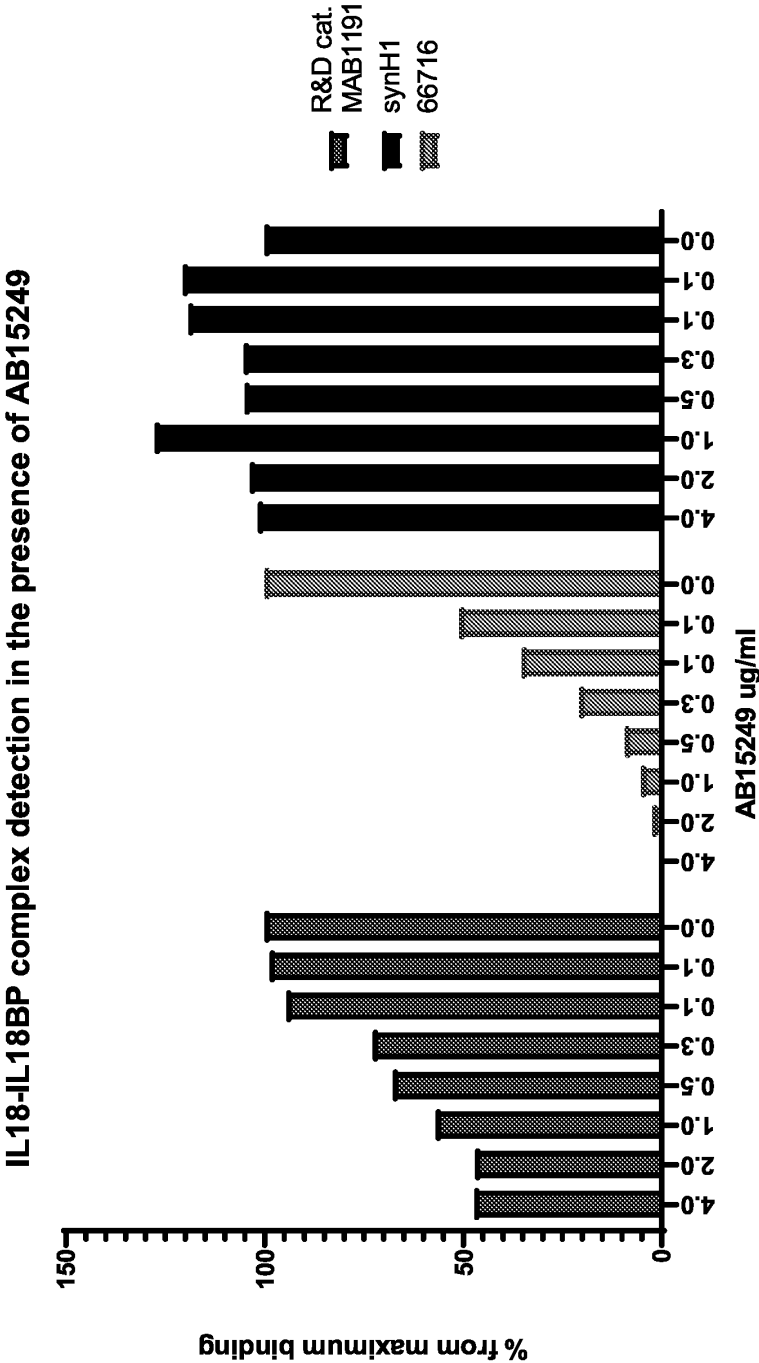


Figure 55

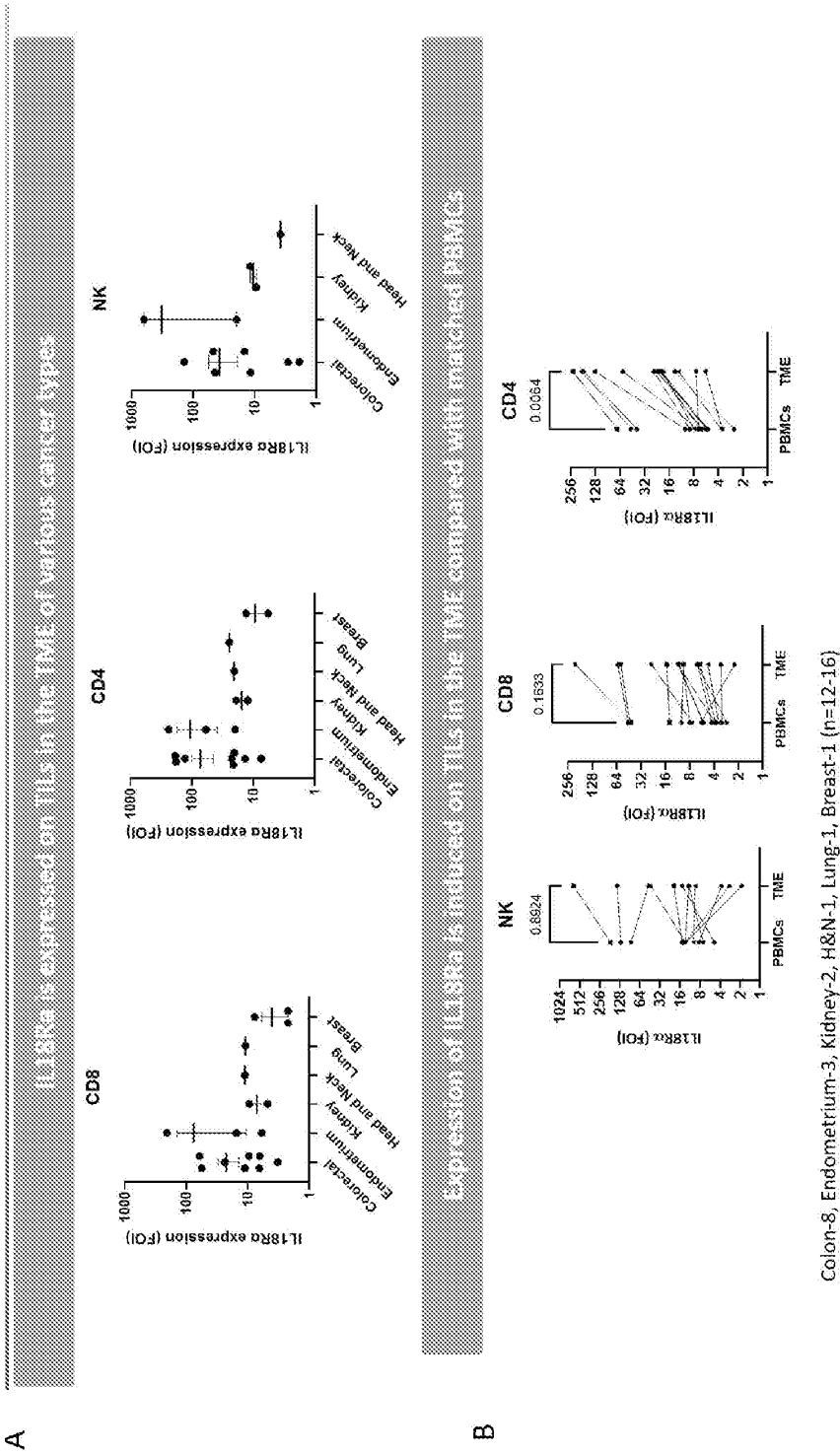


Figure 56

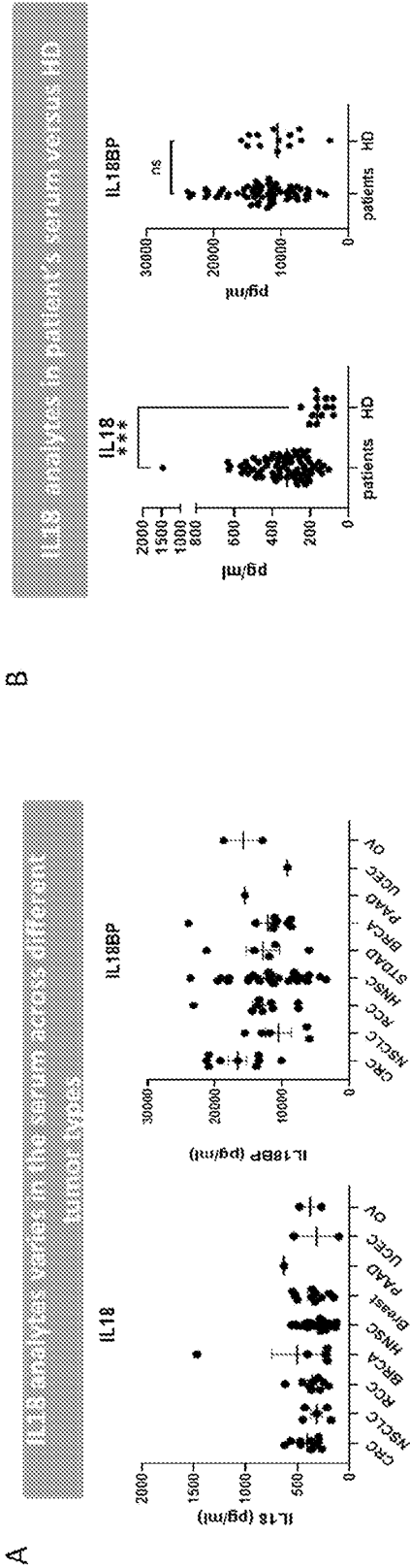


Figure 57

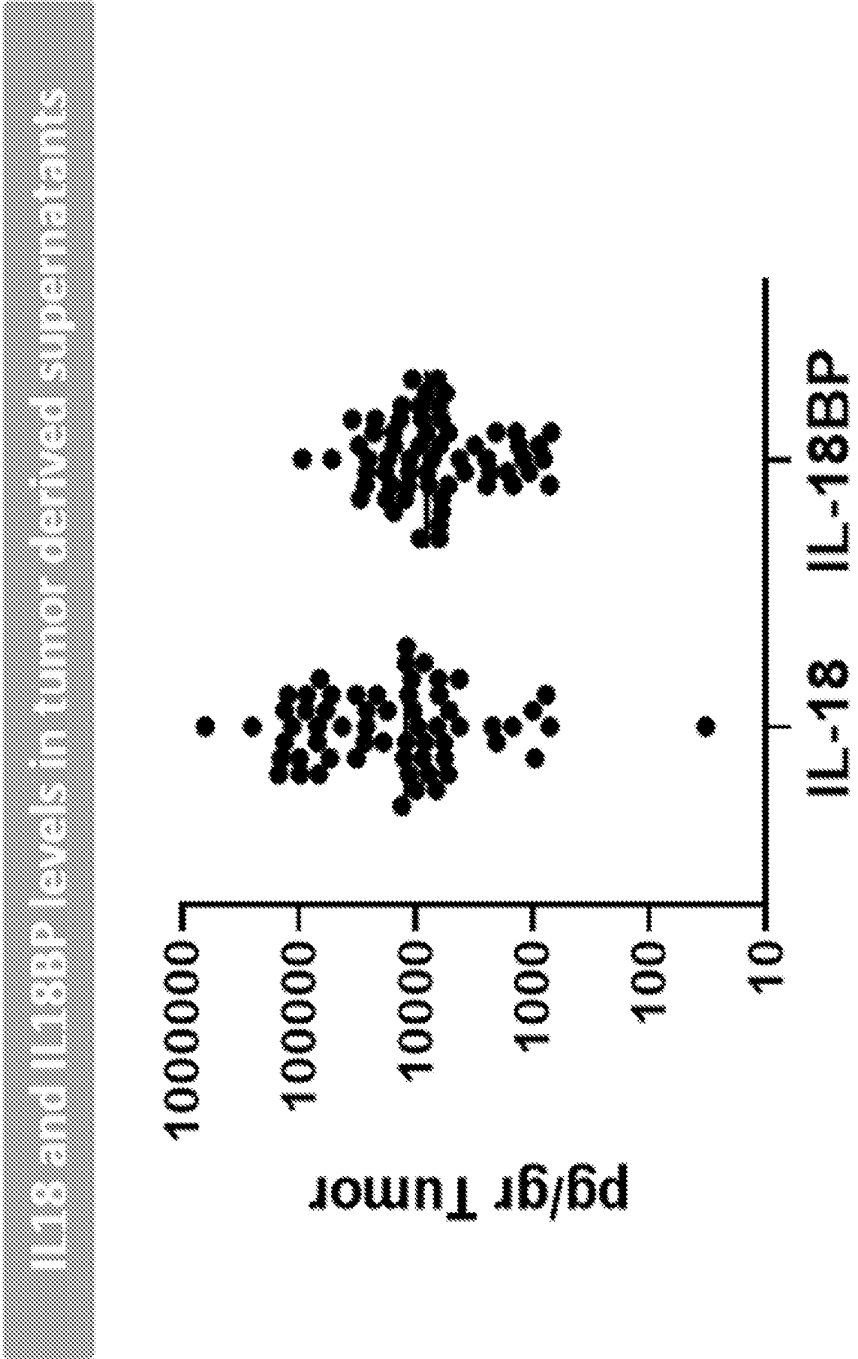


Figure 58

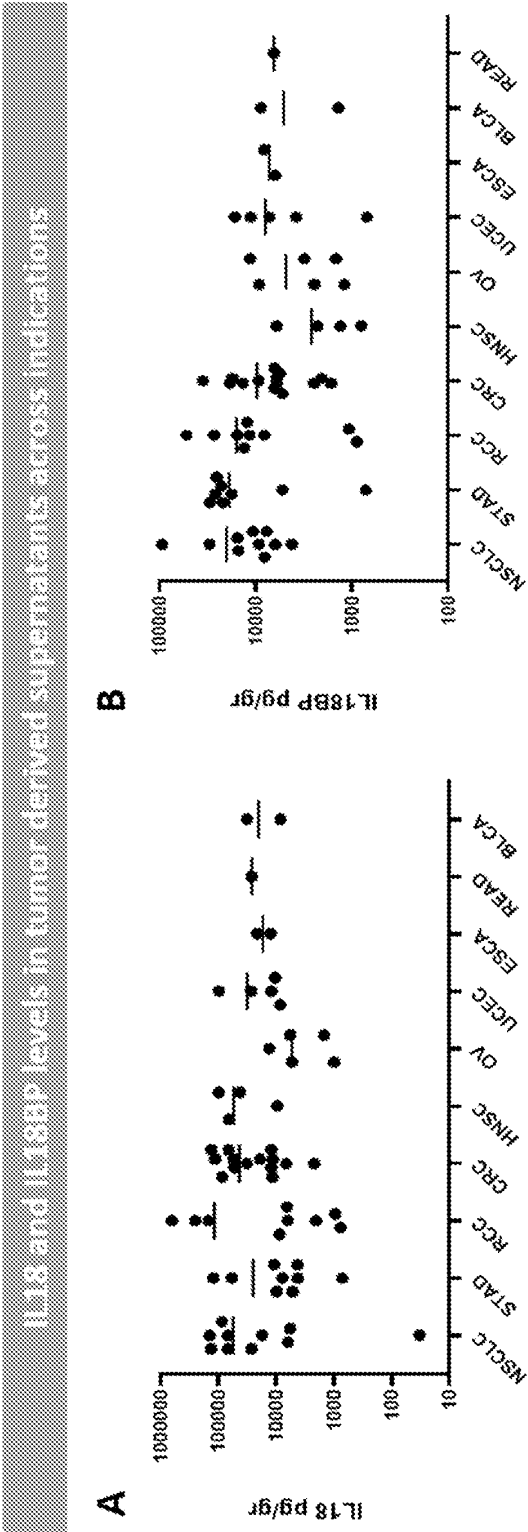


Figure 59

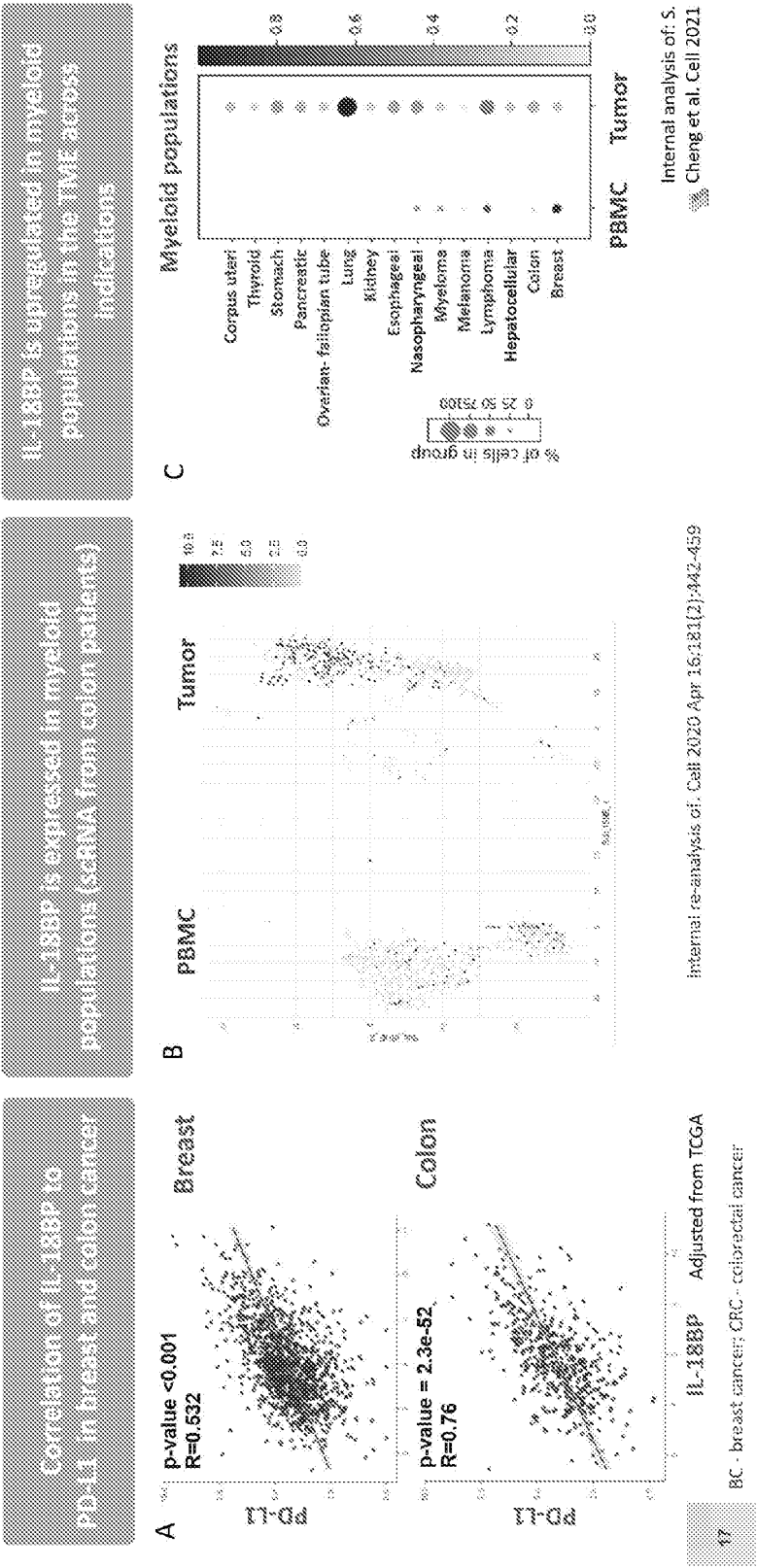


Figure 60

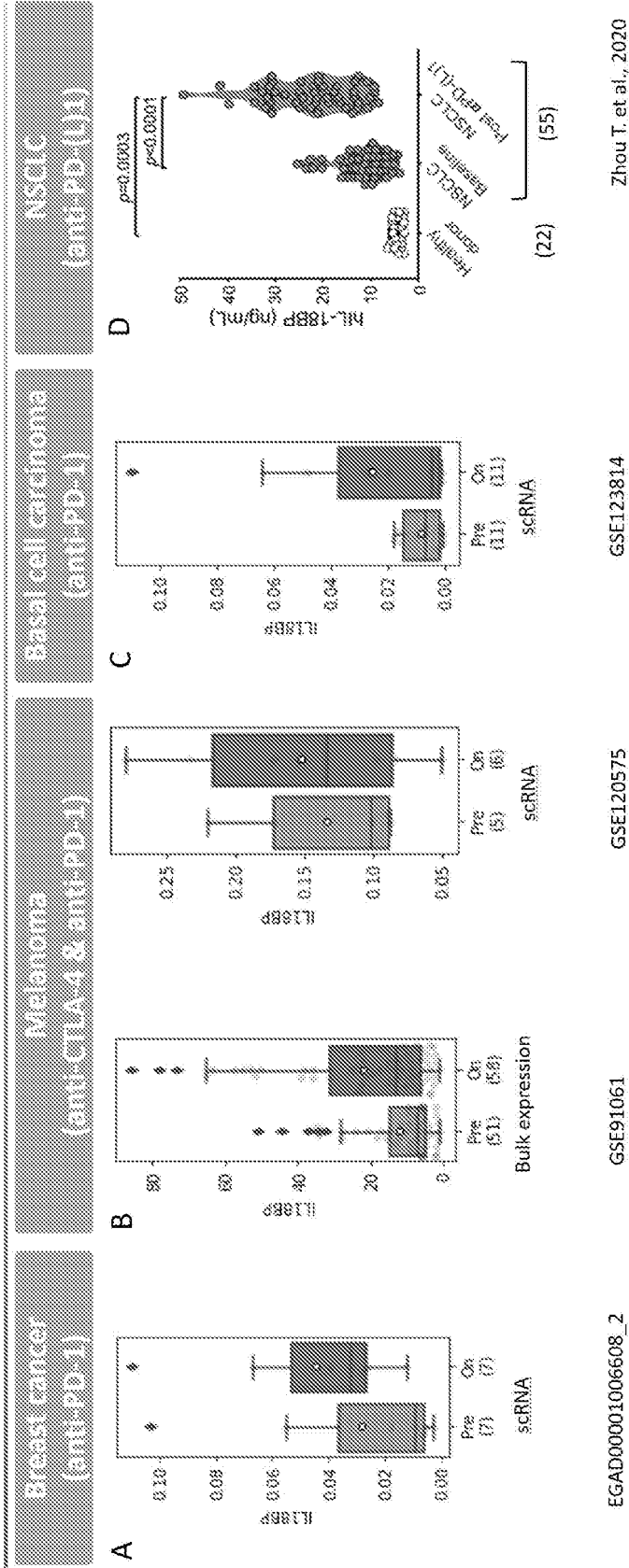
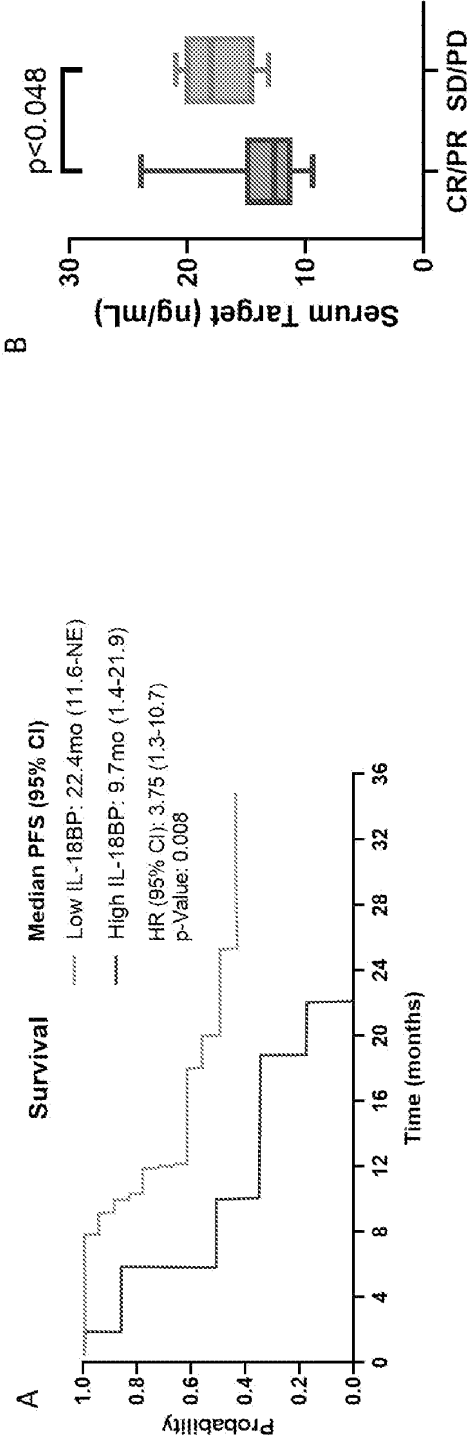


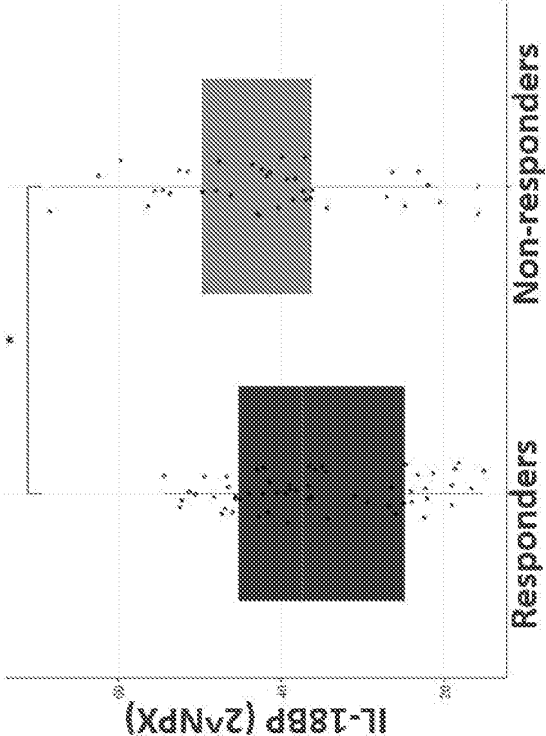
Figure 61

High levels of IL-18BP are associated with poor objective responses and PFS to pembrolizumab + lenvatinib combo treatment (RCC)



Adjusted from: Lee CH. Et al. KN146 biomarker, ESMO, 2020, poster 719P

Figure 62



Analyzed from: Mehta A. et al 2022

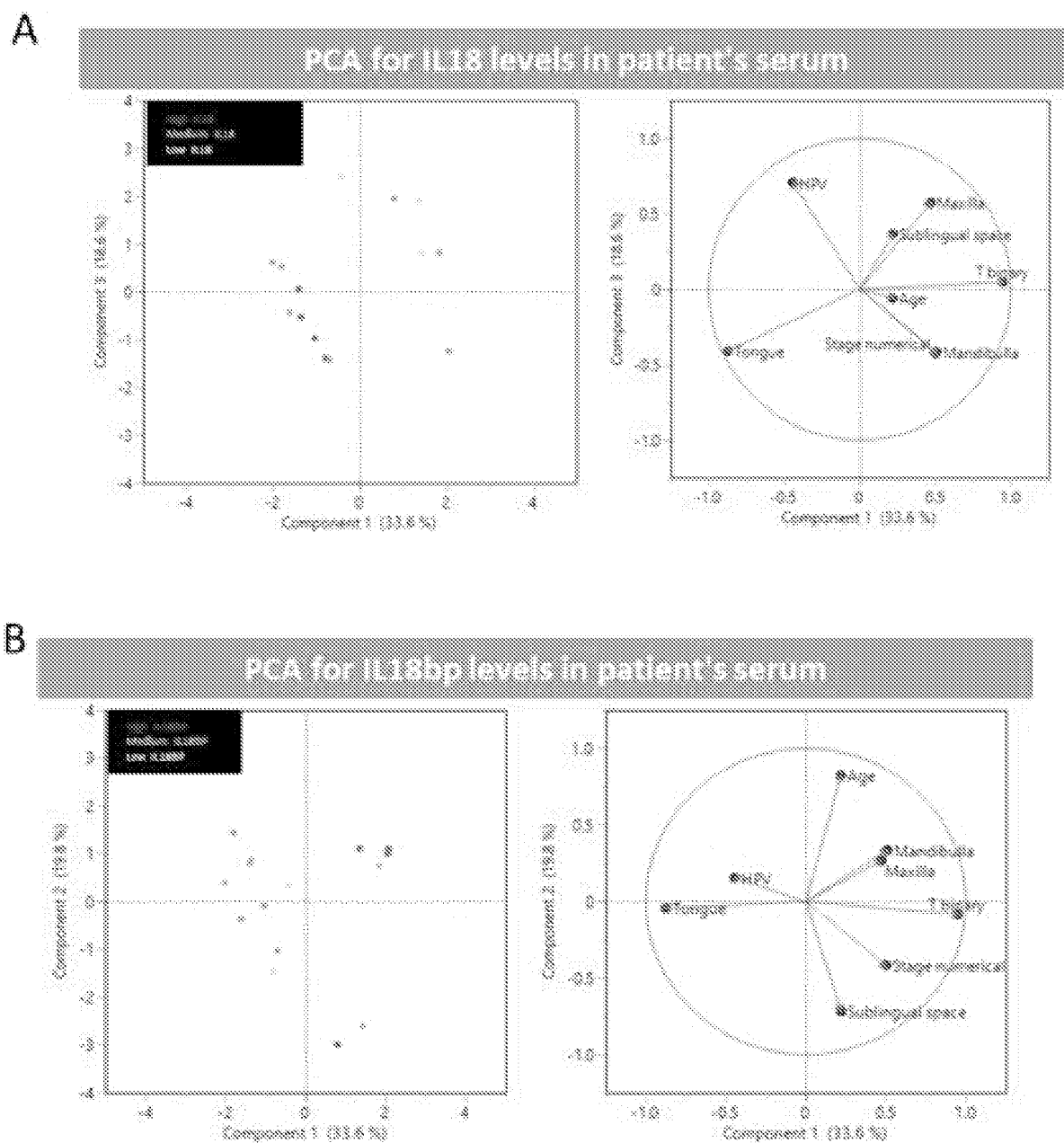
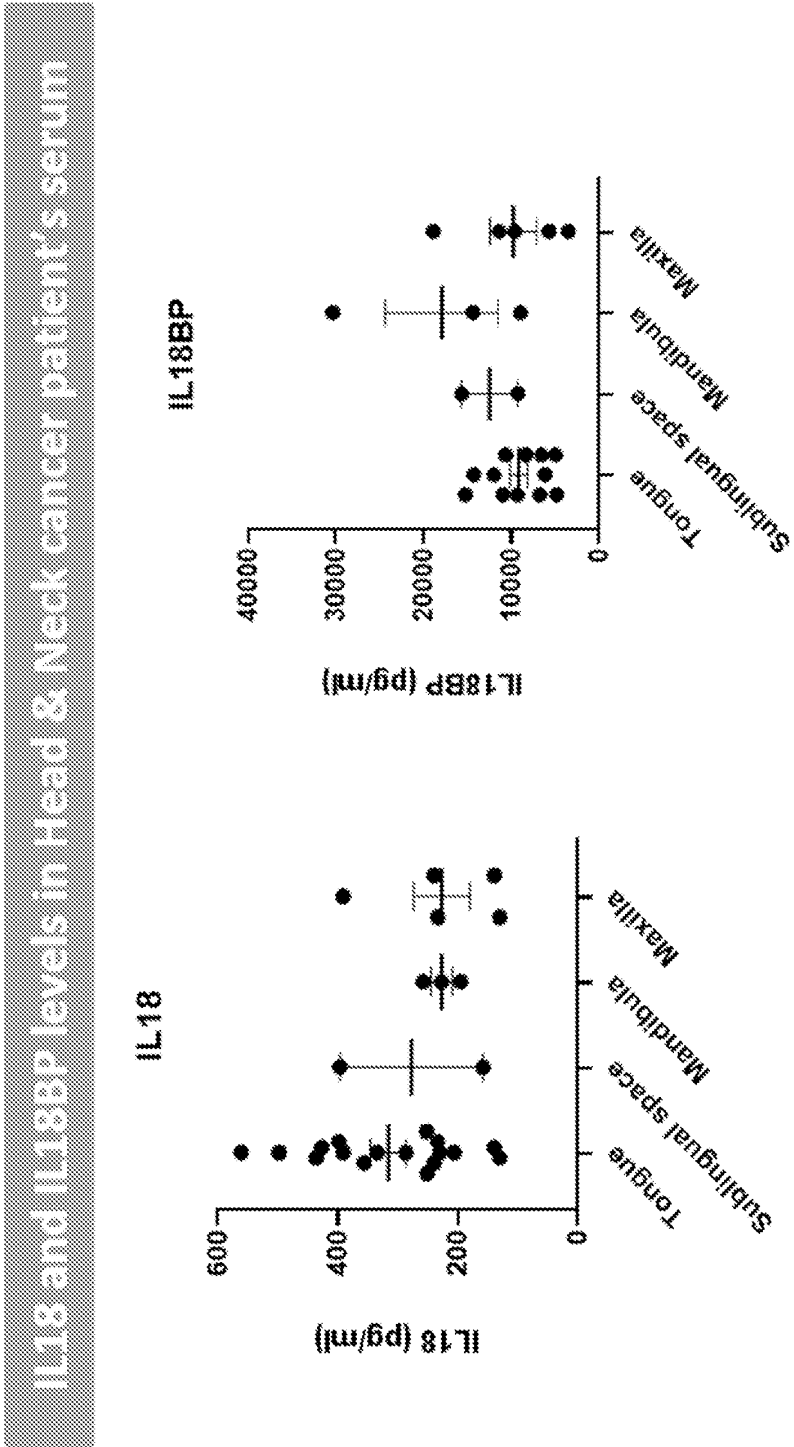
Figure 63

Figure 64



Average Plasma levels of IL18BP and IL18 at Baseline are Higher in Patients Responding to Therapy

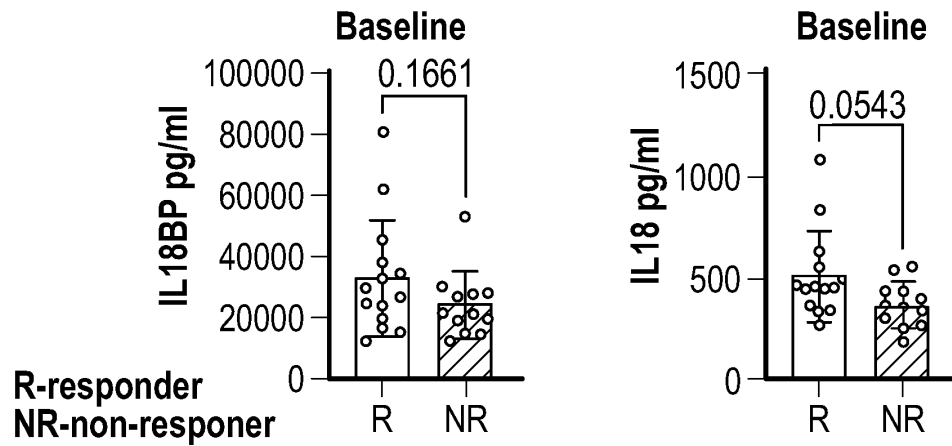


FIG. 65A

IL18 and IL18BP levels in Plasma Increase in Non-responding Patients Following Single Treatment with Anti-PD-1

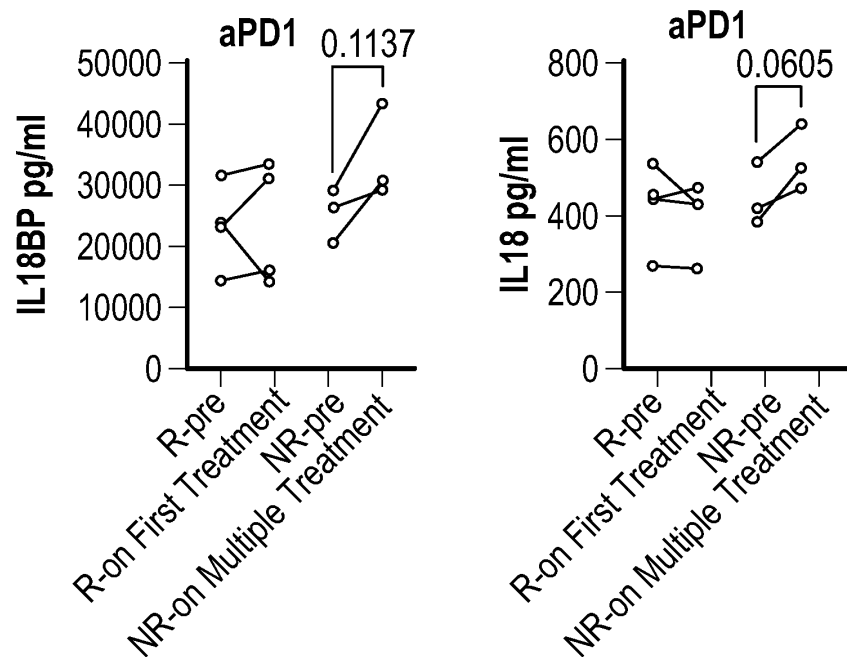


FIG. 65B

IL18 and IL18BP Levels in Plasma Increase in Responding Patients Following Single Treatment with Anti-PD-1+Chemotherapy

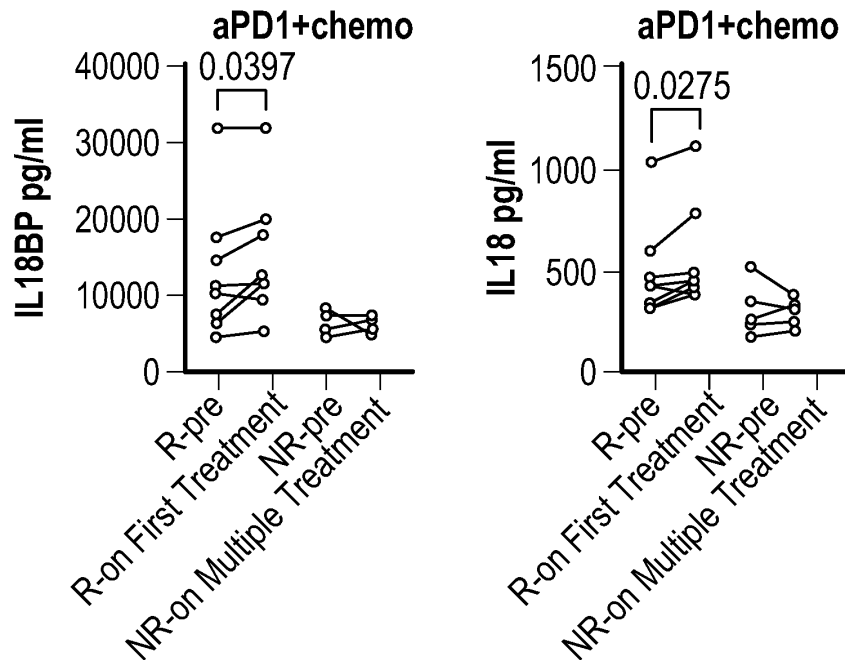


FIG. 65C

Percent of Change in IL18 and IL18BP From Baseline in R/NR Following Combo Treatment with aPD1+Chemotherapy or Anti-PD-1

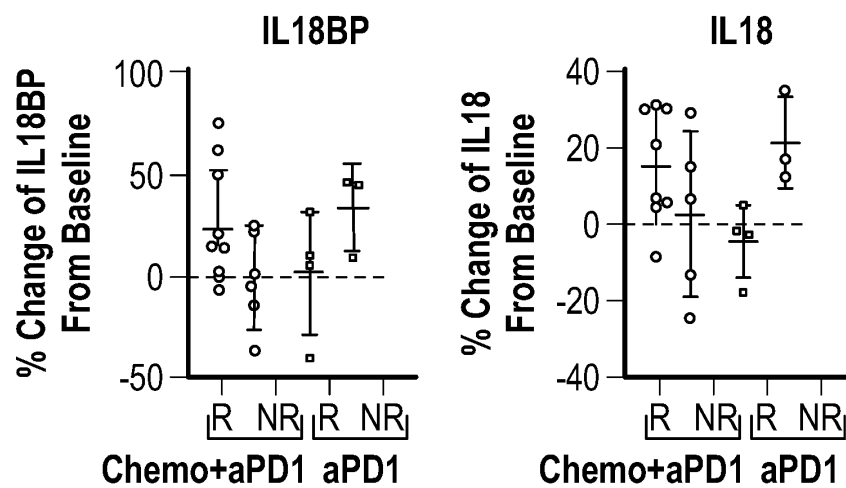


FIG. 65D

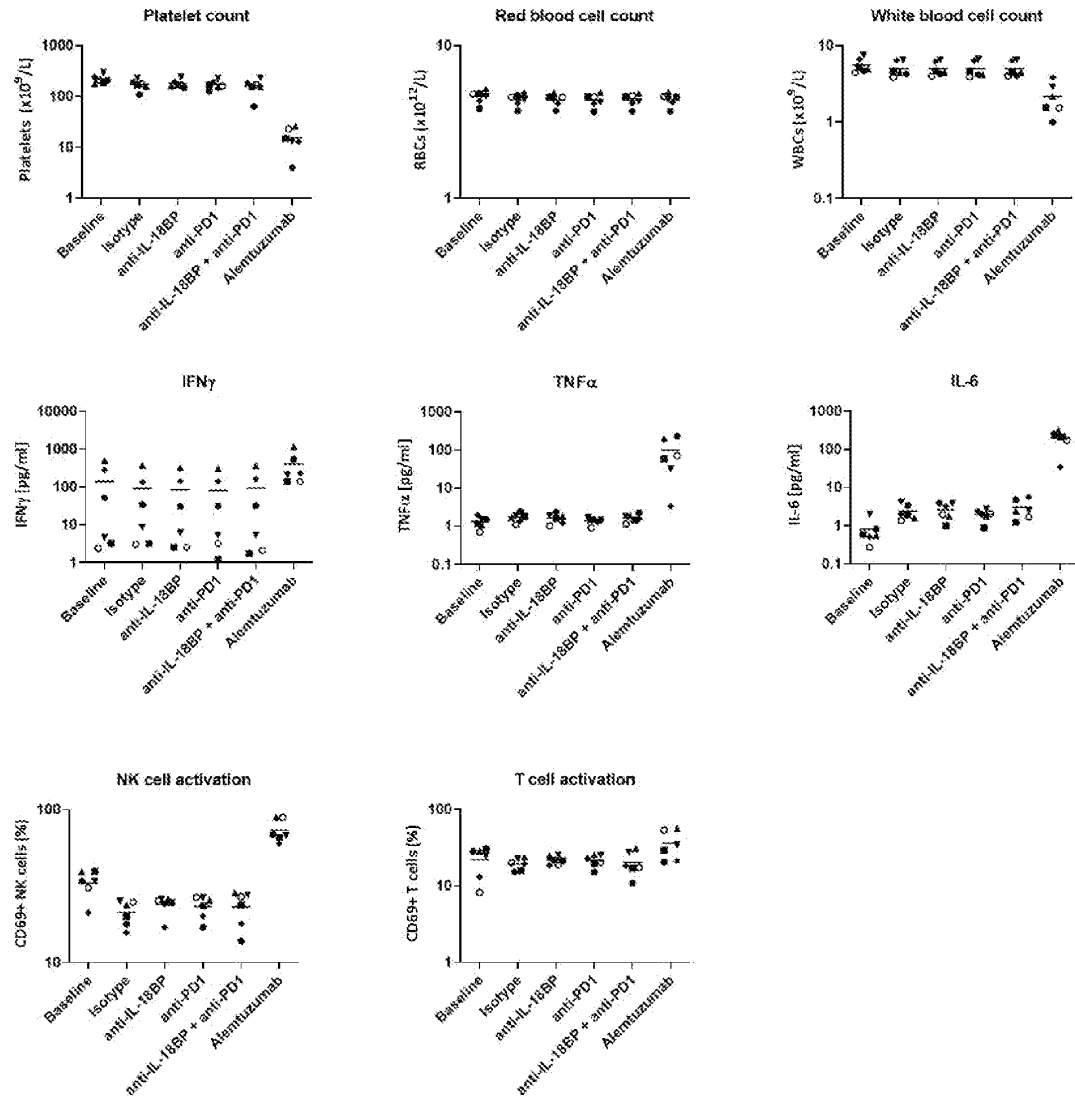
Figure 66

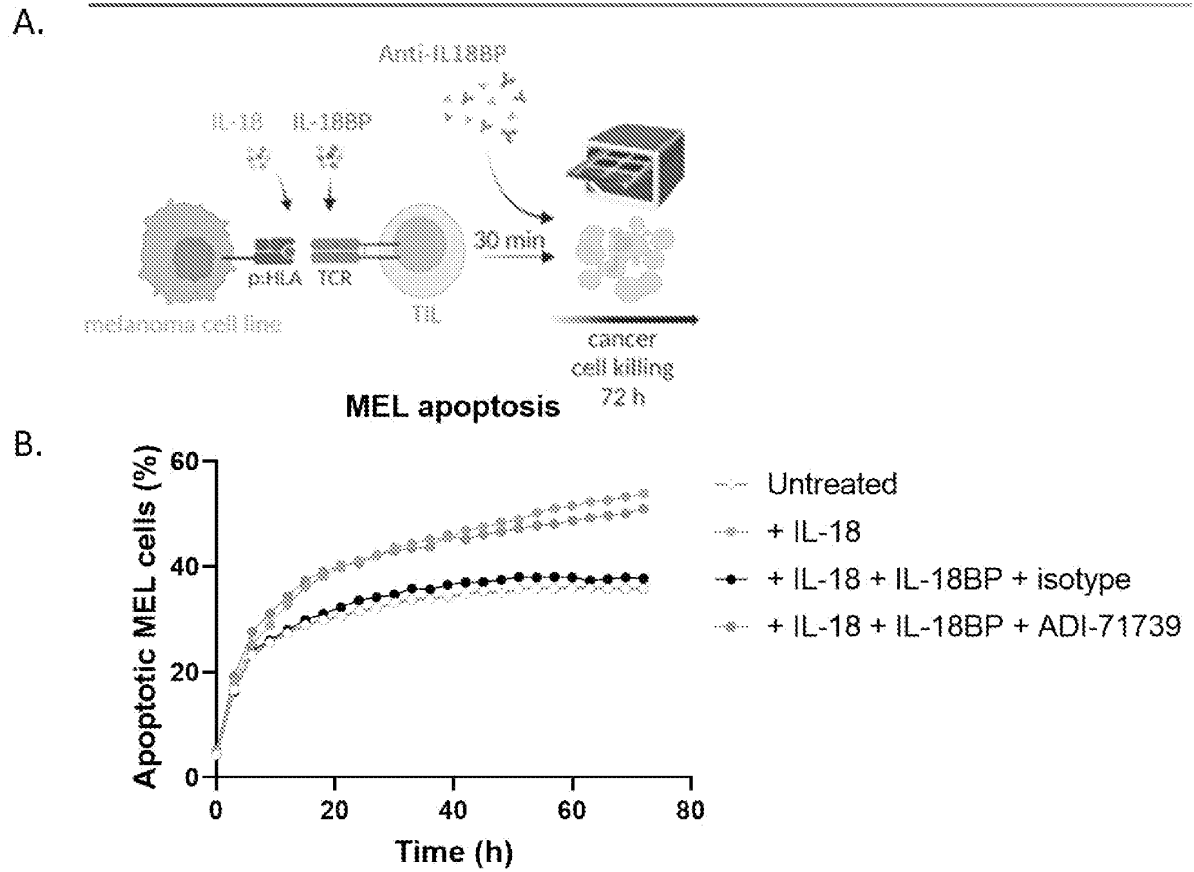
Figure 67

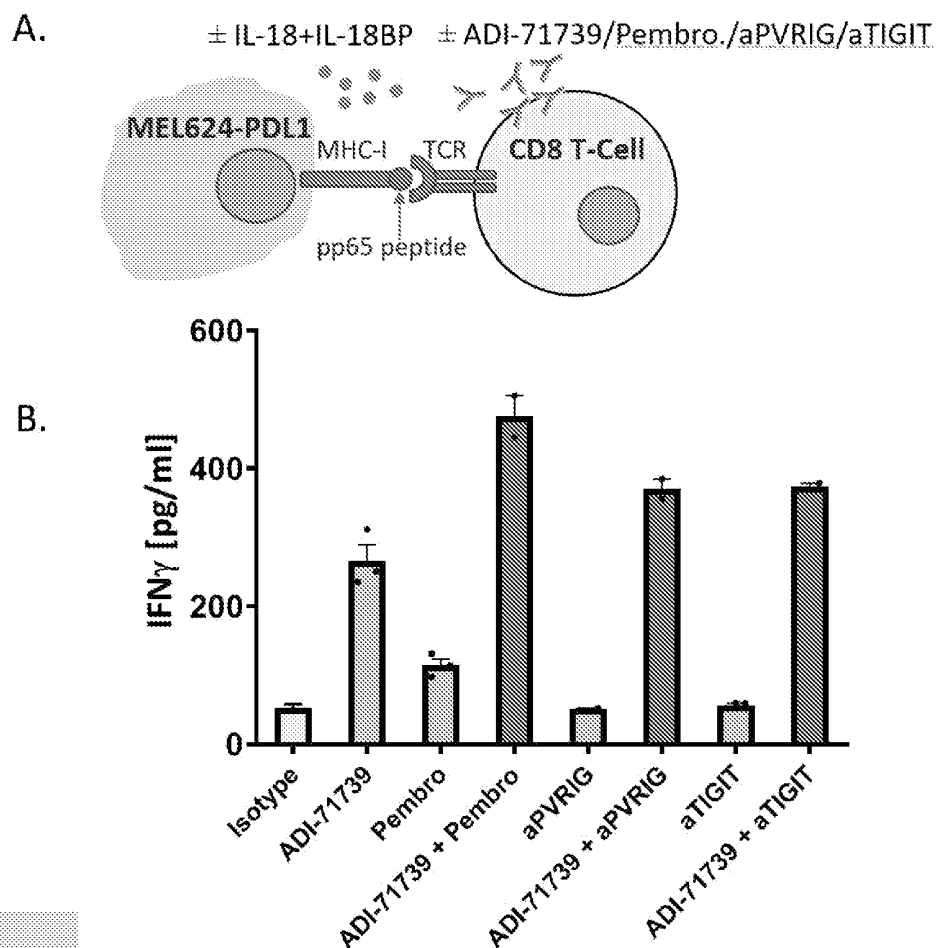
Figure 68

Figure 69

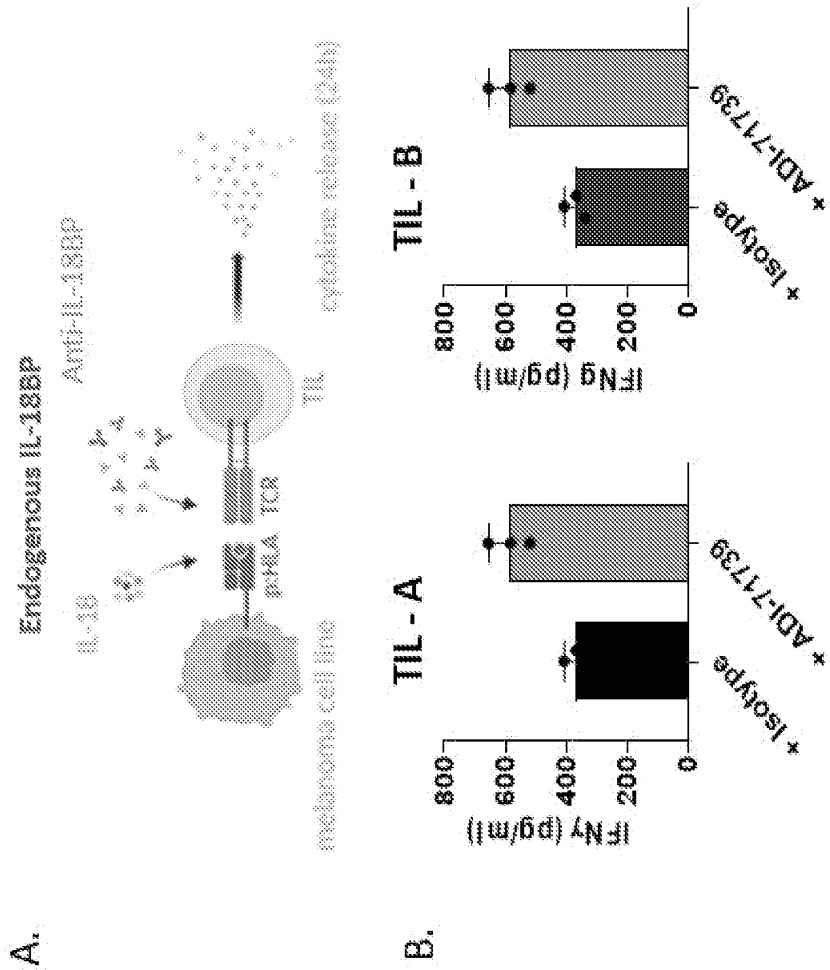


Figure 70

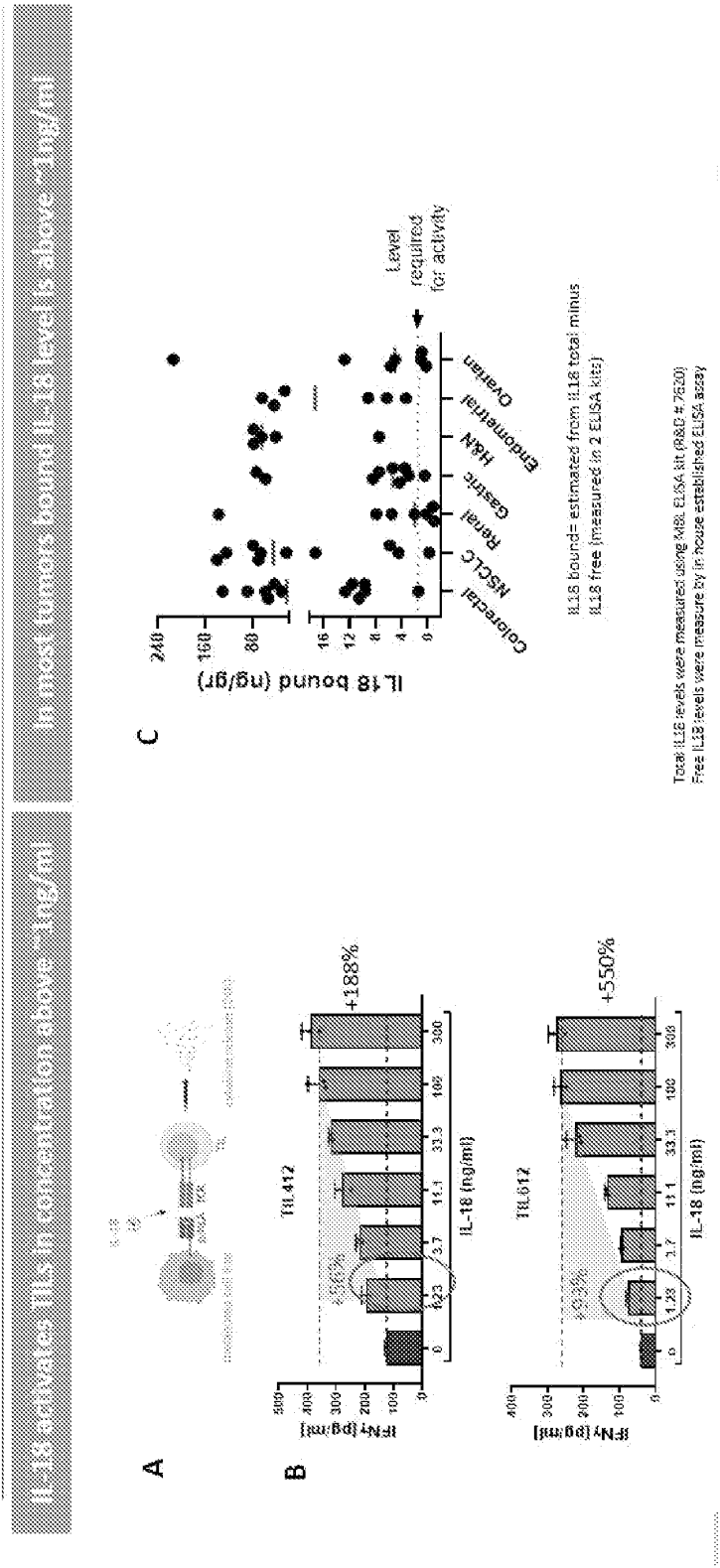
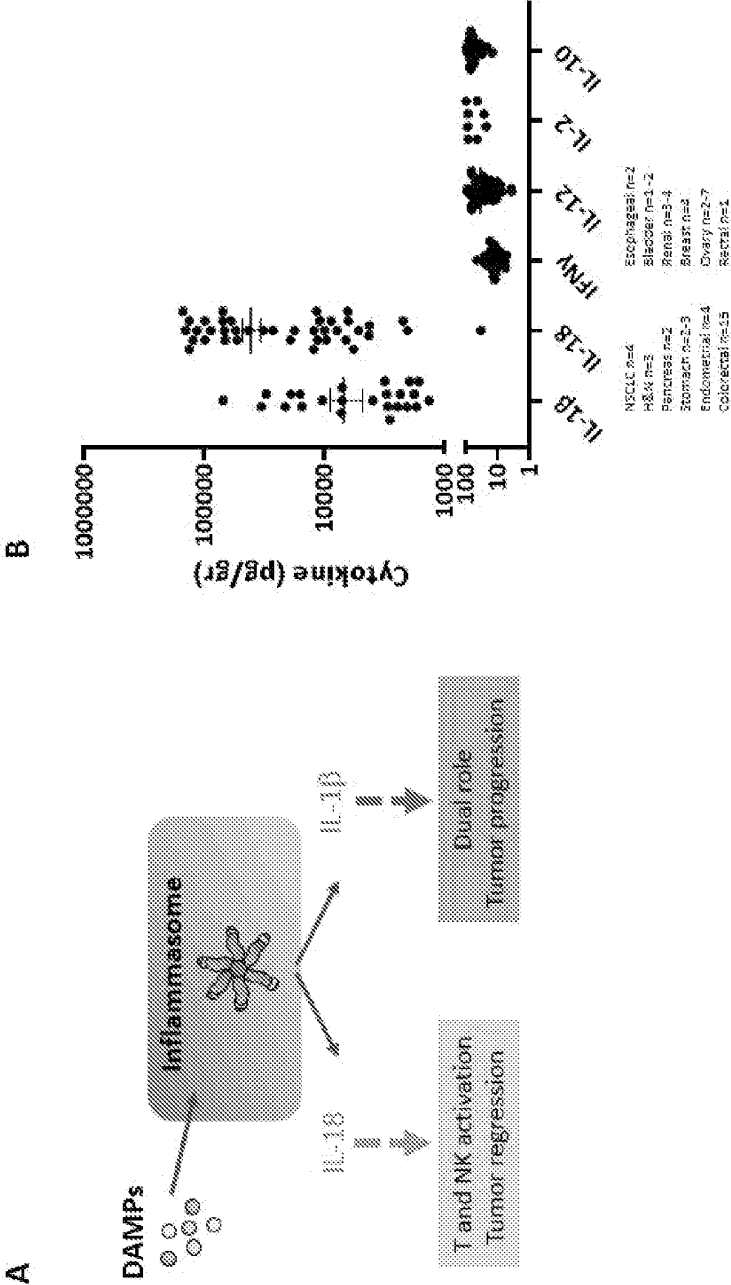
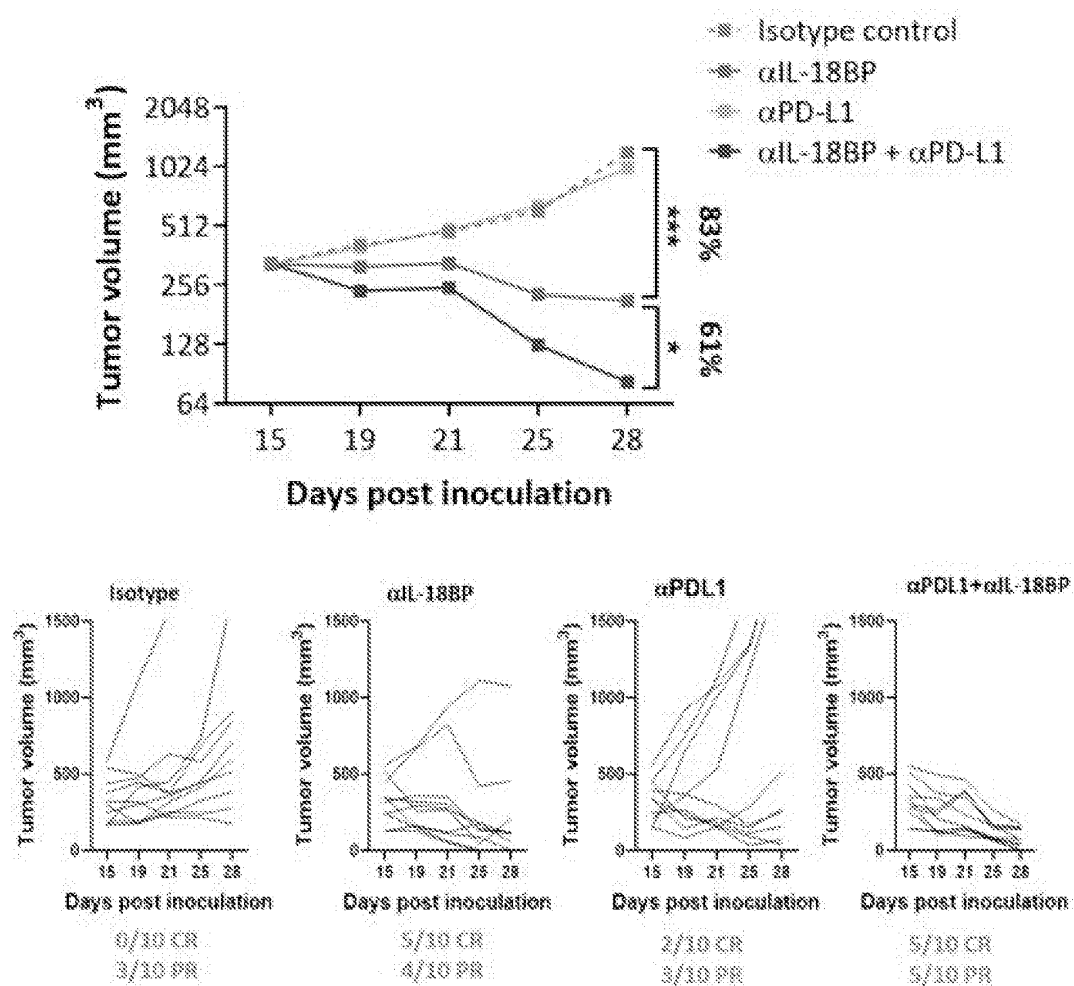
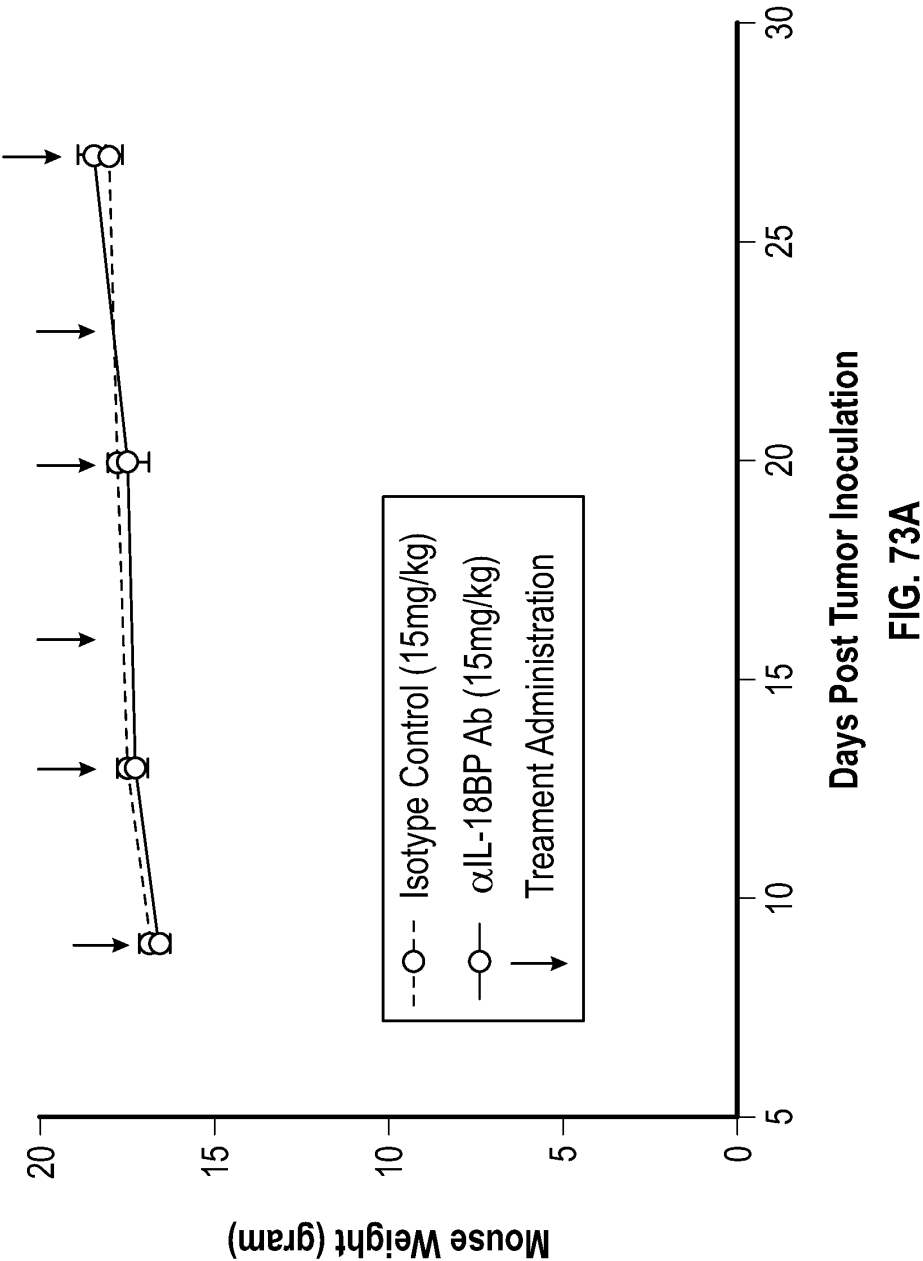


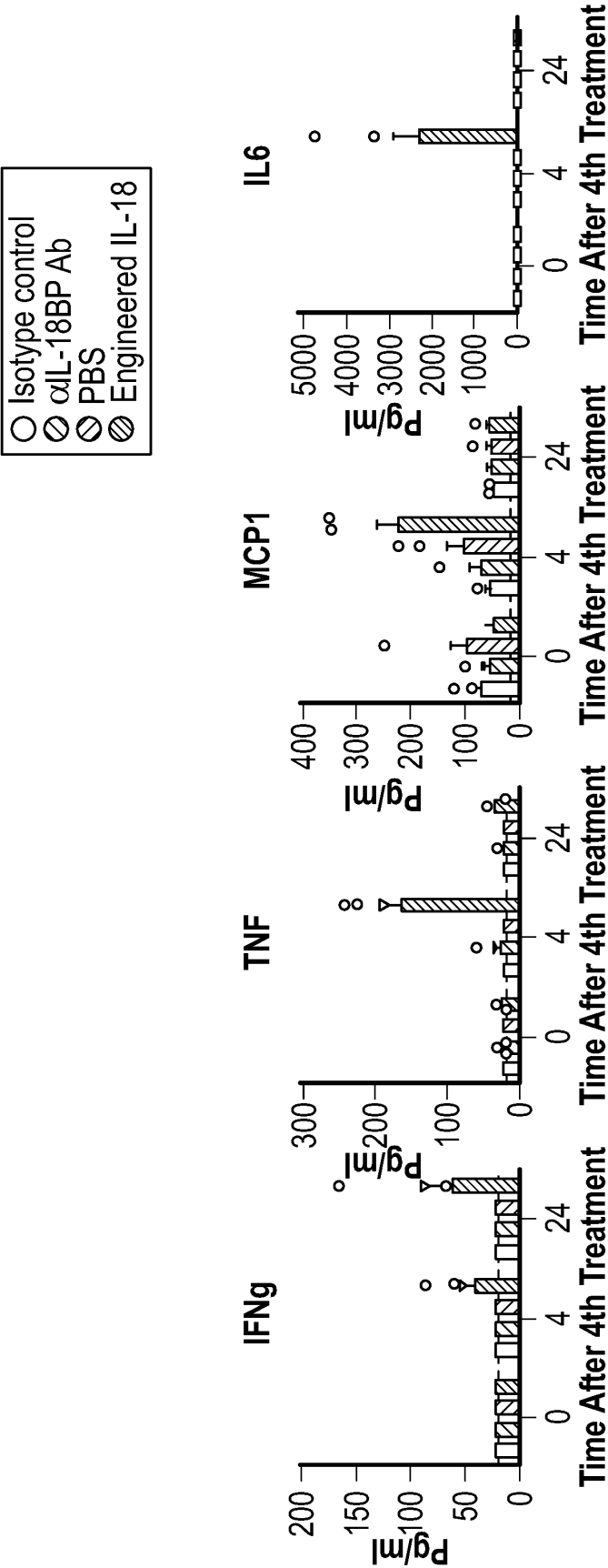
Figure 71



Human IL18 ELISA kit (MEL7620)
Human Th1/Th2/Th17 cytokine Cytometric Bead Array (CBA) (BD 560484)
Human Inflammatory Cytokine Cytometric Bead Array (CBA) (BD 551811)

Figure 72





* Engineered IL-18 Does Not Bind to IL18BP But Retains its Binding to IL-18R

FIG. 73B

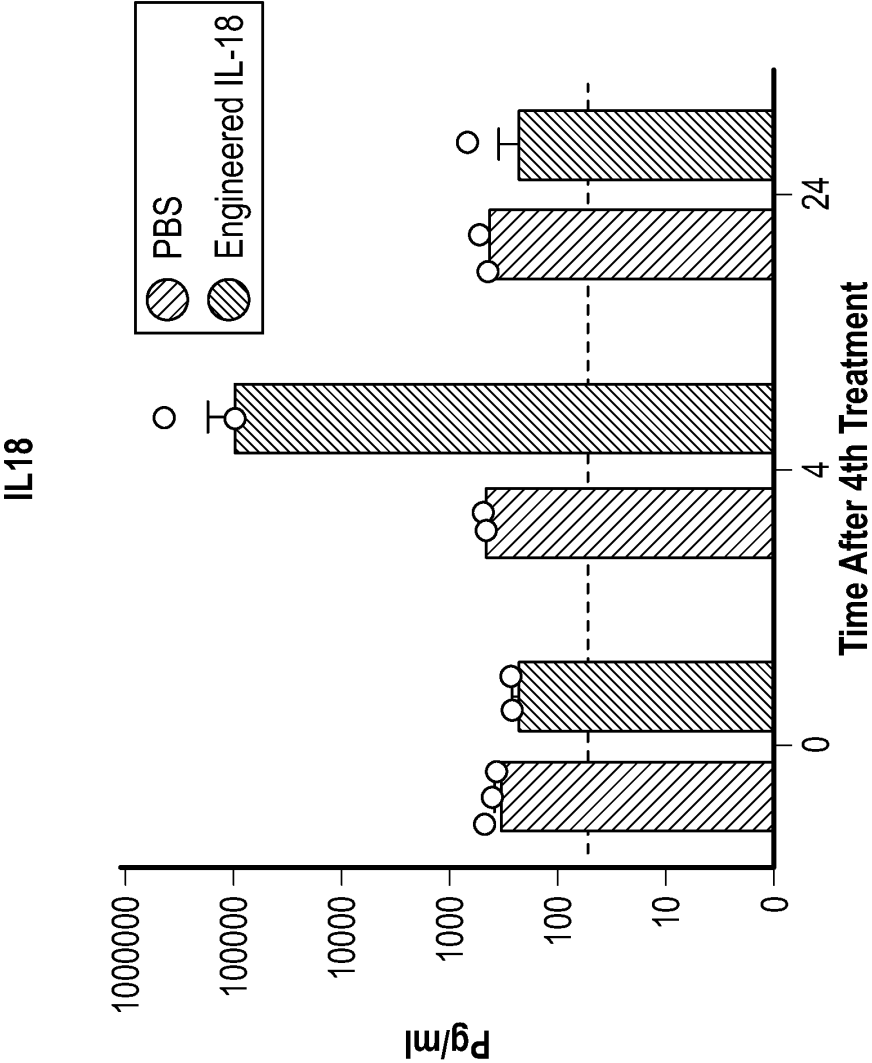


FIG. 73C

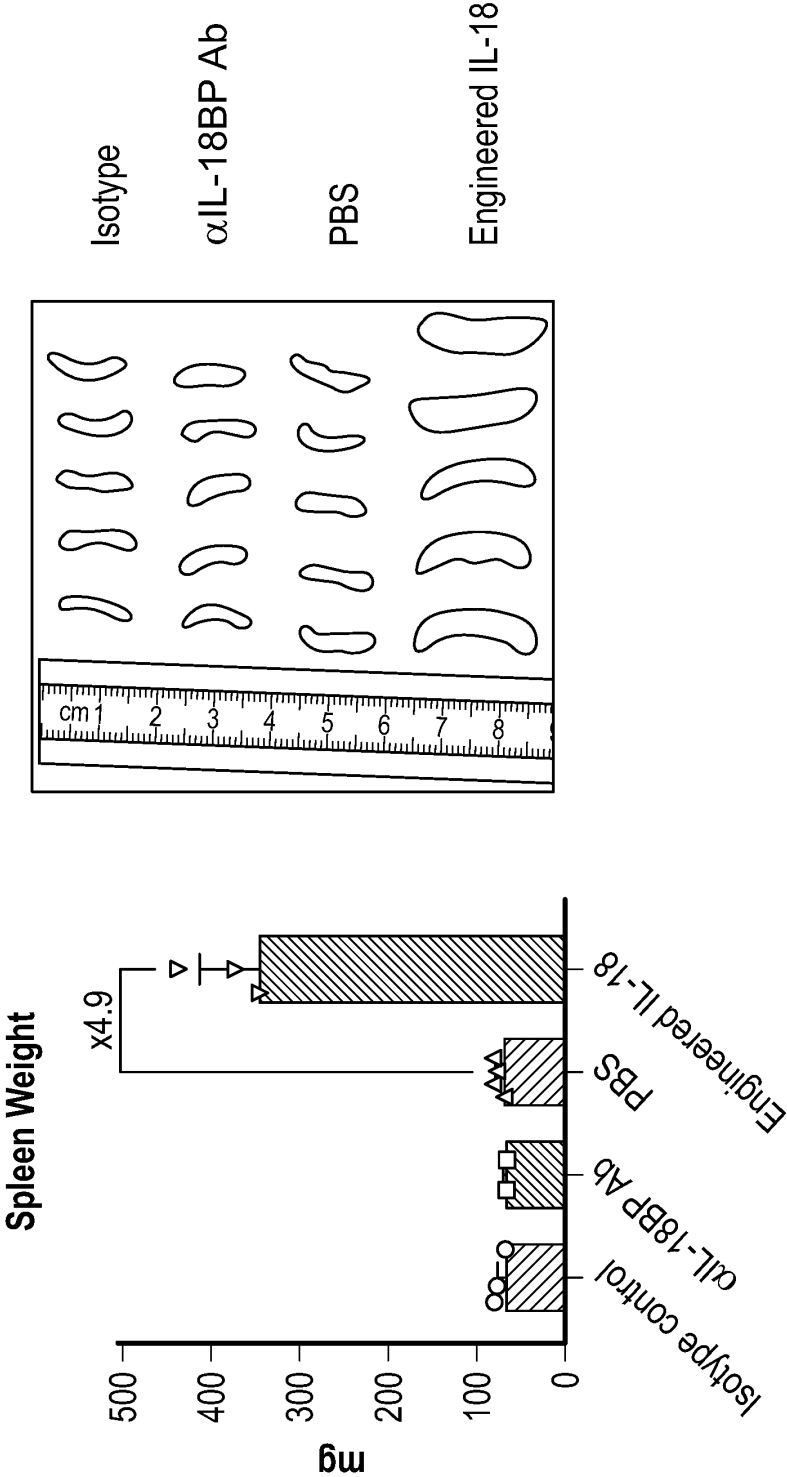


FIG. 73D

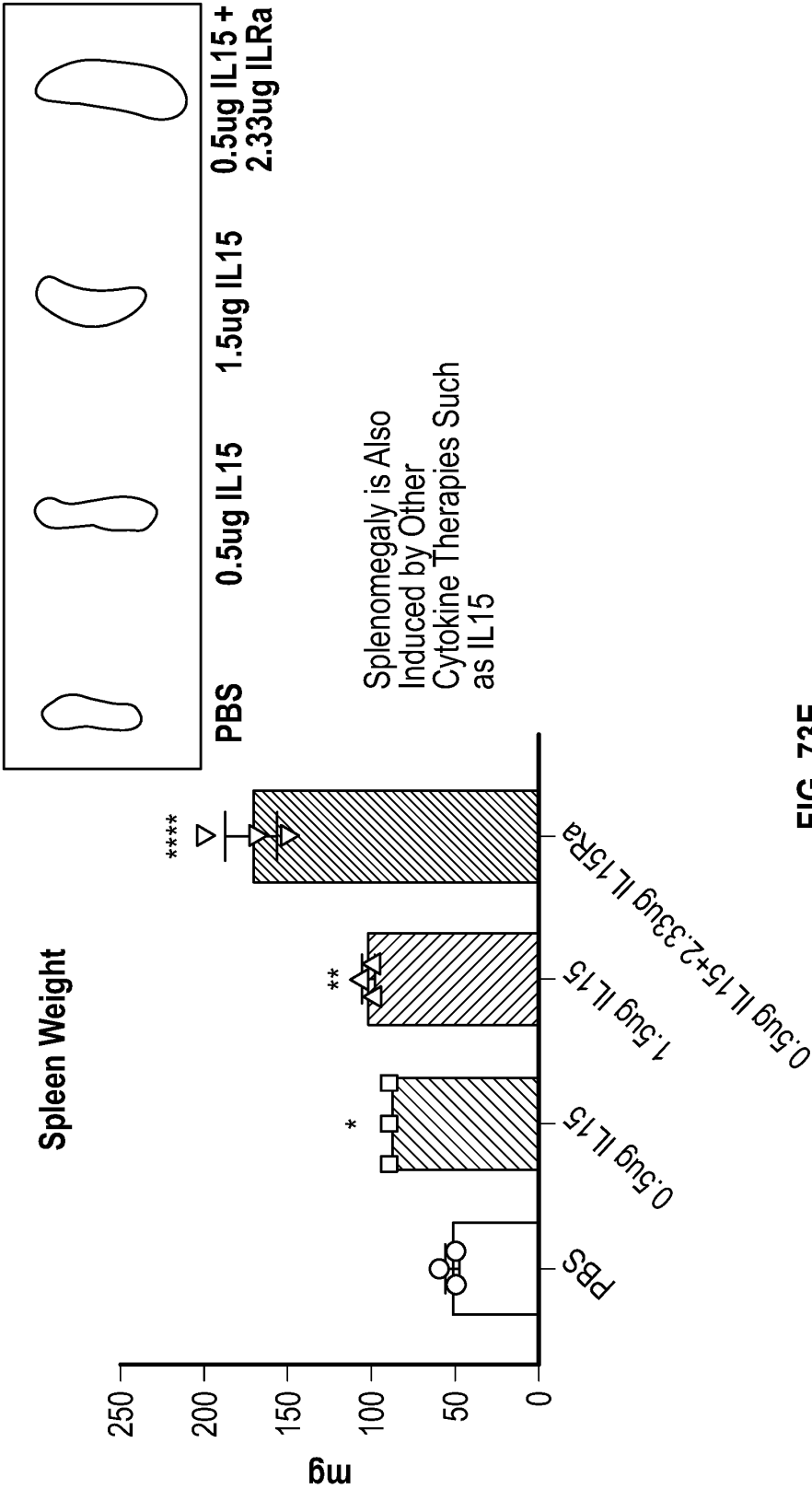
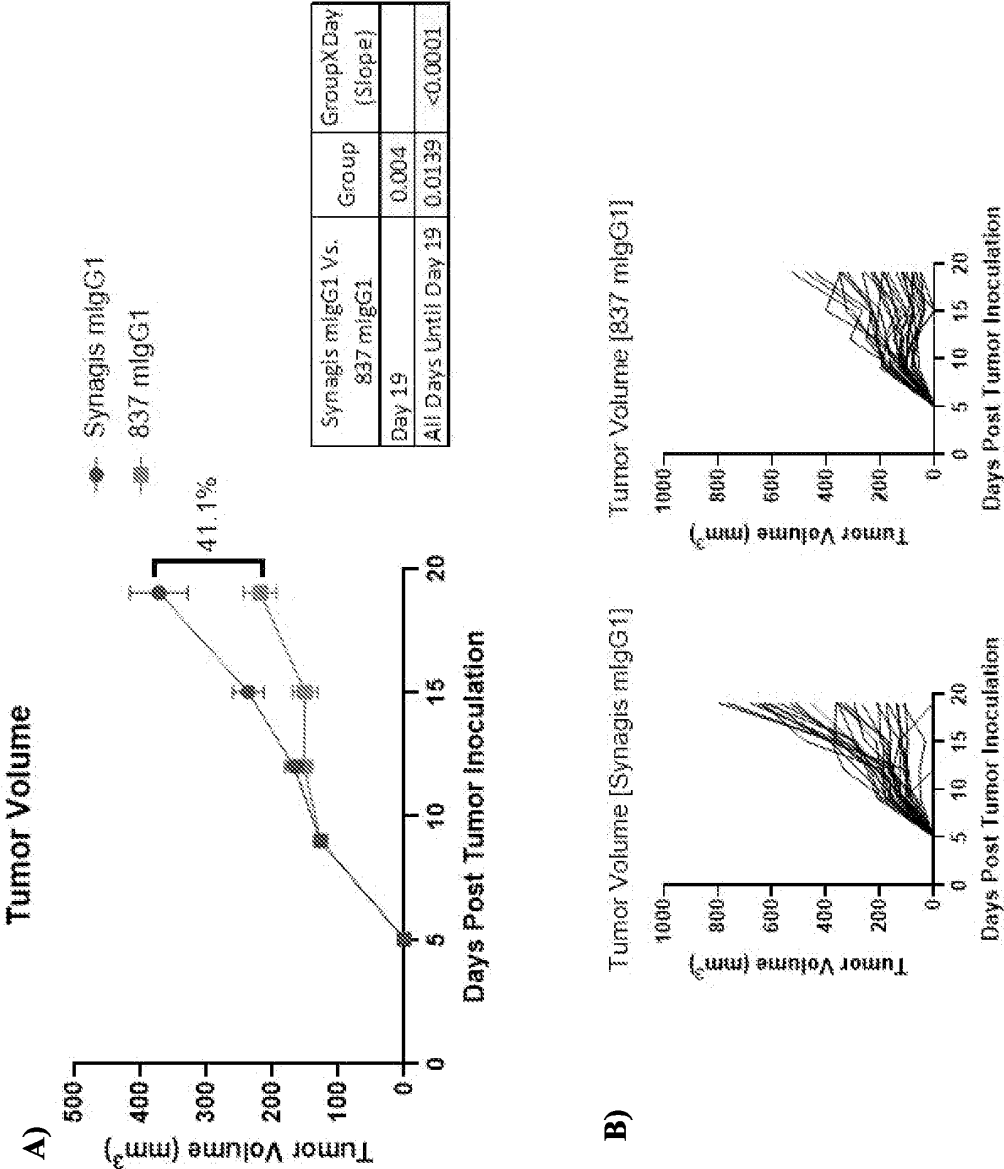


Figure 74



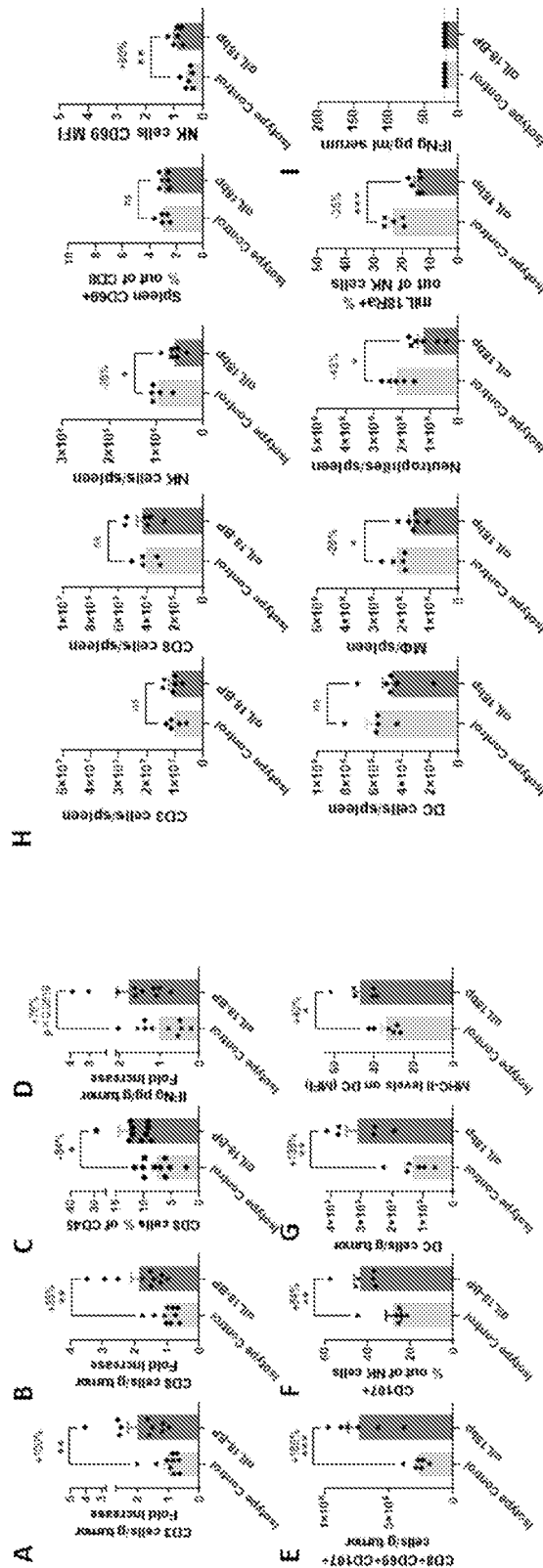
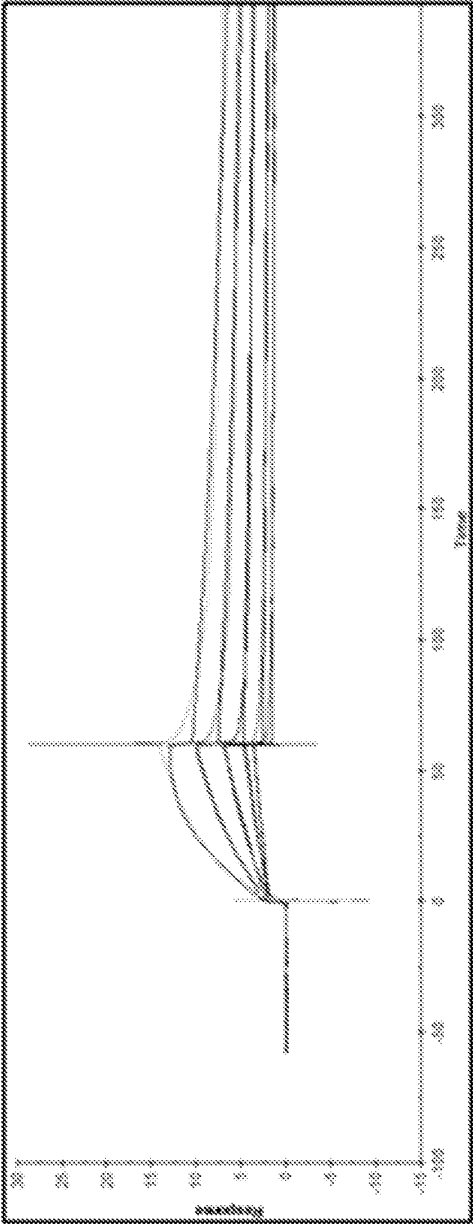


Figure 75

Figure 76



Curve	ka (1/Ms)	kd (1/s)	KD (M)
	9.22E+06	0.002519	2.73E-10

Figure 77

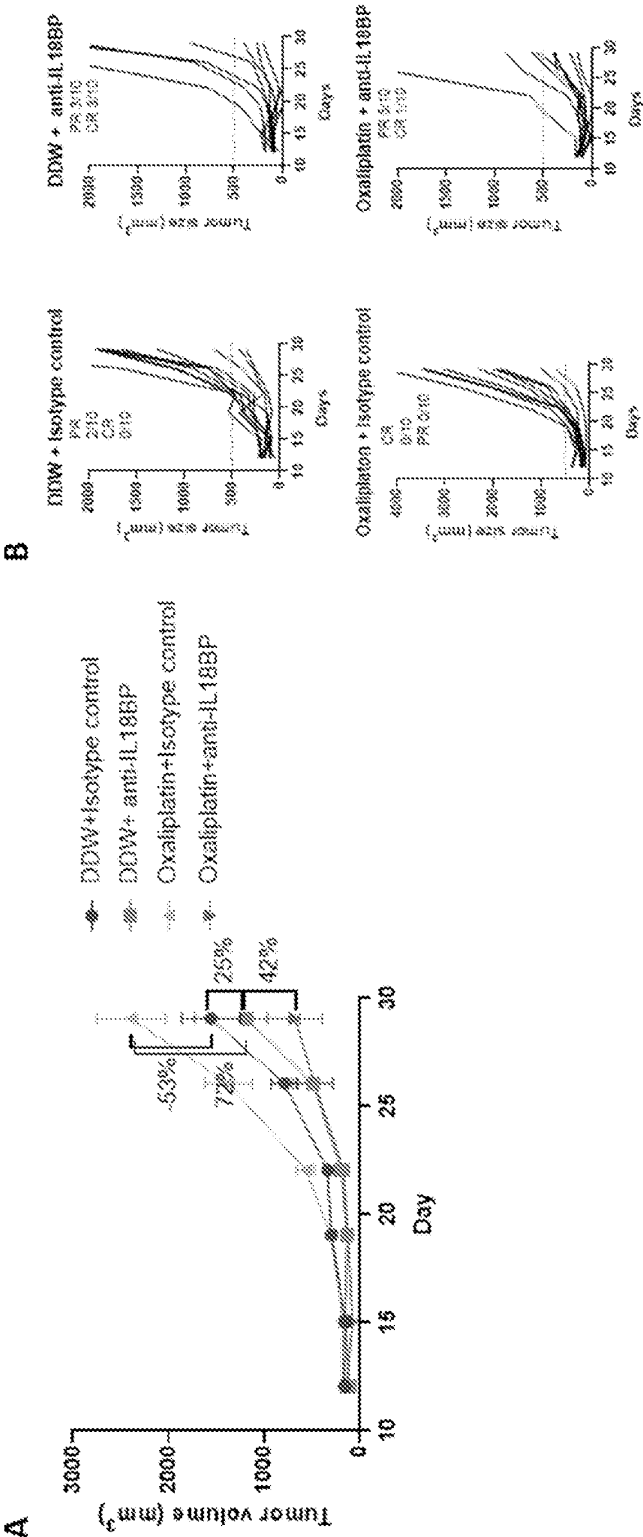


Figure 78

