

Figure 1A

[illegible]

Figure 1B

Human IgG4 constant region (Wild Type)

ASTKGPVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYTCNVVDHFKPSNTRKVDKRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGCSFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6)

Human IgG4 constant region (S241P hinge mutant)

ASTKGPVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYTCNVVDHFKPSNTRKVDKRVESKYGPPCP[CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGCSFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 7)

Human kappa light chain

RTVAADPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 8)

Human lambda light chain

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTIPSKQSNNKYAASSVLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 9)

Figure 2

Human TIGIT extra-cellular domain

MMTCTIETTCNISAEKGCISILQCHLSSTTAQVTQVNWEQQDQLLAICNADLCWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPD
CTYTGRIFLEVLESSVAEHGARFQIP (SEQ ID NO: 10)

Cynomolgus macaque TIGIT extra-cellular domain

MMTCTIETTCNISAKKGCISVILQCHLSSTMAQVTQVNWEQHDHSLLAIRNAELGWHIYPAFKDRVAPGPGGLGLTLQSLTMNDTGEYECTYHT
YPDGTYGRIFLEVLESSVAEHSARFQIP (SEQ ID NO: 11)

Human PVRIg extra-cellular domain

TPEVVVQVRMEATELSSFTIRCGFLGSCISLVTVSWGPNCGAGCTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTECCCK
EASFPEGSWEACGSLPPSSDPGLSAPPTAPILRAD (SEQ ID NO: 12)

Cynomolgus macaque PVRIg extra-cellular domain

TPEVVVQVQMEATELSSFTVHCGLPGSISLVTVSWGPGDGAGGTKLAVLHPELGTQWAPARQARWETQSSISLALEDSCASSPEANTTTC
CKFASTPEGSWESCGSLPPSSDPGLSAPPTVPILRAD (SEQ ID NO: 13)

Human PD-1 extra-cellular domain

PGWFLDSPDRPWNPPTFSPALLVVTEDGNATFTCSFNTSEFVLNWYRMSPSNQTDKLAAPEDRSQPGQDCRFRVTQLPNGRDFHMSVVR
ARRNDSGTLYLCCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPRPAGQFQTLV (SEQ ID NO: 14)

Cynomolgus PD-1 extra-cellular domain

PGWFLESFDRPWNPPTFSPALLVVTEDGNATFTCSFNSASEFVLNWYRMSPSNQTDKLAAPEDRSQPGQDCRFRVTQLPNGRDFHMSVVR
ARRNDSGTLYLCCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPRPAGQFQALV (SEQ ID NO: 15)

Figure 3A: CPA.9.018

What	sequence	SEQ ID NO:
Variable heavy (vn) domain	QVQLVESGGGLVOPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAFIRYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVY YCAKEMILVQDYYMDVWGGQTTVTSS	16
vhCDR1	GFTSSYG	17
vhCDR2	IRYDGSNK	18
vhCDR3	AKEMILVQDYYMDV	19
Full length HC (IgG4(S241P); CPA.9.018.H4(S241P))	QVQLVESGGGLVOPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAFIRYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVY YCAKEMILVQDYYMDVWGGQTTVTSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYTCNV/DHKPSNTKVDKRVESKVGPPCPAPAEFLGGPSVFLPPKPD TLMISRTPEVTCVWVDVSEDPEVQFNWVVDGVEV HNAKTPREEQFNSTYRWVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSEFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	20
Variable light (vl) domain	DVVMQTQSPSLPVSPGEPASISCRSSQNLHHRNGINYNWYLOKPGQSPQLLYWGSNRASGVDRFSGSGSGTDFTLKISRVEADVGVVYCMQ GLQIPPTFGQGTVDIKR	21
vlCDR1	QNLHHRNGINYNWYLOKPGQSPQLLYWGSNRASGVDRFSGSGSGTDFTLKISRVEADVGVVYCMQ	22
vlCDR2	WGS	23
vlCDR3	MQGLQIPPT	24
Full length light chain ((CPA.9.018.H4(S241P)))	DVVMQTQSPSLPVSPGEPASISCRSSQNLHHRNGINYNWYLOKPGQSPQLLYWGSNRASGVDRFSGSGSGTDFTLKISRVEADVGVVYCMQ GLQIPPTFGQGTVDIKRVTVAAPSVFIPTPSDEQLKSGTASVCLNNFYPREAKVQWIKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	25

Figure 3B : CPA.9.027

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	26
vhCDR1	GFTSSYA	27
vhCDR2	ISYDGSNK	28
vhCDR3	ARDPLPLHYGMDV	29
Full length HC (IgG4(S241P); CPA.9.027.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPELGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSEQDEPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRW/SVLT/LHQDW/LNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCVMHEALHINHYTQKSLSPGK	30
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLSLQLGGGTQLAVLG	31
vICDR1	SSNMGRRP	32
vICDR2	SQN	33
vICDR3	AVWDDSLSLQ	34
Full length light chain (CPA.9.027.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLSLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	35

Figure 3C: CPA.9.049

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	36
vhCDR1	GFTSSYA	37
vhCDR2	ISYDGSNK	38
vhCDR3	ARDPLPLHYGMDV	39
Full length HC (IgG4(S241P); CPA.9.049.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFGLGSPVFLFPPK PKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRW/SVLT/LHQDW/LNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESINGQPENNYKTTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	40
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLFSLLLGGGTQLAVLG	41
vlCDR1	SSNMGRRP	42
vlCDR2	SQN	43
vlCDR3	AVWDDSLFSL	44
Full length light chain (CPA.9.049.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLFSLLLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	45

Figure 3D: CPA.9.057

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWIQQPGKGLWIGSIYSGSTYYNP SLKSRVTISVDTSKNQFS KLKLS SVTAADTAVYYCARGGAAAGNPFDIWGGQGTMTVTSS	46
vhCDR1	GGSISSSSYY	47
vhCDR2	IYSGST	48
vhCDR3	ARGGAAAGNPFDI	49
Full length HC (IgG4(S241P); CPA.9.057.H4(S241P))	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWIQQPGKGLWIGSIYSGSTYYNP SLKSRVTISVDTSKNQFS KLKLS SVTAADTAVYYCARGGAAAGNPFDIWGGQGTMTVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTPPSSSLGKTYYTCNV/DHKPSNTKVDKRVEKYGPPCPCPAPEFELGGPSVFLPPKPKDT LMISRTPETCVWVDVSDQEDPEVQFNWYVDGVGVHNAKTPREEQFNSTYRVWSVLTVLHQDW/LNGKEYCKVSNKGLPS SIEKTSKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRITVDK SRWQEGNVSFCSVMHEALHNHYTQKSLSLSPGK	50
Variable light (vl) domain	QSVLTQPPSVSGTPGQQRVTISCSGSSNIGSNEVYWHQQLTGTAPKLLIYRNTQRP SGVDPDRFSGSKSGTSASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLG	51
vICDR1	SSNIGSNF	52
vICDR2	RNT	53
vICDR3	ATWDDSLSAWV	54
Full length light chain (CPA.9.057.H4(S241P))	QSVLTQPPSVSGTPGQQRVTISCSGSSNIGSNEVYWHQQLTGTAPKLLIYRNTQRP SGVDPDRFSGSKSGTSASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWIKADSSPYKAGVET TTPSKQSNKNKYAASSYSLTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	55

Figure 3E: CPA.9.059

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGIIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSIVYSGGSTIYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCYARGARYSGQYPYWGQGTLVTVSS	56
vhCDR1	GFTVSSNY	57
vhCDR2	IYSGGST	58
vhCDR3	ARGARYSGQYPY	59
Full length HC (IgG4(S241P); CPA.9.059.H4(S241P))	EVQLVETGGGIIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSIVYSGGSTIYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCYARGARYSGQYPYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYTCNVLDHKSNTKVDKRVESYGPCCPAPAEFLGGPSVFLPPKP KDTLMISRTPETVCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGG LPSSIEKTIKAKAQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRLT VDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	60
Variable light (vl) domain	DIQLTQSPSFLSASVGDRTITCRASHDISSLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFGSGSGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFTFGQGKVEIKR	61
vlCDR1	HDISL	62
vlCDR2	AAS	63
vlCDR3	LQLDSFPTWT	64
Full length light chain (CPA.9.059.H4(S241P))	DIQLTQSPSFLSASVGDRTITCRASHDISSLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFGSGSGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFTFGQGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	65

Figure 3F: CPA.9.083

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTPLYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	66
vhCDR1	GFTSSYA	67
vhCDR2	ISYDGTVP	68
vhCDR3	ARDPLPLHYGMDV	69
Full length HC (IgG4(S241P); CPA.9.083.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLEWVAVISYDGTPLYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFLLGPPSVFLPPK PKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRW/SVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESINGQPENNYKTTTPPVLDSDGSFFLYSRL TVDKSRWQEGRNPFSCVMHEALHINHYTQKSLSPGK	70
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDGDRRLQLGGGTQLAVLG	71
vlCDR1	SSNMGRRP	72
vlCDR2	SQN	73
vlCDR3	AVWDGDRRLQ	74
Full length light chain (CPA.9.083.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDGDRRLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGV ETTPSKQSNKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	75

Figure 3G: CPA.9.086

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYAGEVKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	76
vhCDR1	GFTSSYA	77
vhCDR2	ISYAGEVK	78
vhCDR3	ARDPLPLHYGMDV	79
Full length HC (IgG4(S241P); CPA.9.086.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYAGEVKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVDKRVESKYGPPCPPAPEELGGPSVFLPPK PKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPREEQNFSTYRW/SVLT/LHQDW/LNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESINGQPENNYKTTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	80
Variable light (vl) domain	QSALTQPRASGNPQORVTISCGSSSNMGRRPVNWYQQIPGTAPKLLYSQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDIGRVLQLGGGTQLAVLG	81
vICDR1	SSNMGRRP	82
vICDR2	SQN	83
vICDR3	AVWDDIGRVLQ	84
Full length light chain (CPA.9.086.H4(S241P))	QSALTQPRASGNPQORVTISCGSSSNMGRRPVNWYQQIPGTAPKLLYSQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDIGRVLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	85

Figure 3H: CPA.9.089

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVROAPGKGLEWVAVISYDRTPTVYYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	86
vhCDR1	GFTSSYA	87
vhCDR2	ISYDRTPV	88
vhCDR3	ARDPLPLHYGMDV	89
Full length HC (IgG4(S241P); CPA.9.089.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVROAPGKGLEWVAVISYDRTPTVYYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVKRVEISKYGPCCPAPEELGGPSVFLFPK PKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRW/SVLT/LHQDW/LNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESINGQPENNYKTTTPPVLDSDGSFFLYSRL TVDKSRWQEGRNPFSCVMHEALHINHYTQKSLSPGK	90
Variable light (vl) domain	QSALTQPRASGNPQORVTISCSGSSNMGRRPVNWYQQIPGTAPKLLYSQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLG	91
vICDR1	SSNMGRRP	92
vICDR2	SQN	93
vICDR3	ATWDDSLPRLN	94
Full length light chain (CPA.9.089.H4(S241P))	QSALTQPRASGNPQORVTISCSGSSNMGRRPVNWYQQIPGTAPKLLYSQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNINKYAASSVLSLTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	95

Figure 31: CPA.9.093

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYEGDRKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSS	96
vhCDR1	GFTSSYA	97
vhCDR2	ISYEGDRK	98
vhCDR3	ARDPLPLHYGMDV	99
Full length HC (lgG4(S241P); CPA.9.093.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYEGDRKYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTTKTYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFGLGSPSVFLPPK PKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRW/SVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLTCLVKGFYPSDIAVEWESINGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCVMHEALHINHYTQKSLSPGK	100
Variable light (vl) domain	QSALTQPRASGNPGQRTVITSCGSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFGGGTKLAVLG	101
vICDR1	SSNMGRRP	102
vICDR2	SQN	103
vICDR3	ATWDDSTPHGV	104
Full length light chain (CPA.9.093.H4(S241P))	QSALTQPRASGNPGQRTVITSCGSSSNMGRRPVNWYQQIPGTAPKLLIYQNRPSGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNINKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	105

Figure 31: CPA.9.101

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSIVYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARGAPLEGGQPYWGQGLTVTVSS	106
vhCDR1	GFTVSSNY	107
vhCDR2	IYSGGST	108
vhCDR3	ARGAPLEGGQPY	109
Full length HC (IgG4(S241P); CPA.9.101.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSIVYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARGAPLEGGQPYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVLEPPKPK DTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHREALHNYTQKSLSPGK	110
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASHAIALFSWYQQKPGKAPKLLIYAASLTQGTGPSRFGSGSASGTEFTLTISSLQPEDFAT YYCLQDSFPTWTFGGQTKVEIKR	111
vlCDR1	HAIALS	112
vlCDR2	AAS	113
vlCDR3	LQLDSFPTWT	114
Full length light chain (CPA.9.101.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASHAIALFSWYQQKPGKAPKLLIYAASLTQGTGPSRFGSGSASGTEFTLTISSLQPEDFAT YYCLQDSFPTWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFPYPREAKVQWVKVDNALQSGNSQESVTEQ DSKDSYSTLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	115

Figure 3K: CPA.9.103

What	sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSVIYSGGSTYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYVCARGARPNQYPYWGGGLTVTVSS	116
vhCDR1	GFTVSSNY	117
vhCDR2	IYSGGST	118
vhCDR3	ARGARPNQYPY	119
Full length HC (IgG4(S241P); CPA.9.103.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSVIYSGGSTYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYVCARGARPNQYPYWGGGLTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGLHTFPAVLQSSGLYSLSSVTPVSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVLEFPKPK DTLMISRTPETVTCVVVDVSDQEDPEVFQFNWVDGVVEVHNAKTKPREEQFNSTYRVVSVLTVHQDWLNGKEYKCKVSNKGL PSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSRLTV DKSRWQEGNVFSCSVMHREALHNYTQKSLSPGK	120
Variable light (vl) domain	DIQLTQSPSFLASVGDRTVITCRASHGKISLFSWYQQKPGKAPKLLIYAASLTQIGVPSRFSGSASGTEFTLTISLQPEDFATY YCLQLDSFPTWTFGQGTKEIKR	121
vICDR1	HGKSL	122
vICDR2	AAS	123
vICDR3	LQLDSFPTWT	124
Full length light chain (CPA.9.103.H4(S241P))	DIQLTQSPSFLASVGDRTVITCRASHGKISLFSWYQQKPGKAPKLLIYAASLTQIGVPSRFSGSASGTEFTLTISLQPEDFATY YCLQLDSFPTWTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	125

Figure 3L:
BM26 hlgG4 [BM26-H4] (WO2016/028656A1, Clone 31C6)

W/hat	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVNHVWVKQPGQGLEWIGVIDPYNDGAKYNEKFGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPGYGFVWAGTITVTSSASTKGPSVFLA PCSRSTSESTAAAGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVDPHKNSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPKP	126
vhCDR1	GYTSSVY	127
vhCDR2	IDPYNDGA	128
vhCDR3	ARGGPGYGFV	129
Full length HC (lgG4(S241P))	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVNHVWVKQPGQGLEWIGVIDPYNDGAKYNEKFGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPGYGFVWAGTITVTSSASTKGPSVFLA PCSRSTSESTAAAGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVDPHKNSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPKP KDTLMISRTPETVTCVWDVDSQEDPEVQFNWVVDGVEVHNAKTKPREEQFNSTYRVSVLTVHLHQQDWLNGKEYCKVSNKG LPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLT VDKSRWQEGNVFSCSVMHREALNHHTQKSLSLSPGK	130
Variable light (vl) domain	DIQMTQSPASLSASVGETVITTCRASEHIYSYLSWYQQKQKGKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSKINSIQPEDFG TYQCQHHFGSPLTFGAGTTLELK	131
vICDR1	EHYSY	132
vICDR2	NAK	133
vICDR3	QHHFGSPLT	134
Full length light chain	DIQMTQSPASLSASVGETVITTCRASEHIYSYLSWYQQKQKGKSPQLLVYNAKTLAEGVPSRFSGSGGTQFSKINSIQPEDFG TYQCQHHFGSPLTFGAGTTLELKRTVAAPSVFIFFPSDEQLKSGTASWCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVYTKSFNRGEC	135

Figure 3M:
BM29 IgG4 (BM29-H4) (US2016/0176963A1, Clone 22G2)

W/hat	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGGLV ¹³⁶ KPSETLSITCTVSGSVSSGIYWSWIRQPPGKGLWIGIYVYSGSTINYNPSLKSRTVISVDTSKNQFSIKLS SVTAADTAVYVCARDYVSGNYNVDYFEFGVDYWGQGT ¹³⁷ TVVSS	136
vhCDR1	GGSVSSGIY ¹³⁷	137
vhCDR2	IYSGST ¹³⁸	138
vhCDR3	ARDYVSGNYNVDYFEFGVDV ¹³⁹	139
Full length HC (IgG4(S241P))	QVHLQESGPGGLV ¹⁴⁰ KPSETLSITCTVSGSVSSGIYWSWIRQPPGKGLWIGIYVYSGSTINYNPSLKSRTVISVDTSKNQFSIKLS SVTAADTAVYVCARDYVSGNYNVDYFEFGVDYWGQGT ¹⁴¹ TVVSSASTKGPSEPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLG ¹⁴² TKTYTCNV ¹⁴³ DHKPSNTKVDKRVESKYGPPCPAPEFLGGPSV FLPPPKD ¹⁴⁴ TLMIKRTPEVTCWVDVSDQEPVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKC KVSNGKGLPSSIEK ¹⁴⁵ TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYK ¹⁴⁶ TTIPPVLDSDGSEF FLYSRLTVD ¹⁴⁷ KSRWDQEGNIVFSCSV ¹⁴⁸ MHEALHNHYTQKLSLS ¹⁴⁹ PGK	140
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPARFSGSGGTDF ¹⁴¹ LTISSL ¹⁴² EPEDFAVY YCCQRSNWPPLE ¹⁴³ TFGPGTKVDIK	141
vICDR1	QSVSSY ¹⁴²	142
vICDR2	DAS ¹⁴³	143
vICDR3	QQRSNWPPLE ¹⁴⁴ TF	144
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPARFSGSGGTDF ¹⁴⁵ LTISSL ¹⁴⁶ EPEDFAVY YCCQRSNWPPLE ¹⁴⁷ TFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASV ¹⁴⁸ VCLLNNFYPREAKVQW ¹⁴⁹ KYD ¹⁵⁰ NALQSGNSQESVTE QDSKDS ¹⁵¹ TYSLSS ¹⁵² LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	145

Figure 3N: CHA.9.536.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGVTFTYTLHWVRQAPGQGLEWMGGINPNNGGTSYAQKFGQGRVMTMRDTSSTVYMESSLRS EDTAVYVCARSGYYDYSFAYWGQGTLTVSS	146
vhCDR1	GYTFTYTLH	147
vhCDR2	GINPNNGGTS	148
vhCDR3	SGYYDYSFAY	149
Full length HC (IgG4(S241P); CHA.9.536.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGVTFTYTLHWVRQAPGQGLEWMGGINPNNGGTSYAQKFGQGRVMTMRDTSSTVYMESSLRS EDTAVYVCARSGYYDYSFAYWGQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGKTYTCNVDHKPSNTKVDKRVEKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQF NWWYVDGVEVHNAKTPREEQFNSTYRVSVLTIVLHODWLNKGEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	150
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCRASQDVKNNAVWVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	151
vlCDR1	RASQDVKNNAV	152
vlCDR2	SPSYRYT	153
vlCDR3	QQHYSTPFT	154
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRTVITCRASQDVKNNAVWVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSFIIPPSDEQLKSGTASVWCLLNIFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	155

Figure 30: CHA.9.536.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGGGLEW/GGINPNNGGTSYAQKFGGRVTMTVDTS TVYMEISSLRSEDTAVYCAAGSGYDYSFAWGGGLTVYSS	156
vhCDR1	GYTFEYTLH	157
vhCDR2	GINPNNGGTS	158
vhCDR3	SGYDYSFAY	159
Full length HC (IgG4(S241P) CHA.9.536.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGGGLEW/GGINPNNGGTSYAQKFGGRVTMTVDTS TVYMEISSLRSEDTAVYCAAGSGYDYSFAWGGGLTVYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPP KPKDTLMISRTPETVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNQKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSR LTVDKSRW/QEGNVFCSVMHEALHNHYTQKSLSLSPGK	160
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCCQHYSTPETFQGQTKLEIK	161
vlCDR1	RASQDVKNNAV	162
vlCDR2	SPSYRYT	163
vlCDR3	QQHYSTPFT	164
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCCQHYSTPETFQGQTKLEIKRTVAAPSFIIPPSDEQLKSGTASVCLLNINFPYBREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	165

Figure 3P: CHA.9.536.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFGGRVTMTVDTS TVYMEISSLRSEDTAVYVCAGSGYDYSAFWGQGLTVTVSS	166
vhCDR1	GYTFEYTLH	167
vhCDR2	GINPNNGGTS	168
vhCDR3	SGYDYSAFW	169
Full length HC (IgG4(S241P); CHA.9.536.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFGGRVTMTVDTS TVYMEISSLRSEDTAVYVCAGSGYDYSAFWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLPPP KPKDTLMISRTEPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNQKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHREALHNYTQKSLSPGK	170
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQGTKLEIK	171
vlCDR1	RASQDVKNNAV	172
vlCDR2	SPSYRYT	173
vlCDR3	QQHYSTPFT	174
Full length light chain (CHA.9.536.4.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALOS GNSQESVTEQDSKDSYSLSTLTLSKADYKEHKHVACEVTHQGLSSPVTKSFNRGEC	175

Figure 3Q: CHA.9.536.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGLEWIGGINPNNGGTSYAQKFQGRATLTVDTS TAYMELSLRSED TAVY CAGSGYDY SFAYWGQGLTVTVSS	176
vCDR1	GYTFEYTLH	177
vCDR2	GINPNNGGTS	178
vCDR3	SGYDYSFAY	179
Full length HC (IgG4(S241P); CHA.9.536.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGLEWIGGINPNNGGTSYAQKFQGRATLTVDTS TAYMELSLRSED TAVY CAGSGYDY SFAYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTITCTNVDHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPP KPKDTLMISRTPETVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSN KGLPSSIEKTTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSR LTVDKSRW/QEGNVFSCVMHEALHNHYTQKSLSLSPGK	180
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTL TISLQPEDFATYYCQGHYSTPETFQGGTKLEIK	181
vICDR1	RASQDVKNNAV	182
vICDR2	SPSYRYT	183
vICDR3	QQHYSTPFT	184
Full length light chain (CHA.9.536.5.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTL TISLQPEDFATYYCQGHYSTPETFQGGTKLEIKRTVAAPSFIIPPSDEQLKSGTASVCLLNINFPYBREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	185

Figure 3R: CHA.9.536.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDTS TAYMELSLRSED TAVY CAGSGYDY SFAYWGQGLTVTVSS	186
vhCDR1	GYTFTEYTLH	187
vhCDR2	GINPNNGGTS	188
vhCDR3	SGYDYDFAY	189
Full length HC (IgG4(S241P); CHA.9.536.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDTS TAYMELSLRSED TAVY CAGSGYDY SFAYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTITCTNVDHKPSNTKVDKRVESKYGPPCPAPEFLGGPSVFLFPP KPKDTLMISRTPETVTCVVDVDSQEDPEVQGFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHREALHNYTQKSLSLSPGK	190
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFGGGKLEIK	191
vlCDR1	RASQDVKNNAV	192
vlCDR2	SPSYRYT	193
vlCDR3	QQHYSTPFT	194
Full length light chain (CHA.9.536.6.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFGGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALOS GNSQESVTEQDSKDSYSLSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC	195

Figure 35: CHA.9.536.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSED TAVY CAGSGYDYSFAYWGQGLTVTVSS	196
vhCDR1	GYTFTEYTLH	197
vhCDR2	GINPNNGGTS	198
vhCDR3	SGYDYSFAY	199
Full length HC (IgG4(S241P); CHA.9.536.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSED TAVY CAGSGYDYSFAYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPP KPKDTLMISRTPETVTCVVVDVSQEDPEVQGFNFWYDGVGVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNKGKEYCKVSN KGLPSSIEKTTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHREALHNYTQKSLSLSPGK	200
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQHHYSTPETFQGQTKLEIK	201
vlCDR1	RASQDVKNNAV	202
vlCDR2	SPSYRYT	203
vlCDR3	QQHYSTPFT	204
Full length light chain (CHA.9.536.7.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISLQPEDFATYYCQHHYSTPETFQGQTKLEIKRTVAAPSFIIPPSDEQLKSGTASVCLLNINNYPREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	205

Figure 3T: CHA.9.536.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYCAAGSGYDYSFAYWGQGLTVTVSS	206
vHCDR1	GYTFTEYTLH	207
vHCDR2	GINPNNGGTS	208
vHCDR3	SGYDYDFAY	209
Full length HC (IgG4(S241P); CHA.9.536.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGGGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYCAAGSGYDYSFAYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTCTYTCNVDHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPETVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHQDWLNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNVFSCSVMHREALHNYTQKSLSLSPGK	210
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQGTKLEIK	211
vLCDR1	RASQDVKNNAV	212
vLCDR2	SPSYRYT	213
vLCDR3	QQHYSTPFT	214
Full length light chain (CHA.9.536.8.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNNAVWYQQKPKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPRKAVQWVKVDNALOS GNSQESVTEQDSKDSYSLSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC	215

Figure 3U: CHA.9.560.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYVCARGNGYVGMIDYWGQGTLTVSS	216
vCDR1	GYFTNYGMN	217
vCDR2	WINTYTGEP	218
vCDR3	NGYVGMIDY	219
Full length HC (IgG4(S241P); CHA.9.560.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYVCARGNGYVGMIDYWGQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTYTCNVDHKPSNTKVDKRVESKYPPCPPAPFELGGPSVFLF PPKPDITLMISRTPEVTCVWDVSEQEDPEVQFNWVDGVEVHNAKTKPREQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTSKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVAMHEALHNHYTQKSLSISPGK	220
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTCSRSTGAVTTSNHNANWFQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	221
vICDR1	RSSTGAVTTSNHNAN	222
vICDR2	GTNGRGS	223
vICDR3	ALWFSNHWV	224
Full length light chain (CHA.9.560.1.H4(S241P))	QAWVTQEPSTVSPGGTVTLTCSRSTGAVTTSNHNANWFQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS	225

Figure 3V: CHA.9.560.3

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYCSRGNNGYVGMMDYWGQGTLVTVSS	226
vHCDR1	GYTFITNYGMN	227
vHCDR2	WINTYTGEP	228
vHCDR3	GNNGYVGMMDY	229
Full length HC (IgG4(S241P); CHA.9.560.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYCSRGNNGYVGMMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSGTTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWVDVSEQEDPEVQFNWVDGVEVHNAKTKPREQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTKQSLSLSPGK	230
Variable light (vl) domain	QAWTQEPSLTVSPGGTVTLTQSSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	231
vLCDR1	GSSTGAVTTSNHNAN	232
vLCDR2	GTNGRGS	233
vLCDR3	ALWFSNHWV	234
Full length light chain (CHA.9.560.3.H4(S241P))	QAWTQEPSLTVSPGGTVTLTQSSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	235

Figure 3W: CHA.9.560.4

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYCSRNGNGYVGMMDYWGQGTLVTVSS	236
vHCDR1	GYTFITNYGMN	237
vHCDR2	WINTYTGEP	238
vHCDR3	NGYVGMMDY	239
Full length HC (IgG4(S241P); CHA.9.560.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGEPYAKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYCSRNGNGYVGMMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWVDVSEQEDPEVQFNWVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNYTKQSLSLSPGK	240
Variable light (vl) domain	QAWTQEPSLTVSPGGTVTLTQSGSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	241
vLCDR1	GSSTGAVTTSNHNAN	242
vLCDR2	GTNGRGS	243
vLCDR3	ALWFSNHWV	244
Full length light chain (CHA.9.560.4.H4(S241P))	QAWTQEPSLTVSPGGTVTLTQSGSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLPKAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNKYYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	245

Figure 3X: CHA.9.560.5

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTFTNNGMNWVRQAPGGLEWMGVWINTYGEPTYAQKFGQGRFTTLDTSIS TAYLEISSURSEDTAVYYCSRNGNGYVGMMDYWGQGTLVTVSS	246
vHCDR1	GYTFTNNGMN	247
vHCDR2	WINTYGEPT	248
vHCDR3	NGYVGMMDY	249
Full length HC (IgG4(S241P); CHA.9.560.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTFTNNGMNWVRQAPGGLEWMGVWINTYGEPTYAQKFGQGRFTTLDTSIS TAYLEISSURSEDTAVYYCSRNGNGYVGMMDYWGQGTLVTVSSASTKGPSVFELAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTITCTNVDHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTEPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODW/LNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSR LTVDKSRW/QEGNVFSCVMHEALHNHYTQKSLSLSPGK	250
Variable light (vl) domain	QAWTQEPSLTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	251
vLCDR1	GSSTGAVTTSNHNAN	252
vLCDR2	GTNGRGS	253
vLCDR3	ALWFSNHWV	254
Full length light chain (CHA.9.560.5.H4(S241P))	QAWTQEPSLTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	255

Figure 3Y: CHA.9.560.6

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTFTNNGMNWVRQAPGQGLEWMGVWINTYGEPTYAQKFQGRFTTLDTSIS TAYLEISSURSEDTAVYYCSRNGNGYVGMMDYWGQGTLVTVSS	256
vCDR1	GYTFTNYGMN	257
vCDR2	WINTYGEPT	258
vCDR3	NGYVGMMDY	259
Full length HC (IgG4(S241P); CHA.9.560.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTFTNNGMNWVRQAPGQGLEWMGVWINTYGEPTYAQKFQGRFTTLDTSIS TAYLEISSURSEDTAVYYCSRNGNGYVGMMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITCTNVDHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPP KPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNQKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	260
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPAFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	261
vICDR1	GSSTGAVTTSNHNAN	262
vICDR2	GTNGRGS	263
vICDR3	ALWFSNHWV	264
Full length light chain (CHA.9.560.6.H4(S241P))	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPAFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	265

Figure 32: CHA.9.560.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGGLEWMGVWINTYGEPTYAQKFQGRFTFTLDASTS TAYLEISSURSEDTAVYYCSRNGYVGMMDYWGQGTLVTVSS	266
vHCDR1	GYTFITNYGMN	267
vHCDR2	WINTYGEPT	268
vHCDR3	NGYVGMMDY	269
Full length HC (IgG4(S241P); CHA.9.560.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFITNYGMNWRQAPGGLEWMGVWINTYGEPTYAQKFQGRFTFTLDASTS TAYLEISSURSEDTAVYYCSRNGYVGMMDYWGQGTLVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTEPEVTCVVVDVSDQEDPEVQFQNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNQKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCVMHEALHNYTKQSLSLSPGK	270
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	271
vLCDR1	GSSTGAVTTSNHNAN	272
vLCDR2	GTNGRGS	273
vLCDR3	ALWFSNHWV	274
Full length light chain (CHA.9.560.7.H4(S241P))	QAWVTQEPSTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	275

Figure 3AA: CHA.9.560.8

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNMGMINWVRQAPGQGLEWMGVNITGEPTYAQKFGGRFTTLDASTS TAYLEISSURSEDTAVYCSRNGYVGMMDYWGQGTLTVSS	276
vCDR1	GYTFTNYGMN	277
vCDR2	WINTYGEPT	278
vCDR3	NGYVGMMDY	279
Full length HC (IgG4(S241P); CHA.9.560.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNMGMINWVRQAPGQGLEWMGVNITGEPTYAQKFGGRFTTLDASTS TAYLEISSURSEDTAVYCSRNGYVGMMDYWGQGTLTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVFLFPP KPKDTLMISRTEPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLDHWLNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	280
Variable light (vl) domain	QAWTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRSGVPAFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	281
vICDR1	GSSTGAVTTSNHNAN	282
vICDR2	GTNGRGS	283
vICDR3	ALWFSNHWV	284
Full length light chain (CHA.9.560.8.H4(S241P))	QAWTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGIRGTNGRSGVPAFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	285

Figure 3BB: CHA.9.546.1

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLVWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARWLLSYAMDYWGQGTLVTVSS	286
vhCDR1	GFTSSYIMS	287
vhCDR2	TISGGGTNTY	288
vhCDR3	WLLSYAMDY	289
Full length HC (IgG4(S241P); CHA.9.546.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLVWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARWLLSYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSVWTPVSSSLGTKTYTCNVSDHKPSNTKVDKRVESKYPPCPPAPFELGGPSVFLF PPKPDTLMSRTPEVTCVWDVSDQEDPEVQFNWVDGVEVHNAKTKPREQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKSLSPGK	290
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWVLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGGQTKLEIK	291
vlCDR1	RASQININWLT	292
vlCDR2	KASNLHT	293
vlCDR3	QQGQSYPT	294
Full length light chain (CHA.9.546.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWVLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYLSLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	295

Figure 3C: CHA.9.547.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLVTVSS	296
vhCDR1	GFTSSYIMS	297
vhCDR2	TISGGGTNTY	298
vhCDR3	WLLSYAMDY	299
Full length HC (IgG4(S241P); CHA.9.547.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSVWTPSSSLGTTKTYTCNVDSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS PPKPDTLISRTPETVCVWDVSDQEDPEVQFNWVDGVEVHNAKTPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK	300
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	301
vlCDR1	RASQININWLT	302
vlCDR2	KASNLHT	303
vlCDR3	QQGQSYPT	304
Full length light chain (CHA.9.547.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSYLSLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	305

Figure 3DD: CHA.9.547.2

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	306
vhCDR1	GFTSSYIMS	307
vhCDR2	TISGGGTNTY	308
vhCDR3	WLLSYAMDY	309
Full length HC (IgG4(S241P); CHA.9.547.2.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTKSLSPGK	310
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	311
vlCDR1	RASQININWLT	312
vlCDR2	KASNLHT	313
vlCDR3	QQGQSYPT	314
Full length light chain (CHA.9.547.2.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSPRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRFAKQVQWKVDNALQSGNS QESVTEQDSKDSYISLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	315

Figure 3EE: CHA.9.547.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u>	316
vhCDR1	GFTSSYIMS	317
vhCDR2	TISGGGTNTY	318
vhCDR3	WLLSYAMDY	319
Full length HC (IgG4(S241P); CHA.9.547.3.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSVWTPSSSLGTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTIKAKQPREPKQYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKSLSLSPGK	320
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	321
vlCDR1	RASQININWLT	322
vlCDR2	KASNLHT	323
vlCDR3	QQGQSYPT	324
Full length light chain (CHA.9.547.3.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSYSTLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	325

Figure 3FF: CHA.9.547.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	326
vhCDR1	GFTSSYIMS	327
vhCDR2	TISGGGTNTY	328
vhCDR3	WLLSYAMDY	329
Full length HC (IgG4(S241P); CHA.9.547.4.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSSVTPSSSLGTKYTCNVDPKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVAMHEALHNHYTQKSLSISPGK	330
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGGQTKLEIK	331
vlCDR1	RASQININWLT	332
vlCDR2	KASNLHT	333
vlCDR3	QQGQSYPT	334
Full length light chain (CHA.9.547.4.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGGSGGTDFTLTIS LQPEDFATYYCQQGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	335

Figure 3GG: CHA.9.547.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLVWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSS	336
vhCDR1	GFTSSYIMS	337
vhCDR2	TISGGGTNTY	338
vhCDR3	WLLSYAMDY	339
Full length HC (IgG4(S241P); CHA.9.547.6.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLVWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTKYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKSLSLSPGK	340
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGGTDFLT TISS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	341
vlCDR1	RASQININWLT	342
vlCDR2	KASKSHT	343
vlCDR3	QQGQSYPT	344
Full length light chain (CHA.9.547.6.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGGTDFLT TISS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSYISLTSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	345

Figure 3HH: CHA.9.547.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u>	346
vhCDR1	GFTSSYIMS	347
vhCDR2	TISGGGTNTY	348
vhCDR3	WLLSYAMDY	349
Full length HC (IgG4(S241P) for CHA.9.547.7.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSSVTPSSSLGTKYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPPKDITLMISRTPEVTCVWDVSEQDEPEVQFNWVDGVEVHNAKTPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNYTKQSLSLSPGK	350
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGGTDFTLTISS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	351
vlCDR1	RASQININWLT	352
vlCDR2	KASKSHT	353
vlCDR3	QQGQSYPT	354
Full length light chain for CHA.9.547.7.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRASQININWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGGTDFTLTISS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355

Figure 3II: CHA.9.547.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLIEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u>	356
vhCDR1	GFTSSYIMS	357
vhCDR2	TISGGGTNTY	358
vhCDR3	WLLSYAMDY	359
Full length HC (IgG4(S241P); CHA.9.547.8.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLIEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u> ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSVWTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWDVSEQDEPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKLSLSLSPGK	360
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASKSHTIGVPSRFGSGSGTDFLT TISS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	361
vlCDR1	RASQININWLT	362
vlCDR2	KASKSHT	363
vlCDR3	QQGQSYPT	364
Full length light chain (CHA.9.547.8.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASKSHTIGVPSRFGSGSGTDFLT TISS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365

Figure 3J: CHA.9.547.9

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	366
vHCDR1	GFTSSYIMS	367
vHCDR2	TISGGGTNTY	368
vHCDR3	WLLSYAMDY	369
Full length HC (IgG4(S241P); CHA.9.547.9.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVAMHEALHNHYTQKSLSLSPGK	370
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASKSHITGVPSRFGSGSGTDFTLTIS LQPEDFATYYCQQGOSYPYTFGGGTKLEIK	371
vLCDR1	RASQININWLT	372
vLCDR2	KASKSH	373
vLCDR3	QQGOSYPYT	374
Full length light chain (CHA.9.547.9.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWLTWYQQKPGKAPKLLIKASKSHITGVPSRFGSGSGTDFTLTIS LQPEDFATYYCQQGOSYPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375

Figure 3KK: CHA.9.541.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFGQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGGGTLTVSS	376
vhCDR1	GYTITNYGMN	377
vhCDR2	WINTYGEPT	378
vhCDR3	GNGNPLGMDY	379
Full length HC (IgG4(S241P); CHA.9.541.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFGQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGGGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTIKTYTCNVDPKPSNTKVDKRVESKYPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWDVSEQDEPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGPPEPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK	380
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDFLTITSSL EPEDFAVYYCFQGGSGYPLTFGQGTKLEIK	381
vlCDR1	GNGNPLGMDY	382
vlCDR2	DTSKLAS	383
vlCDR3	FQGGSGYPLT	384
Full length light chain (CHA.9.541.1.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDFLTITSSL EPEDFAVYYCFQGGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	385

Figure 3L: CHA.9.541.3

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGQGLEWMGVWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGGGTLTVSS	386
vhCDR1	GYTITNYGMN	387
vhCDR2	WINTYGEPT	388
vhCDR3	GNGNPLGMDY	389
Full length HC (IgG4(S241P); CHA.9.541.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGQGLEWMGVWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGGGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTITCNVDHKPSNKKVDKRVESKYPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWDVSEQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGPQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVAMHEALHNHYTQKSLSLSPGK	390
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGGTKLEIK	391
vlCDR1	GNGNPLGMDY	392
vlCDR2	DTSKLAS	393
vlCDR3	FQGGSGYPLT	394
Full length light chain (CHA.9.541.3.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREKVKVQWKVDNALQSGNSQ ESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	395

Figure 3NN: CHA.9.541.4

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQFQGRFTMTLDTSTS TVYMEISSLRSEDTAVYVCARGNGNPLGMDYWGQGTILTVSS	396
vhCDR1	GYTITNYGMN	397
vhCDR2	WINTYGEPT	398
vhCDR3	GNGNPLGMDY	399
Full length HC (IgG4(S241P); CHA.9.541.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQFQGRFTMTLDTSTS TVYMEISSLRSEDTAVYVCARGNGNPLGMDYWGQGTILTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTITCNVDHKPSNKTVDKRVESKYPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWDVSEQDEPEVQFNWYDGVGVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGPPEPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKLSLSLSPGK	400
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGTDYTLTISSL EPEDFAVYYCFQGGSGYPLTFGQGTKLEIK	401
vlCDR1	GNGNPLGMDY	402
vlCDR2	DTSKLAS	403
vlCDR3	FQGGSGYPLT	404
Full length light chain (CHA.9.541.4.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGTDYTLTISSL EPEDFAVYYCFQGGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	405

Figure 300 CHA.9.541.5

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMEISSLRSEDTAVYVCARGNGNPLGMDYWGGGTLTVSS	406
vhCDR1	GYTITNYGMN	407
vhCDR2	WINTYGEPT	408
vhCDR3	GNGNPLGMDY	409
Full length HC (IgG4(S241P); CHA.9.541.5.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMEISSLRSEDTAVYVCARGNGNPLGMDYWGGGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTITCNVDHKPSNKTVDKRVESKYPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGPQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVMHENHYTQKSLSLSPGK	410
Variable light (vl) domain	EIVLTQSPATLSLSPGERVTMTCGNGNPLGMDYWYQQKPGQAPRLWYDTSKLASGVPARFSGSGGTDTLTISSM EPEDFAVYYCFQGGSGYPLTFGGGTKLEIK	411
vlCDR1	GNGNPLGMDY	412
vlCDR2	DTSKLAS	413
vlCDR3	FQGGSGYPLT	414
Full length light chain (CHA.9.541.5.H4(S241P))	EIVLTQSPATLSLSPGERVTMTCGNGNPLGMDYWYQQKPGQAPRLWYDTSKLASGVPARFSGSGGTDTLTISSM EPEDFAVYYCFQGGSGYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415

Figure 3PP: CHA.9.541.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGPTYAQFGGRFTITLDTSTSTVYLEISSRSED AVYYCARGNGNPLGMDYWGQGTILVTVSS	416
vhCDR1	GYTITNYGMN	417
vhCDR2	WINTYTGPT	418
vhCDR3	GNGNPLGMDY	419
Full length HC (IgG4(S241P); CHA.9.541.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGPTYAQFGGRFTITLDTSTSTVYLEISSRSED AVYYCARGNGNPLGMDYWGQGTILVTVSS ASTKGPVFPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVQHODWLNQGEYCKVSNKGLPSSIEKTIKSAKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSR	420
Variable light (vl) domain	LTVDKSRWQEGNVFCSVMHEALHNHYTQKSLSLSPGKEIVLTQSPATLSLSPGERATLSCGNGNPLGMDY WYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGGTKLEIK	421
vlCDR1	GNGNPLGMDY	422
vlCDR2	DTSKLAS	423
vlCDR3	FQGGSGYPLT	424
Full length light chain (CHA.9.541.6.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDY WYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425

Figure 3QQ: CHA.9.541.7

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWNVRQAPGQGLEWMGWINTYTGPTYAQKFGGRFTITLDTSTSTVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTILTVSS	426
vhCDR1	GYTITNYGMN	427
vhCDR2	WINTYTGPT	428
vhCDR3	GNGNPLGMDY	429
Full length HC (IgG4(S241P) CHA.9.541.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWNVRQAPGQGLEWMGWINTYTGPTYAQKFGGRFTITLDTSTSTVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTILTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLDHWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSR	430
Variable light (vl) domain	LTVDKSRW/QEGNVFSCVMHEALHNHYTQKSLSLSPGKEIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGTDYTLTISSL	431
vICDR1	EPEDFAVYYCFQGGSGYPLTFGQGTKEIK	432
vICDR2	GNGNPLGMDY	433
vICDR3	DTSKLAS	434
Full length light chain (CHA.9.541.7.H4(S241P))	FQGGSGYPLT	435
	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGTDYTLTISSL	
	EPEDFAVYYCFQGGSGYPLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQ	
	ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	

Figure 3RR: CHA.9.541.8

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGPTYAQKFGGRFTITLDTSTSTVYLEISSRSED AVYYCARGNGNPLGMDYWGQGLTVVSS	436
vhCDR1	GYTITNYGMN	437
vhCDR2	WINTYTGPT	438
vhCDR3	GNGNPLGMDY	439
Full length HC (IgG4(S241P); CHA.9.541.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGQGLEWMGWINTYTGPTYAQKFGGRFTITLDTSTSTVYLEISSRSED AVYYCARGNGNPLGMDYWGQGLTVVSS ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGKTITCNVDHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPPDKDTLMISRTPETVTCVVVDVSQEDPEVQFNNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHODWLNQGEYCKVSNKGLPSSIEKTIKSAKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSR	440
Variable light (vl) domain	LTVDKSRWQEGNVFCSVMHEALHNHYTQKSLSLSPGKEIVLTQSPATLSLSPGERVTMTCGNGNPLGMDY WYQQKPGQAPRLWYDTSKLASGVPARFSGSGSDYTLTISSM EPEDFAVYYCFQGGSGYPLTFGGGTKLEIK	441
vlCDR1	GNGNPLGMDY	442
vlCDR2	DTSKLAS	443
vlCDR3	FQGGSGYPLT	444
Full length light chain (CHA.9.541.8.H4(S241P))	EIVLTQSPATLSLSPGERVTMTCGNGNPLGMDY WYQQKPGQAPRLWYDTSKLASGVPARFSGSGSDYTLTISSM EPEDFAVYYCFQGGSGYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	445

Figure 35S: CHA.9.547.10

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSS	446
vhCDR1	GFTSSYIMS	447
vhCDR2	TISGGGTNTY	448
vhCDR3	WLLSYAMDY	449
Full length HC for CHA.9.547.10.H4 (S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPPKDITLMISRTPEVTCVWDVDSQEDPEVQFNWVDGVEVHNAKTKPREQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNYHTQKSLSPGK	450
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLSWYQQKPGKAPKLLIYKASKSHITGVPSTRFSGSGTDFTLTISS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	451
vlCDR1	RASQININWLS	452
vlCDR2	KASKSH	453
vlCDR3	QQGQSYPT	454
Full length light chain For CHA.9.547.10.H4 (S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWLSWYQQKPGKAPKLLIYKASKSHITGVPSTRFSGSGTDFTLTISS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455

Figure 3T: CHA.9.547.11

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSS	456
vhCDR1	GFTSSYIMS	457
vhCDR2	TISGGGTNTY	458
vhCDR3	WLLSYAMDY	459
Full length HC for CHA.9.547.11.H4 (S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLWVSTISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKWLSSYAMDYWGQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTTKTYTCNVDHPSNTKVDRVESKYGPPCPPAPFELGGPSVFLF PPPKDITLMISRTPEVTCVWDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	460
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGGSGGTDFTLTSS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	461
vlCDR1	RASQININWLS	462
vlCDR2	KASKSHT	463
vlCDR3	QQGQSYPT	464
Full length light chain For CHA.9.547.11.H4 (S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGGSGGTDFTLTSS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	465

Figure 3UU: CHA.9.547.12

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	466
vhCDR1	GFTSSYIMS	467
vhCDR2	TISGGGTNTY	468
vhCDR3	WLLSYAMDY	469
Full length HC For CHA.9.547.12.H4 (S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYPPCPPAPFELGGPSVFLF PPPKDITLMISRTPEVTCVWDVDSQEDPEVQFNWVDGVEVHNAKTKPREQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLY SRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK	470
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQGGQSYPTFGGQTKLEIK	471
vlCDR1	RASQININWLS	472
vlCDR2	KASKSHT	473
vlCDR3	QGGQSYPT	474
Full length light chain for CHA.9.547.12.H4 (S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LQPEDFATYYCQGGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	475

Figure 3VV: CHA.9.547.13

What	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u>	476
vhCDR1	GFTSSYIMS	477
vhCDR2	TISGGGTNTY	478
vhCDR3	WLLSYAMDY	479
Full length HC for CHA.9.547.13.H4 (S241P)	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAIVLQSSGLYSLSVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYPPCPPAPEFLGGPSVFLF PPPKDITLMISRTPEVTCVWDVSEQEDPEVQFNWVDGVEVHNAKTPREEQFNSTYRVSVLTVHQDWLNGKEYCKV SNKGLPSSIEKTIKAKQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCSVAMHEALHNHYTQKSLSLSPGK	480
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSPRFGSGSGTDFLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIK	481
vlCDR1	RASQININWLS	482
vlCDR2	KASKSHT	483
vlCDR3	QQGQSYPT	484
Full length light chain for CHA.9.547.13.H4 (S241P)	DIQMTQSPSSLSASVGDRITITCRASQININWLSWYQQKPGKAPKLLIYKASKSHTGVPSPRFGSGSGTDFLTIS LQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	485

Figure 3WW: CHA.9.543

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWRQSHGKNLEWLG ^{LI} FPYNGGTSYNQNFKGKATLTVDTSSTAY MELLSITSVDSAVYYCARGVRFALDYWGQGTSVSVSS	486
vhCDR1	GYSFTGYTMN	487
vhCDR2	LIFPYNGGTS	488
vhCDR3	GVRFALDY	489
Full length HC for CHA.9.543.H4(S2 41P))	Mouse hybridoma, sequence not available	
Variable light (vl) domain	DVVMVTQTPLSLPVSFQDQVSI ^{CR} SSQSLANSYGN ^{TY} LSWY ^L HKPGQSPQL ^{LI} YEISNRFSGVPDRFSGSGGTDFTLNISTIKP EDLGMYYC ^{LG} THQHPWTFGGGKLEIK	490
vlCDR1	RSSQSLANSYGN ^{TY} LS	491
vlCDR2	EISNRF	492
vlCDR3	LGTHQHPWT	493
Full length light chain for CHA.9.543.H4(S2 41P))	Mouse hybridoma, sequence not available	

Figure 3XX: BM26 mouse IgG1 (BM26-M1) (WO2016/028656A1, Clone 31C6)

W/hat	Sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVMHVVVKQPGQGLEWIGVDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSLTSEDSAVYYCARGGPGYWYFDVWGAGTTVTSS	494
vhCDR1	GYTSSVY	495
vhCDR2	IDPYNDGA	496
vhCDR3	ARGGPGYWYFDV	497
Full length HC	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVMHVVVKQPGQGLEWIGVDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSLTSEDSAVYYCARGGPGYWYFDVWGAGTTVTSSAKTTTPPSVYPLAPGSAQAQTNMVLGQLVKGYFREPVTVTW NSGSLSSGVHTPAVLOSPLYLSSSVTVPSSTWPSSTWCNVAPASSTKVDKIVPRDCGCKPCICTVPEVSSVFIHPPKPKD VLTITLTPKVTCVAVDISKDDPEVQFVWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAP IEKTSKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSRVYVKLVV QKSNWEAGNTFTCSVLHEGLHNHTEKLSHSPGK	498
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQKQKQKSPQLLVYNAKTLAEGVPSRFSGGSGTQFSKINSIQPEDFG TYQCQHHFGSPLTFGAGTTILELK	499
vICDR1	EHYSY	500
vICDR2	NAK	501
vICDR3	QHHFGSPLT	502
Full length light chain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQKQKQKSPQLLVYNAKTLAEGVPSRFSGGSGTQFSKINSIQPEDFG TYQCQHHFGSPLTFGAGTTILELKRAADAAPTYSPFPSSSEQLTSGGASVVCFLNNPYKDIWIKWKIDGSRQNGVINSWTDQ DSKDSYNSMSSLTLTKDEYERHNSYTCEATHKTSTSPVKSFRNEC	503

Figure 3YY: BM29 mouse IgG1 (BM29-M1) (US2016/0176963A1, Clone 22G2)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGGLV KPSETLSLTCTVSGGSVSGIYYWSWIRPPGKGLWIGIYYSGSTNYPNPKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNDYFFGVGVWGGGTTTVSS	504
vhCDR1	GGSVSSGIW	505
vhCDR2	IYSGST	506
vhCDR3	ARDYYVSGNYYNDYFFGVGV	507
Full length HC	QVHLQESGPGGLV KPSETLSLTCTVSGGSVSGIYYWSWIRPPGKGLWIGIYYSGSTNYPNPKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNDYFFGVGVWGGGTTTVSSAKTTPSVVPLAPGSAQTNSMVTGLCLVKGYFPEP VTVTWNSGSLSGVHTPEAVLQSDLYTLSSSVTVPSSTW/PSEITVCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI PPKPDVLTTLTPKVTGVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS AAFPAPIETKTSKGRKAPQVYTIPTPPKEQMAKDVKSLTCMIDTFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVY SKLNVQKSNWEAGNTFTCSVLHEGLHNHTEKSLSHSPGK	508
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIYDASNRAIGIPARFSGSGGTDFTLTISSLEPEDFAVY YCQQRSNWPPLETFGPSTKVDIK	509
vlCDR1	QSVSSY	510
vlCDR2	DAS	511
vlCDR3	QQRSNWPPLETF	512
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIYDASNRAIGIPARFSGSGGTDFTLTISSLEPEDFAVY YCQQRSNWPPLETFGPSTKVDIKRADAAPTVSIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTD QDSKSDSTYSMSSTLTITKDEYERHNSYTCEATHKTTSTSPIVKSFNRNEC	513

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Figure 3AAA

From US20170281764 (JN Biosciences)	What sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:10 from US2017281764)	DVQLVESGGGLVQPGRKLSCAASGFTFSNFGMIHWVROAPEKGLEWVAFISGSS SIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARMRLDYYAMDYWGQ GTSVTVSS	514
vhCDR1 (SEQ ID NO:11 from US2017281764)	NFGMIH	515
vhCDR2 (SEQ ID NO:12 from US2017281764)	FISGSSSIYYADTVKG	516
vhCDR3 (SEQ ID NO:13 from US2017281764)	MRLDYYAMDY	517
Light chain (SEQ ID NO:14 from US2017281764)	DVQITQSPSYLAASPGETITINCRASKISKYLAWYQEKPGKTNKLLIYSGSTLQSGIPS RFSGSGSGTDFTLTISLSEPEDFAMYYCQQHNEYPWTFGGGKLEIK	518
vlCDR1 (SEQ ID NO:15 from US2017281764)	RASKISKYLA	519
vlCDR2 (SEQ ID NO:16 from US2017281764)	SGSTLQS	520
vlCDR3 (SEQ ID NO:17 from US2017281764)	QQHNEYPWT	521

Figure 3BBB

From US20170281764 (JN Biosciences)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:18 from US2017281764)	EVQLQQSGPELVKPGASVKISKCTSGYTFIEYTMHWVKQSHGKNLEWIGINPNNG GTSYNQKFKGRATLTVDKSSSTAYMELRSLTSDSDSAVYYCARPGWYNYAMDYWG QGTSVTVSS	522
vhCDR1	EYTMH	523
(SEQ ID NO:19 from US2017281764)		
Light chain (SEQ ID NO:20 from US2017281764)	GINPNNGGTSYNQKFKG	524
Light chain (SEQ ID NO:22 from US2017281764)	PGWYNYAMDY	525
Light chain (SEQ ID NO:23 from US2017281764)	DIVMTQSHKFMETSVGDRVNITCKASQGVSTAVAWYQQKPGQSPKLLIYSASYRYT GVPDRFTGSGSGTDFITFTISSVQAEDLAVYHCQQHYITPWTFGGCTKLEIK	526
vCDR1	KASQGVSTAVA	527
(SEQ ID NO:23 from US2017281764)		
vCDR2	SASYRYT	528
(SEQ ID NO:24 from US2017281764)		
vCDR3	QQHYITPWT	529
(SEQ ID NO:25 from US2017281764)		

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Figure 3CCC

From US20170281764 (JN Biosciences) What sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:26 from US2017281764)	530
EVQLVESGGGLVKPGGSLKLSCAASGFAFSDYDMSWVRQTPEKRLIEWVAYISDGGY NTYYPDITVKGRFTISRDNAKNTLYLQMSSLKSEDTAIYYCARQILLRYYFDYWGQGT TLTVSS	
vHCDR1 (SEQ ID NO:27 from US2017281764)	531
DYDMS	
vHCDR2 (SEQ ID NO:28 from US2017281764)	532
YISDGGYNTYYPDITVKG	
vHCDR3 (SEQ ID NO:29 from US2017281764)	533
QILLRYYFDY	
Light chain (SEQ ID NO:30 from US2017281764)	534
DIVMSQSPSSLAVSVGEKVTMTCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYW ASTRESGVPDFRFTGSGSGTDFLTITSSVK AEDLAVYYCQQYHSPWTFGGGTGLEIK	
vLCDR1 (SEQ ID NO:31 from US2017281764)	535
KSSQSLLYSSNQKNYLA	
vLCDR2 (SEQ ID NO:32 from US2017281764)	536
WASTRES	
vLCDR3 (SEQ ID NO:33 from US2017281764)	537
QQYHSPWWT	

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Figure 3DDD

From US20170281764 (JN Biosciences)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:35 from US2017281764)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMIWVRQAPGKGLEWVAFISGSS IYYADTVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMLDYYAMDYWGQ GTMVTVSS	538
Light chain (SEQ ID NO:37 from US2017281764)	DIQMTQSPSSLASVGDRTVTITCRASKSISKYLAWYQQKPGKAPKLLIYSGSTLQSGV PSRPSGSGGTDFTLTISSLQPEDFATYYCQQHNEYPWTFGGGTKVEIK	539
From US20170281764 (JN Biosciences)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:34 from US2017281764)	MDSRLNLVFLVLILKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWV RQAPGKGLEWVAFISGSSIIYYADTVKGRFTISRDNKNSLYLQMNSLRAEDTAVY YCARMLDYYAMDYWGQGTMTVSS	540
Light chain (SEQ ID NO:36 from US2017281764)	MRFQVQVLGLLLWISGAQCIDIQMTQSPSSLASVGDRTVTITCRASKSISKYLAWYQ QKPGKAPKLLIYSGSTLQSGVPSRPSGSGGTDFTLTISSLQPEDFATYYCQQHNEYP WTFGGGTKVEIK	541

Figure 3EEE

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG; see also, WO2016011264)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:15 from WO2015009856)	EVQLVESGGGLTQPGKSLKLSCEASGFTFSFTMIWVRQSPGKGLEWVAFIRSGGIVF YADAVRGRFTISRDNAKNLLFLQMNDLKSEDTAMYYCARRPLGHNTFDSWGQGTLVT VSS	542
vhCDR1 (SEQ ID NO:4 from WO2015009856)	GIFFSSFTMH	543
vhCDR2 (SEQ ID NO:5 from WO2015009856)	FIRSGGIVFYADAVRG	544
vhCDR3 (SEQ ID NO:6 from WO2015009856)	RPLGHNTFDS	545
Light chain (SEQ ID NO:13 from WO2015009856)	DIVMTQSPSSLAVSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASI RFTGVPRFTGSGSGTDYTLTITSVQAEDMGQYFCQQGINNPLTFGDDGTKLEIKR	546
vlCDR1 (SEQ ID NO:1 from WO2015009856)	KSSQSLYYSGVKENLLA	547
vlCDR2 (SEQ ID NO:2 from WO2015009856)	ASIRFT	548
vlCDR3 (SEQ ID NO:3 from WO2015009856)	QQGINNPLT	549

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Figure 3FF

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG; see also, WO2016011264)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:16 from WO2015009856)	EVQLQQSGPELVKPGTSMKISKASGYSTGHLMNWVKQSHGKNLEWIGLIIPYNGGTS YNQKFKGKATLTVDKSSSTAYMELLSLTSDDSA VYFC SRGLRGFYAMDYWGQGTSVT VSS	550
vhCDR1 (SEQ ID NO:10 from WO2015009856)	GYSFTGHLMN	551
vhCDR2 (SEQ ID NO:11 from WO2015009856)	LIIPYNGGTSYNQKFKG	552
vhCDR3 (SEQ ID NO:12 from WO2015009856)	GLRGFYAMDY	553
Light chain (SEQ ID NO:14 from WO2015009856)	DVVLTTQPLSLSVSGDQVSISCRSSQSLVNSYGNTELSWY LHKPGQSPQLLIFGISNRFS GVPDRFSGSGGTDFTLKISTIKPEDLGMYCYCLQGTHQPTTFGPGTKLEVK	554
vlCDR1 (SEQ ID NO:7 from WO2015009856)	RSSQSLVNSYGNTELS	555
vlCDR2 (SEQ ID NO:8 from WO2015009856)	GISNRFS	556
vlCDR3 (SEQ ID NO:9 from WO2015009856)	LQGTHQPPT	557

Figure 3GGG

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

Sequences and germlines (GL) of IgH1 ABs									
Ab	VH GL	CDR- H1 ¹ (SEQ ID NOs 558- 562)	CDR- H2 ² (SEQ ID NOs 563- 567)	CDR- H3 ³ (SEQ ID NOs 568- 572)	VL GL	CDR- L1 ⁴ (SEQ ID NOs 579- 582)	CDR- L2 ⁵ (SEQ ID NOs 583- 587)	CDR- L3 ⁶ (SEQ ID NOs 588- 592)	VL Protein (SEQ ID NOs 593-597)
MAB1 -IgG4	4- 39	GSISSS (SEQ ID NO 48)	SIYVSG (SEQ ID NO 36)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VH Protein (SEQ ID NOs 573-577)	RASQS VSSYL A (SEQ ID NO 67)	DASNRA T (SEQ ID NO 67)	QQHFNL PT (SEQ ID NO 63)	EVLTSQSPATLSTSPGERATLSCTRAQSQSVSSYLAWYQOK PGQAPRLLYDASNRATGIPARFSGSGSGTDFTLTSSLEP EDFAVYYCQQHFNLPITFGGGTKVEIK (SEQ ID NO 25)
MAE2 -IgG4	4- 39	GSISSS (SEQ ID NO 49)	SIYVSG (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VH Protein (SEQ ID NOs 573-577)	RASQS VSSYL A (SEQ ID NO 67)	DASNRA T (SEQ ID NO 67)	QQHFNL PT (SEQ ID NO 63)	EVLTSQSPATLSTSPGERATLSCTRAQSQSVSSYLAWYQOK PGQAPRLLYDASNRATGIPARFSGSGSGTDFTLTSSLEP EDFAVYYCQQHFNLPITFGGGTKVEIK (SEQ ID NO 25)
MAR3 -IgG4	4- 39	GSISST (SEQ ID NO 30)	SIYVSG (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VH Protein (SEQ ID NOs 573-577)	RASQS VSSYL A (SEQ ID NO 67)	DASNRA T (SEQ ID NO 67)	QQHFNL PT (SEQ ID NO 63)	EVLTSQSPATLSTSPGERATLSCTRAQSQSVSSYLAWYQOK PGQAPRLLYDASNRATGIPARFSGSGSGTDFTLTSSLEP EDFAVYYCQQHFNLPITFGGGTKVEIK (SEQ ID NO 25)
MAR4 -IgG4	4- 39	GSISST (SEQ ID NO 30)	SIYVSG (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VH Protein (SEQ ID NOs 573-577)	RASQS VSSYL A (SEQ ID NO 67)	DASNRA T (SEQ ID NO 67)	QQHFNL PT (SEQ ID NO 63)	EVLTSQSPATLSTSPGERATLSCTRAQSQSVSSYLAWYQOK PGQAPRLLYDASNRATGIPARFSGSGSGTDFTLTSSLEP EDFAVYYCQQHFNLPITFGGGTKVEIK (SEQ ID NO 25)
MAR5 -IgG4	4- 39	GSISST (SEQ ID NO 30)	SIYVSG (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VH Protein (SEQ ID NOs 573-577)	RASQS VSSYL A (SEQ ID NO 67)	DASNRA T (SEQ ID NO 67)	QQHFNL PT (SEQ ID NO 63)	EVLTSQSPATLSTSPGERATLSCTRAQSQSVSSYLAWYQOK PGQAPRLLYDASNRATGIPARFSGSGSGTDFTLTSSLEP EDFAVYYCQQHFNLPITFGGGTKVEIK (SEQ ID NO 25)

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 Chothia and Chothia numbering systems.⁴ According to the Kabat and Chothia numbering systems.⁵ According to the Kabat, Chothia, and IMGT numbering systems.⁶ According to the Kabat, Chothia, and IMGT numbering systems.

Figure 3HHH

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

		Sequences and germlines (GL) of TIGIT ABPs									
		CDR- H1 ⁷	CDR- H2 ⁸	CDR- H3 ⁹			CDR- L1 ¹⁰	CDR- L2 ¹¹	CDR- L3		
		(SEQ ID NO 588- 602)	(SEQ ID NO 603- 607)	(SEQ ID NO 608- 612)	VL	GL	(SEQ ID NO 613- 627)	(SEQ ID NO 628- 632)	(SEQ ID NO 633- 637)		
MAb6	VH	GNEKGS	SIYNSGTT	ARDGV	VL	GL	RASQS	GASSRA	QOHTV	VL Protein (SEQ ID NO 633-637)	
4gG4	4	YVWG	YVNSLK	LTLNKR	20	VK3-	VSSSY	T(SQ	RPLT	EIVLTQSPGTLSPGERATLS	
39	39	(SEQ ID NO 51)	S (SEQ ID NO 39)	STDI	20	VK3-	(SEQ ID NO 71)	ID (NO 68)	(SEQ ID NO 64)	KPGQAPRLIYGASSRATGIPDRFGSGGIDITLISRL	
										EPHDEAVVYCCQHTVTPPLTFGGGKVEIK (SEQ ID NO 26)	
MAb7	VH	GNEKGS	SIYNSGTT	ARDGV	VL	GL	RASQS	GASSRA	QOHTV	EIVLTQSPGTLSPGERATLS	
4gG4	4	YVWG	YVNSLK	LTLNKR	20	VK3-	VSSSY	T(SQ	RPLT	KPGQAPRLIYGASSRATGIPDRFGSGGIDITLISRL	
31	31	(SEQ ID NO 32)	S (SEQ ID NO 40)	STDI	20	VK3-	(SEQ ID NO 71)	ID (NO 68)	(SEQ ID NO 64)	EPHDEAVVYCCQHTVTPPLTFGGGKVEIK (SEQ ID NO 26)	
MAb8	VH	GNEKGS	SIYNSGTT	ARDGV	VL	GL	RASQS	GASSRA	QOHTV	EIVLTQSPGTLSPGERATLS	
4gG4	4	YVWG	YVNSLK	LTLNKR	20	VK3-	VSSSY	T(SQ	RPLT	KPGQAPRLIYGASSRATGIPDRFGSGGIDITLISRL	
39	39	(SEQ ID NO 53)	S (SEQ ID NO 41)	STDI	20	VK3-	(SEQ ID NO 71)	ID (NO 68)	(SEQ ID NO 64)	EPHDEAVVYCCQHTVTPPLTFGGGKVEIK (SEQ ID NO 26)	
MAb9	VH	GNEKGS	SIYNSGTT	ARDGV	VL	GL	RASQS	GASSRA	QOHTV	EIVLTQSPGTLSPGERATLS	
4gG4	4	YVWG	YVNSLK	LTLNKR	20	VK3-	VSSSY	T(SQ	RPLT	KPGQAPRLIYGASSRATGIPDRFGSGGIDITLISRL	
31	31	(SEQ ID NO 54)	S (SEQ ID NO 42)	STDI	20	VK3-	(SEQ ID NO 71)	ID (NO 68)	(SEQ ID NO 64)	EPHDEAVVYCCQHTVTPPLTFGGGKVEIK (SEQ ID NO 26)	
MAb1	VH	GNEKGS	SIYNSGTT	ARDGV	VL	GL	RASQS	GASSRA	QOHTV	EIVLTQSPGTLSPGERATLS	
4gG4	4	YVWG	YVNSLK	LTLNKR	20	VK3-	VSSSY	T(SQ	RPLT	KPGQAPRLIYGASSRATGIPDRFGSGGIDITLISRL	
31	31	(SEQ ID NO 55)	S (SEQ ID NO 43)	STDI	20	VK3-	(SEQ ID NO 71)	ID (NO 68)	(SEQ ID NO 64)	EPHDEAVVYCCQHTVTPPLTFGGGKVEIK (SEQ ID NO 26)	

⁷ Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems.⁸ According to the Kabat numbering system.⁹ According to the Chothia numbering system.¹⁰ According to the Kabat and Chothia numbering systems.¹¹ According to the Kabat numbering systems.¹² According to the Kabat, Chothia, and IMGT numbering systems.

Figure 3III

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

Sequences and germlines (GL) of LIGHT ABs ¹³									
Ab	CDR- H1 (SEQ ID NOs 638- 642)	CDR- H2 (SEQ ID NOs 643- 647)	CDR- H3 (SEQ ID NOs 648- 652)	CDR- L1 (SEQ ID NOs 653-657)	CDR- L2 (SEQ ID NOs 658- 662)	CDR- L3 (SEQ ID NOs 663- 667)	CDR- L4 (SEQ ID NOs 668-672)	CDR- L5 (SEQ ID NOs 673-677)	CDR- L6 (SEQ ID NOs 678-682)
MAB1 1-IgG4	VH GL 31	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 14)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 15)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QQITYR PPLT (SEQ ID NO 64)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 26)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 2-IgG4	VH GL 31	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 16)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 17)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QQITYR PPLT (SEQ ID NO 64)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 26)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 3-IgG4	VH GL 46	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 18)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 19)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QQITYR PPLT (SEQ ID NO 64)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 26)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 4-IgG4	VH GL 46	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 20)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 21)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QQITYR PPLT (SEQ ID NO 64)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 26)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 5-IgG4	VH GL 46	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 22)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGFLVPSGQSLISLTCTAS GGSEGLYYWGAWIRQPGKGLHWI GSIYSGSYVYNPSLKRVTISVDIS KNQPSLKLSSVTADTAAYVYCARD GVLALNKRSPDWGGQGMVTVSS (SEQ ID NO 23)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QQITYR PPLT (SEQ ID NO 64)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 26)	EVLTQSGTILSLSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGASTRATGIPARFSGSGGTETPLTSSLSQS PEDFAVVYCCQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)

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 3]]]]

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

Sequences and germlines (GL) of IIGII ABPs									
Ab	CDR- H1 (SEQ ID NOs)	CDR- H2 (SEQ ID NOs)	CDR- H3 (SEQ ID NOs)	CDR- L1 (SEQ ID NOs)	CDR- L2 (SEQ ID NOs)	CDR- L3 (SEQ ID NOs)	CDR- L4 (SEQ ID NOs)	CDR- L5 (SEQ ID NOs)	VL Protein (SEQ ID NOs 720-725)
MAB1 6-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)
MAB1 7-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)
MAB1 8-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)
MAB1 9-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)
MAB2 0-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)
MAB2 1-4gG4	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	YIFR6 (SEQ ID NO 68)	EVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKFG QAPRLHYGASTRAIGHPARFSGSGSGTEFTLTISLQSEDFAV YYCQQYVVVWPPETPGGGTKVEIK (SEQ ID NO 27)

15 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 3KKK

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:7 from WO2016028656)	EVQLQESGPGLVKPSQSLSLTCSVTGSSIASDYWGWRKFPGNKMEW/MGFITYSGSTSY NPSLKSRISITRDTSKNQFLQLHSVTDDTATYSCARMPSFITLASLSTWEGYDFWGP GTMVTVSS	726
vhCDR1 (SEQ ID NO:1 from WO2016028656)	SDYWG	727
vhCDR2 (SEQ ID NO:2 from WO2016028656)	FITYSGSTSYNPSLKS	728
vhCDR3 (SEQ ID NO:3 from WO2016028656)	MPSFITLASLSTWEGYDF	729
Light chain (SEQ ID NO:8 from WO2016028656)	DIQMTQSPSLLSASVGDRTVLNCKASQSIHKNLAWYQQKLGAPKFLIYYANSLQTGIPS RFGSGSGTDFLTISGLQPEDVATYFCQQYYSGWTFGGGTKVELK	730
vICDR1 (SEQ ID NO:4 from WO2016028656)	KASQSIHKNLA	731
vICDR2 (SEQ ID NO:5 from WO2016028656)	YANSLQT	732
vICDR3 (SEQ ID NO:6 from WO2016028656)	QQYYSGWT	733

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Figure 3LLL

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:9 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARMPSFITLASLSTWEGYFDYWGQG TMVTVSS	734
vhCDR1 (WO2016028656)	DYWG	735
vhCDR2 (WO2016028656)	FITYSGSTSYNPSLKS	736
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDY	737
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:10 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARMPSFITLASLSTWEGYFDYWGQG TMVTVSS	738
vhCDR1 (from WO2016028656)	SDYWG	739
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	740
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDY	741

Figure 3MMM

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:11 from WO2016028656)	EVQLQESGPGLVKPSFETLSLTCTVSGSSISDYWGWIQQPGKGLWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYDFWGGQGT MVTVSS	742
vhCDR1 (from WO2016028656)	SDYWG	743
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	744
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	745
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:12 from WO2016028656)	EVQLQESGPGLVKPSFETLSLTCTVSGSSISDYWGWIQQPGKGLWWMGFITYSGSTSYN PSLKSRIITISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYDFWGGQGT TMVTVSS	746
vhCDR1 (from WO2016028656)	SDYWG	747
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	748
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	749

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Figure 3000

From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:13 from WO2016028656)	750
EVQLQESGPGLVKPSSETLSLTCTVSGGSISDDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQG TMVTVSS	
vhCDR1 (from WO2016028656)	751
SDYWG	
vhCDR2 (from WO2016028656)	752
FITYSGSTSYNPSLKS	
vhCDR3 (from WO2016028656)	753
MPSFITLASLSTWEGYFDY	
From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:14 from WO2016028656)	754
EVQLQESGPGLVKPSSETLSLTCTVSGGSISDDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQG TMVTVSS	
vhCDR1 (from WO2016028656)	755
SDYWG	
vhCDR2 (from WO2016028656)	756
FITYSGSTSYNPSLKS	
vhCDR3 (from WO2016028656)	757
MPSFITLASLSTWEGYFDY	

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Figure 3PPP

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:15 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSISSDYWGWIQQPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQSLKLHHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFFWGQGT MVTVSS	758
vhCDR1 (from WO2016028656)	SDYWG	759
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	760
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDFF	761
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:16 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSISSDYWGWIQQPGKGLEWIGFITYSGSTSYNP PSLKSRIITISVDTSKNQSLKLHHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFFWGQGT TMVTVSS	762
vhCDR1 (from WO2016028656)	SDYWG	763
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	764
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDFF	765

Figure 3QQQ

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:17 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQQPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDWFVGQ GTMVTVSS	766
vhCDR1 (from WO2016028656)	SDYWG	767
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	768
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	769
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:18 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQQPGKGLEWIGFI TYSGSTSYNPSLKSRTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFI TLASLSTWEGYFDWFVGQGTMTVTVSS	770
vhCDR1 (from WO2016028656)	SDYWG	771
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	772
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	773

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Figure 3RRR

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:19 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSISSDYWGWRQPPGKGLEWIGFI TYSGSTSYNPSLKSRLTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFI TLASLSTWEGYFDWGGQGTMTVSS	774
vhCDR1 (from WO2016028656)	SDYWG	775
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	776
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDW	777
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:20 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSISSDYWGWRQPPGKGLEW/MGFI TYSGSTSYNPSLKSRLTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFI TLASLSTWEGYFDWGGQGTMTVSS	778
vhCDR1 (from WO2016028656)	SDYWG	779
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	780
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDW	781

Figure 3SSS

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:21 from WO2016028656)	EVQLQESGPGGLVKPSETLSLTCAVSGYSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSCLKLHVSVAADTAVYYCARMPSFITLASLSTWEGYFDYWGQ GTMVTVSS	782
vhCDR1 (from WO2016028656)	SDYWG	783
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	784
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	785
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:22 from WO2016028656)	EVQLQESGPGGLVKPSETLSLTCAVSGYSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSCLKLHVSVAADTAVYYCARMPSFITLASLSTWEGYFDYWGQ TMVTVSS	786
vhCDR1 (from WO2016028656)	SDYWG	787
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	788
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	789

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Figure 3TTT

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:37 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDWGGQG TMVTVSSAS	790
vhCDR1 (from WO2016028656)	SDYWG	791
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	792
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFD	793
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:38 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDWGGQG TMVTVSS	794
vhCDR1 (from WO2016028656)	SDYWG	795
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	796
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFD	797

Figure 3UUU

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:39 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWRKPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDWFVGQG TMVTVSS	798
vhCDR1 (from WO2016028656)	SDYWG	799
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	800
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDWF	801
From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:40 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWRKPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDWFVGQG TMVTVSS	802
vhCDR1 (from WO2016028656)	SDYWG	803
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	804
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDWF	805

Figure 3VVV

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:41 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPKGMWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQ GTMVTVSS	806
vhCDR1 (from WO2016028656)	SDYWG	807
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	808
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	809
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:42 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQQPKGMWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQ GTMVTVSS	810
vhCDR1 (from WO2016028656)	SDYWG	811
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	812
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	813

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Figure 3WWW

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:43 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWRQFPKGKLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQPSLKLSSVTADDTAVYYCARMPSFITLASLSTWEGYFDYWGQG TMVTVSS	814
vhCDR1 (from WO2016028656)	SDYWG	815
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	816
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	817
From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:44 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWRKPPGKMEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQPSLKLSSVTAAADTAVYYCARMPSFITLASLSTWEGYFDYWGQG GTMVTVSS	818
vhCDR1 (from WO2016028656)	SDYWG	819
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	820
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	821

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Figure 3XXX

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:45 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCSVTGSSIASDYWGWRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQPSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQG TMVTVSS	822
vhCDR1 (from WO2016028656)	SDYWG	823
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	824
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	825
From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:46 from WO2016028656)	EVQLQQSGAGLLKPSSETLSLTCSVTGSSIASDYWGWRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDYFWGQG GTMVTVSS	826
vhCDR1 (from WO2016028656)	SDYWG	827
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	828
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDY	829

Figure 3YYY		SEQ ID NO:
From WO2016028656 (Table 4, reproduced herein)	Sequence	
What		
Heavy chain		
(SEQ ID NO:47 from	EVQLQESGPGLVKPPGTLSTCSVTGSSIASDYWGWWVRQPGKGLEWIGFITYSGSTSYN	830
WO2016028656)	PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSPFITLASLSTWEGYFDYWGQ	
	GTMVTVSS	
vhCDR1	SDYWG	831
(from WO2016028656)		
vhCDR2	FITYSGSTSYNPSLKS	832
(from WO2016028656)		
vhCDR3	MPSFITLASLSTWEGYFDY	833
(from WO2016028656)		

Figure 3ZZZ

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2016028656)	EVQLQESGPGLVKPSFETLSLTCAVSGSSISDYWGWRQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSCLKLHISVTAADTAVYYCARMPSPFITLASLSTWEGYFDYFWGQGT MVTVSS	834
vhCDR1 (SEQ ID NO: from WO2016028656)	SDYWG	835
vhCDR2 (SEQ ID NO: from WO2016028656)	FITYSGSTSYNPSLKS	836
vhCDR3 (SEQ ID NO: from WO2016028656)	MPSFITLASLSTWEGYFDF	837

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Figure 3AAAA

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:24 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGSSISDYWGWRQPPGKGLEWMGFITYSGSTSYN PSLKSRIITISRDTSKNQFSLKLSHVTAAADTAVYYCARMPSTITLASLSTWEGYFDWGGQ TMVTVSS	838
vHCDR1 (from WO2016028656)	SDYWG	839
vHCDR2 (WO2016028656)	FITYSGSTSYNPSLKS	840
vHCDR3 (WO2016028656)	MPSFITLASLSTWEGYFD	841

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:25 from WO2016028656)	DIQMTQSPSSLSASVGDRTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQGTGVP SRFSGSGGTDFTLTISSIQPEDFATYYCQQYYSGWTFGGGTKVEIK	842
vLCDR1 (from WO2016028656)	KASQSIHKNLAW	843
vLCDR2 (from WO2016028656)	YANSLQT	844
vLCDR3 (from WO2016028656)	QQYYSGW/T	845

Figure 3B BBB

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:26 from WO2016028656)	DIQMTQSPSSLSASVGDRTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGVP RFSGSGSGIDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	846
vICDR1 (from WO2016028656)	KASQSIHKNLAW	847
vICDR2 (from WO2016028656)	YANSLQT	848
vICDR3 (from WO2016028656)	QQYYSGWT	849
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:27 from WO2016028656)	DIQMTQSPSSLSASVGDRTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGIPS RFSGSGSGIDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	850
vICDR1 (from WO2016028656)	KASQSIHKNLAW	851
vICDR2 (from WO2016028656)	YANSLQT	852
vICDR3 (from WO2016028656)	QQYYSGWT	853

Figure 3CCCC

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:28 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKLLIYYANSLQIGVP SRFSGSGGIDFTLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	854
vICDR1 (from WO2016028656)	KASQSIHKNLAW	855
vICDR2 (from WO2016028656)	YANSLQT	856
vICDR3 (from WO2016028656)	QQYYSGWT	857
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:29 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQIGVPS RFSGSGGIDFTLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	858
vICDR1 (from WO2016028656)	KASQSIHKNLAW	859
vICDR2 (from WO2016028656)	YANSLQT	860
vICDR3 (from WO2016028656)	QQYYSGWT	861

Figure 3DDDD		
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What		
Light chain		
(SEQ ID NO:30 from	DIQMTQSPSSLASVGDRTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQTGIPS	862
WO2016028656)	RFSGSGSGTDFTLTISSLQPEDVATYYCQYYSGWTFGGGTKVEIK	
vICDR1	KASQSIHKNLAW	863
(from WO2016028656)		
vICDR2	YANSLQT	864
(from WO2016028656)		
vICDR3	QQYYSGWT	865
(from WO2016028656)		
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What		
Light chain		
(SEQ ID NO:48 from	DIQMTQSPSSLASVGDRTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP	866
WO2016028656)	SRFSGSGSGTDFTLTISSLQPEDFATYYCQYYSGWTFGGGTKVEIK	
vICDR1	KASQSIHKNLAW	867
(from WO2016028656)		
vICDR2	YANSLQT	868
(WO2016028656)		
vICDR3	QQYYSGWT	869
(WO2016028656)		

Figure 3EEEE

From WO2016028656 (Table 4, reproduced herein)			
What	sequence		SEQ ID NO:
Light chain (SEQ ID NO:49 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQGTGVP RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK		870
vICDR1 (from WO2016028656)	KASQSIHKNLAW		871
vICDR2 (WO2016028656)	YANSLQT		872
vICDR3 (WO2016028656)	QQYYSGWT		873
From WO2016028656 (Table 4, reproduced herein)			
What	sequence		SEQ ID NO:
Light chain (SEQ ID NO:50 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQGTGVP SRFSGSGSGTDFTLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK		874
vICDR1 (from WO2016028656)	KASQSIHKNLAW		875
vICDR2 (WO2016028656)	YANSLQT		876
vICDR3 (WO2016028656)	QQYYSGWT		877

Figure 3FFF

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:51 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK	878
vICDR1 (from WO2016028656)	KASQSIHKNLAW	879
vICDR2 (WO2016028656)	YANSLQT	880
vICDR3 (WO2016028656)	QQYYSGWT	881
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:52 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGIPS RFSGSGSGTDFLTISSLQPEDFATYYCQQYYSGWTFGGG IKVEIK	882
vICDR1 (from WO2016028656)	KASQSIHKNLAW	883
vICDR2 (WO2016028656)	YANSLQT	884
vICDR3 (WO2016028656)	QQYYSGWT	885

Figure 3GGGG		SEQ ID NO:
From WO2016028656 (Table 4, reproduced herein)		
What	sequence	
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWRQFPGNKLEWMGYISNSGSAS YNPSLKSRIISITRDTSKNQFFLQLNSVTIEDTATYYCATLIYYDYGGAMNFWGQGTSVT VSS	886
vhCDR1 (from WO2016028656)	GYSITSDYAWN	887
vhCDR2 (WO2016028656)	YISNSCSASYNPSLKS	888
vhCDR3 (WO2016028656)	LIYYDYGGAMNF	889

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Figure 3HHHH

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO.
Light chain (SEQ ID NO: 62 from WO2016028656)	DIVMTQSIHKFMSTSVGDRVSITCKASQGVSTTVAWYQQKPGQSPKLLINYSASYRYTGVPDRFTG SGSGTDFITFISSVQSEDLAVYYCQHYYSIPWTFGGGTKLEIK	890
vICDR1 (from WO2016028656)	KASQGVSTTV A	891
vICDR2 (WO2016028656)	SASYRYT	892
vICDR3 (WO2016028656)	QHYYSTPWT	893
vICDR2 variant (WO2016028656)	YASNLQT	894
vICDR2 variant (WO2016028656)	YASSLQT	895
vICDR2 variant (WO2016028656)	YASTLQT	896
vICDR2 variant (WO2016028656)	YATTLQT	897
vICDR2 variant (WO2016028656)	YASYLQT	898
vICDR2 variant (WO2016028656)	YANQLQT	899
vICDR2 variant (WO2016028656)	YAGSLQT	900
vICDR2 variant (WO2016028656)	YASQLQT	901
vICDR2 variant (WO2016028656)	YADSLQT	902

Figure 3IIII	
From WO2016028656 (Table 4, reproduced herein)	
What	sequence
Light chain (SEQ ID NO: 62 from WO2016028656)	DI VMTQSIHKFNSTSVGDRVSI TCKASQGVSTTVAWYQQKPGQSPKLLIYSA SRYTGTGVPDRFTG SGSGTDFITFISSVQSEDLAVYYCQHYYSTPWTFGGGKLEIK
vHCDR1 (from WO2016028656)	KASQGVSTTV A
vHCDR2 (WO2016028656)	SASRYT
vHCDR3 (WO2016028656)	QHYYSTPW T
vHCDR3 variant (WO2016028656)	QYYYS GFT
vHCDR3 variant (WO2016028656)	QYYYS GYT
vHCDR3 variant (WO2016028656)	QYYYS GIT
vHCDR3 variant (WO2016028656)	QYYYS GVT
vHCDR3 variant (WO2016028656)	QYYYS GLT
	SEQ ID NO:
	903
	904
	905
	906
	907
	908
	909
	910
	911

Figure 3]]]]

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWRQFPGNKLEWMGYISNSGSAS YNPSLKSRISITRDTSKNQFFLQLNSVTIEDTATYYCATLIYYDYGGMNFWGQGTSVT VSS	912
vHCDR1 (from WO2016028656)	GYSITSDYAWN	913
vHCDR2 (WO2016028656)	YISNSGSASYNPSLKS	914
vHCDR3 (WO2016028656)	LIYYDYGGMNFW	915
vHCDR3 variant (WO2016028656)	MPSFITLASLSTFEGYFDF	916
vHCDR3 variant (WO2016028656)	MPSFITLASLSTYEGYFDF	917
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	918
vHCDR3 variant (WO2016028656)	MPSFITLASLSTVEGYFDF	919
vHCDR3 variant (WO2016028656)	MPSFITLASLSTLEGYFDF	920

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Figure 3KKKK

From WO2016028656 (Table 4, reproduced herein)

What	Heavy chain (SEQ ID NO: 94 from WO2016028656)	sequence	SEQ ID NO:
vHCDR1 (from WO2016028656)		EVQLQQSGPELVKPGSSVKMISCKASGYTSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEK FKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWVGAGTITVYSS	921
vHCDR2 (WO2016028656)		SYVMH	922
vHCDR3 (WO2016028656)		YIDPYNDGAKYNEKFK	923
		GPYGVYFDV	924
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	925
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	926
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	927
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	928
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	929
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	930
vHCDR2 variant (WO2016028656)		YIDPYNIGAKYNEKFG	931
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	932
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	933
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	934
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	935
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	936
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	937
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	938
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	939
vHCDR2 variant (WO2016028656)		YIDPYNDIAGYNEKFKG	940

Figure 3LLLL

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:94 from WO2016028656)	DIQMTQSPASLSASVGETIVTITCRASEHIYSYLSWYQOKQKSPQLLVYNAKTLAEGVPSRFSGSG SGTQFSLKINSLQPEDFGTYYCQHIFGSPLTFGAGTILELK	941
vICDR1 (from WO2016028656)	RASEHIYSYLS	942
vICDR2 (WO2016028656)	NAKTLAE	943
vICDR3 (WO2016028656)	QHIFGSPLT	944
vLCDR2 variant (WO2016028656)	AAKTLAE	945
vLCDR2 variant (WO2016028656)	YAKTLAE	946
vLCDR2 variant (WO2016028656)	WAKTLAE	947
vLCDR2 variant (WO2016028656)	SAKTLAE	948
vLCDR2 variant (WO2016028656)	TAKTLAE	949
vLCDR2 variant (WO2016028656)	IAKTLAE	950
vLCDR2 variant (WO2016028656)	VAKTLAE	951
vLCDR2 variant (WO2016028656)	NNKTLAE	952
vLCDR2 variant (WO2016028656)	NIKTLAE	953
vLCDR2 variant (WO2016028656)	NLLTLAE	954
vLCDR2 variant (WO2016028656)	NIKTLAE	955
vLCDR2 variant (WO2016028656)	NVKTLAE	956

Figure 3MMMM

From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:124 from WO2016028656)	957
EVQLVQSGAEVKKPKASVKVSKASGYTFSSVMHWVRQAPGQRLIEWIGYIDPYNDGAKYS QKFQGRVLTTRDTSASTAYMELSSLRSEDTAVYYCARGGPGYGYFDVWGQGTTIVSS	
vhCDR1 (from WO2016028656)	958
SYVMHW	
vhCDR2 (from WO2016028656)	959
YIDPYNDGAKYSQKFQ	
vhCDR3 (from WO2016028656)	960
GGPYGWYFDV	
From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:125 from WO2016028656)	961
EVQLVQSGAEVKKPKASVKVSKASGYTFSSVMHWVRQAPGQRLIEWIGYIDPYNDGAKYS QKFQGRVLTSDKSASTAYMELSSLRSEDTAVYYCARGGPGYGYFDVWGQGTTIVSS	
vhCDR1 (from WO2016028656)	962
SYVMH	
vhCDR2 (from WO2016028656)	963
YIDPYNDGAKYSQKFQ	
vhCDR3 (from WO2016028656)	964
GGPYGWYFDV	

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Figure 3NNNN

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:126 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYMHVWRQAPGQGLEWIGYIDPYNNDGAKY AQKFQGRVTLTRDTSTSTVYMELSSLRSEDTAVYYCARGGPGYGYFDVWGQGTTITVSS	965
vhCDR1 (from WO2016028656)	SYVMH	966
vhCDR2 (from WO2016028656)	YIDPYNNDGAKY AQ	967
vhCDR3 (SEQ ID NO:13 from WO2016028656)	GGPYGWYFDV	968
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:127 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYMHVWRQAPGQGLEWIGYIDPYNNDGAKY AQKFQGRVTLTSDKSTSTVYMELSSLRSEDTAVYYCARGGPGYGYFDVWGQGTTITVSS	969
vhCDR1 (from WO2016028656)	SYVMH	970
vhCDR2 (from WO2016028656)	YIDPYNNDGAKY AQKFQ	971
vhCDR3 (from WO2016028656)	GGPYGWYFDV	972

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Figure 30000

From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:128 from WO2016028656)	973
	EVQLVQSGAEVKKPKCSVKVSKASGYTFSSVYMHVVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVLTLSDKSTSTAYMELSSLRSEDTAVYYCARGGPGYGYFDVWGQGTTITVSS
vhCDR1 (from WO2016028656)	974
	SYVMH
vhCDR2 (from WO2016028656)	975
	YIDPYNDGAKYAQKFQ
vhCDR3 (from WO2016028656)	976
	GGPYGWYFDV
From WO2016028656 (Table 4, reproduced herein) What	SEQ ID NO:
Heavy chain (SEQ ID NO:129 from WO2016028656)	977
	EVQLVQSGAEVKKPKCSVKVSKASGYTFSSVYMHVVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVLTLSDKSISTAYMELSLRSDTAVYYCARGGPGYGYFDVWGQGTTITVSS
vhCDR1 (from WO2016028656)	978
	SYVMH
vhCDR2 (from WO2016028656)	979
	YIDPYNDGAKYAQKFQ
vhCDR3 (from WO2016028656)	980
	GGPYGWYFDV

Figure 3PPPP

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:130 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITTCRASEHIYSYLSWYQQKPGKAPKLLIYNNAKTAEGVPSRFSG SCSGTDFLTITSSLPEDFATYYCQHHFGSPLTFGQGTREIK	981
vICDR1 (from WO2016028656)	RASEHIYSYLS	982
vICDR2 (from WO2016028656)	NAKTAE	983
vICDR3 (from WO2016028656)	QHHFGSPLT	984
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:131 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITTCRASEHIYSYLSWYQQKPGKAPKLLIYNNAKTAE GVPSRFSGSGTGFTLTSSLPEDFATYYCQHHFGSPLTFGQGTREIK	985
vICDR1 (from WO2016028656)	RASEHIYSYLS	986
vICDR2 (from WO2016028656)	NAKTAE	987
vICDR3 (from WO2016028656)	QHHFGSPLT	988

Figure 3QQQQ		
From WO2016028656 (Table 4, reproduced herein)		
What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:132 from WO2016028656)	DIQMTQSPSSLSASVGDRVTTCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSG SGSGTDFLTITSSLPEDVATYYCQHHFGSPLTFGQGTREIK	989
vICDR1 (from WO2016028656)	RASEHIYSYLS	990
vICDR2 (from WO2016028656)	NAKTLAE	991
vICDR3 (from WO2016028656)	QHHFGSPLT	992
From WO2016028656 (Table 4, reproduced herein)		
What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:133 from WO2016028656)	DIQMTQSPSSLSASVGDRVTTCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSG SGSGTQFTLTITSSLPEDVATYYCQHHFGSPLTFGQGTREIK	993
vICDR1 (from WO2016028656)	RASEHIYSYLS	994
vICDR2 (from WO2016028656)	NAKTLAE	995
vICDR3 (from WO2016028656)	QHHFGSPLT	996

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Figure 3RRRR

From WO2016028656 (Table 4, reproduced herein)			SEQ ID NO:
What	sequence		
Heavy chain	EVQLVQSGAEVKKPKASVKVCKASGYTSSVVMHWVVRQAPGQGLEWIGYIDPYNDGAKYA		997
(SEQ ID NO: 129 from	QKFQGRVTLTSDKSISTAYMELSLRLSDDTVVYYCARGGPYGWYFDVWGQGTTITVSS		
WO2016028656)			
vhCDR2 variant	YIDPYNDGAKYAQKFTQG		998
(from WO2016028656)			
vhCDR2 variant	YIDPYNDGAKYSQKFTQG		999
(from WO2016028656)			
From WO2016028656 (Table 4, reproduced herein)			SEQ ID NO:
What	sequence		
Heavy chain	EVQLVQSGAEVKKPKASVKVCKASGYTSSVVMHWVVRQAPGQGLEWIGYIDPYNDGAKYAQ		1000
(SEQ ID NO: 129 from	KFQGRVTLTSDKSISTAYMELSLRLSDDTVVYYCARGGPYGWYFDVWGQGTTITVSS		
WO2016028656)			
vhCDR3 variant (from	GGPYGAYFDV		1001
WO2016028656)			
vhCDR3 variant (from	GGPYGDYFDV		1002
WO2016028656)			
vhCDR3 variant (from	GGPYGEYFDV		1003
WO2016028656)			
vhCDR3 variant (from	GGPYGFYFDV		1004
WO2016028656)			
vhCDR3 variant (from	GGPYGGYFDV		1005
WO2016028656)			
vhCDR3 variant (from	GGPYGYFDV		1006
WO2016028656)			
vhCDR3 variant (from	GGPYGKYFDV		1007
WO2016028656)			
vhCDR3 variant (from	GGPYGNYFDV		1008
WO2016028656)			
vhCDR3 variant (from	GGPYGQYFDV		1009
WO2016028656)			
vhCDR3 variant (from	GGPYGRYFDV		1010
WO2016028656)			
vhCDR3 variant (from	GGPYGSYFDV		1011
WO2016028656)			
vhCDR3 variant (from	GGPYGTIYFDV		1012
WO2016028656)			
vhCDR3 variant (from	GGPYGVYFDV		1013
WO2016028656)			
vhCDR3 variant (from	GGPYGYFDV		1014

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Figure 3SSSS

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	1015
VH 18G10	QVQLMESGPGLVQPSQTLSTCTVSGFPLTSYTVHWVRQPPGKGLEWIGAIWSSGSTDYNSA	
(SEQ ID NO:136 from	LKRLNINRDSSKSQVFLKMNSLQTEDTAIFYCTKSGWAFDYWGQGVMTVSS	
WO2016028656)		
VL 18G10	DIQMTQSPSLLSASVCGDRVTLNCLIASQNIYKSLAWYQLKLEAPKLLIYNANSLQAGIPSRFSG	1016
(SEQ ID NO:137 from	SGSGTDFALTISGLQPEDVATYFCQQYSGGYTFGAGTKLELK	
WO2016028656)		
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	1017
VH 11A11	EVQLVESGGDLVQPGRSLKISCVASGFTESDYMAWVRLAPQKGLEWVASISYEGSRTHYGD	
(SEQ ID NO:138 from	SVRGRFIISRDNPKNILYLQMNSLGSDDTATYFCARHTGTLDWLVIYWGQGTILVIVSS	
WO2016028656)		
VL 11A11	NIVMAQSPKSMISAGDRVTMNCKASQNVDDNNIAWYQQKPGQSPKLLIFYASNRYSGVPDR	1018
(SEQ ID NO:139 from	FTCGGYGTDFTLTIKSVQAEDAAFPYQCRIYNNEPTFCGSKLEIK	
WO2016028656)		

Figure 4A

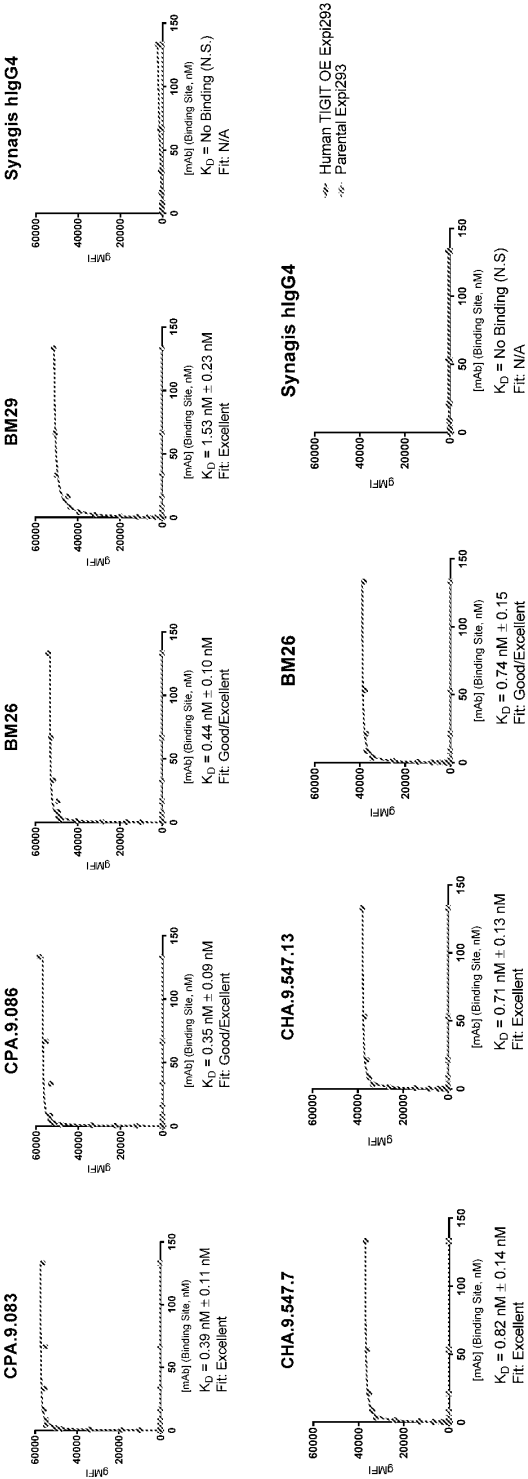


Figure 4B

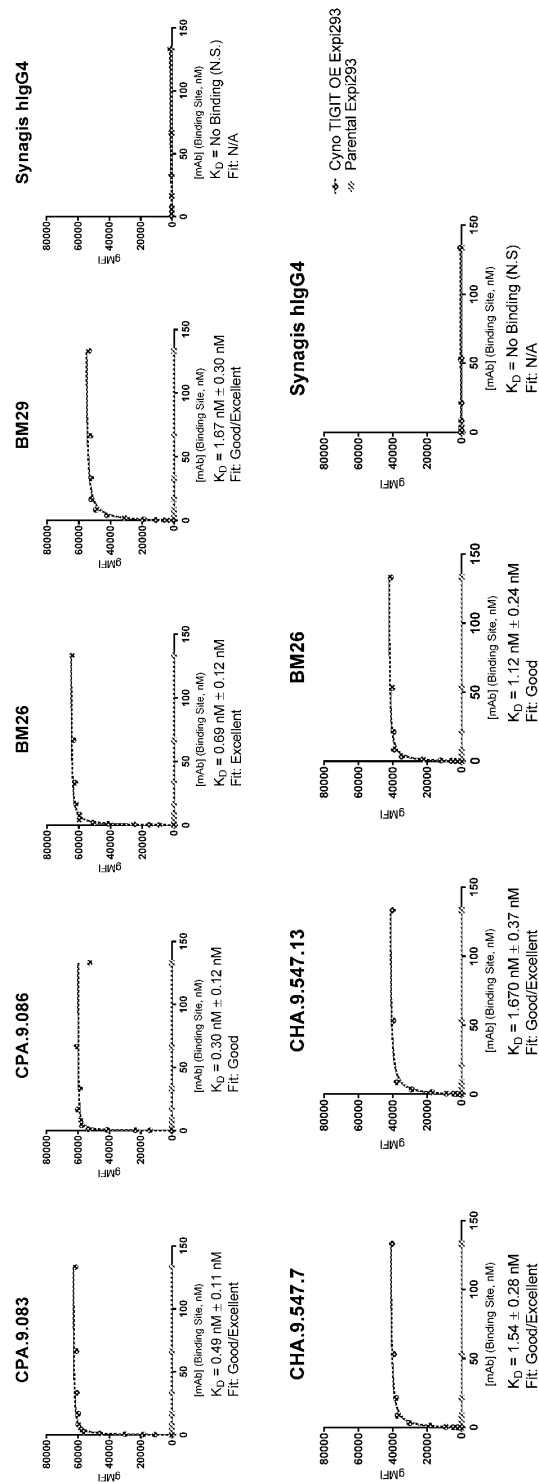
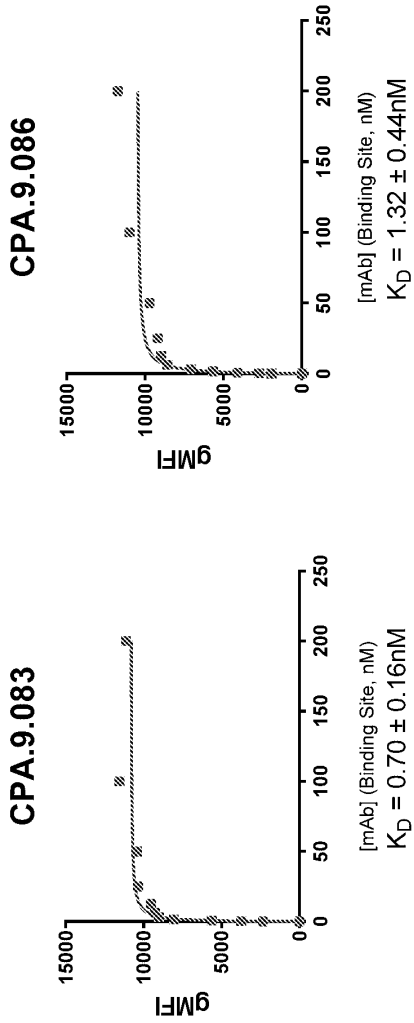


Figure 4C



What	sequence	SEQ ID NO.
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFIDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFFQGRVTMTIRDTSTSTVYMELSSLRSDDTAIVYYCAREDKTARNAMDYWGQGTLVTVSS	1019
vhCDR1	GYTFIDYN	1020
vhCDR2	DYPYIGGS	1021
vhCDR3	AREDKTARNAMDY	1022
Full length HC (IgG4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTFIDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFFQGRVTMTIRDTSTSTVYMELSSLRSDDTAIVYYCAREDKTARNAMDYWGQGTLVTVSSASTIKGPSVFPLAPCSRSTSESTAAAGCLVKDYFPELPTVSWNSGALTSGVHTFPPAVLQSSGLYSLSVTVTPSSSLGKITYICNVDPHKPSNTKVDKRVESKYGPPCPAPAPEFLGGPSVLEFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLFHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPGK	1023
Full length HC for CHA.7.518.1.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRVSENINYSNLAWYQQKPKAPKLLIYEATNLAEGVPSRFSGSGCTDFTLTISSLQPEDFATYYVQCQHEFWGTPYTFGGGTKLEIK	1024
Variable light (vl) domain	ENIYSN	1025
vlCDR1	EAT	1026
vlCDR2		1027
vlCDR3	QHEFWGTPYT	1028
Full length light chain for CHA.7.518.1.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRVSENINYSNLAWYQQKPKAPKLLIYEATNLAEGVPSRFSGSGCTDFTLTISSLQPEDFATYYVQCQHEFWGTPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKFSNRGEC	1029

Figure 5B CHA.7.538.1.2		What	sequence	SEQ ID NO.
Variable heavy (vh) domain	vHCDR1	Full length HC (IgG4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASCYAFNXLJEWVRQAPGQGLEWIGVINPGSGGIYAAQKFGQGRVTMTADTISTIVY MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS	1029
			GYAFINYL	1030
			INPGSGGI	1031
			ARSETHDTWFAY	1032
Full length light (vL) domain	vLCDR1	Full length HC for CHA.7.538.1.2. H4(S241P)	QVQLVQSGAEVKKPGASVKVSCKASCYAFNXLJEWVRQAPGQGLEWIGVINPGSGGIYAAQKFGQGRVTMTADTISTIVY MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAAAGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTITTCNVDPKHPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLIHQDWLNGKEYKCKVSN KGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGRVFSQVMHEALHNHYTQKSLSLSPGK	1033
			DIQMTQSPSSLSASVGRVTITCKASQSVRIAFAWFQQKPGKAPKALIVLASTRHTGVPSTRFSGSGGTDFTLTISSVQPEDFA TYYCLOHWNNYPYTFGGQGTKLEIK	1034
			QSVRIA	1035
			LAS	1036
Full length light chain for CHA.7.518.1.H 4(S241P)	vLCDR3	Full length light chain for CHA.7.518.1.H 4(S241P)	LQHWNNYPYT	1037
			DIQMTQSPSSLSASVGRVTITCKASQSVRIAFAWFQQKPGKAPKALIVLASTRHTGVPSTRFSGSGGTDFTLTISSVQPEDFA TYYCLOHWNNYPYTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSSTYSLSSTLTLSKADVEKHKVYACEVTHQGLSSPVTKSFNRGEC	1038

[illegible]

Figure 5D

From Zhu (WO 2017/041004) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFISDWMHWVKQRPQGLEWIGYINPSTGYTEY NQKPKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARCSSGSWFAYWGQGTLVTVSA	1047
vhCDR1 (SEQ ID NO:34 from WO 2017/041004)	SDWMH	1048
vhCDR2 (SEQ ID NO:35 from WO 2017/041004)	YINPSTGYTEYNQKFKD	1049
vhCDR3 (SEQ ID NO:36 from WO 2017/041004)	GSSGSWFAY	1050
Light chain (SEQ ID NO:33 from WO 2017/041004)	DIVLTQSPASLAVSLCQRATISCRASQSVSTSSYSYMHWYQQKPKQPPKLLIKYASNLESGVPA RFGSCSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGTKLEIK	1051
viCDR1 (SEQ ID NO:37 from WO 2017/041004)	RASQSVSTSSYSYMH	1052
viCDR2 (SEQ ID NO:38 from WO 2017/041004)	YASNLES	1053
viCDR3 (SEQ ID NO:39 from WO 2017/041004)	QHSWEIPYT	1054

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Figure 5E

From Zhu (WO 2017/041004) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFISDWMMHWVKQRPQGQLEWIGYINPSTCYTEY NQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARCGSSGSWFAYWGQGCTLVTVSA	1055
vhCDR1 (SEQ ID NO:34 from WO 2017/041004)	SDWMH	1056
vhCDR2 (SEQ ID NO:35 from WO 2017/041004)	YINPSTGYTEYNQKFKD	1057
vhCDR3 (SEQ ID NO:36 from WO 2017/041004)	GSSGSWFAY	1058
Light chain (SEQ ID NO:40 from WO 2017/041004)	DVVMTQTPLTISVTICQPASISCKSSQSLNSDGKTYLNWLLQRPQSPKRLIYLVSKLID SGVPDRFTCSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPTFCGCTKLEIK	1059
vlCDR1 (SEQ ID NO:41 from WO 2017/041004)	KSSQSLNSDGKTYLN	1060
vlCDR2 (SEQ ID NO:42 from WO 2017/041004)	LVSKLDS	1061
vlCDR3 (SEQ ID NO:43 from WO 2017/041004)	WQGTHTFPRT	1062

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Figure 5F

From WO 2018/017864 (334M5 antibody)		SEQ ID NO.
What	sequence	
Heavy chain (SEQ ID NO:30 from WO 2018/017864)	EVQLQQSV AELVRPGTSVTISCKASGYTFINYWLGWVKQRPGHGLEWIGDIFPGGDYPNY NEKFKGKATLTADTSSTAYMQLSSLTSEDSSVYFCTRGYFDVWVGAGTTVTSS	1063
vHCDR1 (SEQ ID NO:31 from WO 2018/017864)	TNYWLG	1064
vHCDR2 (SEQ ID NO:32 from WO 2018/017864)	DIFPGGDYPNYNEKFKG	1065
vHCDR3 (SEQ ID NO:33 from WO 2018/017864)	TRGYFDV	1066
Light chain (SEQ ID NO:25 from WO 2018/017864)	DIQMTQSPSSLSVSAAGEKVTMSCKS5QSLNSENQKNYLAWFQQKPCQPPKMLIYGASTR ESGVPRDRTCSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPFTFGSGTKLEIKR	1067
vLCDR1 (SEQ ID NO:26 from WO 2018/017864)	KSSQSLNSENQKNYLA	1068
vLCDR2 (SEQ ID NO:27 from WO 2018/017864)	GASTRES	1069
vLCDR3 (SEQ ID NO:28 from WO 2018/017864)	QNIDHSYP	1070

Figure 7A

Pembrolizumab (Anti-PD1 hlgC4)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVLSGGGFVQPGGSLKLSCAA <u>SGFTSSY</u> AMSWVRQNPERRLVWVAITIGGGRNTYYPDSVKGRFTISR DNAKNITLYLQMSSLRSEDAMYYCTIQGYDGYTWFAFWGQGTILTVSS	1071
vhCDR1	GFTTSSYA	1072
vhCDR2	ITGGGRNT	1073
vhCDR3	TRQGYDGYTWFAW	1074
Full length HC	EVQLVLSGGGFVQPGGSLKLSCAA <u>SGFTSSY</u> AMSWVRQNPERRLVWVAITIGGGRNTYYPDSVKGRFTISR DNAKNITLYLQMSSLRSEDAMYYCTIQGYDGYTWFAFWGQGTILTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYEPPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTCNVVDHFKPSNTHKVD KRVEKYGPPCPCPAPEFLGGPSVFLFPPKPKDITLMISRTPVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVHLQDWLNGKEYCKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTIPVLDSDGSHFLYSRLITVDKSRWQEGNVTFSCSVMIHE ALHNITYTQKSLSPGK	1075
Variable light (vl) domain	DIVLTQSPSTSLAVSLGQRATISCRASEVDNSGISFMINWVQQKPGQPPKLLIYAASNPVGSVGPARGSCSGGT DFSLNIHPMEEDDTAMVFCQOSKEVPWTFGGGTGLEIKR	1076
vlCDR1	ESVDNSGISF	1077
vlCDR2	AAS	1078
vlCDR3	QOSKEVPWT	1079
Full length light chain	DIVLTQSPSTSLAVSLGQRATISCRASEVDNSGISFMINWVQQKPGQPPKLLIYAASNPVGSVGPARGSCSGGT DFSLNIHPMEEDDTAMVFCQOSKEVPWTFGGGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWVKVDNALQSGNSQESVTEQDSKDSTYSLSSTLLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C	1080

Figure 7B	
Pembrolizumab (Anti-PD1 from WO2016028656)	
What	sequence
Full length HC (SEQ ID NO:33 from WO2016028656)	QVQLVQSGVEVKKPGASVKVSCKASCYTFNYYMYWVRQAPCQGLEWMGGINPNSNGGTNINEKFKNRV TLITDSSTTTAYMELKSLQFDDTA VYVCARRDYRFDMGFDYWGQGTITVYSSASTKGPSVFPLAPCSRSTSES TAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHDKPSNTK VDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDITLMISRTPETCVVVDVSDQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKGLTPSSIEKTSKAKGQPREPQVYVTLPPSQEE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSRLTVDKSRWQEGNVFSCSYM HEALTHHNYTQKSLSLGK
Full length light chain (SEQ ID NO:34 from WO2016028656)	EIVLTQSPATLSLSPGERATLSCRASKGVSTGYSLHWYQQKPGQAPRLIYLASYLESGVPARISGSGGTD FTLTISLSLEPEDFAVYYCQHSRDLP LITGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAK VQWKYDNNALQSGNSQESVTEQDSKDSYSLSSITLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 7C

Nivolumab (Anti-PD1 hIgG4)		SEQ ID NO:
What	sequence	
Variable heavy (vh) domain	QVQLVESGGGVVQPGSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAIVWYDGSKRYYADSVKGRFTI SRD NSKNITLFLQ MNSLRAEDTAVYYCAINDDYWGQGTLVTVSS	1083
vhCDR1	GITFSNSG	1084
vhCDR2	IWYDGSKR	1085
vhCDR3	ATNDDY	1086
Full length HC	QVQLVESGGGVVQPGSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAIVWYDGSKRYYADSVKGRFTI SRD NSKNITLFLQ MNSLRAEDTAVYYCAINDDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTISCVHTFPAPVLQSSGLYSLSSVTVTPSSSLGTYICTCNVDHDKPSNTKVDKRVES KYGPPCPAPAEFLGGPSVFLPPKPKDITLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVYSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMIKNQV SLTCLVKGFPYPSDIAVEWESNCPENNYKTTPTPVLDSGSHFLYSRLTVDKSRWQEGNVFSCSVMEALHN HYTQKSLSLSLGK	1087
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRAIGIPARFSGSGTDFTLTIT SSLEPEDFAVYYCQSSNWPRITFGQGTKEIKRTVAAPSVFHPSPDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1088
vlCDR1	QSVSSY	1089
vlCDR2	DAS	1090
vlCDR3	QSSNWPRIT	1091
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRAIGIPARFSGSGTDFTLTIT SSLEPEDFAVYYCQSSNWPRITFGQGTKEIKRTVAAPSVFHPSPDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1092

Figure 7D			
Nivolumab (Anti-PD1 from WO2016028656)			
What	sequence	SEQ ID NO:	
Full length heavy chain	QVQLVESGGGVVQPGRSLRLDCKASGITFSNCGMHWVRQAPCKGLEWVAVIWYDCSKRYYADSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVKDKRVES KYGPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVYTLPPSQEEMTKNQV SLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHN HYTQKSLSLGK	1093	
Full length light chain	EIVLTQSPATLSLSPGERATLSCRAQSQSVSSYLAWYQQKPGQAPRLIYDASNRAICIPARFSGSGTDFTLTIT SSLEPEDFAVYYCQQSSNWPRFTIGQGTKVEIKRTVAAPSVHFFPSDEQLKSGTASVVCCLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1094	
(SEQ ID NO:35 from WO2016028656)			
(SEQ ID NO:36 from WO2016028656)			

Figure 7E

Cemiplimab (REGN2810; anti-PD1)	
What	sequence
Variable heavy (vh) domain (SEQ ID NO:1 from US20170174779)	EVQLLESGGVLVQPGCSLRISCAASGFTTSNFGMTWVRQAPGKGLEWVSGISGGRDITYF ADSVKGRFTISRDN SKNTLYLQMNSLKGEDTAVYCVKWGNIYFDYWGQGTILVTVSS
vhCDR1 (SEQ ID NO:3 from US20170174779)	GFTTSNFG
vhCDR2 (SEQ ID NO:4 from US20170174779)	ISGGGRDT
vhCDR3 (SEQ ID NO:5 from US20170174779)	VKWGNIYFDY
Variable light (vl) domain (SEQ ID NO:2 from US20170174779)	DIQMTQSPSSLSASVGDSTITTCRASISNITELNIWYQQKPKAPNLLIYAASLHCGVPS RFSGCSGTDFLTIRTLQPEDFATYCCQSSNTPFTFGPGTVWDFR
vlCDR1 (SEQ ID NO:6 from US20170174779)	LSINTF
vlCDR2 (SEQ ID NO:7 from US20170174779)	AAS
vlCDR3 (SEQ ID NO:8 from US20170174779)	QQSSNTPFT

Figure 7F		
Cemiplimab (REGN2810; anti-PD1)		
What	sequence	SEQ ID NO:
Full length heavy chain	EVQLLESGGVLVQPGGSLRLSCAASGFTFSNFGMTWVRQAPGKGLEWVSGISGGRDITYFADSVKGRFTISR DNSKNTILYLQMNSLKGEDTAVVYCVKWCNIFYDYWGQGLTVYSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVIVTPSSSLGKTYTCNVVDHFKPSNLIKVDKRV ESKYGPPCPAPAEFLGGPSVFLPPPKDITLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALH NHVTQKSLSLGK	1103
(SEQ ID NO:9 from US20170174779)		
Full length light chain	DIQMTQSPSSLSASVGDSITHTCRASISNTFLNWWYQQKPGKAPNLLIYAASLHGGVPSRFSGSGGTIDFILT RTIQPEDFAITYCQQSSNTPFTFGPTVVDERRIVAAPSVTHPPSPDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNAIQSGNSQESVTEQDSKDSITYSLSSITLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1104
(SEQ ID NO:10 from US20170174779)		

Figure 8

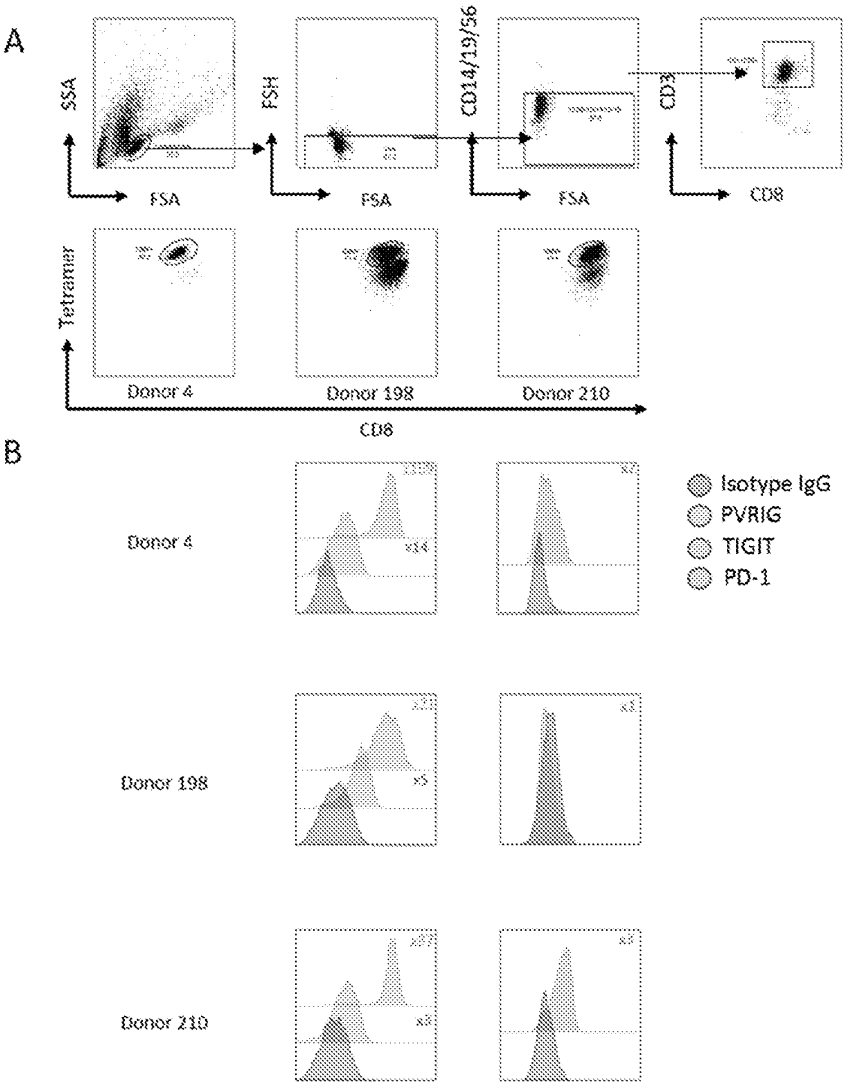


FIGURE 9

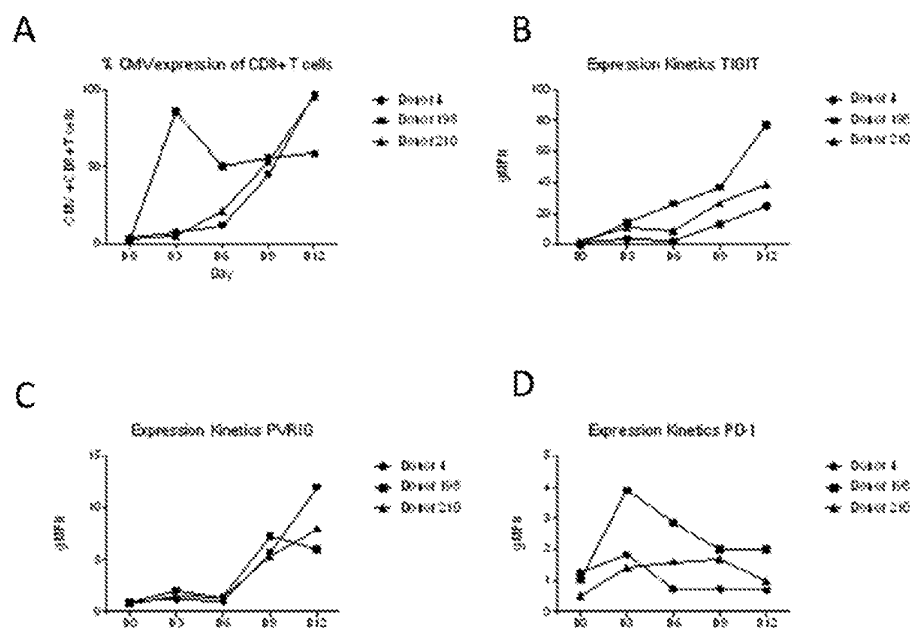


FIGURE 10

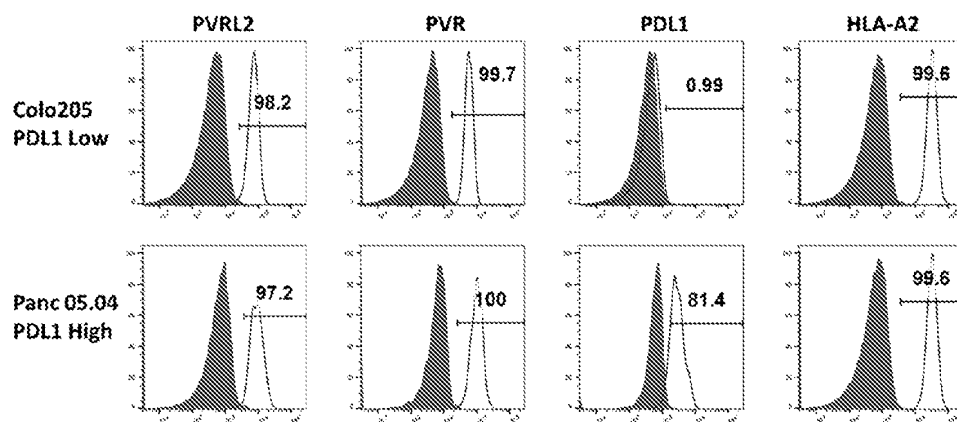


FIGURE 11A

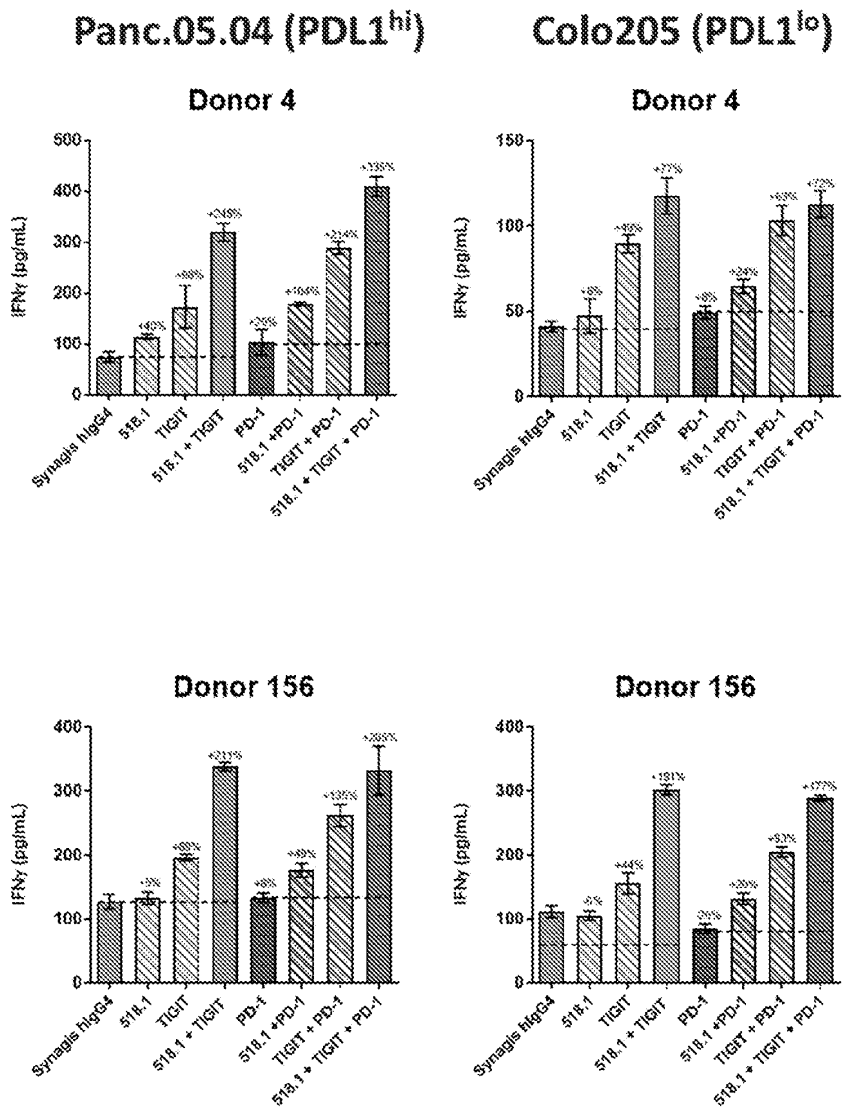


Figure 11B

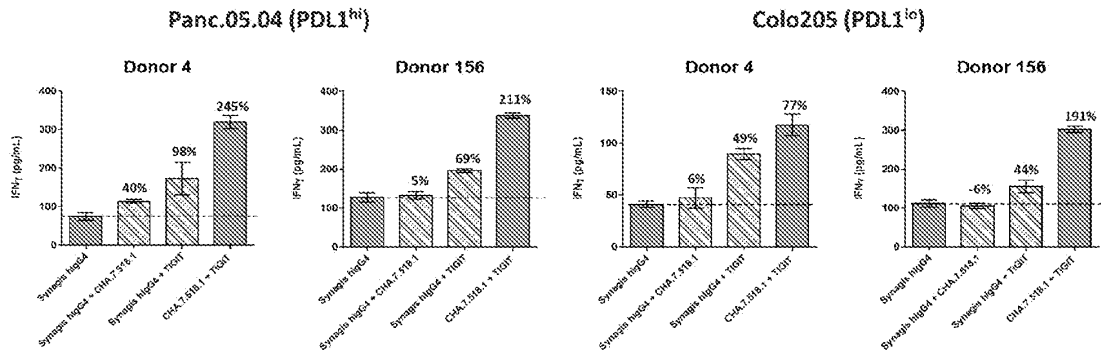


Figure 11C

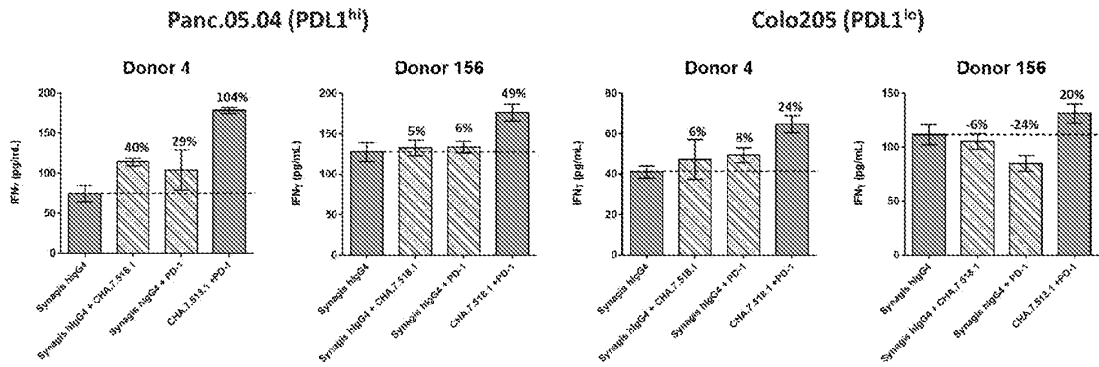


Figure 11D

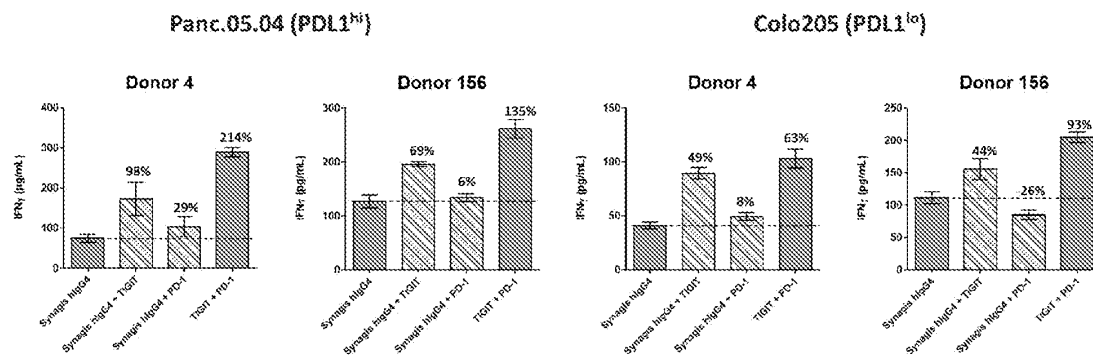


Figure 12

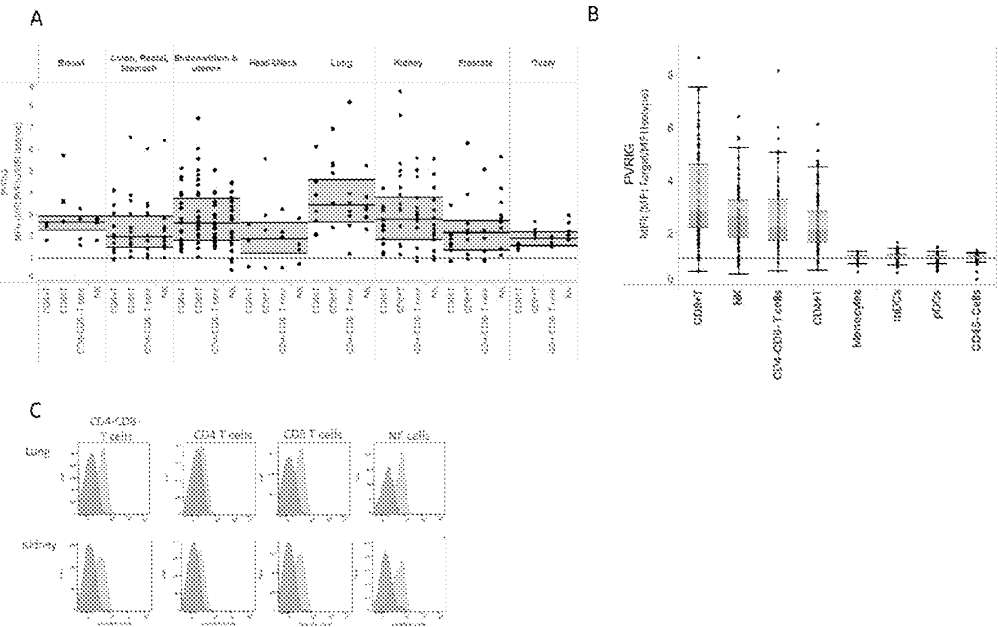


Figure 13

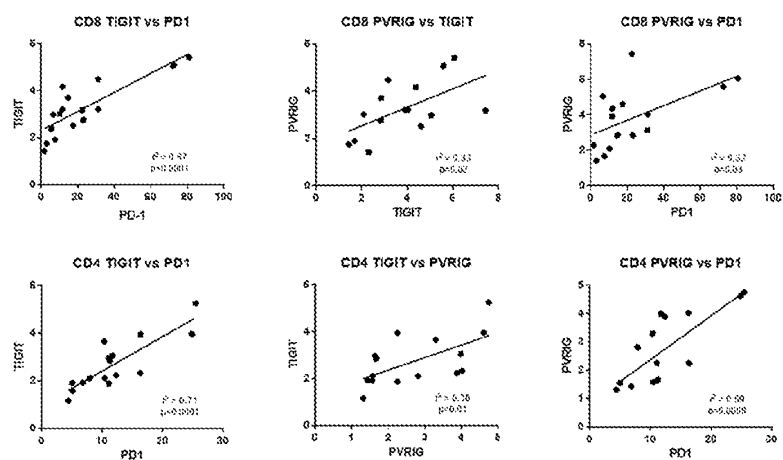


Figure 14

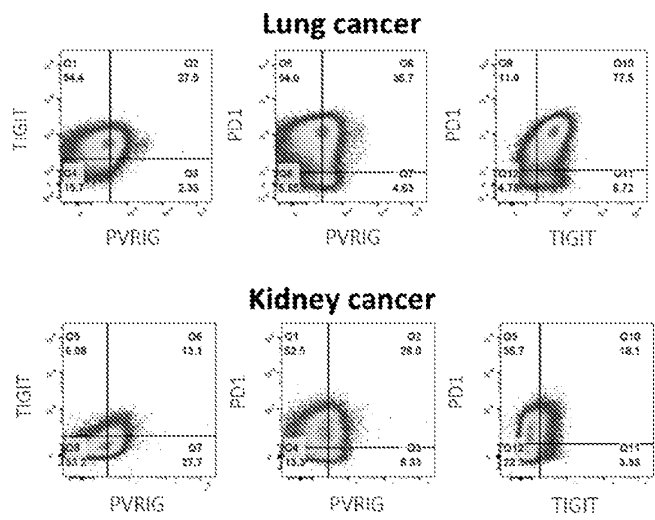


Figure 15

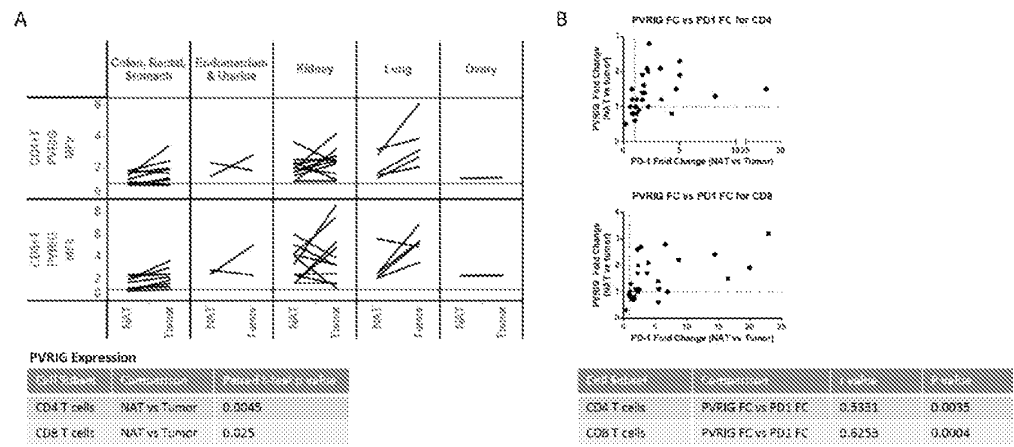


Figure 16

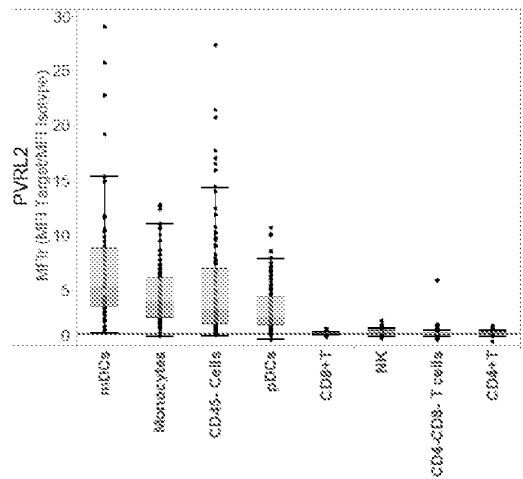


Figure 17

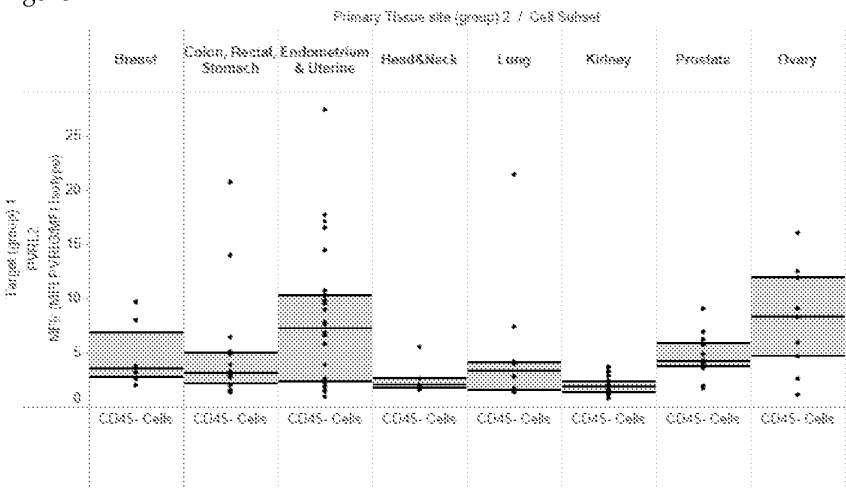


Figure 18

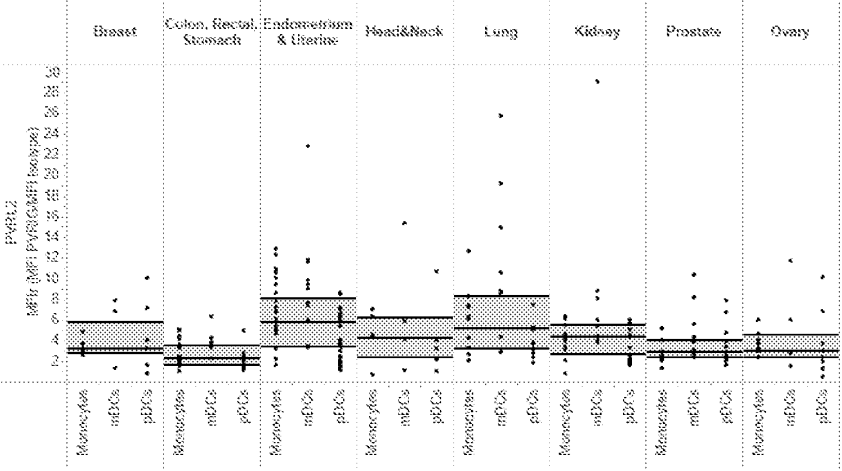


Figure 19

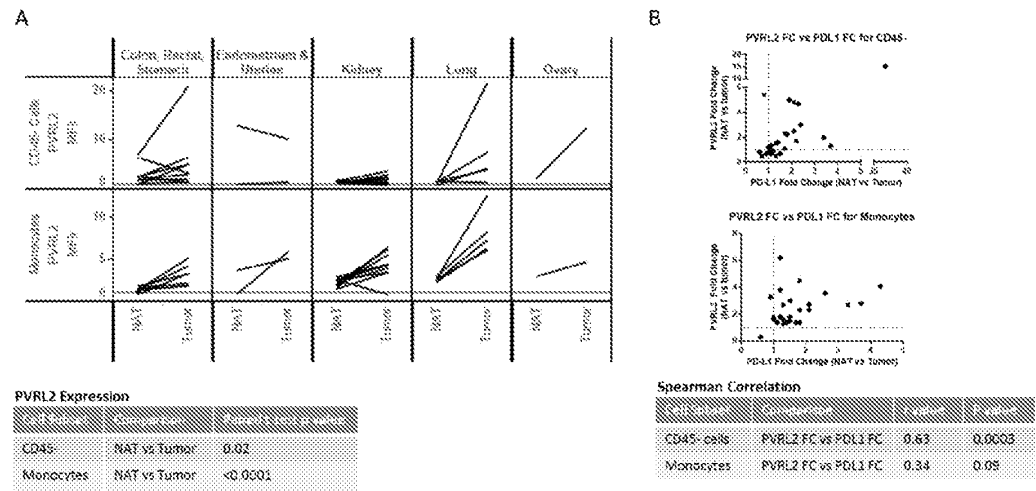


Figure 20

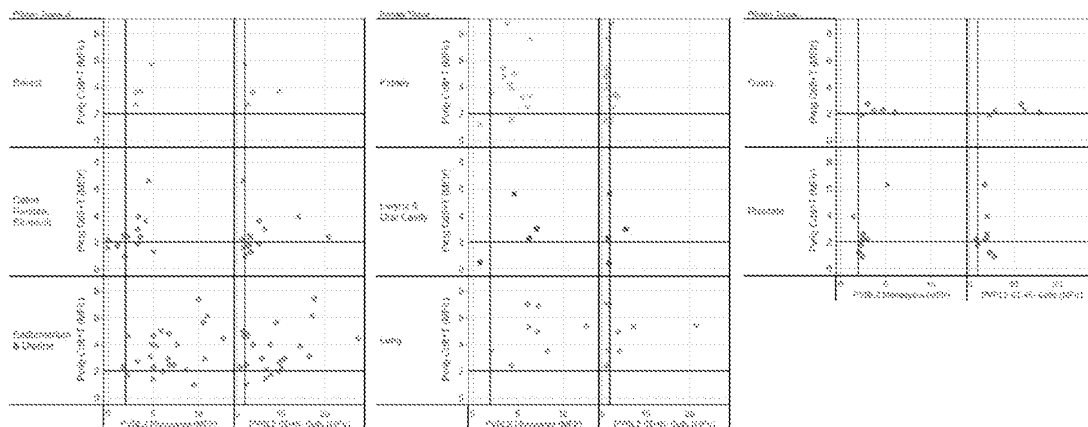


Figure 21A

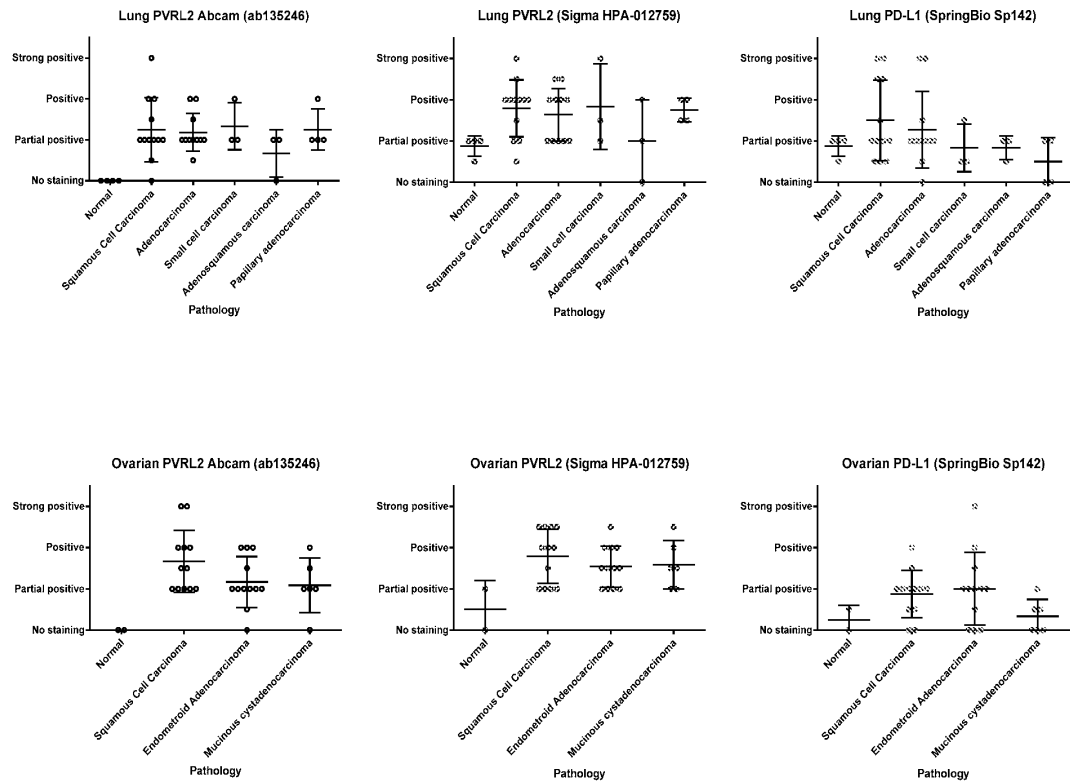


Figure 21B

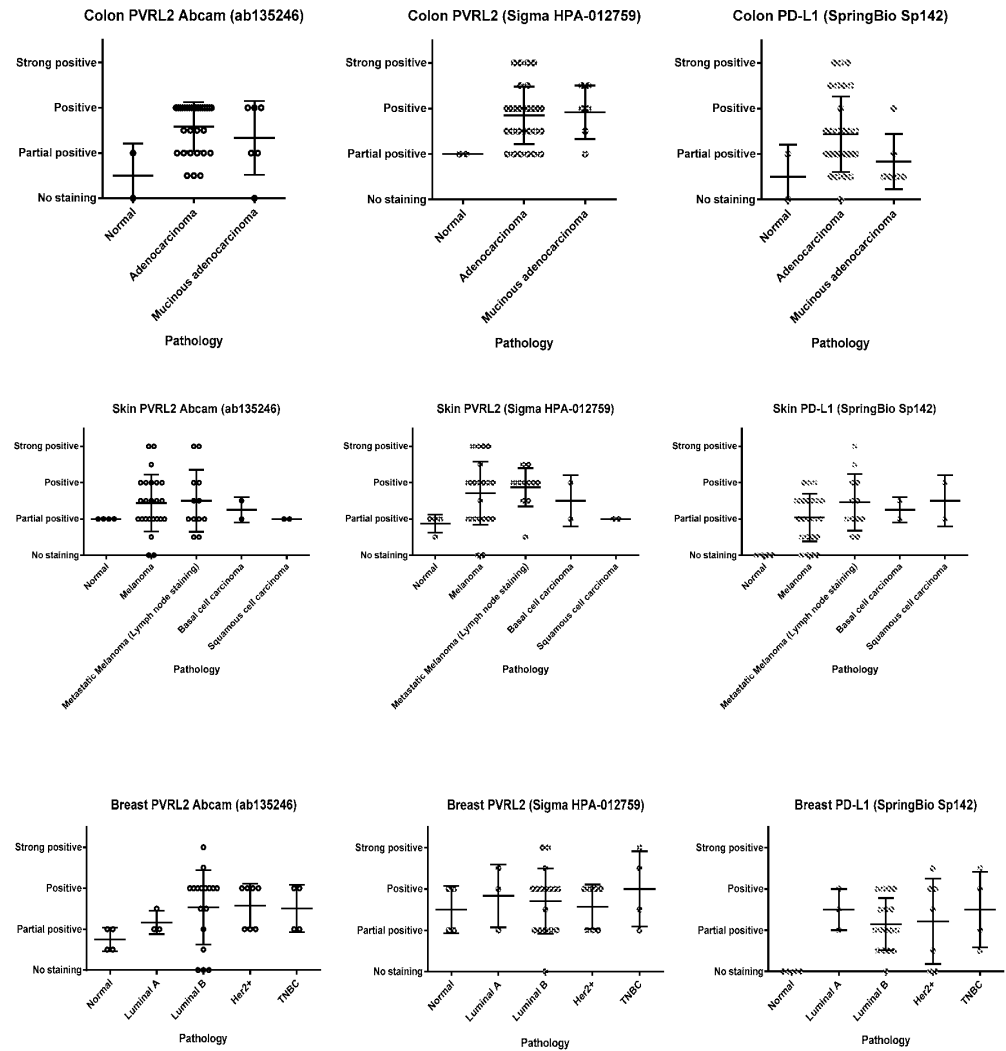


Figure 22

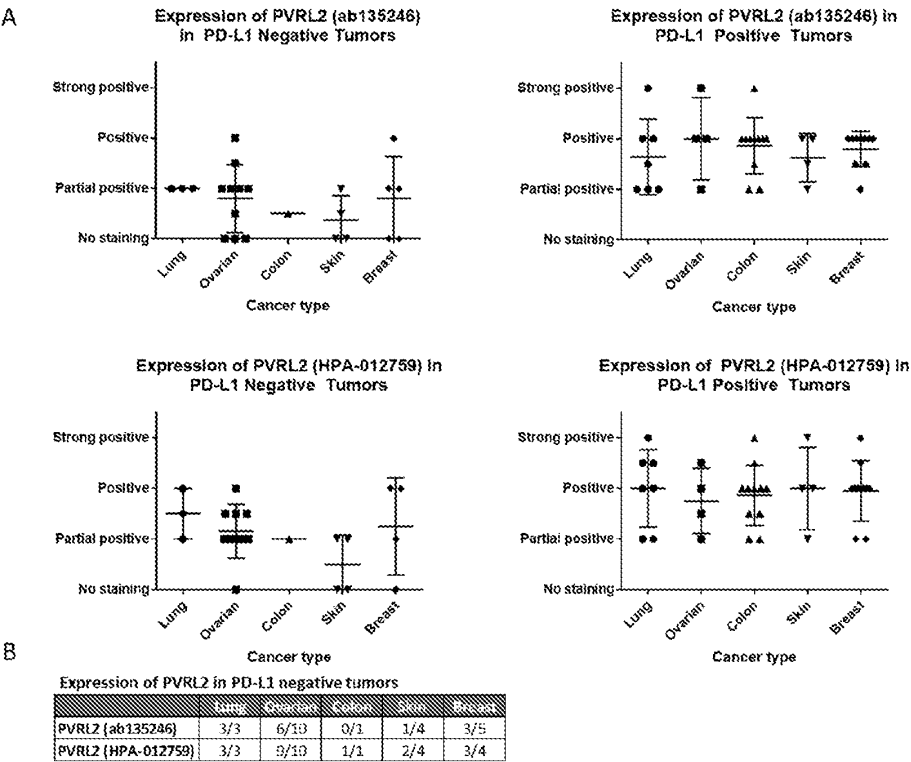


Figure 23

A. PVRL2 (HPA-012759)

B. PD-L1 (SP142)

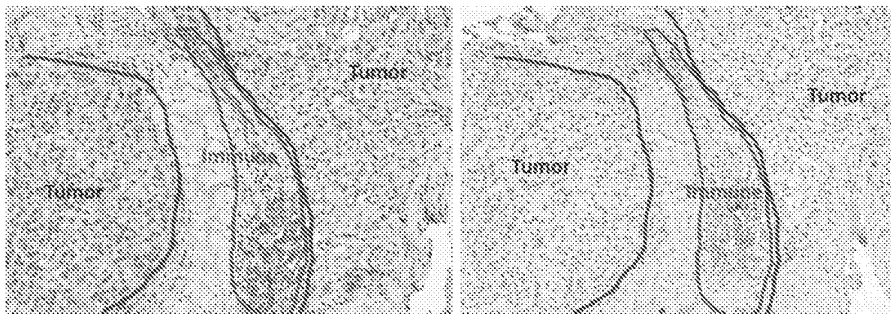


Figure 24

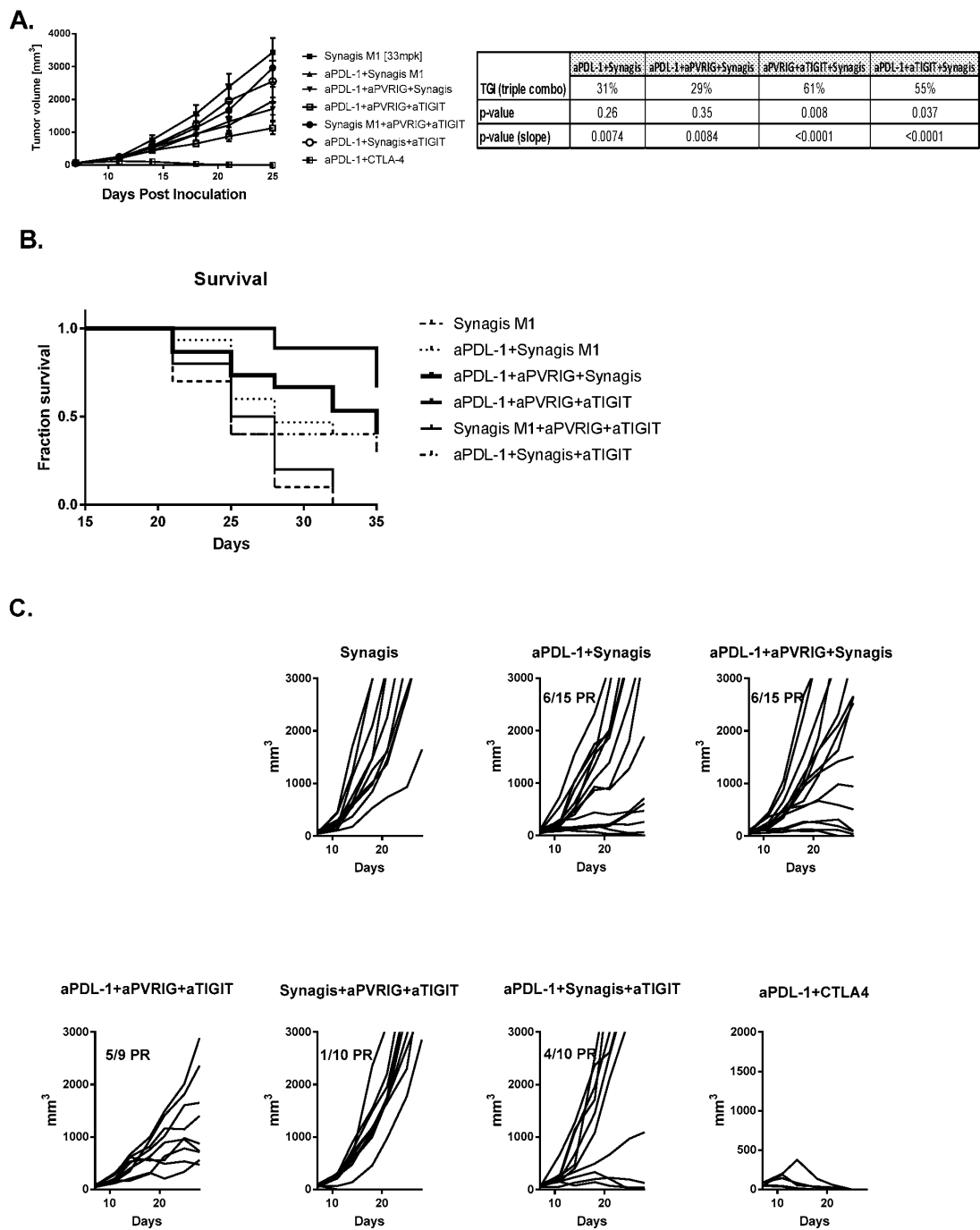


Figure 25

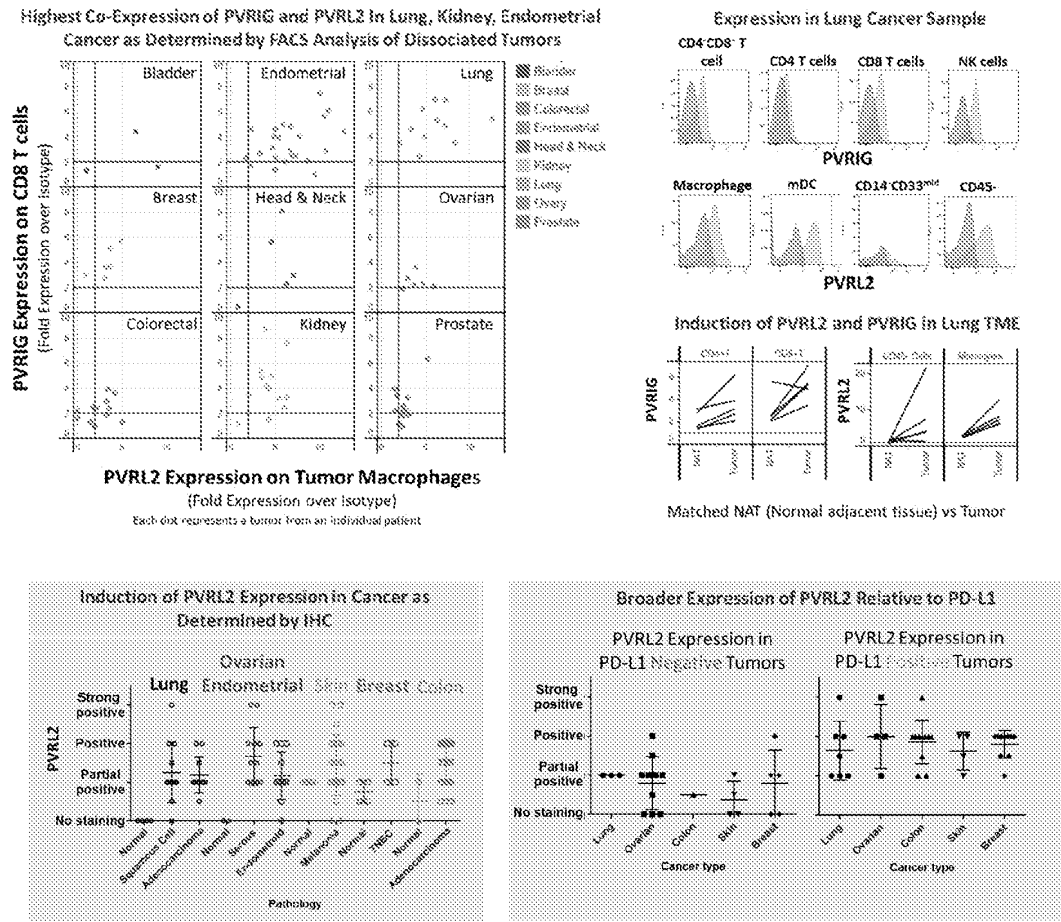
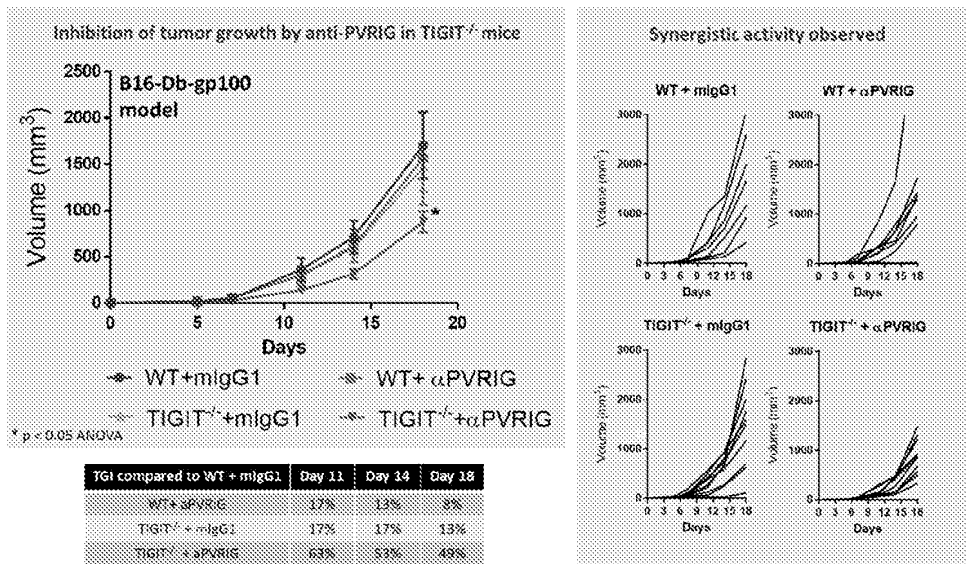


Figure 26

PVRIG ANTIBODY BLOCKADE REDUCED TUMOR GROWTH IN TIGIT^{-/-} MICE



PVRIG BLOCKING ANTIBODIES REDUCE TUMOR GROWTH AND INCREASE SURVIVAL IN COMBINATION WITH PD1 PATHWAY BLOCKADE

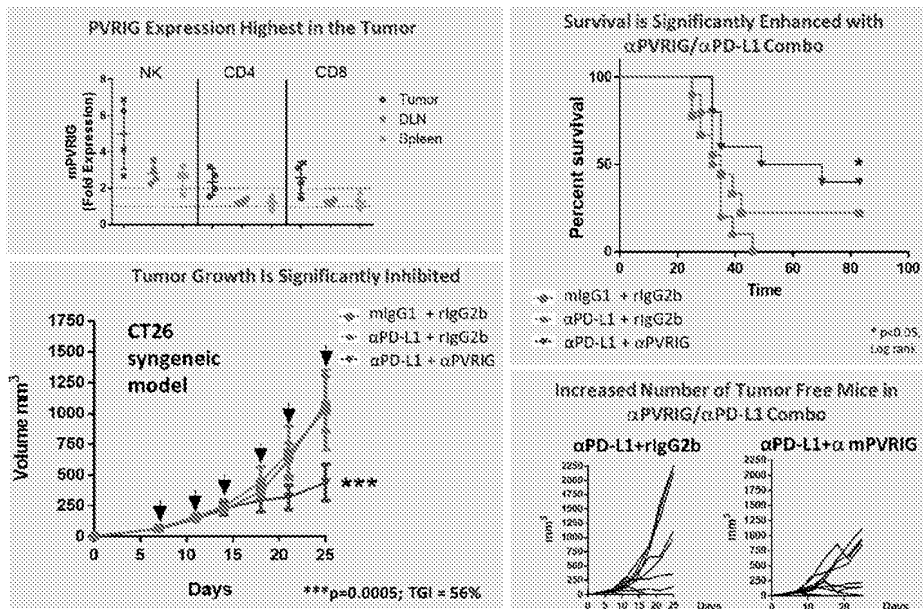


Figure 27

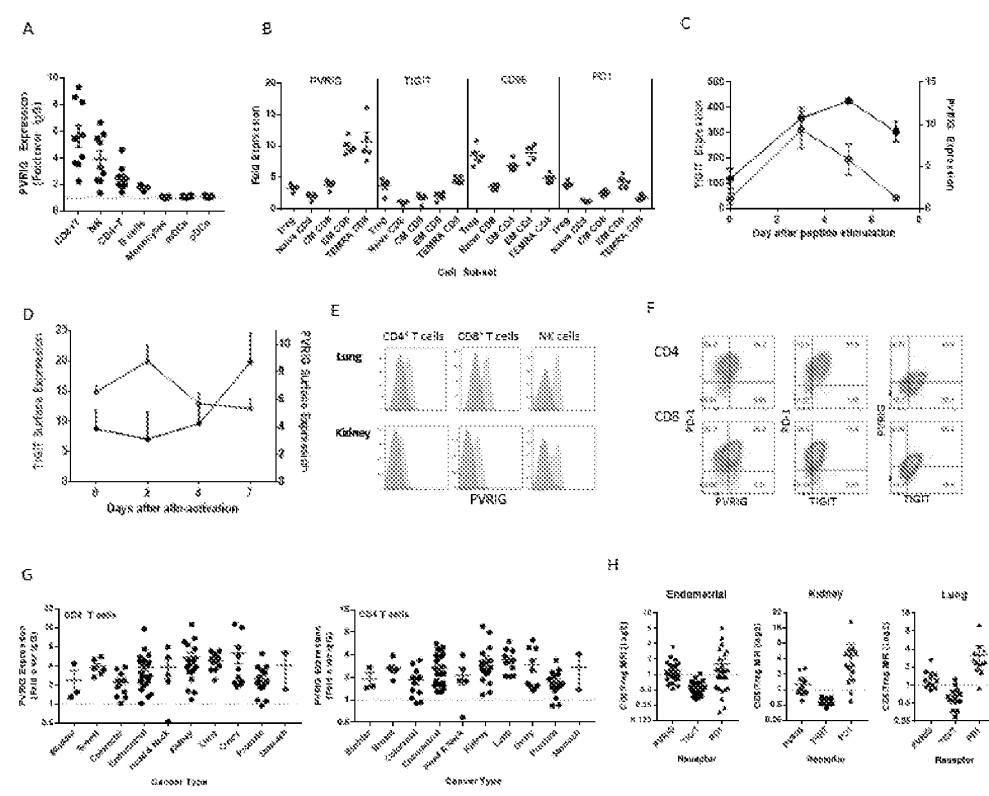


Figure 28F

	All Tumors				PD-L1+				PD-L1-		
Tissue Type	PVRL2+	Total	% Positive		PVRL2+	Total	% Positive		PVRL2+	Total	% Positive
Lung											
Normal	1	4	25		N/A	N/A	N/A		N/A	N/A	N/A
Adenocarcinoma	8	14	57		3	5	60		5	9	56
Squamous cell carcinoma	8	13	62		5	7	71		3	6	50
Ovarian											
Normal	0	2	0		N/A	N/A	N/A		N/A	N/A	N/A
Serous cystadenocarcinoma	8	12	67		2	3	67		6	9	67
Mucinous cystadenocarcinoma	4	6	67		1	1	100		3	5	60
Endometrioid adenocarcinoma	8	12	67		3	4	75		5	8	63
Colon											
Normal	0	2	0		N/A	N/A	N/A		N/A	N/A	N/A
Adenocarcinoma	16	30	53		8	14	57		7	16	44
Skin											
Normal	0	4	0		N/A	N/A	N/A		N/A	N/A	N/A
Melanoma-Primary	3	24	13		1	4	25		2	20	10
Metastatic melanoma	1	12	8		1	4	25		0	8	0
Renal											
Normal	0	3	0		N/A	N/A	N/A		N/A	N/A	N/A
Clear cell carcinoma	8	20	40		0	0	N/A		8	20	40
Papillary renal cell carcinoma	2	7	29		1	1	100		1	6	17
Breast											
TNBC	1	3	33		0	0	N/A		1	3	33
Invasive ductal carcinoma	19	30	63		6	10	60		13	20	65

Figure 29

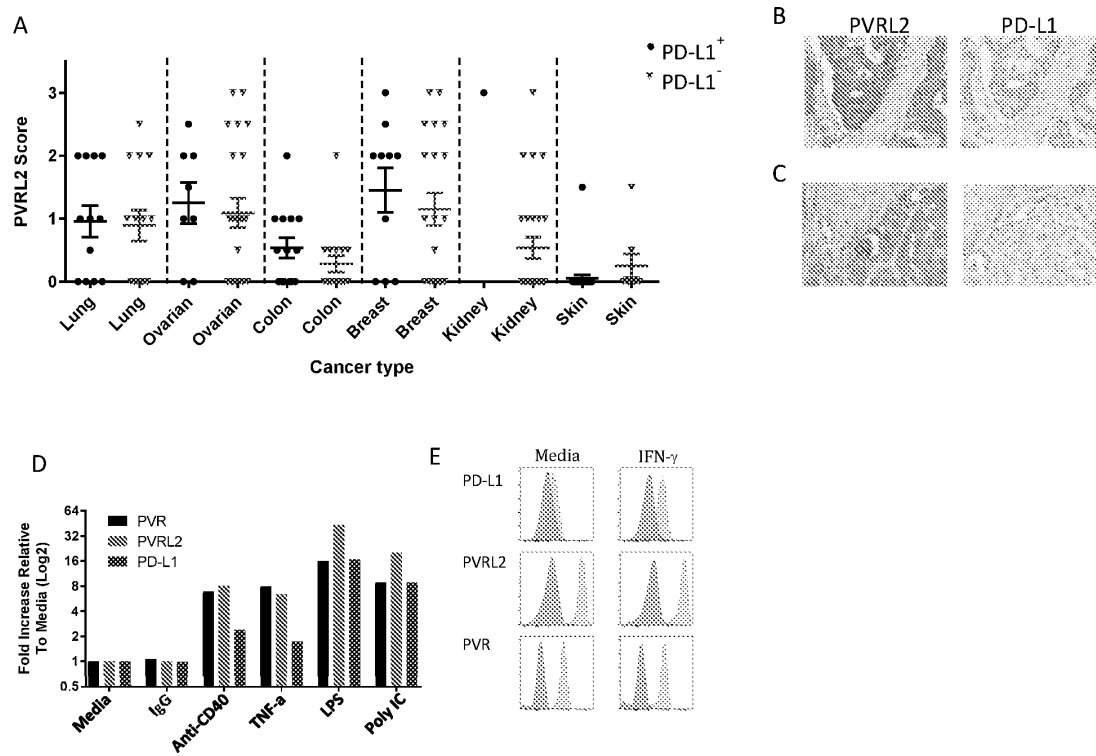


Figure 30

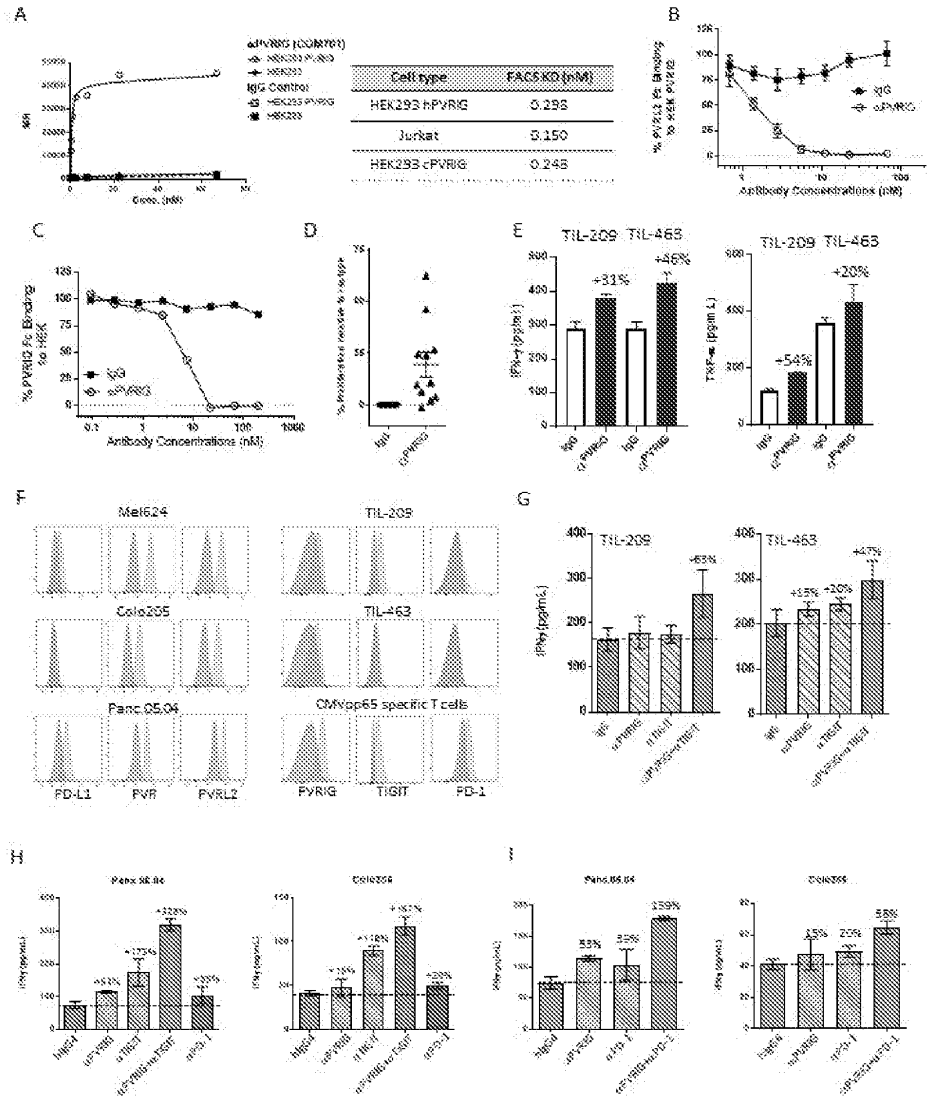


Figure 31

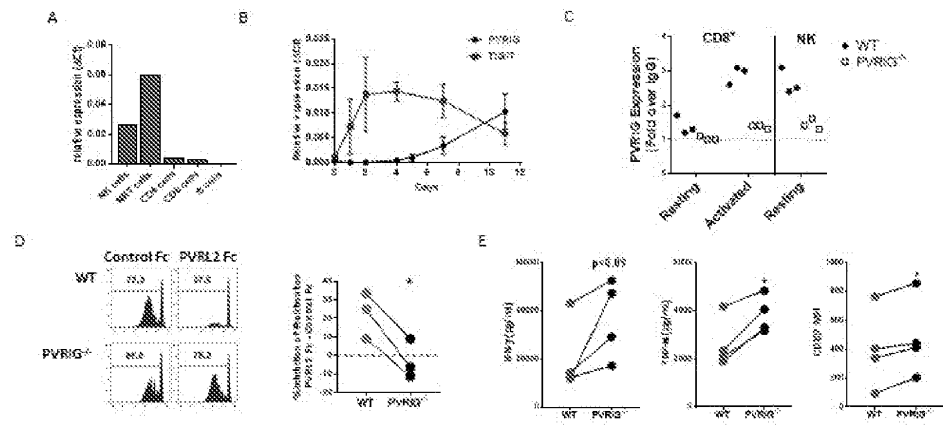


Figure 32

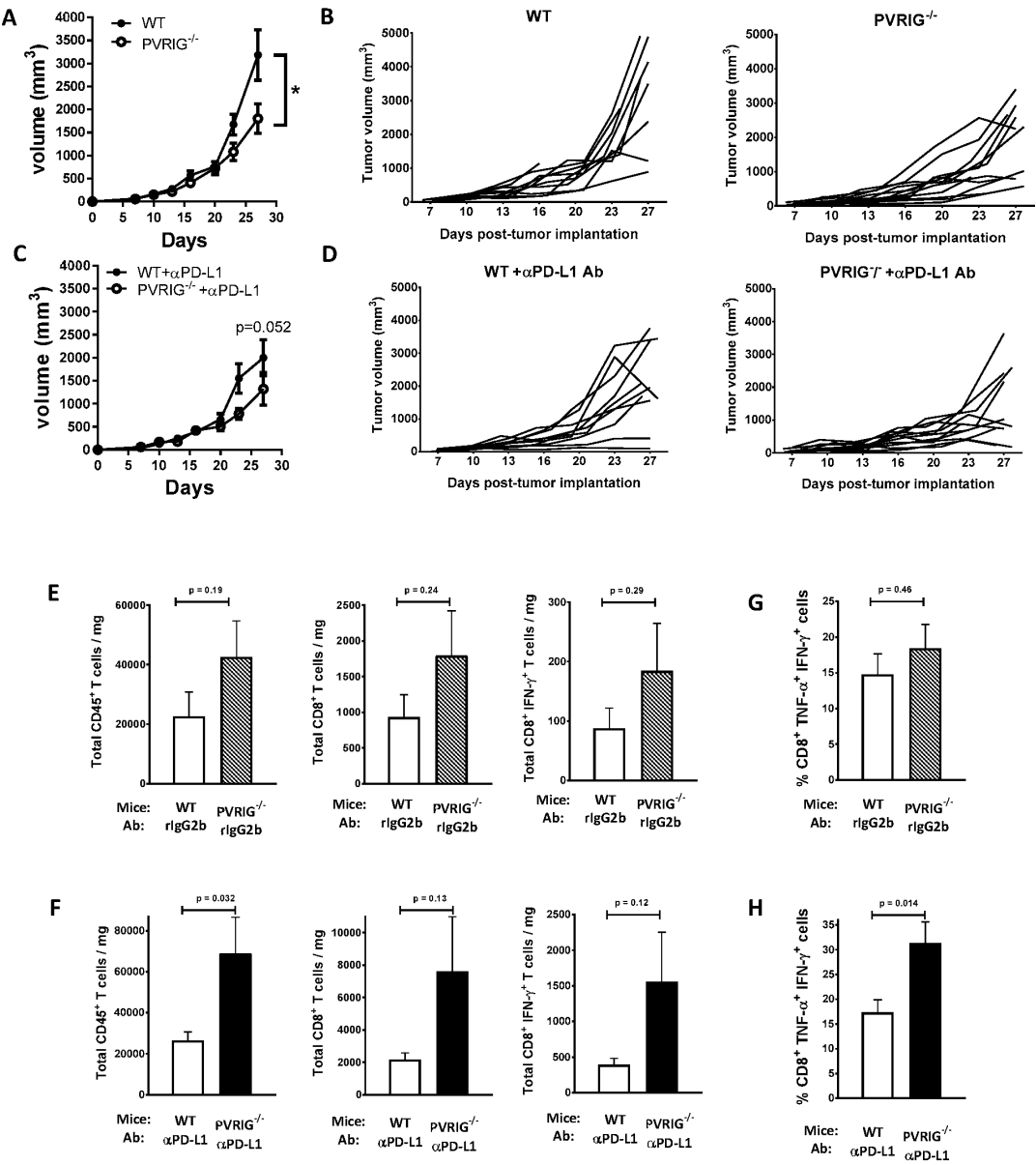


Figure 33

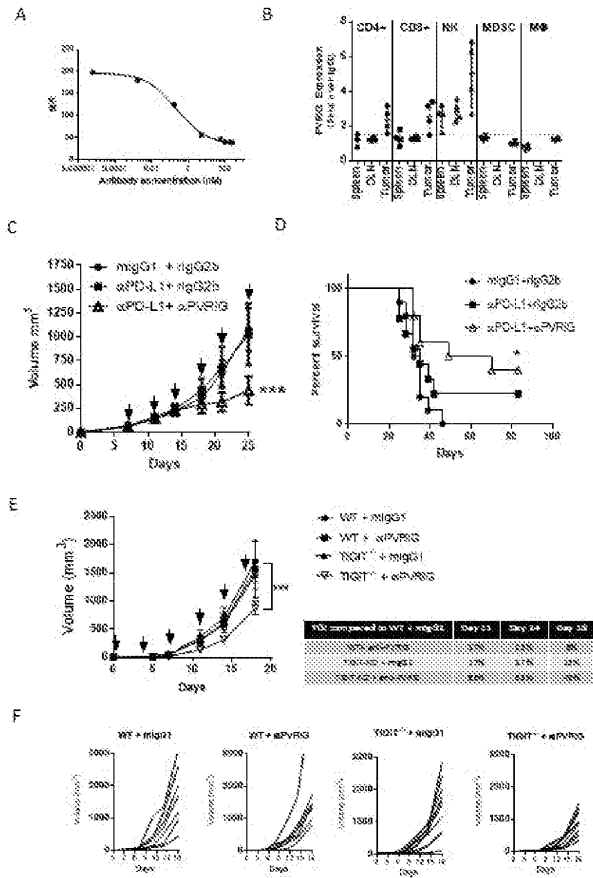


Figure 34

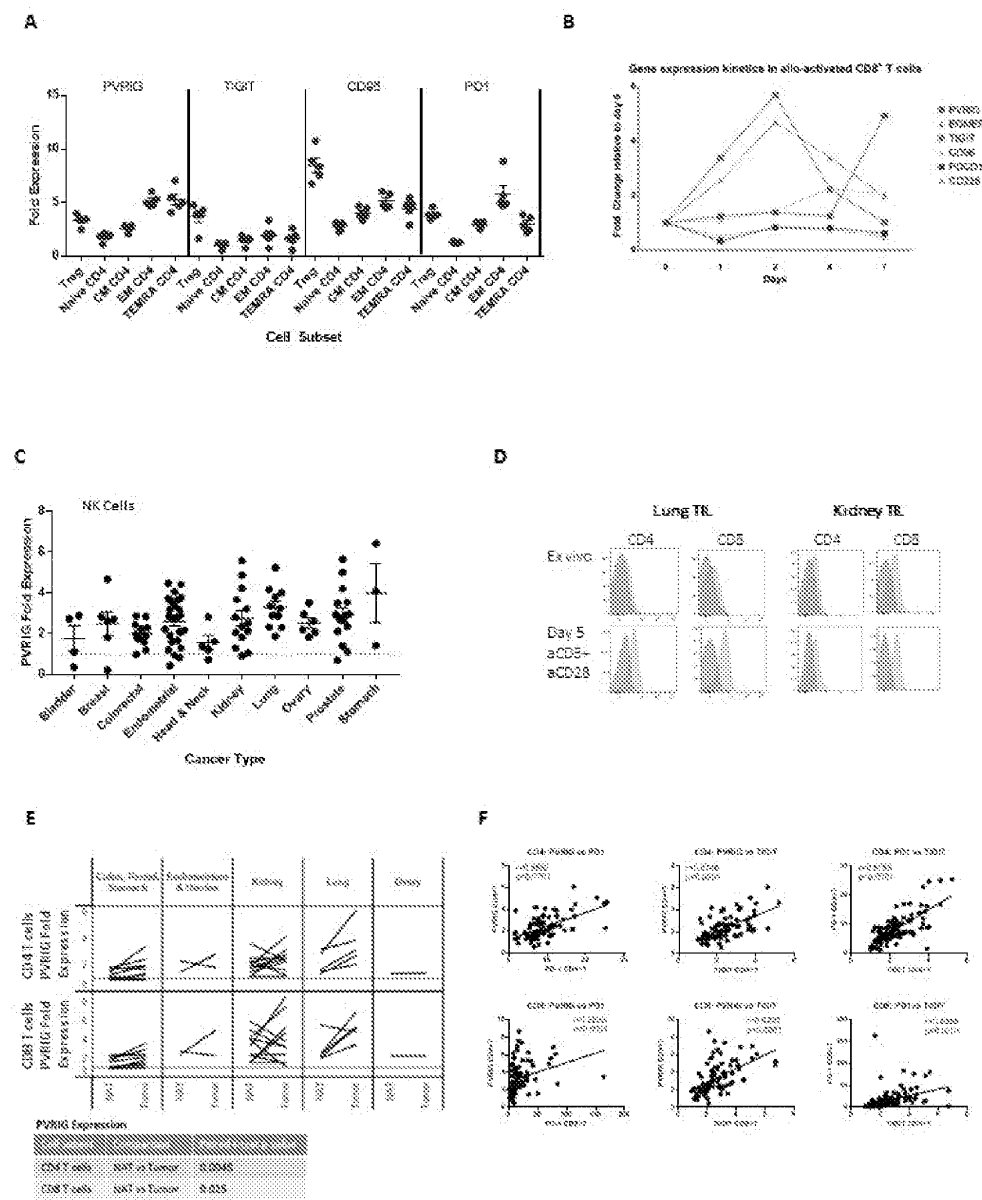


Figure 35

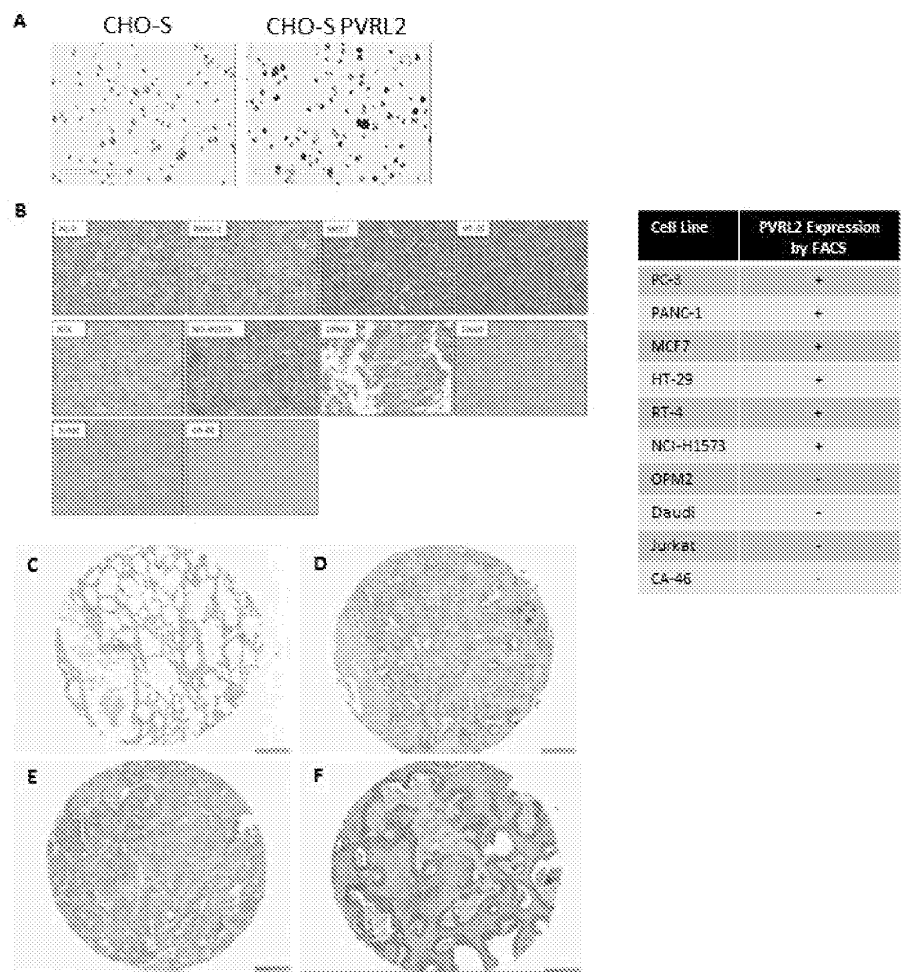


Figure 36

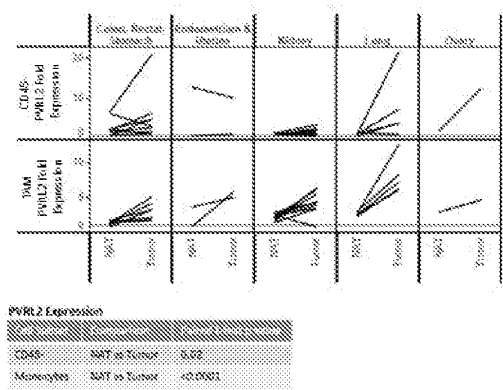


Figure 37

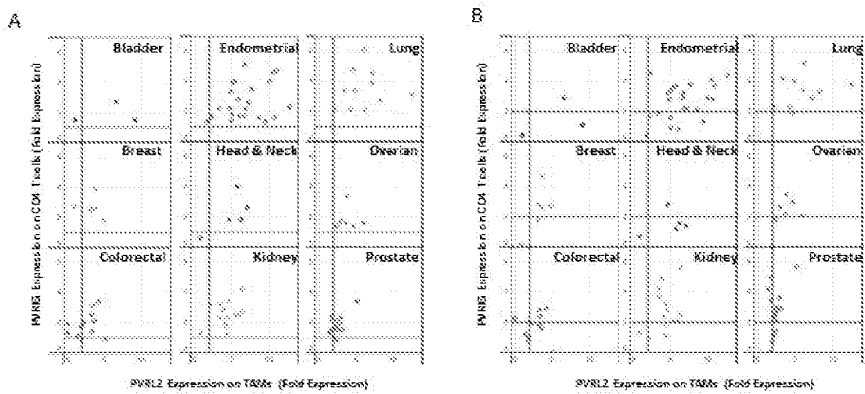


Figure 38

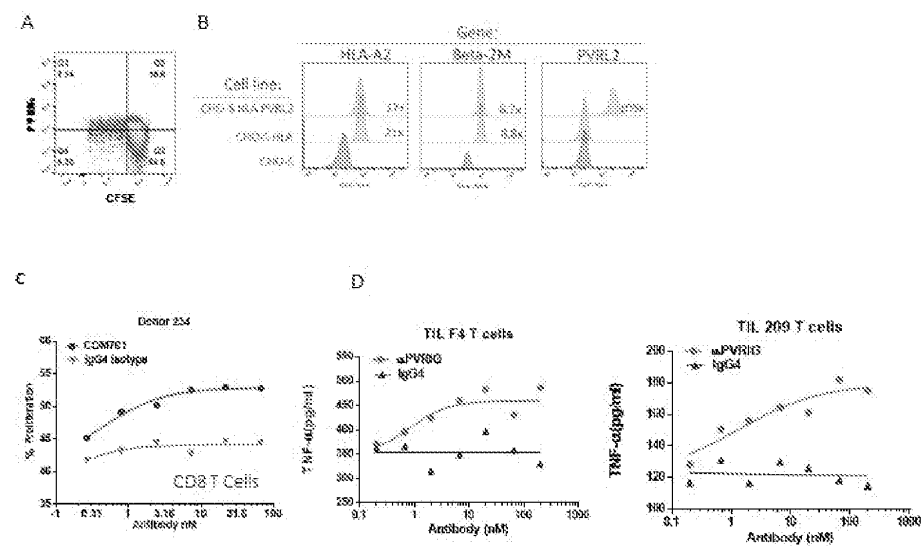


Figure 39

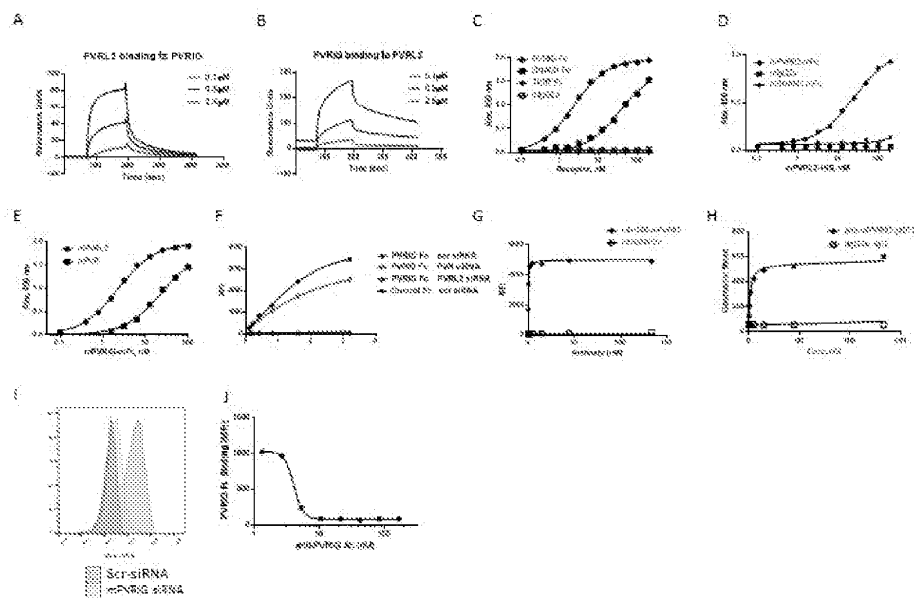


Figure 40

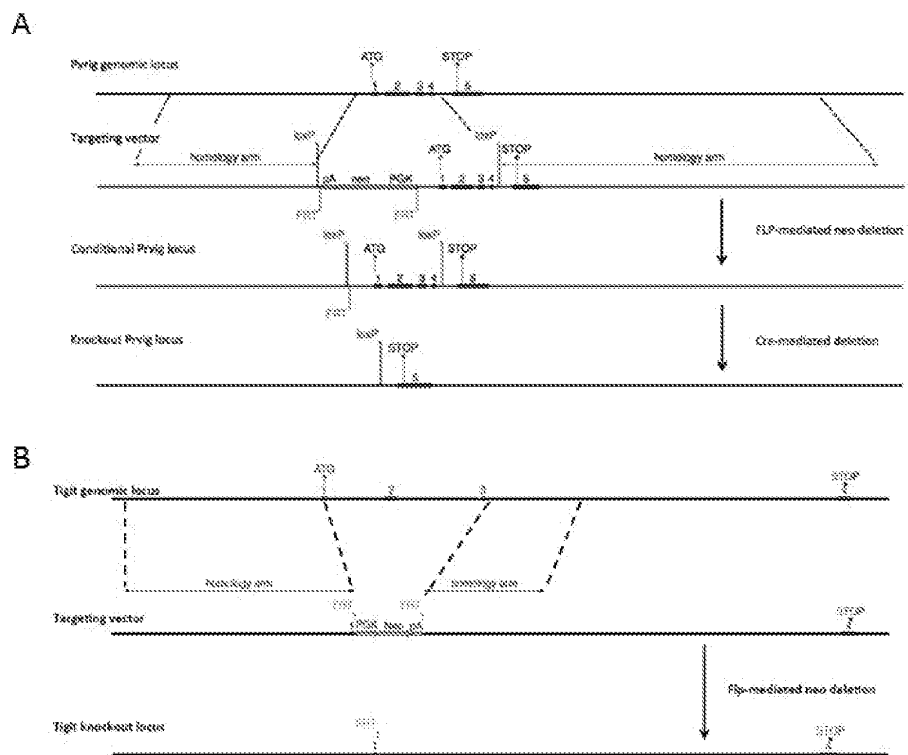


Figure 41

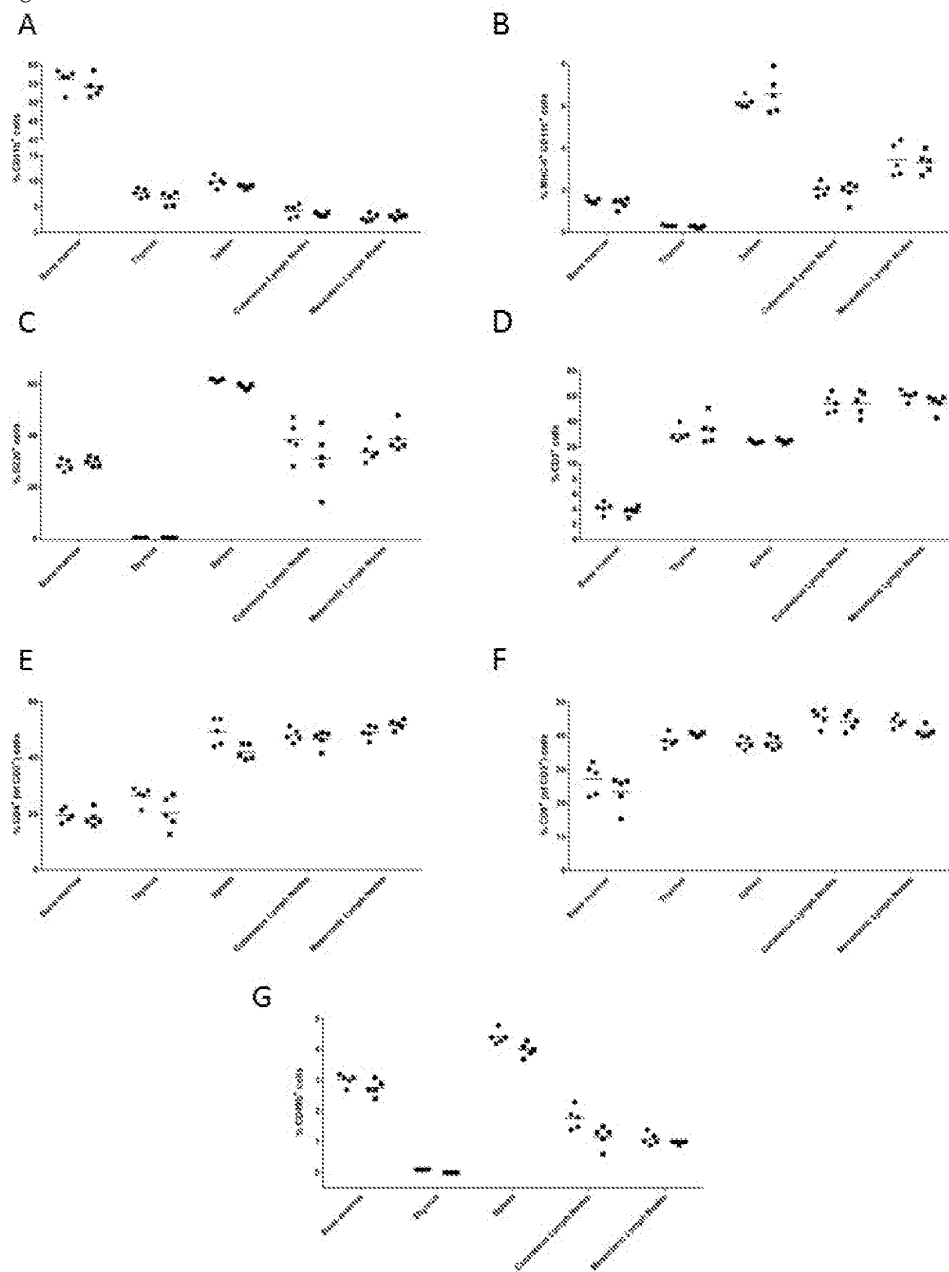


Figure 41 (cont.)

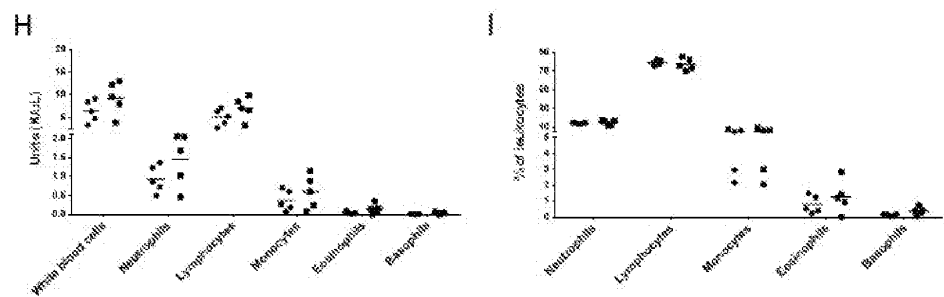


Figure 42

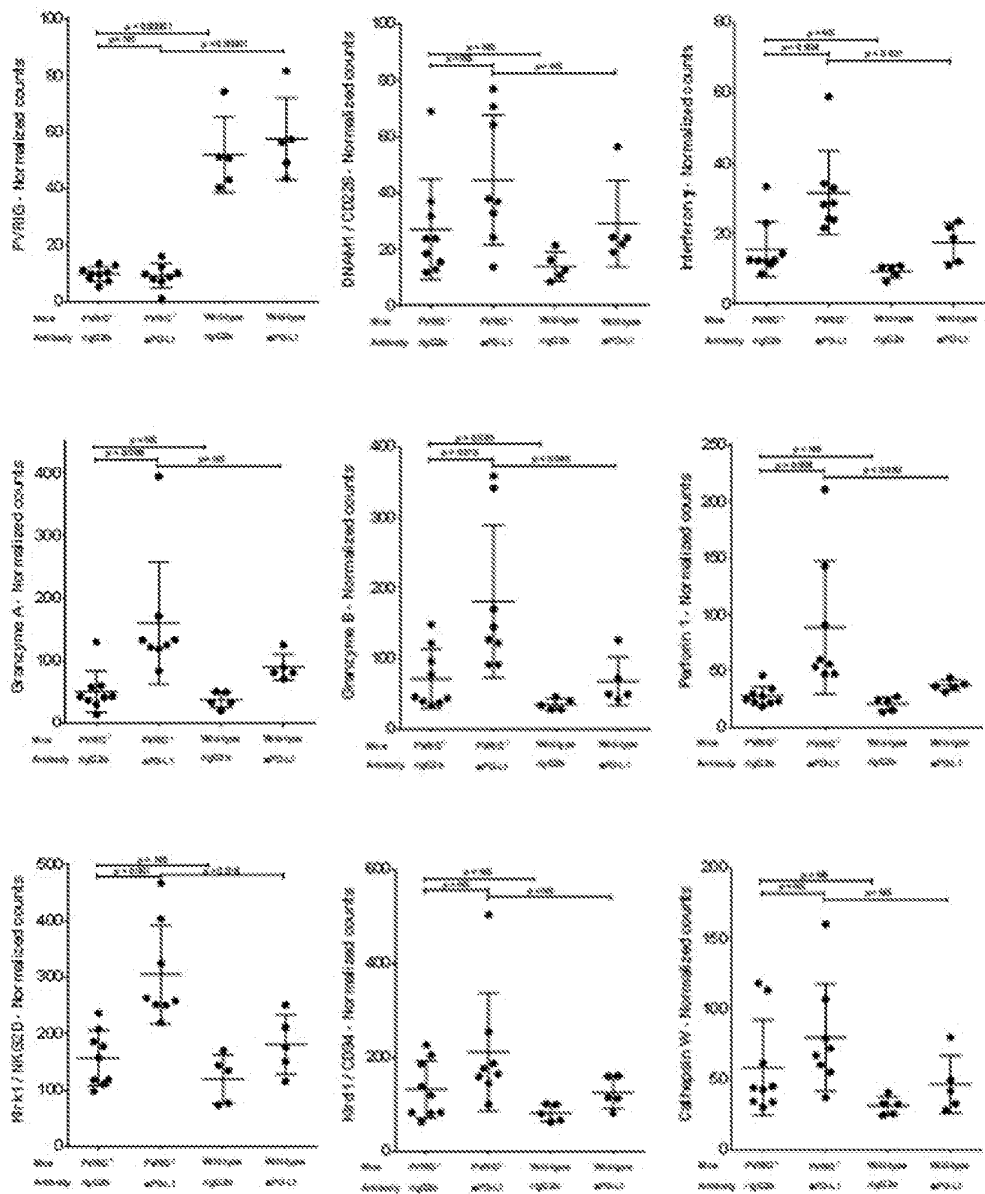


Figure 43

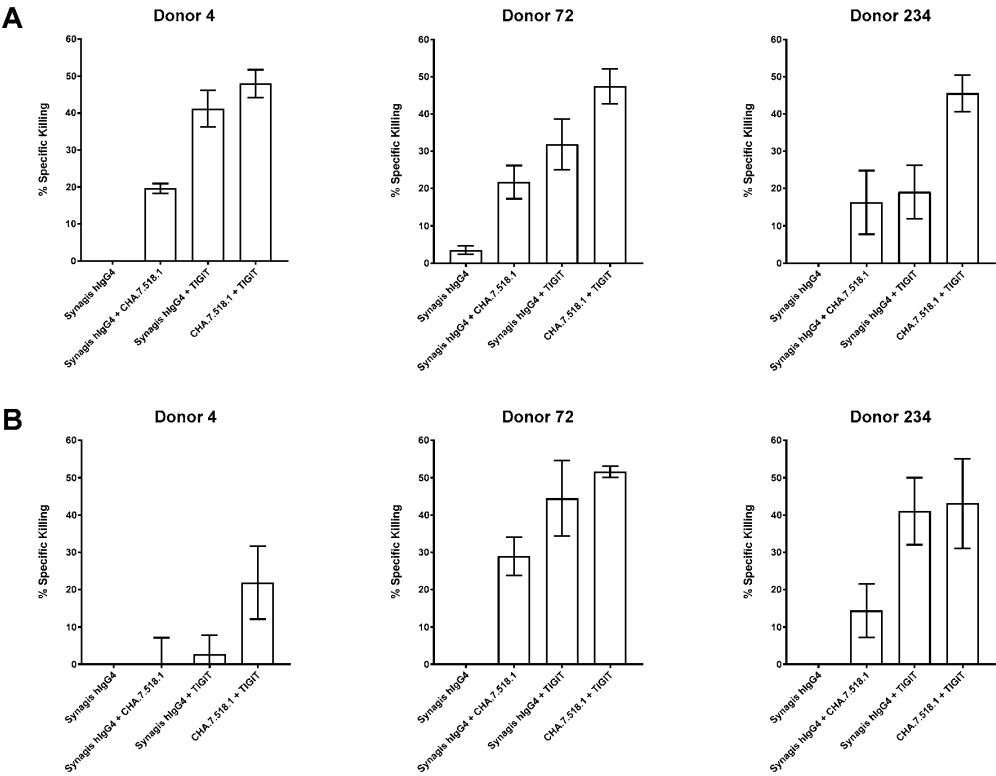


Figure 44

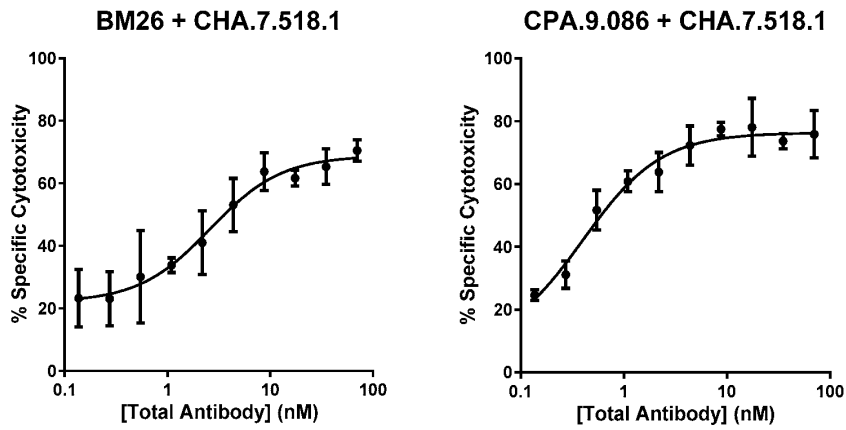


Figure 45
CPA9.086 CDR sequences

Definition	H-CDR1	H-CDR2	H-CDR3	L-CDR1	L-CDR2	L-CDR3
MGT	GFTFSYA (SEQ ID NO:1105)	ISYAGEVK (SEQ ID NO:1107)	ARDPLPLHYGMDV (SEQ ID NO:1109)	SSNIMGRRP (SEQ ID NO:1111)	SQN (SEQ ID NO:1113)	AVWDDIGRVLQ (SEQ ID NO:1115)
Kabat	SYAMH (SEQ ID NO:1106)	VISYAGEVKYADSVKG (SEQ ID NO:1108)	DPLPLHYGMDV (SEQ ID NO:1110)	SGSSSNMIGRRPVN (SEQ ID NO:1112)	SQNQRPS (SEQ ID NO:1114)	AVWDDIGRVLQ (SEQ ID NO:1116)

Figure 46

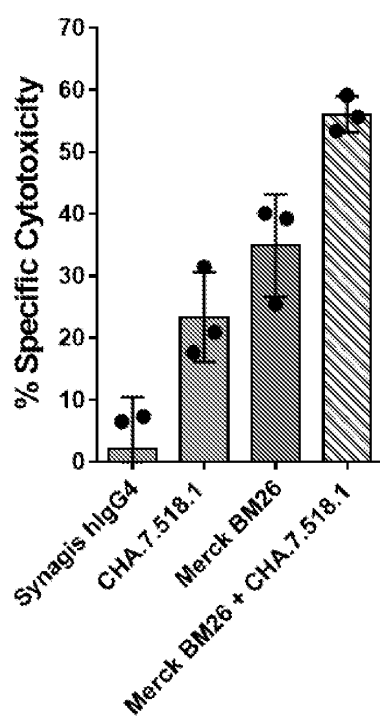
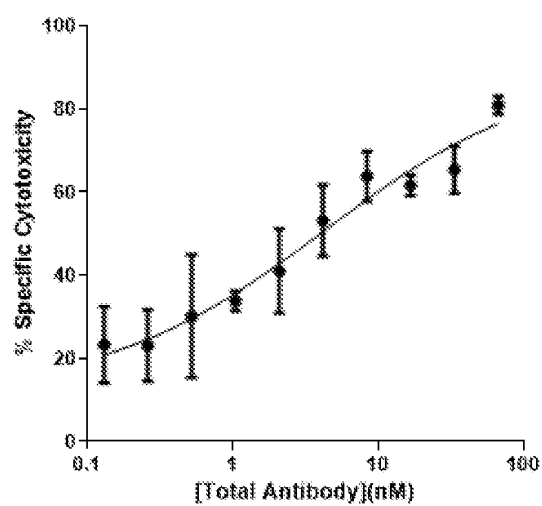
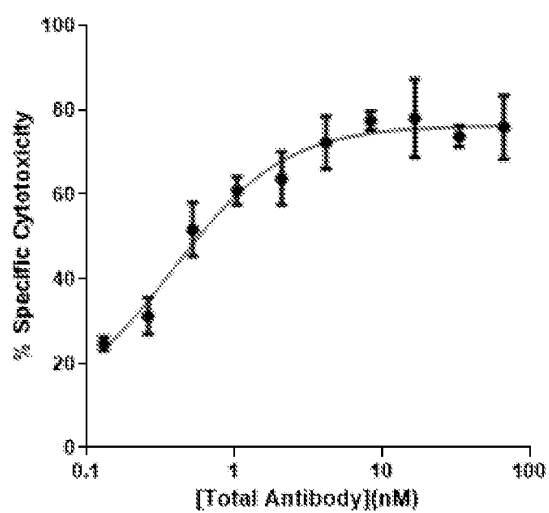
Merck BM26 + CHA.7.518.1**Merck BM26 + CHA.7.518.1****CPA.9.086 + CHA.7.518.1**

Figure 47

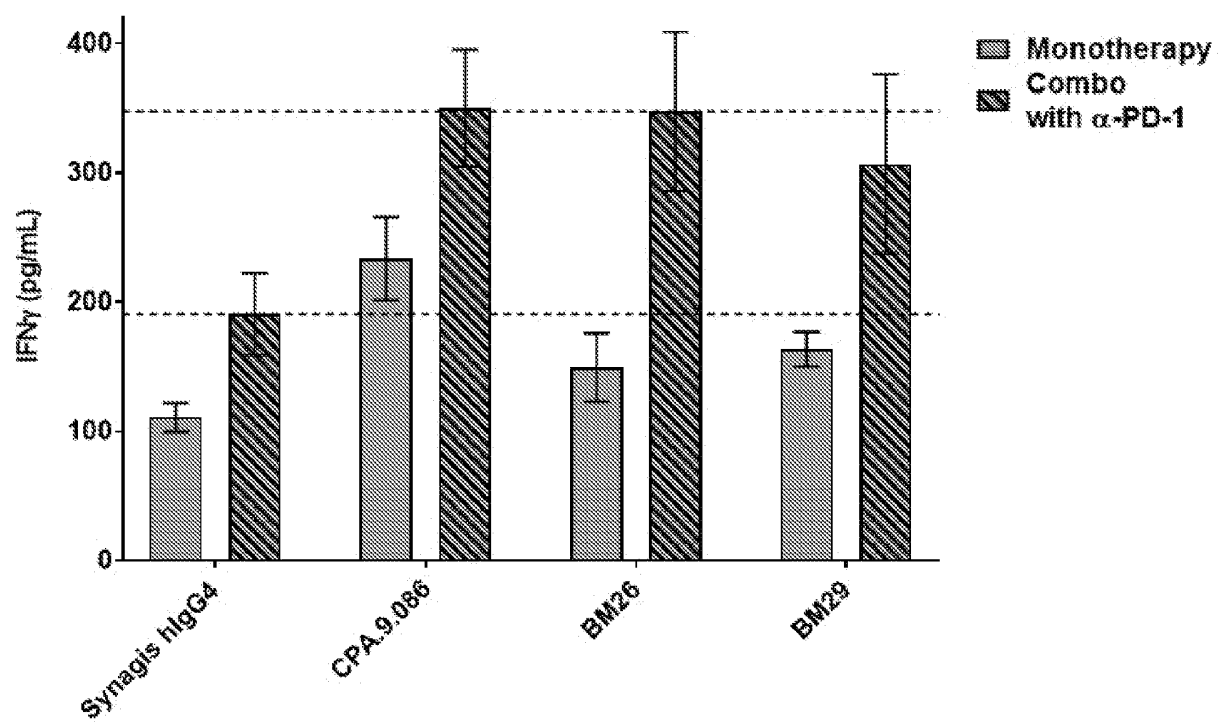


Figure 48

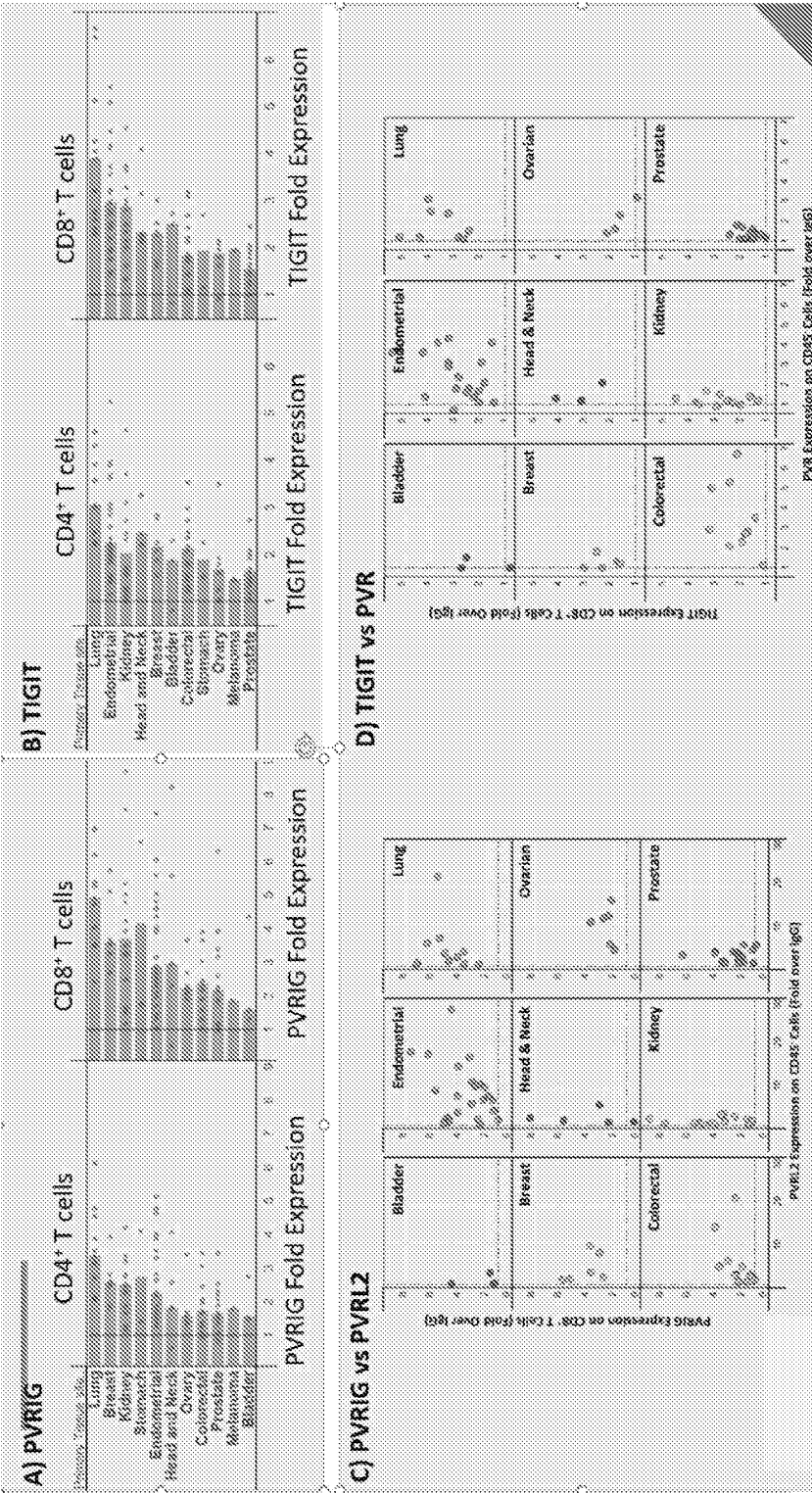


Figure 49

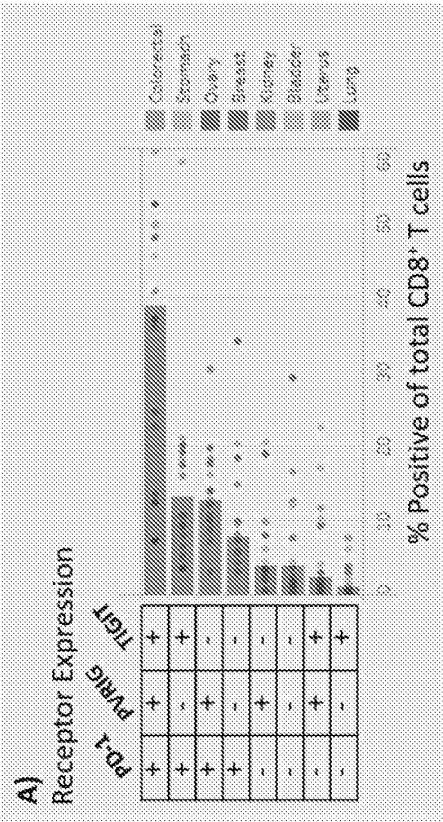
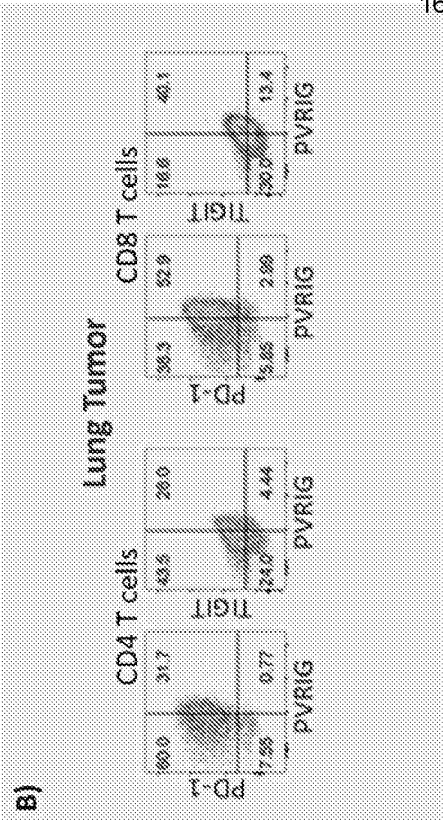


Figure 49 (cont.)

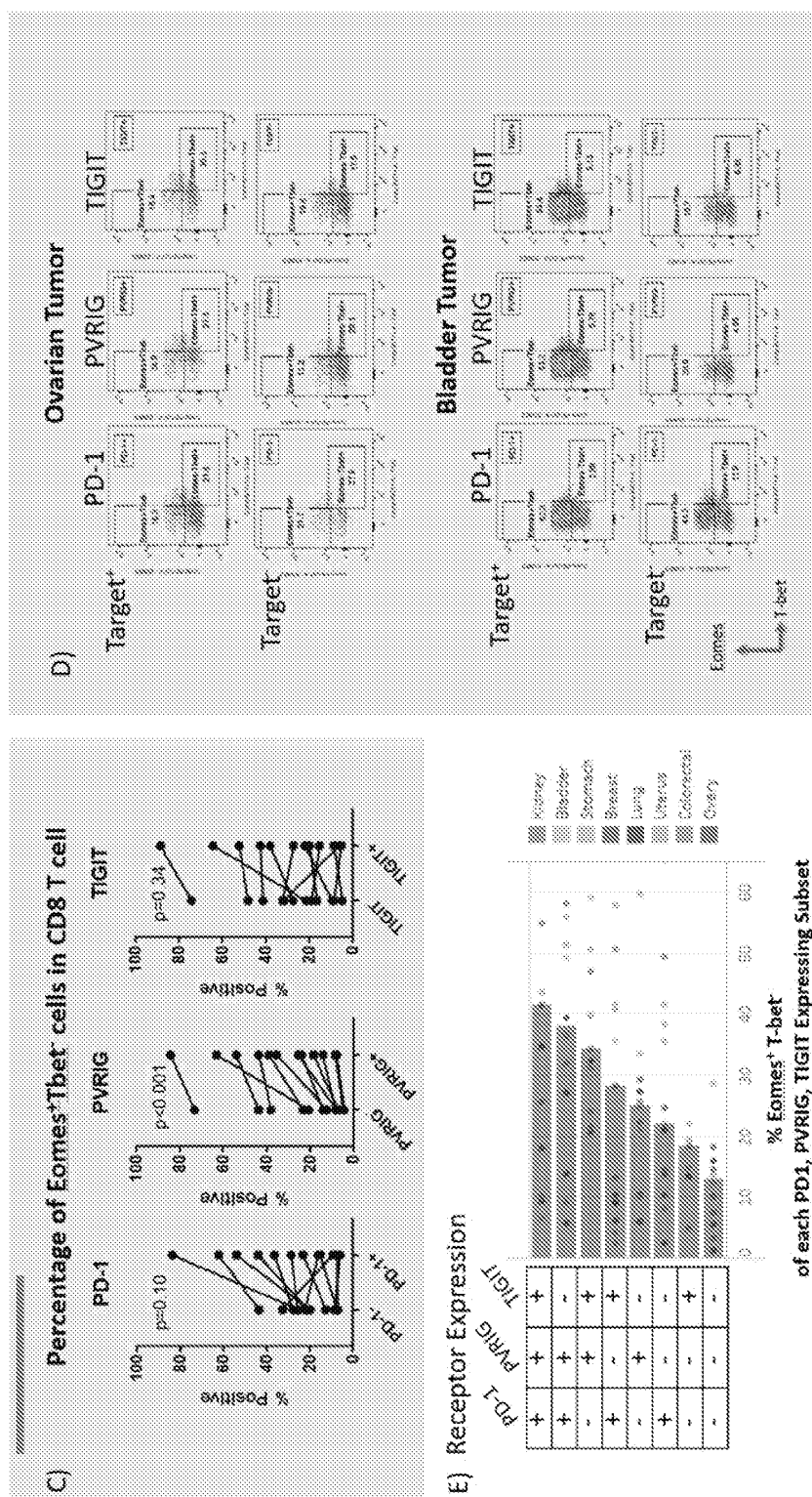


Figure 50

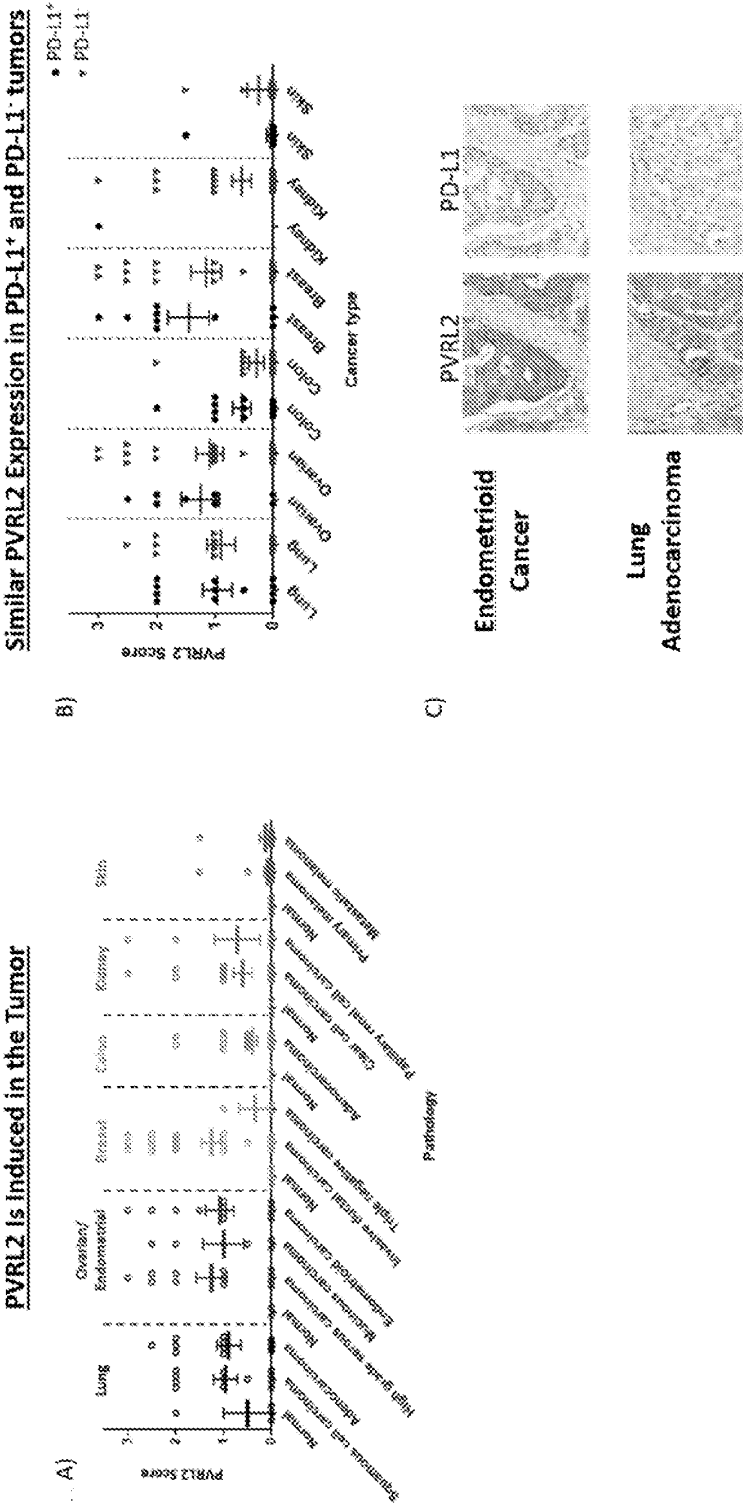


Figure 51

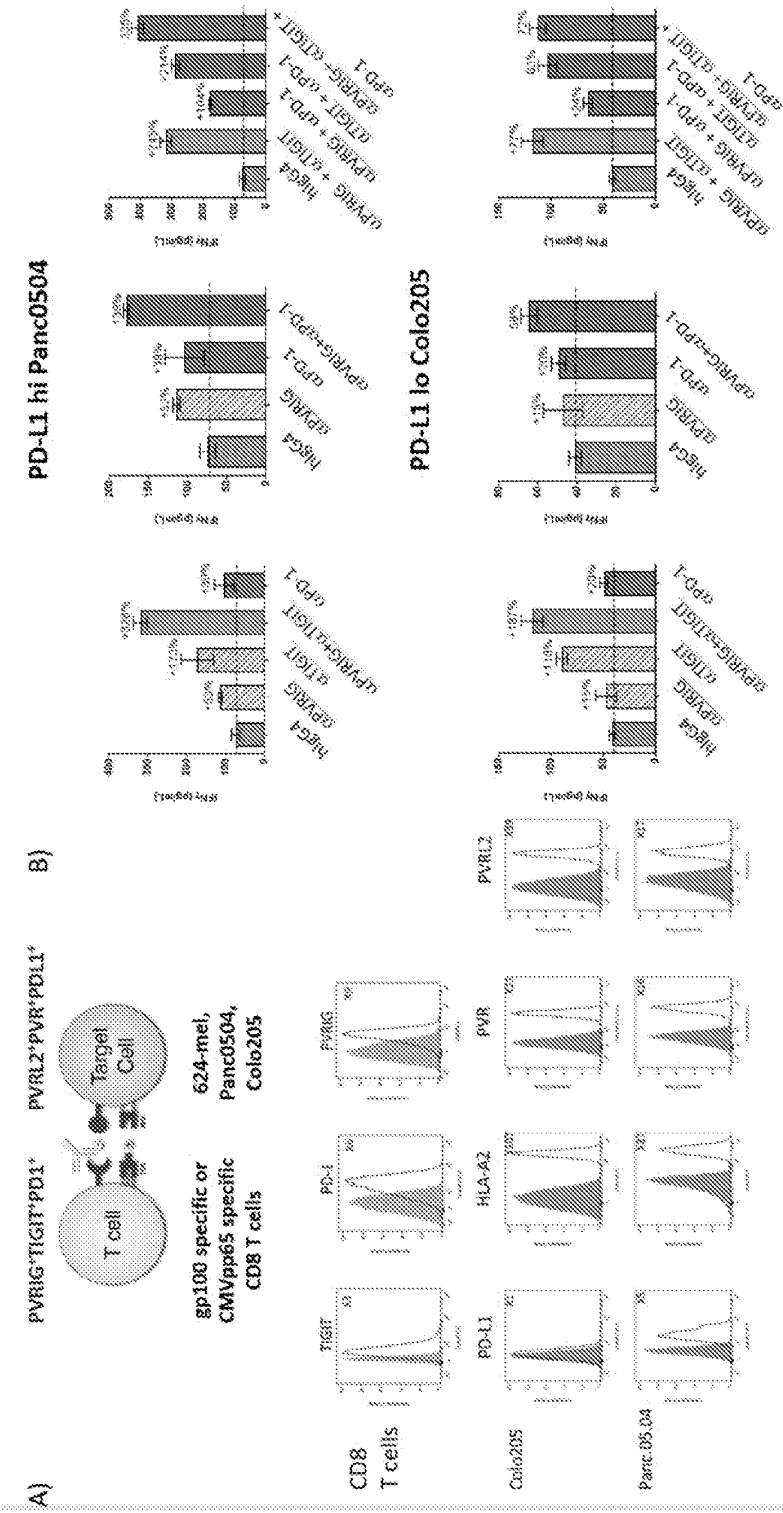


Figure 52

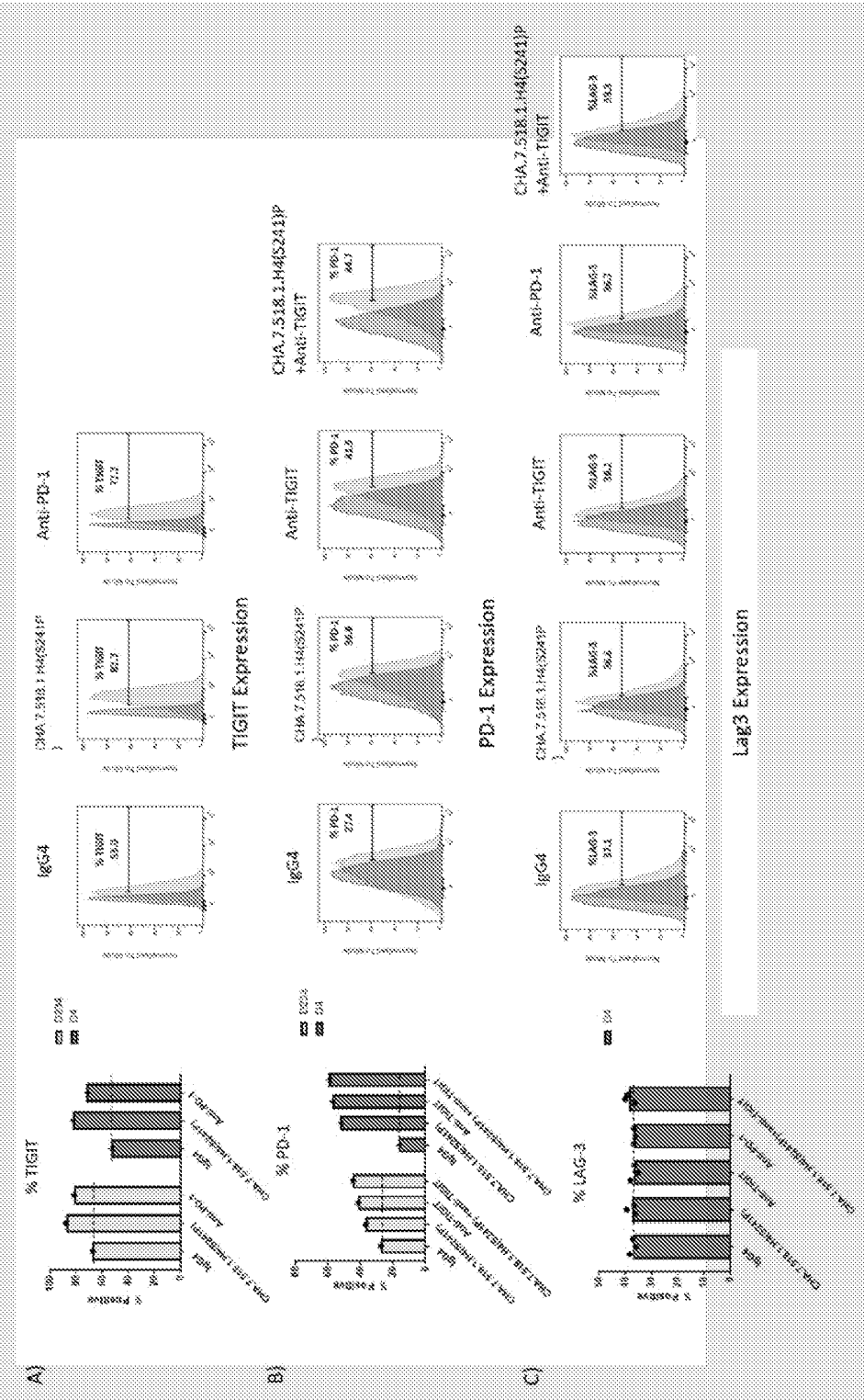


Figure 53

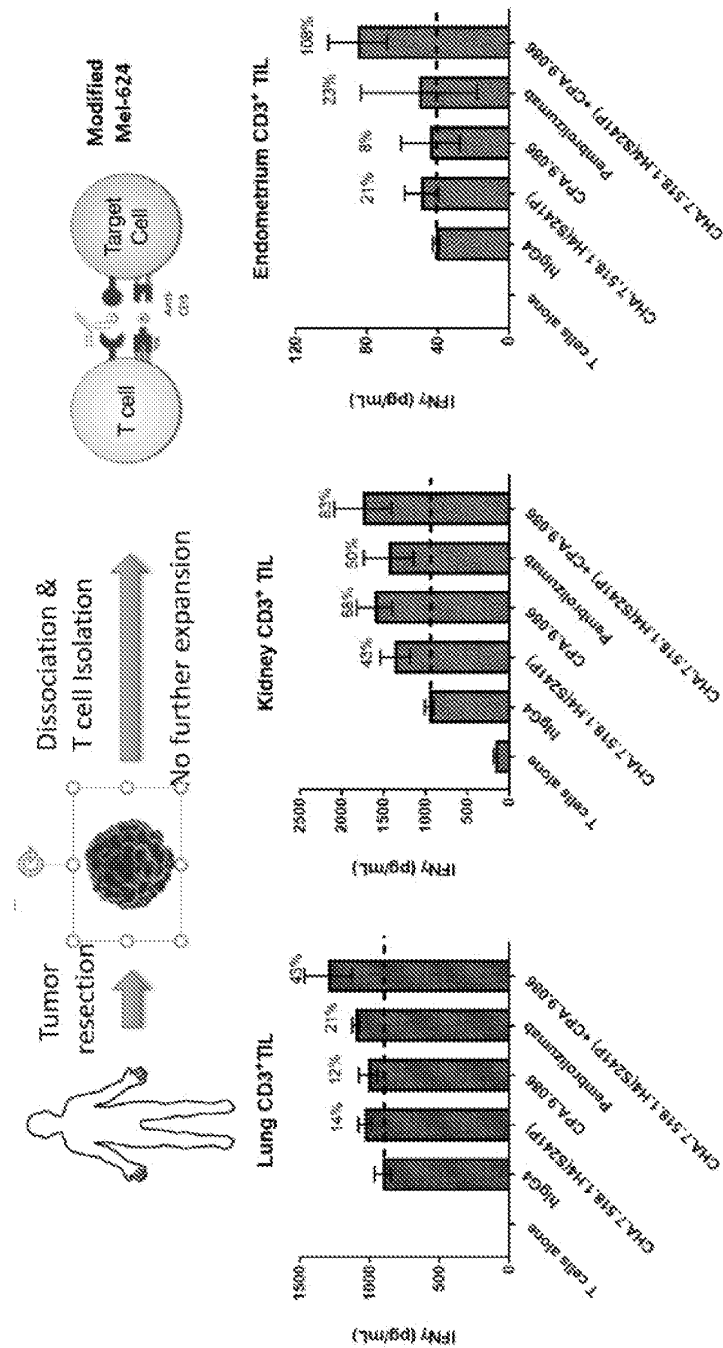


Figure 54

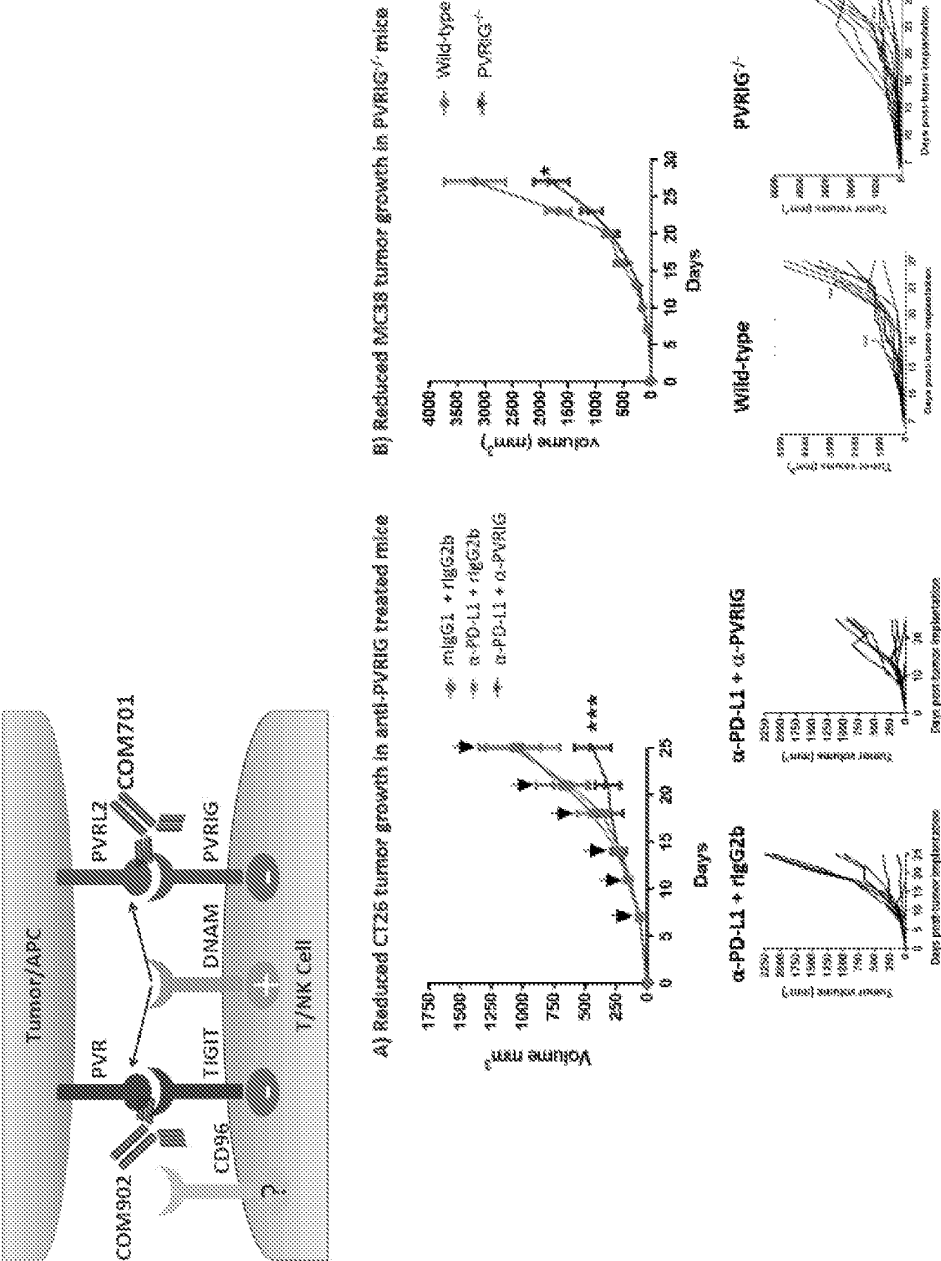


Figure 55

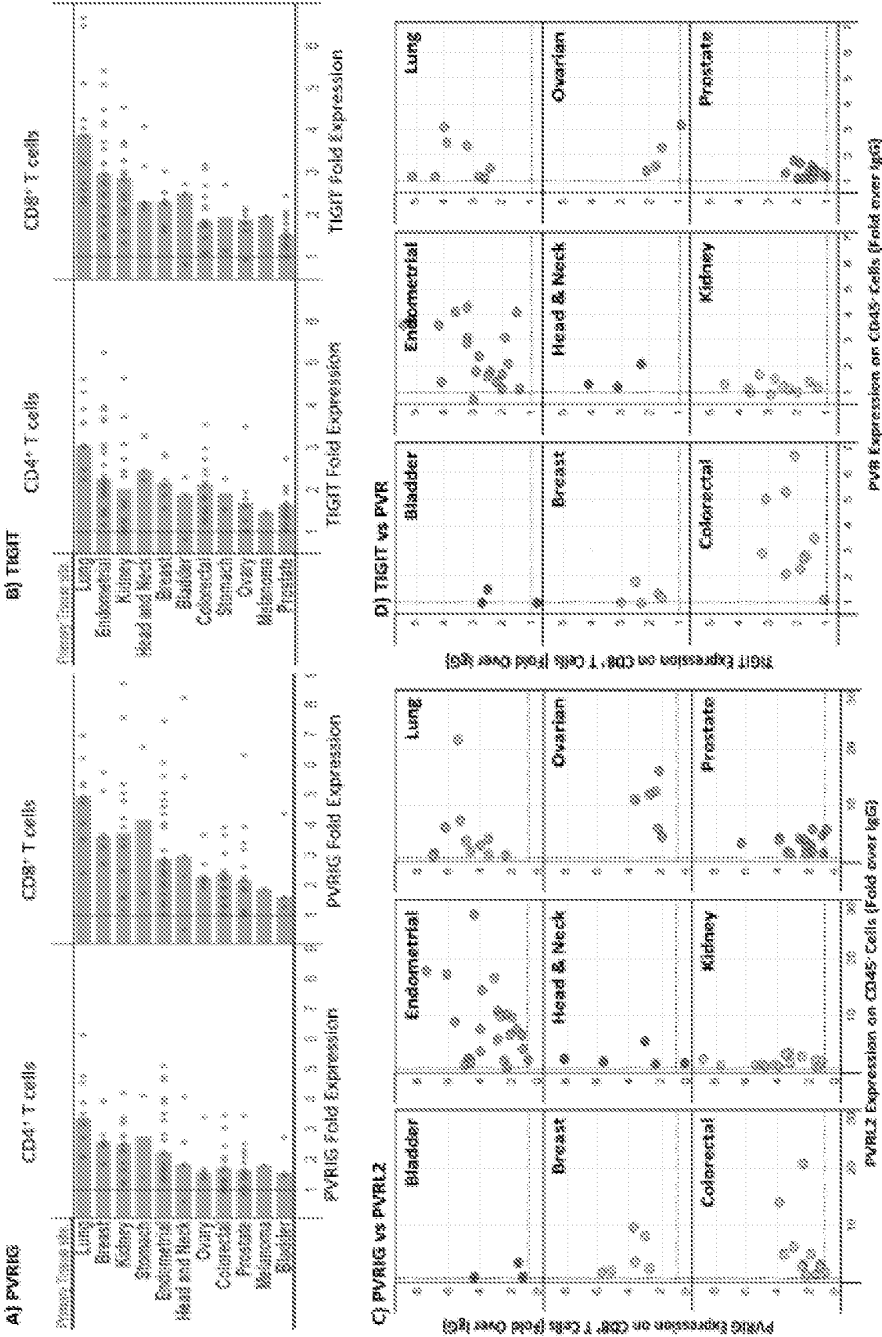


Figure 56

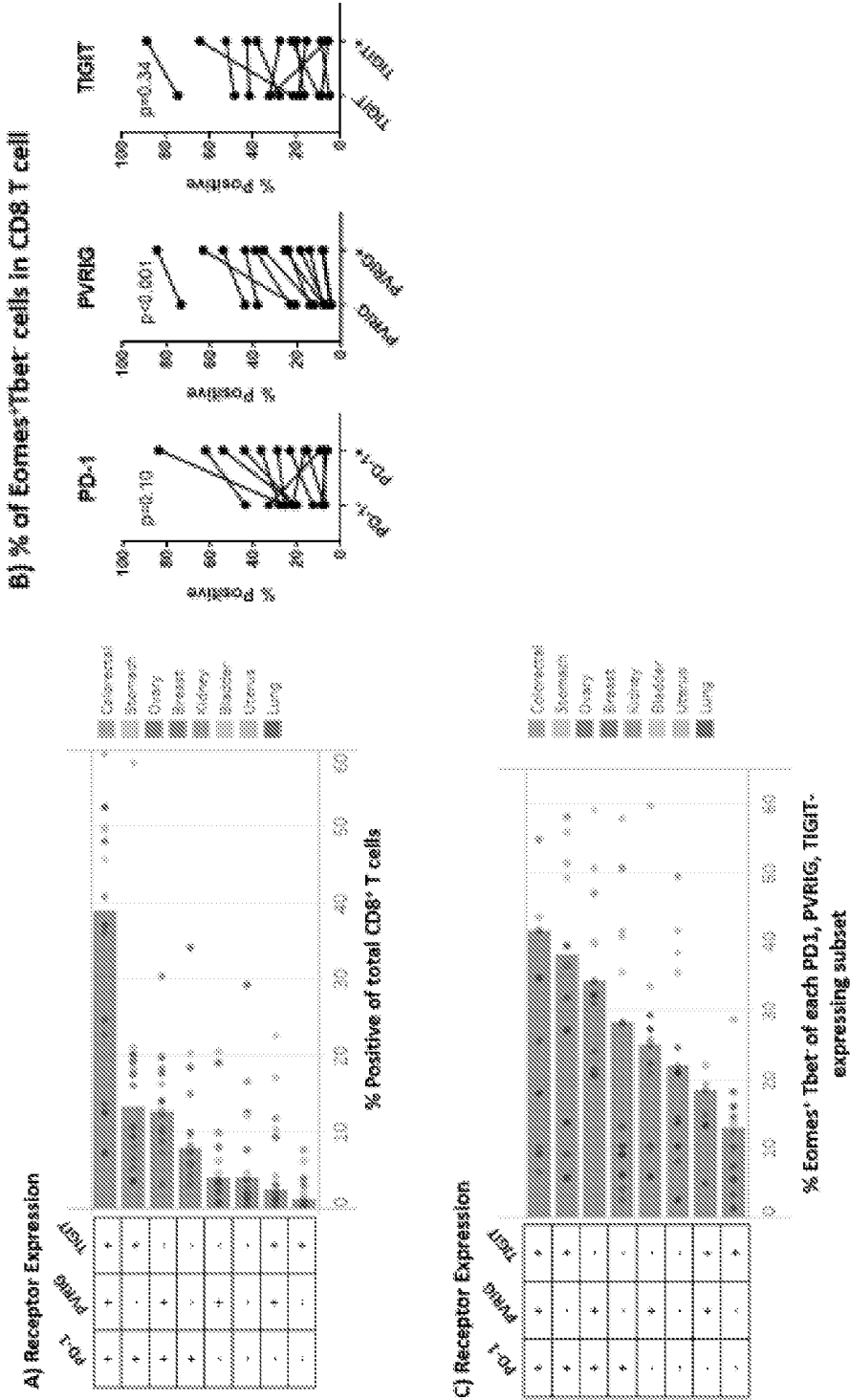


Figure 57

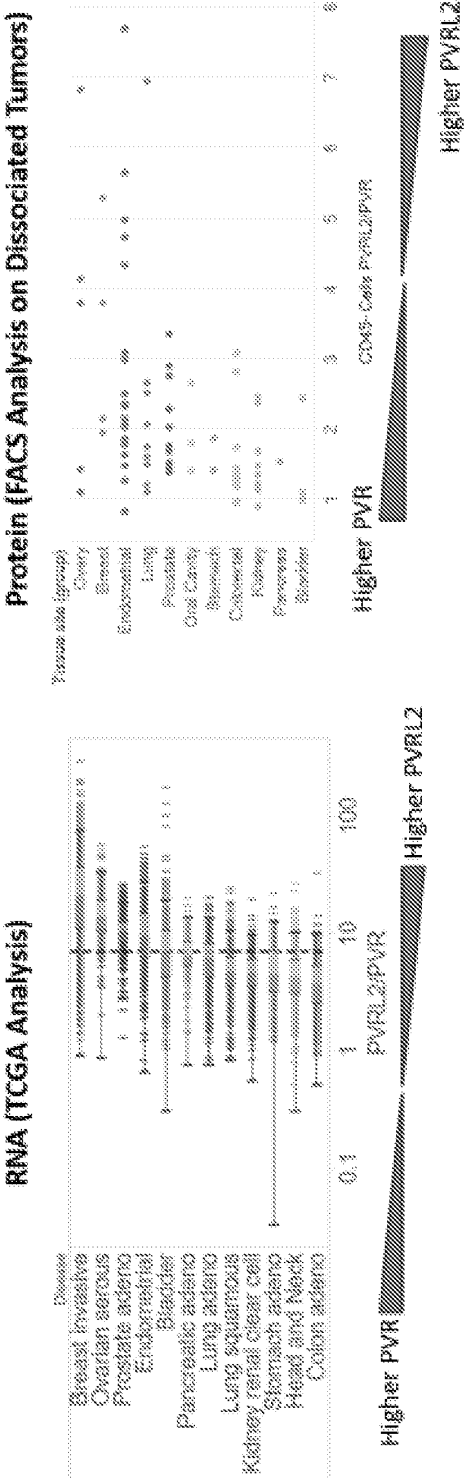


Figure 58

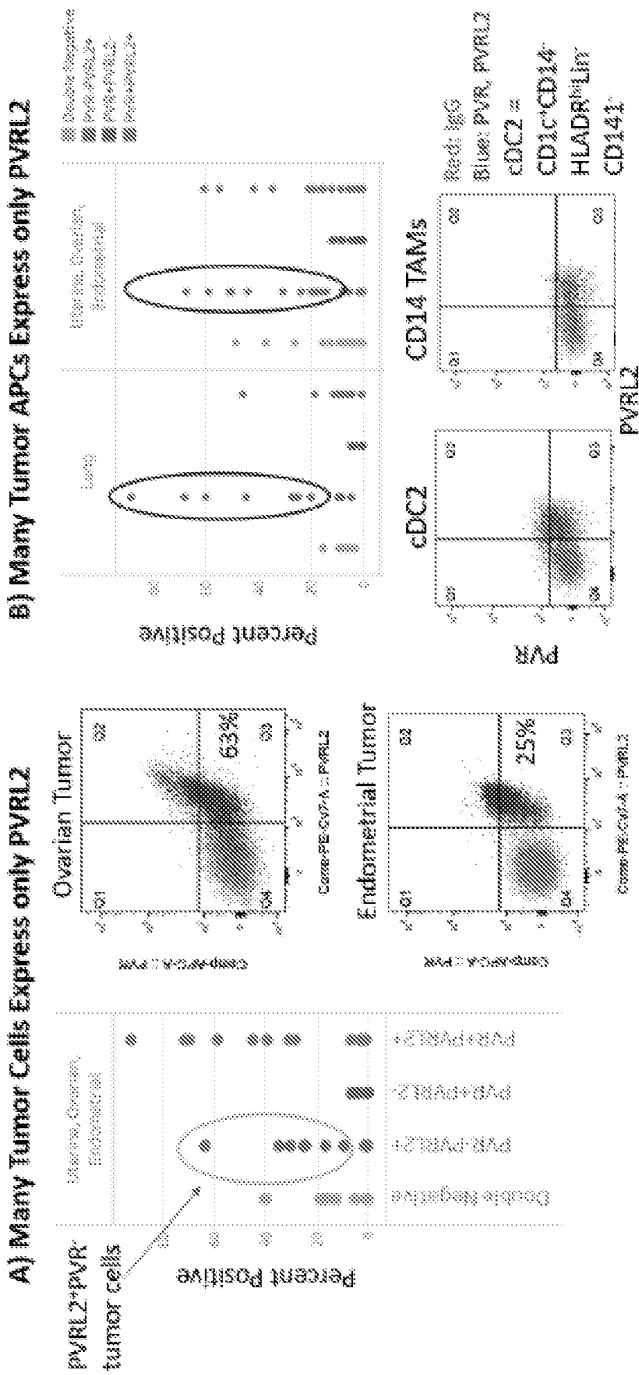


Figure 59

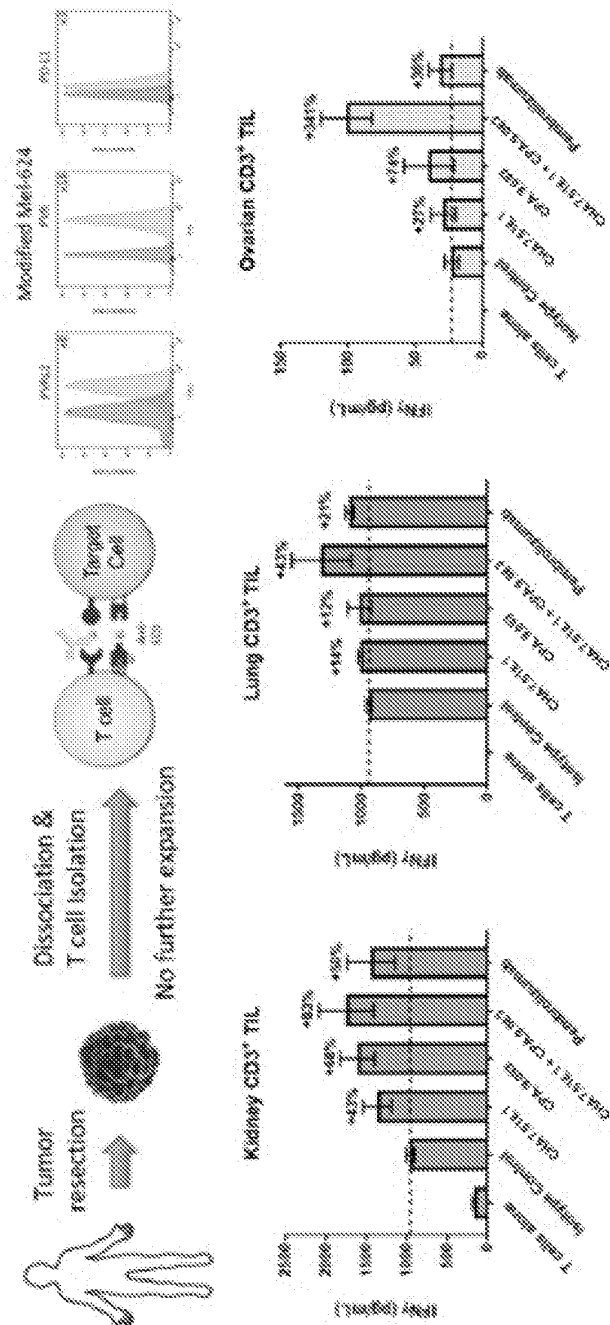


Figure 60

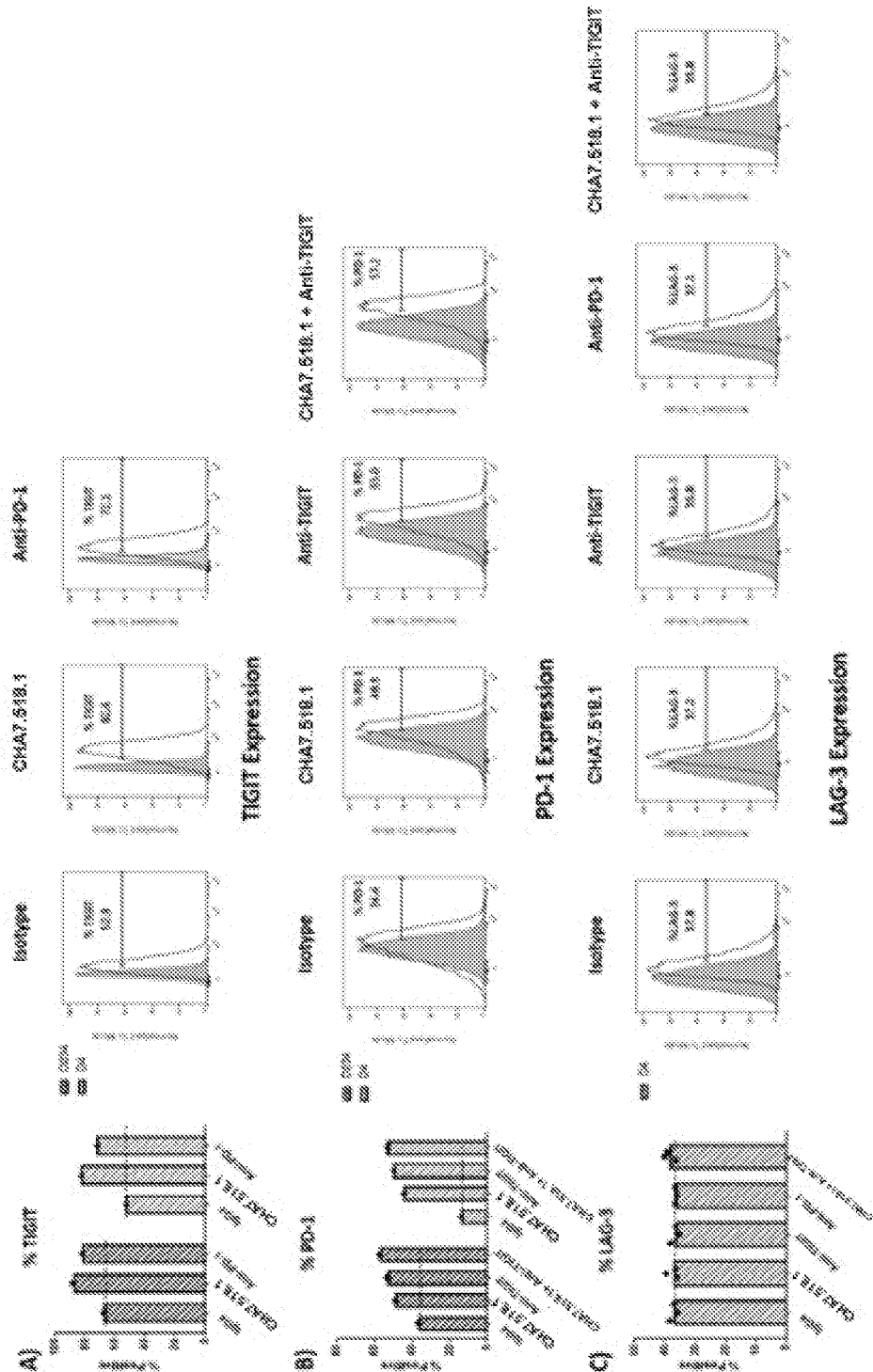


Figure 61A

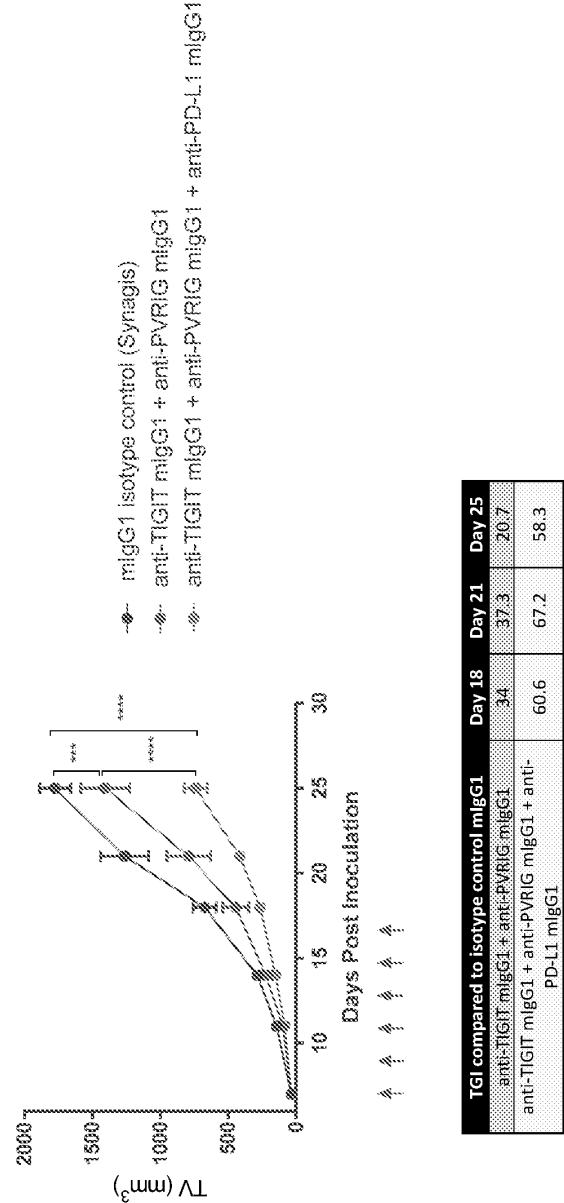


Figure 61B

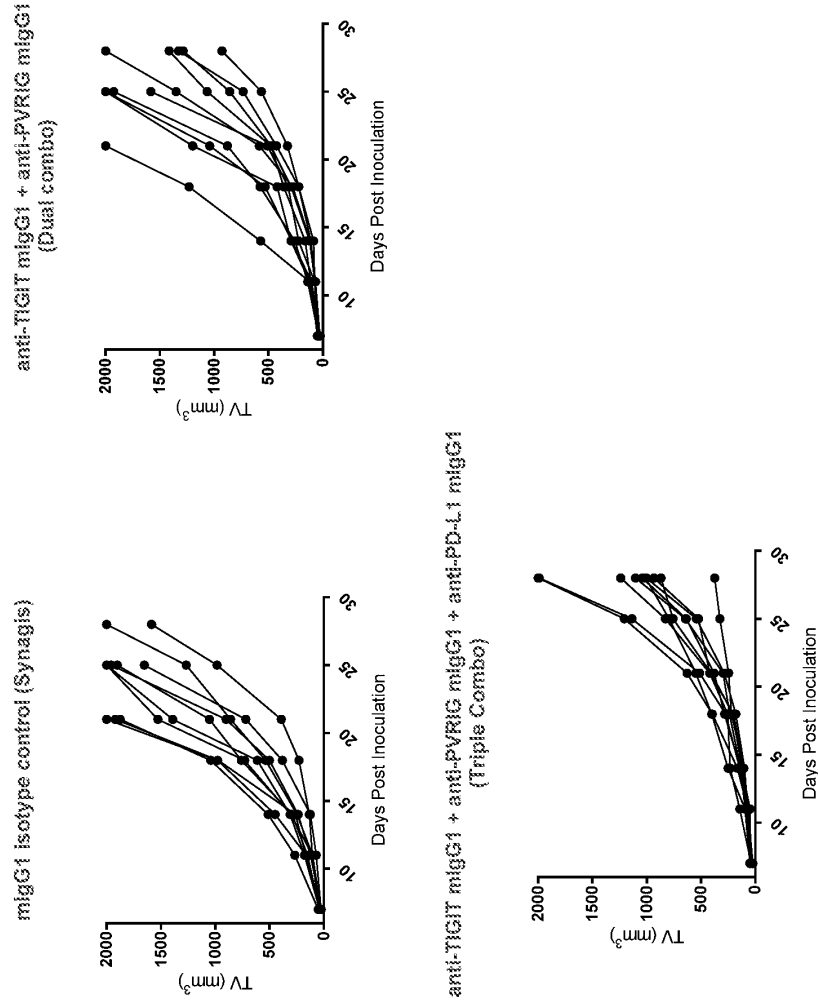
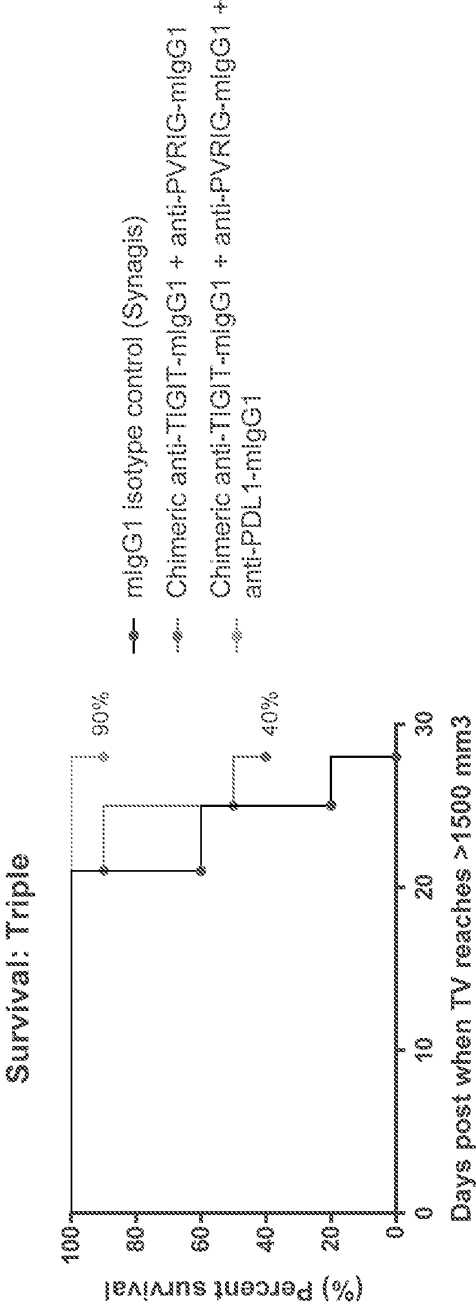


Figure 61C



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Figure 62A

From W02017100541 (Medimmune, LLC; also US20170306025; Durvalumab)		SEQ ID NO:
What	sequence	
Heavy chain		
(SEQ ID NO:2 from W02017100541)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDQSEKYYV	1117
vhCDR1	DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLLVTVSS	
(SEQ ID NO:3 from W02017100541)	RYWMS	1118
vhCDR2	NIKQDCSEKYYVDSVKG	1119
(SEQ ID NO:4 from W02017100541)	EGGWFGELAFD	1120
vhCDR3		
(SEQ ID NO:5 from W02017100541)		
Light chain		
(SEQ ID NO:1 from W02017100541)	EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPD	1121
vlCDR1	RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSIPWTFGQGTKVEIK	
(SEQ ID NO:6 from W02017100541)	RASQRVSSSYLA	1122
vlCDR2	DASSRAT	1123
(SEQ ID NO:7 from W02017100541)	QQYGSLPWT	1124
vlCDR3		
(SEQ ID NO:8 from W02017100541)		

Figure 62B

Figure 62B

From US20170281764 (JN Biosciences)	What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:34 from US2017281764)		EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEW/AWISPYGGSTYYADS VKGRFTISADTSKNTAYLQNINSLRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSAASTKGPS VFPLAPSSKSTSGGTAAAGCLVKDYFPEPTVSWNSGALTSQVHTFPAVLQSSGLYSLSVVTVTP SSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLIHQDWLNGK EYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG DIQMTQSPSSLSASVGDRTVITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGS GSGTDFLTITSLQPEDFATYYCQQLYFTPTTGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	1125
Light chain (SEQ ID NO:36 from US2017281764)			1126

Figure 62C

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)	What sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGGTLVTVSA	1127
vhCDR1 (SEQ ID NO:17 from WO2015009856)	GFTFSDSWIH	1128
vhCDR2 (SEQ ID NO:18 from WO2015009856)	A WISPYGGSYYADSVKG	1129
vhCDR3 (SEQ ID NO:19 from WO2015009856)	RHWPGGFDY	1130
Light chain (SEQ ID NO:24 from WO2015009856)	DIQMTQSPSSLSASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGGTDFLTITSLQPEDFATYYCQQLYHPATFGGQGTKVEIKR	1131
vlCDR1 (SEQ ID NO:20 from WO2015009856)	RASQDVSTAVA	1132
vlCDR2 (SEQ ID NO:21 from WO2015009856)	SASFLYS	1133
vlCDR3 (SEQ ID NO:22 from WO2015009856)	QQYLYHPAT	1134

Figure 62D

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)	
What	sequence
Heavy chain (SEQ ID NO: 40 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWV A WISPYGG STYY ADSVKGRFTISADTSKNTA YLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSSASTK (SEQ ID NO:40), or
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLASVGDRTTTCRASQDVSTA VA WYQKPGKAPKLLIYSASFL YSG VPSRFGSGSGTDFTLTISSLQPEDF ATYYCQQYL YHPATFGGQGTKVEIKR (SEQ ID NO:24).
From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)	
What	sequence
Heavy chain (SEQ ID NO: 41 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGG STYYADSVKGRFTISADTSKNFA YLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSS
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLASVGDRTTTCRASQDVSTA VAWYQKPGKAPKLLIYSASFL YSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYL YHPATFGGQGTKVEIKR

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Figure 62E

From US20160222117 (GENENTECH, INC.)			SEQ ID NO:
What	sequence		
Heavy chain (SEQ ID NO:20 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA		1139
Heavy chain (SEQ ID NO:23 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA		1140
Heavy chain (SEQ ID NO:24 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWILPYGGSS YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA		1141
From US20160222117 (GENENTECH, INC.)			SEQ ID NO
What	sequence		
Light chain (SEQ ID NO:21 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYLHPATFGQGTKVEIKR		1142
Light chain (SEQ ID NO:26 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYVNPWFYGGGTKVEIKR		1143
Light chain (SEQ ID NO:27 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYAPPWFYGGGTKVEIKR		1144

Figure 62F

From US20160222117 (GENENTECH, INC.) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:28 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYVTPWTFGGGTKVEIKR	1145
Light chain (SEQ ID NO:29 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVINTFLAWYQQKPGKAPKLLIYSASTLASGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYVTPRITFGGGTKVEIKR	1146
Light chain (SEQ ID NO:30 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQGYGVPRTFGGGTKVEIKR	1147
Light chain (SEQ ID NO:31 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYLIPTPTFGGGTKVEIKR	1148
Light chain (SEQ ID NO:32 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYFETPTTFGGGTKVEIKR	1149
Light chain (SEQ ID NO:33 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYVTPPTFGGGTKVEIKR	1150
Light chain (SEQ ID NO:34 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQFFYTPPTFGGGTKVEIKR	1151

Figure 62G

From US20160222117 (GENENTECH, INC.)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:35 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQSLFTPTTFGGGTKEIKR	1152
Light chain (SEQ ID NO:36 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQSLYTPPTTFGGGTKEIKR	1153
Light chain (SEQ ID NO:37 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQSWYHPPTTFGGGTKEIKR	1154
Light chain (SEQ ID NO:38 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQYFVIPPPTTFGGGTKEIKR	1155
Light chain (SEQ ID NO:39 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQYVWYTPYTPYTFGGGTKEIKR	1156
Light chain (SEQ ID NO:40 from US20160222117)	DIQMTQSPSSLASVGDRLVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQSYFIPPPTTFGGGTKEIKR	1157

Figure 62H

From WO2013079174 (Merck; Avelumab or A09-246- 2)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO2013079174)	EVQLLESGGGLVQPFGSLRLSCAASGFTFSSYIMMWVRQAPGKGLWVSSINPSCGITYADT VKGRFTISRDN SKNTLYLQMNSLRAEDTA VYYCARIKLGIVTTVDYWGQGTLVTVSSASTKG PSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYMCNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	1158
Light chain (SEQ ID NO: from WO2013079174)	QSALTQPA SVSGSPCQSITISCTGTSSDVGGYNVYVSWYQQHPGKAPKLMYDVSNRPSGVSNR FSGSKSGNTASLTISGLQAEDEADYYCSSYTSSTRVFGTGKVTVLGQPKANPTVTLFPSSSE LQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQW KSHRSYSCQVTHEGSTVEKTVAPTECS	1159

Figure 62I

From US8217149 (Hoffman La Roche; Atezolizumab)		SEQ ID NO:
What	sequence	
Heavy chain (VH) (SEQ ID NO:20 from US8217149)	EVQLVESGGGLVQP ^{CG} SLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYCGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSA	1160
Light chain (VL) (SEQ ID NO:21 from US8217149)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKGAPKWKYSASFLYSGVPSRFSGS GSGTDFLTITSLQPEDEATYYC QQYLYH PATFGQGTKVEIKR	1161
Atezolizumab (alternate sequence))		185/264
What	sequence	SEQ ID NO:
Heavy chain (from IMGT database or DrugBank database)	EVQLVESGGGLVQP ^{CG} SLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYCGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFSQSVMEALH NHYTQKSLSLSPGK	1162
Light chain (from IMGT database or DrugBank database)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKGAPKLLIYSASFLYSGVPSRFSG SGSGTDFLTITSLQPEDFATYYCQQYLYHPATFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSLSPVTKSFNRGEC	1163

Figure 63A

CPA.7.001

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSS	1164
vhCDR1	GGTFSSYA	1165
vhCDR2	IIPIFGTA	1166
vhCDR3	AREEVSSPYGMDV	1167
Full length HC	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	1168
Variable light (vl) domain	QAVVTQEPSTVSPGGTTLTCGTSTGAVTSGHYPYWFFQKPGQAPKTLIVDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYC LLSYSGASW VFGGGTKLTVLG	1169
vlCDR1	TGAVTSGHY	1170
vlCDR2	DTG	1171
vlCDR3	LLSYSGASWV	1172
Full length light chain	QAVVTQEPSTVSPGGTTLTCGTSTGAVTSGHYPYWFFQKPGQAPKTLIVDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYC LLSYSGASW VFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT PSKQSNINKYAASSYSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1173

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Figure 63B
CPA. 7.003

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKVSGFSLSHFSMHVWRQVPKGLEW/LGGFDPEEGGTIPAKQFQGRITMTEDTSTETAYMELSSLRSEDATVYYCATGIWYSSGWPVVDYWGPGTLTVSS	1174
vhCDR1	<u>GFSLSHFS</u>	1175
vhCDR2	<u>FDPEEGGT</u>	1176
vhCDR3	<u>ATGIWYSSGWPVDY</u>	1177
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTSSVAISVIRQAPGGQGLEWMGGIPIFGTANYAQKFGGRVTITADKSTSTAYMELSSLRSEDATVYYCARGPWYDSSGYSSAYYMDVWGQGTITVYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSMHEALHNHYTQKSLSLSPGK	1178
Variable light (vl) domain	DVVMTQSPSLSPVTPGGPASISCRSSQSLDSSGYNYVDWYVYLPKPGQSPQLLSLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYCMQALQTPITFGQGTRLEIKR	1179
vlCDR1	<u>QSLDSSGYNY</u>	1180
vlCDR2	<u>LGS</u>	1181
vlCDR3	<u>MQALQTPIT</u>	1182
Full length light chain	DVVMTQSPSLSPVTPGGPASISCRSSQSLDSSGYNYVDWYVYLPKPGQSPQLLSLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYCMQALQTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNIPYREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1183

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Figure 63C
CPA. 7.004

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHHWRQAPGKGLWMGGFDPEDGETVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATVSRVRGVINYYMMIDV WGKGTTVTVSS	1184
vhCDR1	<u>GYTLTSL</u>	1185
vhCDR2	<u>FDPEDGET</u>	1186
vhCDR3	<u>ATVSRVRGVINYYMMIDV</u>	1187
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHHWRQAPGKGLWMGGFDPEDGETVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATVSRVRGVINYYMMIDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSLSLTGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTC PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSMHEALHNYTKQKLSLSPGK	1188
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLYRNGINNYLDWYLQKPGQSPQLLLYLGSNRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKR	1189
vlCDR1	<u>QSLYRNGN</u>	1190
vlCDR2	<u>LGS</u>	1191
vlCDR3	<u>MQALQTPPT</u>	1192
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLYRNGINNYLDWYLQKPGQSPQLLLYLGSNRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSVYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1193

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Figure 63D
CPA. 7.006

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVRRPGSSVRVCKPSGGTGTGTAFTWVRQAPGGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSED ¹ TAVVYCARGFEYSDGLLDDWGQGTLLVTVSS	1194
vhCDR1	<u>GGTGTGTA</u>	1195
vhCDR2	<u>ITPISAT</u>	1196
vhCDR3	<u>ARGFEYSDGLLDD</u>	1197
Full length HC	QVQLVQSGAEVRRPGSSVRVCKPSGGTGTGTAFTWVRQAPGGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSED ¹ TAVVYCARGFEYSDGLLDDWGQGTLLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCTCPPCAP ELLGGPSVF ² LPPKPKD ³ TLMI ⁴ SRTP ⁵ EVTCVVDVSHEDPEVKFNWVDGVGVHNAKTKPREEQYNSTYRVSVLT ⁶ LH QDWLNGKEYKCKVSNKALPAPIEKTI ⁷ SKAGQP ⁸ REPQV ⁹ YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NIN ¹⁰ YKTT ¹¹ PPVLDSDG ¹² SFFLYSKLTVDKSRWQQGNV ¹³ FSCSV ¹⁴ MHEALHNHYTQKSLSLSPGK	1198
Variable light (vl) domain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGV ¹ PD ² RFSGSGGTDF ³ TLKI SRVEAEDVGVVYCMQ ⁴ HMEF ⁵ PLTFGGGTKEIKR	1199
vlCDR1	<u>QSLFYSDDGNTY</u>	1200
vlCDR2	<u>RLS</u>	1201
vlCDR3	<u>MQHMEFPLT</u>	1202
Full length light chain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGV ¹ PD ² RFSGSGGTDF ³ TLKI SRVEAEDVGVVYCMQ ⁴ HMEF ⁵ PLTFGGGTKEIKRTVAAPS ⁶ VF ⁷ IFPP ⁸ DEQLKSGTASV ⁹ CLLN ¹⁰ FP ¹¹ Y ¹² PREAKV ¹³ QW ¹⁴ KVDN ALQSGNSQESVTEQDSK ¹⁵ DTYSL ¹⁶ STLTLSKADY ¹⁷ EKH ¹⁸ KVYACEV ¹⁹ THQGL ²⁰ SSP ²¹ VTK ²² SFNRGEC	1203

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Figure 63E
CPA. 7.008

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSGTLSTLCVSSGSISSINWWTWVRQPGKGLEWIGEIYHSGTSYNSLSKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYWGQGLTVTVSS	1204
vhCDR1	<u>SGSISSTNW</u>	1205
vhCDR2	<u>IYHSGST</u>	1206
vhCDR3	<u>ARVGPAAIY</u>	1207
Full length HC	QVQLQESGPGLVKPSGTLSTLCVSSGSISSINWWTWVRQPGKGLEWIGEIYHSGTSYNSLSKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYWGQGLTVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKV/DKKVEPKSCDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLTQHQQDWLNG KEYCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1208
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSSGISKRFASRSRGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQTLTVLG	1209
vlCDR1	<u>SNNVGYEG</u>	1210
vlCDR2	<u>RNN</u>	1211
vlCDR3	<u>SAWDSSLNAV</u>	1212
Full length light chain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSSGISKRFASRSRGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQTLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	1213

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Figure 63F
CPA. 7.009

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIVAQKFQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATAKPGIAGVAGQNYYYMDV/WGKGTITVTVSS	1214
vhCDR1	<u>GYTLTELS</u>	1215
vhCDR2	<u>FDPEGET</u>	1216
vhCDR3	<u>ATAKPGIAGVAGQNYYYMDV</u>	1217
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIVAQKFQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATAKPGIAGVAGQNYYYMDV/WGKGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV/PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRWVSIVTLVHQDWLNGKEYCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK	1218
Variable light (vl) domain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLLYRNGNINYLWDWYLQKPGQSPQLLLYLGSNIRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKR	1219
vlCDR1	<u>QSLLYRNGNIN</u>	1220
vlCDR2	<u>LGS</u>	1221
vlCDR3	<u>MQALQTPPT</u>	1222
Full length light chain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLLYRNGNINYLWDWYLQKPGQSPQLLLYLGSNIRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSVYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1223

Figure 63G
CPA. 7.010

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGKSLRLSCAASGFTSSYAMIHVWRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCASSPIGYSYGYWGGMDVWGQGTITVTVSS	1224
vhCDR1	<u>GFTSSYA</u>	1225
vhCDR2	<u>ISYDGSNK</u>	1226
vhCDR3	<u>ASSPIGYSYGYWGGMDV</u>	1227
Full length HC	EVQLVESGGGLVQPGKSLRLSCAASGFTSSYAMIHVWRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCASSPIGYSYGYWGGMDVWGQGTITVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVK DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	1228
Variable light (vl) domain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKGPSPPQHLLTFQSDSDKQKQSGVPSRFSGSKDASANA GILISGLQSEDEADYYCLIIWHTSGWVFGGGTQLTVLG	1229
vlCDR1	<u>SGIDVRTNK</u>	1230
vlCDR2	<u>FQSDSDK</u>	1231
vlCDR3	<u>LIWHTSGWV</u>	1232
Full length light chain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKGPSPPQHLLTFQSDSDKQKQSGVPSRFSGSKDASANA GILISGLQSEDEADYYCLIIWHTSGWVFGGGTQLTVLGPQKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK ADSSPVKAGVETITPTSPKQSNKYYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS	1233

Figure 63H
CPA.7.011

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWRQAPGKGLEWMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGPAAAGVGYYYMIDV WGKGTTVTVSS	1234
vhCDR1	<u>GYTLTELS</u>	1235
vhCDR2	<u>FDPEGET</u>	1236
vhCDR3	<u>ATGPAAAGVGYYYMIDV</u>	1237
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWRQAPGKGLEWMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGPAAAGVGYYYMIDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSLSLTGTQTYICNVNHPKNTKVDKKVEPKSCKTHTC PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK	1238
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGQGKVEIKR	1239
vlCDR1	<u>QSLLYRNGYNY</u>	1240
vlCDR2	<u>LGS</u>	1241
vlCDR3	<u>MQALQTPPT</u>	1242
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGQGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWVKVDNA LQSGNSQESVTEQDSKDSVYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1243

Figure 63I
CPA7.012

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVVYCARDVMMVCSSTSCYFYGMIDVWGQGTITVTVSS	1244
vhCDR1	<u>GFTSSYA</u>	1245
vhCDR2	<u>ISYDGSNK</u>	1246
vhCDR3	<u>ARDVMMVCSSTSCYFYGMIDV</u>	1247
Full length HC	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVVYCARDVMMVCSSTSCYFYGMIDVWGQGTITVTVSSASTKGPSVPEPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKKEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNKGKEYCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGK	1248
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKGKAPKLLIYDASNLEAGVPSRFGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTREIKR	1249
vlCDR1	<u>QDIRDY</u>	1250
vlCDR2	<u>DAS</u>	1251
vlCDR3	<u>QQFENLPIT</u>	1252
Full length light chain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKGKAPKLLIYDASNLEAGVPSRFGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1253

Figure 63J
CPA. 7.013

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHVVRQAPGKGLEWMGGFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGGYSGGFNYYYMDV WGKGTTVTVSS	1254
vhCDR1	<u>GYTLTSL</u>	1255
vhCDR2	<u>FDPEDGET</u>	1256
vhCDR3	<u>ATGGYSGGFNYYYMDV</u>	1257
Full length HC	QVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHVVRQAPGKGLEWMGGFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGGYSGGFNYYYMDVWGKGTTVTVSSASTKGPSVFLPASPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV/PSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK	1258
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGNINYLWYLQKPGQSPQLLILYLGSNIRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKR	1259
vlCDR1	<u>QSLLYRNGNIN</u>	1260
vlCDR2	<u>LGS</u>	1261
vlCDR3	<u>MQALQTPPT</u>	1262
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGNINYLWYLQKPGQSPQLLILYLGSNIRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1263

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Figure 63K
CPA. 7.014

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLWMMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGVTITYYYGMDVWVGQGTITVTSS	1264
vhCDR1	<u>GYTLTELS</u>	1265
vhCDR2	<u>FDPEDEGET</u>	1266
vhCDR3	<u>ATGVTITYYYGMDV</u>	1267
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLWMMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGVTITYYYGMDVWVGQGTITVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGWVFGCSVMHEALHNHYTQKSLSLSPGK	1268
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLYSNGNMFLDWYLQKPGQSPRLISLGSNRA SGVPDRFSGSGSGTDFTLK SRVEAEDVGIYYCMQALQTPPTFGQGTKEIKR	1269
vlCDR1	<u>QSLYSNGNNE</u>	1270
vlCDR2	<u>LGS</u>	1271
vlCDR3	<u>MQALQTPPT</u>	1272
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLYSNGNMFLDWYLQKPGQSPRLISLGSNRA SGVPDRFSGSGSGTDFTLK SRVEAEDVGIYYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1273

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Figure 63L
CPA. 7.015

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QITLKSGGVVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLWVAFIKYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCARDLFDWWDGMDVWGQGTTVTVSS	1274
vhCDR1	<u>GFTSSYG</u>	1275
vhCDR2	<u>IRYDGSNK</u>	1276
vhCDR3	<u>ARDLDFWWDGMDV</u>	1277
Full length HC	QITLKSGGVVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLWVAFIKYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVVYCARDLFDWWDGMDVWGQGTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVWTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGWVFCSSVMHEALHNHYTQKSLSLSPGK	1278
Variable light (vl) domain	EVLTSQSPGTLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLIYGASYRATGIPDRFSGSGGTDFNLTISRLEP EDFAVYCCQQVSSPMYTFGLGTLKLEIKR	1279
vlCDR1	<u>QSVSSMY</u>	1280
vlCDR2	<u>GAS</u>	1281
vlCDR3	<u>QQVSSPMYT</u>	1282
Full length light chain	EVLTSQSPGTLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLIYGASYRATGIPDRFSGSGGTDFNLTISRLEP EDFAVYCCQQVSSPMYTFGLGTLKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSITYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1283

Figure 63M
CPA.7.017

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCSKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDMAADGMADFVWGQGLTVTVSS	1284
vhCDR1	<u>GGTFNNYG</u>	1285
vhCDR2	<u>IPLFGTT</u>	1286
vhCDR3	<u>ARDMAADGMADFV</u>	1287
Full length HC	QVQLVQSGAEVKKPGSSVKVCSKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDMAADGMADFVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV/PSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCP APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1288
Variable light (vl) domain	QSVLTQPPSVSGTPGQKVIISCGSSNNIGRHFVFWYQQLPGTAPKLLYKNDERPSGVPDRFSGSKGTSAVLAVSGLRS EDEADYYC SSWDAALNGV /FGGGTKLTVLG	1289
vlCDR1	<u>SSNIGRHF</u>	1290
vlCDR2	<u>KND</u>	1291
vlCDR3	<u>SSWDAALNGV</u>	1292
Full length light chain	QSVLTQPPSVSGTPGQKVIISCGSSNNIGRHFVFWYQQLPGTAPKLLYKNDERPSGVPDRFSGSKGTSAVLAVSGLRS EDEADYYC SSWDAALNGV /FGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNINIKYAASSYLSTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	1293

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Figure 63N
CPA. 7.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAPGKGLWMMGGFDPEDGETIVAQKFQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATEVPMVRGARRYYYYMDVWGKGTITVTVSS	1294
vhCDR1	<u>GYTLTSL</u>	1295
vhCDR2	<u>FDPEGET</u>	1296
vhCDR3	<u>ATEVPMVRGARRYYYYMDV</u>	1297
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAPGKGLWMMGGFDPEDGETIVAQKFQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATEVPMVRGARRYYYYMDVWGKGTITVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQYICNVNHNKPSNTKV/DKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGK	1298
Variable light (vl) domain	DVVMQTQSPFLFVTPGEPASISCRSSQTLLYNENNYLDWVYVKPGQSPQLLIVLGSTRASGVPDFSGGGSGTDFLTII SRVEAEDVGLYCMQGLQTPPTFGQGTRLEIKR	1299
vlCDR1	<u>QTLLYNENNY</u>	1300
vlCDR2	<u>LGS</u>	1301
vlCDR3	<u>MQGLQTPPT</u>	1302
Full length light chain	DVVMQTQSPFLFVTPGEPASISCRSSQTLLYNENNYLDWVYVKPGQSPQLLIVLGSTRASGVPDFSGGGSGTDFLTII SRVEAEDVGLYCMQGLQTPPTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLINFPREAKVQWVKV/DNA LQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1303

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Figure 630
CPA.7.019

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKSETLSLTCSVSGGISNSNYWGWIRPPGKGLEWIGGIYSGTYYNPSPLESRVTISEDTSKNQIS LKLSVTAADTAVVYCARGAWELSLGDFDPWGPGLTVSS	1304
vhCDR1	<u>GGGISNSNY</u>	1305
vhCDR2	<u>IYSGSI</u>	1306
vhCDR3	<u>ARGAWELSLGDFDP</u>	1307
Full length HC	QVQLQESGPGLVKSETLSLTCSVSGGISNSNYWGWIRPPGKGLEWIGGIYSGTYYNPSPLESRVTISEDTSKNQIS LKLSVTAADTAVVYCARGAWELSLGDFDPWGPGLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDITLMISRTPEVTCWVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NINYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1308
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVDPDRFSGSRGTSASLAITGL QAEDEADYVCQSYDSSLVYWVFGGGTQLTVLG	1309
vlCDR1	<u>SSNIGAGYD</u>	1310
vlCDR2	<u>GNN</u>	1311
vlCDR3	<u>QSYDSSLVYW</u>	1312
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVDPDRFSGSRGTSASLAITGL QAEDEADYVCQSYDSSLVYWVFGGGTQLTVLGPAAKPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETITTPSKQSNKNKYAASSYLSLTPEQWKSHRYSVCQVTHEGSTVEKTVAPTECS	1313

Figure 63P
CPA. 7.021

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVKPGGSLRLSCAASGFTFTGSSMNWVRQAPGKGLEWVAVISFDGTEIHVADSVKGRFTISRDNKST VFLQMINSRLRPDDTALYYCAKSGNIYFYSGMDVWGQGTTVTVSS	1314
vhCDR1	<u>GFTEGTSS</u>	1315
vhCDR2	<u>ISFDGTEI</u>	1316
vhCDR3	<u>AKSGNIYFYSGMDV</u>	1317
Full length HC	EVQLVESGGGVVKPGGSLRLSCAASGFTFTGSSMNWVRQAPGKGLEWVAVISFDGTEIHVADSVKGRFTISRDNKST VFLQMINSRLRPDDTALYYCAKSGNIYFYSGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSLSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSLSPGK	1318
Variable light (vl) domain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESQVPSRFSGGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTVEIKR	1319
vlCDR1	<u>QSSISGW</u>	1320
vlCDR2	<u>EIS</u>	1321
vlCDR3	<u>QQYYSYPLT</u>	1322
Full length light chain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESQVPSRFSGGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1323

Figure 63Q
CAP. 7.022

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAPGKGLWMMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGVPAAGVYYYYYMDVWVGKGTTVVSS	1324
vhCDR1	<u>GYTLTSL</u>	1325
vhCDR2	<u>FDPEGET</u>	1326
vhCDR3	<u>ATGVPAAIGVYYYYYMDV</u>	1327
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHWVRQAPGKGLWMMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATGVPAAGVYYYYYMDVWVGKGTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKKEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTKISKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGK	1328
Variable light (vl) domain	DVVMITQSPPLSPVTPGEPASISCRSSQSLSYNGYNILDWY/LQKPGQSPQLLISLGSNRSAGV/PDRFSGSGSGTDFTLK SRVEAEDVGVVYCMQALQSPVTFGGGTKEIKR	1329
vlCDR1	<u>QSLSYNGYN</u>	1330
vlCDR2	<u>LGS</u>	1331
vlCDR3	<u>MQALQSPV</u>	1332
Full length light chain	DVVMITQSPPLSPVTPGEPASISCRSSQSLSYNGYNILDWY/LQKPGQSPQLLISLGSNRSAGV/PDRFSGSGSGTDFTLK SRVEAEDVGVVYCMQALQSPVTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSYSTYLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1333

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Figure 63R
CPA.7.023

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWRQAPGKGLEWMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATDSRDGPAARGGYVYMDVWGQGTITVTVSS	1334
vhCDR1	<u>GYTLTELS</u>	1335
vhCDR2	<u>FDPEGET</u>	1336
vhCDR3	<u>ATDSRDGPAARGGYVYMDV</u>	1337
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWRQAPGKGLEWMGGFDPEDGETIVAQKQGRV/TMTEDTS TDTAYMELSSLRSEDTAVVYCATDSRDGPAARGGYVYMDVWGQGTITVTVSSASTKGPSVPLAPSSKSTSGGTAALG CLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTP/PSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYR VW/SVLT/LHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHHEALHNHYTQKSLSLSPGK	1338
Variable light (vl) domain	DVVMITQSPPLSPVTLGQPA SISCSSQSLLYINGNYLDWY/LQKPGQSPQLLYLGSNRRASGVPDFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGQGKVEIKR	1339
vlCDR1	<u>QSLLYINGNY</u>	1340
vlCDR2	<u>LGS</u>	1341
vlCDR3	<u>MQALQTPPT</u>	1342
Full length light chain	DVVMITQSPPLSPVTLGQPA SISCSSQSLLYINGNYLDWY/LQKPGQSPQLLYLGSNRRASGVPDFSGSGGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGQGKVEIKRTVAAPSV/IFPPSDEQLKSGTASVCLINNFYPREAKVQWVKVDNA LQSGNSQESVTEQDSKDSVYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1343

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Figure 63S
CPA.7.024

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSVAISWVROAPGGQGLEWMGGIPIFGTANVAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDAYVYDSSGYNPDADFIDWGGGTMTVTSS	1344
vhCDR1	<u>GGTFFSSYA</u>	1345
vhCDR2	<u>IPIFGTA</u>	1346
vhCDR3	<u>ARDAVYVDSSGYNPDADFID</u>	1347
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSVAISWVROAPGGQGLEWMGGIPIFGTANVAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDAYVYDSSGYNPDADFIDWGGGTMTVTSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNIGKEVKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK	1348
Variable light (vl) domain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLHNSGYNLDWYLQKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVVYCMQGLQTPRTFGRGTKLEIKR	1349
vlCDR1	<u>QSLHNSGYN</u>	1350
vlCDR2	<u>LGS</u>	1351
vlCDR3	<u>MQGLQTPRT</u>	1352
Full length light chain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLHNSGYNLDWYLQKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVVYCMQGLQTPRTFGRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWVKVDNALOSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1353

Figure 63T

CPA.7.033

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDIARRVRGVPPYYVYAMDVWGGQGTITVVS	1354
vhCDR1	<u>GGTFSSA</u>	1355
vhCDR2	<u>IPIYGIIT</u>	1356
vhCDR3	<u>ARDDIARRVRGVPPYYVYAMDV</u>	1357
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDIARRVRGVPPYYVYAMDVWGGQGTITVVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1358
Variable light (vl) domain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPILFIEASTLVPGIPRFSGSGFGTDFTLTIKNMESDAAYVFCIQHDNLPITFGGGTKVDIKR	1359
vlCDR1	<u>QDIDDD</u>	1360
vlCDR2	<u>EAS</u>	1361
vlCDR3	<u>LQHDNLPIT</u>	1362
Full length light chain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPILFIEASTLVPGIPRFSGSGFGTDFTLTIKNMESDAAYVFCIQHDNLPITFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1363

Figure 63U

CPA.7.034

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPKGASVKVKSGYLTIELSMHWVRQAPGKGLEWMGGFDPEDEGEIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDATVYYCATEDPGVPAGPYYYGMDVWGGQGTTVTVSS	1364
vhCDR1	<u>GYLTIELS</u>	1365
vhCDR2	<u>FDPEDEGEI</u>	1366
vhCDR3	<u>ATEDPGVPAGPYYYGMDV</u>	1367
Full length HC	EVQLVQSGAEVKKPKGASVKVKSGYLTIELSMHWVRQAPGKGLEWMGGFDPEDEGEIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDATVYYCATEDPGVPAGPYYYGMDVWGGQGTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGLVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCDKTH TCPPCPAPELLGGPSVFLPPKPKDTLMISRTPETVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	1368
Variable light (vl) domain	DVVMTQSPPLVLPVTPGEPASISCRSSQSLLYINGVHYLDWVYVQRPGSQPLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCM <u>QALQTPPI</u> TFGGGTKVEIKR	1369
vlCDR1	<u>QSLLYINGVHY</u>	1370
vlCDR2	<u>LGS</u>	1371
vlCDR3	<u>MQALQTPPI</u>	1372
Full length light chain	DVVMTQSPPLVLPVTPGEPASISCRSSQSLLYINGVHYLDWVYVQRPGSQPLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCM <u>QALQTPPI</u> TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	1373

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Figure 63V

CPA.7.036

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDTARRVRGVPPYYYYAMDVWGQGTTVTVSS	1374
vhCDR1	<u>GGTFSSA</u>	1375
vhCDR2	<u>IPIYGIIT</u>	1376
vhCDR3	<u>ARDDTARRVRGVPPYYYYAMDV</u>	1377
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDTARRVRGVPPYYYYAMDVWGQGTTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCDKTH TCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK	1378
Variable light (vl) domain	DIVMTQTPLSIPVTPGEPASISCRPSQLSDSDGNTYLDWYVLRKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVVYCYCMQRLQFPLTFGGGTKVEIKR	1379
vlCDR1	<u>QSLSDSDGNTY</u>	1380
vlCDR2	<u>ILS</u>	1381
vlCDR3	<u>MQRLQFPLT</u>	1382
Full length light chain	DIVMTQTPLSIPVTPGEPASISCRPSQLSDSDGNTYLDWYVLRKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVVYCYCMQRLQFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	1383

Figure 63W

CPA.7.040

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVKSGYLTIELSMHWVRQAPGKGLEWMGGFDPEGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAGVYYYYYMDVWGKGTITVYSS	1384
vhCDR1	<u>GYLTIELS</u>	1385
vhCDR2	<u>FDPEGET</u>	1386
vhCDR3	<u>ATGVPAAGVYYYYYMDV</u>	1387
Full length HC	EVQLVQSGAEVKKPGASVKVKSGYLTIELSMHWVRQAPGKGLEWMGGFDPEGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAGVYYYYYMDVWGKGTITVYSSASTKGPSVFPLAPSSKSTSGGTAAAGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1388
Variable light (vl) domain	DVVMTQSPVLSLPVTPGEPASISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSDFTLK ISRVEAEDYGVYYC <u>MQAVQNPPITFGQGT</u> KVDIKR	1389
vlCDR1	<u>QSLLYRNGYN</u>	1390
vlCDR2	<u>WGS</u>	1391
vlCDR3	<u>MQAVQNPPIT</u>	1392
Full length light chain	DVVMTQSPVLSLPVTPGEPASISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSDFTLK ISRVEAEDYGVYYC <u>MQAVQNPPITFGQGT</u> KVDIKR ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1393

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Figure 63X

CPA.7.046

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDTARRVRGVPPYYYYAMDVWGQGTTVTVSS	1394
vhCDR1	<u>GGTFSSA</u>	1395
vhCDR2	<u>IPIYGIIT</u>	1396
vhCDR3	<u>ARDDTARRVRGVPPYYYYAMDV</u>	1397
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGIITDYAQKFQGRVTITITDESTSTAYMELSSLTSEDITAVVYCARDDTARRVRGVPPYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	1398
Variable light (vl) domain	DVVMQTQSPAFLSVTPGERVTLSCKASQTMMNNYLAWYQQKPGQAPRLIIYDASTRATDTPPRFSGSGSGTEFTLTISVQSEDFALYYCQQYGDWLPIITFGQGTRLEIKR	1399
vlCDR1	<u>QTMNNY</u>	1400
vlCDR2	<u>DAS</u>	1401
vlCDR3	<u>QQYGDWLPIIT</u>	1402
Full length light chain	DVVMQTQSPAFLSVTPGERVTLSCKASQTMMNNYLAWYQQKPGQAPRLIIYDASTRATDTPPRFSGSGSGTEFTLTISVQSEDFALYYCQQYGDWLPIITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVKQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1403

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Figure 63Y

CPA.7.047

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYLTIELSMHWVRQAPGKGLEWMGGFDPEDEGEIYIAQKFGGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWVGKTTTVVSS	1404
vhCDR1	<u>GYLTIELS</u>	1405
vhCDR2	<u>FDPEDEGEI</u>	1406
vhCDR3	<u>ATAFPEATISYYYMDV</u>	1407
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYLTIELSMHWVRQAPGKGLEWMGGFDPEDEGEIYIAQKFGGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWVGKTTTVVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLVSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSPDIAVEWESENGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1408
Variable light (vl) domain	DVVMTQSPVLSPLPVTPGEPAISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIWVGSYRASGVPDRFSGSGSDTFTLKISRVEAEDYGVVYCMQAVQNPPITFGQGTKEIKR	1409
vlCDR1	<u>QSLLYRNGYN</u>	1410
vlCDR2	<u>WGS</u>	1411
vlCDR3	<u>MQAVQNPPIT</u>	1412
Full length light chain	DVVMTQSPVLSPLPVTPGEPAISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIWVGSYRASGVPDRFSGSGSDTFTLKISRVEAEDYGVVYCMQAVQNPPITFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1413

Figure 63Z

CPA.7.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSKASGGTFSSAISVWRQAPGGQFEWMGGIPIYGIIIDYAKFQGRVTITTDSTST AYMELSSLTSEDIAVYVCARDDTARRVRGVPYPPYYAMDVWGGQGTTVTVSS	1414
vhCDR1	<u>GGTFSSA</u>	1415
vhCDR2	<u>IPIYGIT</u>	1416
vhCDR3	<u>ARDDTARRVRGVPYPPYYAMDV</u>	1417
Full length HC	QMQLVQSGAEVKKPGSSVKVSKASGGTFSSAISVWRQAPGGQFEWMGGIPIYGIIIDYAKFQGRVTITTDSTST AYMELSSLTSEDIAVYVCARDDTARRVRGVPYPPYYAMDVWGGQGTTVTVSSASTKGPSPFLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCDKTH TCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRV VSVLT/LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1418
Variable light (vl) domain	DIVMTQTPLSIPVTPGEPASMSCRSSRLSDSDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDFRSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLIFGGGKTKVEIKR	1419
vlCDR1	<u>RSLLSDSDGNTH</u>	1420
vlCDR2	<u>SLS</u>	1421
vlCDR3	<u>MQRKEFPLI</u>	1422
Full length light chain	DIVMTQTPLSIPVTPGEPASMSCRSSRLSDSDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDFRSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLIFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYIPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1423

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Figure 63AA

CPA.7.050

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRQAPGGGLEWMGGIIPIFGTANVAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGPWYYDSSGYSSAYYMDVWGQGTITVTVSS	1424
vhCDR1	<u>GGTFFSSYA</u>	1425
vhCDR2	<u>IIPIFGTA</u>	1426
vhCDR3	<u>ARGPWYYDSSGYSSAYYMDV</u>	1427
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRQAPGGGLEWMGGIIPIFGTANVAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGPWYYDSSGYSSAYYMDVWGQGTITVTVSSASTKGPVFLPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDWSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	1428
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLHSDGYNLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKR	1429
vlCDR1	<u>QSLHSDGYN</u>	1430
vlCDR2	<u>LGS</u>	1431
vlCDR3	<u>MQALHTPGVT</u>	1432
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLHSDGYNLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1433

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Figure 63BB
CPA.7.028

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QLQLQESGPGLVKPSSETLSLTCTVTGSSISSSYWAWIRQPPGKGLEWIGGIYSGSTYNNVLSLRVTISQDTSKNQFS LKLTSTVTAADTAVYYCARGAWELRLGDWFDPPWGQGLTVTVSS	1434
vhCDR1	GGSISSSY	1435
vhCDR2	IYSGST	1436
vhCDR3	ARGAWELRLGDWFDPP	1437
Full length HC	QLQLQESGPGLVKPSSETLSLTCTVTGSSISSSYWAWIRQPPGKGLEWIGGIYSGSTYNNVLSLRVTISQDTSKNQFS LKLTSTVTAADTAVYYCARGAWELRLGDWFDPPWGQGLTVTVSSASTKPSVFLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELGGPSVFLPFPKPKDTLMISRTPETVCVVVDSHEDPEVKFNWVVDGVEVHNAKTTPREEQYNSTYRVVSVLTVLH QDWLNGKEYCKVKVSNKALPAPIEKTIISKAKGQPREPQVYTYLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	1438
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQQLPGTAPKLLIYGYSNRPSPGVPDFSGSKSGTSASLITGL QAEDEADYYCQSYDSSLSVYVFFGGGTQLTLVGPQKAA	1439
vlCDR1	SSNIGAGYD	1440
vlCDR2	GYS	1441
vlCDR3	QSYDSSLSVYV	1442
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQQLPGTAPKLLIYGYSNRPSPGVPDFSGSKSGTSASLITGL QAEDEADYYCQSYDSSLSVYVFFGGGTQLTLVGPQKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETITTPSKQSNKNKAAASYLSLTPEQWKSHRVSCQVTHEGTVETKVAPECS	1443

Figure 63CC
CPA.7.030

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGGGWQPGGSLRLSCAASRFTEDYAMHWVRQPPGKGLVWVSGISWKGGINYADSVKGRFTISRDNAAQ NSLYLQMNSLRAEDTALYYCVKDPITLVATDRAFNWGGQTMVTVSS	1444
vhCDR1	RFTEDYA	1445
vhCDR2	ISWKGGL	1446
vhCDR3	VKDPTLVATDRAFN	1447
Full length HC	QVQLQESGGGWQPGGSLRLSCAASRFTEDYAMHWVRQPPGKGLVWVSGISWKGGINYADSVKGRFTISRDNAAQ NSLYLQMNSLRAEDTALYYCVKDPITLVATDRAFNWGGQTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1448
Variable light (vl) domain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLHNSGYNVLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYCMQYLTQPTDFTGGQTKLEIKRAAPS	1449
vlCDR1	QSLHNSGYN	1450
vlCDR2	LGS	1451
vlCDR3	MQYLQTPDT	1452
Full length light chain	DVVMQTQSPPLSPVTPGEPASISCRSSQSLHNSGYNVLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYCMQYLTQPTDFTGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1453

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Figure 63DD
CPA.7.041

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPQGFEWMGGIPIYGITDYAQKFQGRVTITTTDESTST AYMELSSLTSEDTAIVYCARDDTARRVRGVPPYYVYAMDVWGQGTITVTVSS	1454
vhCDR1	GGTFSSA	1455
vhCDR2	IPIYGIT	1456
vhCDR3	ARDDTARRVRGVPPYYVYAMDV	1457
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPQGFEWMGGIPIYGITDYAQKFQGRVTITTTDESTST AYMELSSLTSEDTAIVYCARDDTARRVRGVPPYYVYAMDVWGQGTITVTVSSASTKGPSVFLAPSSKSTSGGTAALGC LVKDYFEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHHKPSNTKVDKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1458
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQNISSLHWYQQKPGQSPKLLINYASQSFSGVPSRFSGSGGTDFTLTIDSLEPE DAATYFCHQSSSLPTFGGGTKVEIRRTVAAPS	1459
vlCDR1	QNISS	1460
vlCDR2	YAS	1461
vlCDR3	HQSSSLPT	1462
Full length light chain	QSVLTQPPSVSGAPGQQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSPGVPDFSGSKSGTSASLITGL QAEDEADYCCSYDSSLSVYVWFGGGTQLTVLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETITTPSKQSNKNKYAASSVLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS	1463

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Figure 63EE
CPA.7.016

What	sequence	SEQ. ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKTSGGTFSSAISWVRQAPGQGFQWVGGLPIYGITDYAQKFQGRVTITTDSTSTAYMELSLTSEDYAVYCARDDTARRVRGVPIYYYAMDVWGQGTITVVS	1464
vhCDR1	GGTFSSA	1465
vhCDR2	IPIYGIT	1466
vhCDR3	ARDDTARRVRGVPIYYYAMDV	1467
Full length HC	EVQLVQSGAEVKKPGSSVKVCKTSGGTFSSAISWVRQAPGQGFQWVGGLPIYGITDYAQKFQGRVTITTDSTSTAYMELSLTSEDYAVYCARDDTARRVRGVPIYYYAMDVWGQGTITVVSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	1468
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSVLAWYQQKPGQAPRLIYDASNRTGIPARFSGSGSGTDFTLTISLSQSEDFAVYYCQQYDDWPQTGGQTRLEIKRTVAAPS	1469
vlCDR1	QSVSSY	1470
vlCDR2	DAS	1471
vlCDR3	QQYDDWPQT	1472
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQSVSVLAWYQQKPGQAPRLIYDASNRTGIPARFSGSGSGTDFTLTISLSQSEDFAVYYCQQYDDWPQTGGQTRLEIKRTVAAPSDFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1473

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Figure 63FF
CPA.7.020

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKV5CKASGGTFSSAISWVRQAPGQGFEWVGGLIPIYIGITDYAQKFQGRVTITTTDES TSTAYMELSLTSEDYAVYCARDDETARRVRGVPYVYVYAMDVWGQGTITVTVSS	1474
vhCDR1	GGTFSSSA	1475
vhCDR2	IIPYIGIT	1476
vhCDR3	ARDDTARRVRGVPYVYVYAMDV	1477
Full length HC	QMQLVQSGAEVKKPGSSVKV5CKASGGTFSSAISWVRQAPGQGFEWVGGLIPIYIGITDYAQKFQGRVTITTTDES TSTAYMELSLTSEDYAVYCARDDETARRVRGVPYVYVYAMDVWGQGTITVTVSSASTKGPSVFPPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKV EPKCDKTHCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTRP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFLLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSL SLSPGK	1478
Variable light (vl) domain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEVAVYQQKPGQAPRLIYDTERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYCCQRRDWPIITFGGQGTIRLEIKRTVAAPS	1479
vlCDR1	QNVYGE	1480
vlCDR2	DTF	1481
vlCDR3	QQRRDWPIIT	1482
Full length light chain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEVAVYQQKPGQAPRLIYDTERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYCCQRRDWPIITFGGQGTIRLEIKRTVAAPSVEPPEDEQLKSGTASVCLLNINFPYPREAKVQWVNDN ALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	1483

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Figure 63GG
CPA.7.038

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFFSSAISWVRQAPQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDYAVYCARDDTARRVRGVPPYYVYAMDVWGGQGTTVTVSS	1484
vhCDR1	GGTFSSA	1485
vhCDR2	IPIYGIT	1486
vhCDR3	ARDDTARRVRGVPPYYVYAMDV	1487
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFFSSAISWVRQAPQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDYAVYCARDDTARRVRGVPPYYVYAMDVWGGQGTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGC LVKDYFEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHHKPSNTKV/DKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV/FSCVMHEALHNHYTQKSLSLSPGK	1488
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTTCQASRDIDSLSWYQQKPKGAPKLLIFDASNLKTGVSSRFSGSGGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKEIKRTVAAPS	1489
vlCDR1	RDIDSL	1490
vlCDR2	DAS	1491
vlCDR3	HQYDNLPLT	1492
Full length light chain	DIQMTQSPSSLSASVGDRTTTCQASRDIDSLSWYQQKPKGAPKLLIFDASNLKTGVSSRFSGSGGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKEIKRTVAAPSVEFPPSPDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1493

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Figure 63HH
CPA.7.044

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVKSCASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDSTSTAYMELSSLTSEDITAVYVCARDDTARRVRGVPPYYVYAMDVWGGQGTTVTVSS	1494
vhCDR1	GGTFSSA	1495
vhCDR2	IPIYGIT	1496
vhCDR3	ARDDTARRVRGVPPYYVYAMDV	1497
Full length HC	QMQLVQSGAEVKKPGSSVKVKSCASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDSTSTAYMELSSLTSEDITAVYVCARDDTARRVRGVPPYYVYAMDVWGGQGTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHHKPSNTKVDKVEPKSCDKHTCPPCPAPELLGSPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTKSKAKGQPREPQVYITLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK	1498
Variable light (vl) domain	EIVMTQSPATLSLSPGERATLSCRASESVTFLAWYQQKPGQAPRLITDASNRATGIPGRFSGSGSDTFTLTSSLEPEDFAVYYCHQHTNWPLTFGGGKLEIKRTVAAPS	1499
vlCDR1	ESVTF	1500
vlCDR2	DAS	1501
vlCDR3	HQHTNWPLT	1502
Full length light chain	EIVMTQSPATLSLSPGERATLSCRASESVTFLAWYQQKPGQAPRLITDASNRATGIPGRFSGSGSDTFTLTSSLEPEDFAVYYCHQHTNWPLTFGGGKLEIKRTVAAPSIFPPDEQLKSGTASVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1503

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Figure 63II
CPA.7.045

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEDGETIYAQFQGRVTMTEDTS TDTAYMELSLRSEDATVYYCATEVGYCSGGSCYISYYGMDVWGGQGTTVTVSS	1504
vhCDR1	GYTLTSL	1505
vhCDR2	FDPEDGET	1506
vhCDR3	ATEVGYCSGGSCYISYYGMDV	1507
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEDGETIYAQFQGRVTMTEDTS TDTAYMELSLRSEDATVYYCATEVGYCSGGSCYISYYGMDVWGGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDK THTCPPCPAPELGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSIVTLVHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1508
Variable light (vl) domain	DVVMTQSPISLPVTPGEPASISCRSSQSLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTGLEIKRTVAAPS	1509
vlCDR1	QSLYRNGHNF	1510
vlCDR2	LGS	1511
vlCDR3	MQALQTPPT	1512
Full length light chain	DVVMTQSPISLPVTPGEPASISCRSSQSLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSVYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1513

Figure 63JJ

CHA.7.502

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLVESGGDLVQPGGSRKLSCTAS <u>GFTFSNFG</u> MHWVRQAPEKGLEWVAY <u>ISSGS</u> <u>STIYYADTVKGRFTISRDNPENTLFLQMTSLRSED</u> TAMYYC <u>TRLDYYTNSYSMDH</u> WG QGTSVTVSS	1514
vhCDR1	GFTFSNFG	1515
vhCDR2	ISSGSSTI	1516
vhCDR3	TRLDYYTNSYSMDH	1517
Variable light (vl) domain	QIVLTQSPALMSASPGEKVTLTCSASS <u>SLPY</u> IYWYQQKPGSSPKPWY <u>LTS</u> NLASGVP ARFSGSRSGTSYSLTISSEVAEDAATYYC <u>QQWSSNPFT</u> FGSGTKLEIK	1518
vlCDR1	SSLPY	1519
vlCDR2	LTS	1520
vlCDR3	QQWSSNPFT	1521

Figure 63KK

CHA.7.503

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELAKPGASVKMSCKASGYTFTSNWMHWVKQRPQGGLIEWIGYINP SNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTADS AVYYC <u>ALMISAWLPYWG</u> QGTLVTVSA	1522
vhCDR1	GYTFTSNW	1523
vhCDR2	INPSNGYT	1524
vhCDR3	ALMISAWLPY	1525
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRAS <u>QSVSASSYSY</u> VHWYQKPGQPPKLLIKY <u>ASSLE</u> SGVPARFSGSGSGTDFTLNHPVEEEDTATYYC <u>LHTWEIPYTF</u> GGGKLEIK	1526
vlCDR1	QSVSASSYSY	1527
vlCDR2	YAS	1528
vlCDR3	LHTWEIPYT	1529

Figure 63LL

CHA.7.506

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELTRPGASVNLSCKASGYTFTSYWMQWVKQRPGQGLEWIGAIYPGDGDTRFNQKFKGKATLTADESSSTAYMQLSSLASEDSAVYYCATYYRYDDYWGQGTTLTVSS	1530
vhCDR1	GYTFTSYW	1531
vhCDR2	IYPGDGDT	1532
vhCDR3	ATYYRYDDY	1533
Variable light (vl) domain	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPTRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK	1534
vlCDR1	SSVSY	1535
vlCDR2	DTS	1536
vlCDR3	QQWSSNPYT	1537

Figure 63MM

CHA.7.508

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPDLVKPGASMKISCKASGYTFIDYNIHWVVKQSQGKSLDWIGYIYPYNG GTGYNQKFKNKATLTVDSSTAYMEVRSLTFEDSAVYFCAREADYYGNRGQFDYW GQGLTVTVSA	1538
vhCDR1	GYTFIDYN	1539
vhCDR2	IYPYNGGT	1540
vhCDR3	AREADYYGNRGQFDY	1541
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASENIFSNLAWYQQKQKSPQLLVYGEANLAD GVPSRFSGSGGTQYSLKINSLSQSEDFGNYYCQHFWGTPYTFGGGTTLEIK	1542
vlCDR1	ENIFSN	1543
vlCDR2	GEA	1544
vlCDR3	QHFWGTPYT	1545

Figure 63NN

CHA.7.510

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGTGVGWIRQPSGKGLEWLTHIWWNDNKFYNTFLKSRLTISKETSNNQVFLKIASVDTADAATYYCARMAYGNLWFFVNWGQ GTLVAVST	1546
vhCDR1	GFSLNTSGTG	1547
vhCDR2	IWWNDNK	1548
vhCDR3	ARMAYGNLWFFVN	1549
Variable light (vl) domain	DIVLTQSPASLAVSLGQRASISCRASRSVTISGYSYMYWYQQKPGQPPRLLFYLASNL ASGVPARFSGSGSGTDFTLNHPVEEEDAAIYYCQHSRELPYTFGGGTKLEIK	1550
vlCDR1	RSVTISGYSY	1551
vlCDR2	LAS	1552
vlCDR3	QHSRELPYT	1553

Figure 6300

CHA.7.512

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKKPRETVKISCKASGYTFTDYS SMHWVKQAPGKGLKWMGW <u>INTETGEPT</u> <u>YADDFKGRFAFSL</u> <u>EASASSAYLQINILKDE</u> <u>TATYFCARSRGGY</u> <u>EDYYALDYW</u> <u>GQGTSVT</u> <u>VSS</u>	1554
vhCDR1	GYTFTDYS	1555
vhCDR2	INTETGEP	1556
vhCDR3	ARSRGGYEDYYALDY	1557
Variable light (vl) domain	DIQMTQSPASLSASVGESVTITCRASGNIHY LAWYQQKQKSPQLLVYNA <u>KNLAD</u> <u>GVPSR</u> <u>FGSGSGTQFSLKIN</u> <u>SLQPEDFGSY</u> <u>YCOHFWIS</u> <u>PPTFGG</u> <u>GTKLEIK</u>	1558
vlCDR1	GNIHY	1559
vlCDR2	NAK	1560
vlCDR3	QHFWISPPT	1561

Figure 63PP

CHA.7.514

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLRQSGADLVKPGASVKLSCTASG FN IKDTYIDWVKQRPEQGLDWIGRID PANG NT KYDPKFQGKATIIDTSSNTAYLQLSNLTSEDTAVYYC ARYGSYPYFDY WGRGTTL AVSS	1562
vhCDR1	GFNIKDTY	1563
vhCDR2	IDPANGNT	1564
vhCDR3	ARYGSYPYFDY	1565
Variable light (vl) domain	SIVMTQTPKFLLISAGDRVITICKAS QSVRND VAWYQQKPGQSPKLLMY YAS NRYT GVPDRFTGSGYGTDFTFTISTVQAEDLAVYFC QQDYSSPPT FGGGTKLEIK	1566
vlCDR1	QSVRND	1567
vlCDR2	YAS	1568
vlCDR3	QQDYSSPPT	1569

Figure 63QQ

CHA.7.516

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVRPGVSVKISCKVSGYTFTDYVMHWVKQSHAKSLEWIGIIISPYSG NTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDAIYYCAREGDLPMFAYWGQG TLVTVSA	1570
vhCDR1	GYTFTDYV	1571
vhCDR2	ISPYSGNT	1572
vhCDR3	AREGDLPMFAY	1573
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVSYIYWYQQNPGSSPRLLIYDTSILASGVPF RFGSGSGTSYSLTISRMEAEDAATYYCQQWTSYPLTFGSGTKLELK	1574
vlCDR1	SSVSY	1575
vlCDR2	DTS	1576
vlCDR3	QQWTSYPLT	1577

Figure 63RR

CHA.7.518

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYNINWVKQSHGKSLEWIGYIYPYIGGS GYNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVVYC <u>AREDKTARNAMDY</u> WGQG TPVTVSS	1578
vhCDR1	GYTFTDYN	1579
vhCDR2	IYPYIGGS	1580
vhCDR3	AREDKTARNAMDY	1581
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTIICRVSENIYSNLAWYQQKQKGKSPQLLVYEATNLAEG VPSRFSGSGGTQYSLKINSLSQSEDFGSYYCQHFWGTPYTFGGGTKEIK	1582
vlCDR1	ENIYSN	1583
vlCDR2	EAT	1584
vlCDR3	QHFWGTPYT	1585

Figure 6355

CHA.7.520_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWNWRQFPGNKLEWMGYISYSG STSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARHYRYPYAMDYWGQG TSVTVSS	1586
vhCDR1	GYSITSDYA	1587
vhCDR2	ISYSGST	1588
vhCDR3	ARHYRYPYAMDY	1589
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVY FASTRESGVDPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	1590
vlCDR1	QSLNSSNQKNY	1591
vlCDR2	FAS	1592
vlCDR3	QQHYSTPFT	1593

Figure 63TT

CHA.7.520_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQP <small>SL</small> SITCTVSGFSLTSFGVHWVRQSPGKGLEWLGVIWSGGT TVYDAAFISRLSISKDNSKSQVFFKMNSLQTNDTAIYYCARKRGNFYVMDYWGQGT SVTVSS	1594
vhCDR1	GFSLTSFG	1595
vhCDR2	IWSGGT	1596
vhCDR3	ARKRGNFYVMDY	1597
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQ <small>SL</small> LNSSNQKNYLAWYQQKPGQSPKLLVY FASTRESGVPRFIGSGSGTDFTLTITSVQAEDLADYFCQ <small>Q</small> HYSTPFTFGSGTKLEIK	1598
vlCDR1	QSLNSSNQKNY	1599
vlCDR2	FAS	1600
vlCDR3	QQHYSTPFT	1601

Figure 63UU

CHA.7.522

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGSELVRPGTSVKLSCKASGYTFTSYVHWVRQRHGQGLEWIGNVYPG SGSTNYDEKFKSKGTLTVDTSSSTAYMHLSSLTSEDSAVYYCTRGVLRFLDYWGQG TTLTVSS	1602
vhCDR1	GYTFTSYW	1603
vhCDR2	VYPGSGST	1604
vhCDR3	TRGVLRFLDY	1605
Variable light (vl) domain	DIVMTQAAPSPVPTPGESVSISCRSSKSLHSNGNTYLYWFLQRPQGSPHLLIYRMS NLASGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK	1606
vlCDR1	KSLHSNGNTY	1607
vlCDR2	RMS	1608
vlCDR3	MQHLEYPLT	1609

Figure 63VV

CHA.7.524

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPEVVRPGVSVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGIISYSGNTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAREGDLPMFAYWGQGTLVTVSA	1610
vhCDR1	GYKFPDYV	1611
vhCDR2	ISYSGNT	1612
vhCDR3	AREGDLPMFAY	1613
Variable light (vl) domain	QIVLTQSPAIMSASPGEKVTMTCNASSSVSYMYWYQQKPISSPRLLIYDTSNLSAGVPVRFSGSGSGTSYSLTIGRMEAEDAATYYCQQWSSYPLTFGAGTKVEVK	1614
vlCDR1	SSVS	1615
vlCDR2	DTS	1616
vlCDR3	QQWSSYPLT	1617

Figure 63WW

CHA.7.526

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLTAYNINWVRQPPGKGLEWLGMIWGDGNTDYN SPLKSRITISKDNSK SQVFLKMDSLQTD TARYYCARDLKVRRDSPYTMDYWGQGTSVTVSS	1618
vhCDR1	GFSLTAYN	1619
vhCDR2	IWGDGNT	1620
vhCDR3	ARDLKVRRDSPYTMDY	1621
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASNRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK	1622
vlCDR1	QSVLYSSNQKNY	1623
vlCDR2	WAS	1624
vlCDR3	HQYLSSYT	1625

Figure 63XX

CHA.7.527

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLSLTCTVTGYSLTSDYAWNWRQFPGNKLEWMGYITYSG GTTYNPSLKSRIITRDTSKNQFFLQLTSVTTEDTATYYCARRGSGTTVVGDWYFDV WGAGTTVTVSS	1626
vhCDR1	GYSLTSDYA	1627
vhCDR2	ITYSGGT	1628
vhCDR3	ARRGSGTTVVGDWYFDV	1629
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKYYLAWYQQKPGQSPKLLIYW ASTRESGVPRFTGSGSGTDFTPTISSVTAEDLAVYYCQQFYTPYTFGGGTKLEMK	1630
vlCDR1	QSLLYSFNQKYY	1631
vlCDR2	WAS	1632
vlCDR3	QQFYTPYT	1633

Figure 63YY

CHA.7.528

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQVQQSGPELVKPGASVKISCKASGYTFTKSNMHWVKQSHGKSLEWIGYIYPYNG GTGYNQNFKSKATLTVDISSSTAYMELRSLTLEDSAVYLCAREADYYGNRGQFDYW GQGTLVTVSA	1634
vhCDR1	GYTFTKSN	1635
vhCDR2	IYPYNGGT	1636
vhCDR3	AREADYYGNRGQFDY	1637
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASDNIFSNLAWYHQKQKSPHLLVYGATNLAD GVPSRFSGSGGTQYSLKINSLSQSEDFGDYYCQHFHWGTPYTFGGGKLEIK	1638
vlCDR1	DNIFSN	1639
vlCDR2	GAT	1640
vlCDR3	QHFHWGTPYT	1641

Figure 63ZZ

CHA.7.530

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELMRPGTSVKVSCKASGYAFTNHLIEWIKQRPQGQGLEWIGVINPGSDSTDYNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSLYYNSWFVYWGQ GTLVTVSA	1642
vhCDR1	GYAFTNHL	1643
vhCDR2	INPGSDST	1644
vhCDR3	ARSLYYNSWFVY	1645
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKRGKSPQLLVYNAKTLVEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYQCQHHYGTPYTFGGGTKLEIK	1646
vlCDR1	ENIYSY	1647
vlCDR2	NAK	1648
vlCDR3	QHHYGTPYT	1649

Figure 63AAA

CHA.7.534

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGAELVKPGASVRLSCTAS <u>GFSIRD</u> TYJHWVKQRPEQGLDWIGKIDPANGKSEYDPKFQGRATMTTDTSSNTAYLQLSSLTSEDTAVYYCTRYGYYPYFDVWGAGTTVTVFS	1650
vhCDR1	GFSIRDY	1651
vhCDR2	IDPANGKS	1652
vhCDR3	TRYGYYPYFDV	1653
Variable light (vl) domain	SIVMTQTPKFLLVSAGDRVAITCKASQSVRHDVVWYQQKPGQSPKLLIYYASSRYTGVPDRFTGSGYGTDFTFITSTVQAEDLALYFCLQDFSSPWTFGGGTKLEIK	1654
vlCDR1	QSVRHD	1655
vlCDR2	YAS	1656
vlCDR3	LQDFSSPWT	1657

Figure 63BBB

CHA.7.535

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKTSGYTFTKNTMHWVRQSHGKSLEWIGGINPNSGGASFNQKFMGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARDGYDGDWFFDVWGAGTTVTVSS	1658
vhCDR1	GYTFTKNT	1659
vhCDR2	INPNSGGA	1660
vhCDR3	ARDGYDGDWFFDV	1661
Variable light (vl) domain	DIQMNQSPFSLSASLGDTVITICHASQNIYVWLSWYQQKPGNIPKLLIYKASDLHTGVPSRFSGSGSGTDFTLNISLQPEDATYYCQQGQSYPRTFGGGTKLEIK	1662
vlCDR1	QNIYVW	1663
vlCDR2	KAS	1664
vlCDR3	QQGQSYPRT	1665

Figure 63CCC

CHA.7.537

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLIGHGVNWIRQPPGKGLEWLGVWGDGN IDYNSALKSRLSISKDNSKSQVFLKMNSLQDDTARYFC <u>AVNSAMDY</u> WGQGTAVT VSS	1666
vhCDR1	GFSLIGHG	1667
vhCDR2	IWGDGNT	1668
vhCDR3	AVNSAMDY	1669
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLNCTASENVASFVSWYQQKPEQSPKLLIY <u>GTS</u> NRYT GVPDRFTGSGSATDFTLTISSVQAEDLGDYHCGQSYNYPFTFGSGTKLEIE	1670
vlCDR1	ENVASF	1671
vlCDR2	GTS	1672
vlCDR3	GQSYNYPFT	1673

Figure 63DDD

CHA.7.538_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELVRPGASVKVSCKTS <u>GYAFTNYL</u> IEWVKQRPGQGLEWIGVINPGSGG <u>GIYYNDKFKVKT</u> LTADKSSSTAYMQLSSLTSDDSAVYFC <u>ARSETHDTWFAY</u> WGQGTLVTVSA	1674
vhCDR1	GYAFTNYL	1675
vhCDR2	INPGSGGI	1676
vhCDR3	ARSETHDTWFAY	1677
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIA <small>VAWFQ</small> QKPGQSPKALIYLA <small>STRHTG</small> VPDRFTGSGSGTDFTLTISNVQSEDLADYFC <u>LQHWNYPYT</u> FGGGTKLEIKR	1678
vlCDR1	QSVRIA	1679
vlCDR2	LAS	1680
vlCDR3	LQHWNYPYT	1681

Figure 63EEE

CHA.7.538_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYPG GGYTNYNEKFKGKATLTADTSSSTAYMQLSLTSEDSAIYYCASPYYGSSYGFAFWG QGTLVTVSA	1682
vhCDR1	GYTFTNYW	1683
vhCDR2	IYPGGGYT	1684
vhCDR3	ASPYYGSSYGFAF	1685
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTG VPDRFTGSGSGTDFTLTISNVQSEDLADYFC LQHWNYPYTFGGGTKLEIKR	1686
vlCDR1	QSVRIA	1687
vlCDR2	LAS	1688
vlCDR3	LQHWNYPYT	1689

Figure 63FFF

CHA.7.543

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSGFSLSGYG IKWVRQPPGKGLEWLGTIWGDGS IDYNSALKSRLSISKDNSKSQVFLKMTSLQTDDTARYYC ASDSLGITFGYWGQGTLV TVSA	1690
vhCDR1	GFSLSGYG	1691
vhCDR2	IWGDGST	1692
vhCDR3	ASDSLGITFGY	1693
Variable light (vl) domain	DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGV PSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPLTFGAGTKLELK	1694
vlCDR1	QDISNY	1695
vlCDR2	YTS	1696
vlCDR3	QQGNTLPLT	1697

Figure 63GGG

CHA.7.544

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSGFSLTSYAITWVRQPPGKGLEWLGVIWPGGGT NYNSALKSRLSISKDNSKSHFLKMNLSLTDDTARYYCVRSYDGYLDWYFDVWGTG TTVTVSS	1698
vhCDR1	GFSLTSYA	1699
vhCDR2	IWPGGGT	1700
vhCDR3	VRSYDGYLDWYFDV	1701
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLSCKASENVGTYVSWYQQKPDQSPKLLIYGASNRYT GVPDRFTGSGSATDFTLISSVQAEDLSDYHCGQSYSPYTFGGGKLEII	1702
vlCDR1	ENVGTY	1703
vlCDR2	GAS	1704
vlCDR3	GQSYSPYT	1705

Figure 63HHH

CHA.7.545

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYS GVSTFPDDFKGRFAFSLETSASTAYLQINNLNKEDSATYFCARLGMGSTTGAGYFDV WGTGTTVTSS	1706
vhCDR1	GYTFTTYG	1707
vhCDR2	INTYSGVS	1708
vhCDR3	ARLGMGSTTGAGYFDV	1709
Variable light (vl) domain	DIVLTQSPAIMASAPGKVTMTCSASSSVSSWYLHWYQQKSGASPKLWIYGTSNLA SGVPARFSGSGSGTSYSLTSSVEAEDAATYYCQQYRSDPYTFGSGTKLEIK	1710
vlCDR1	SSVSSWY	1711
vlCDR2	GTS	1712
vlCDR3	QQYRSDPYT	1713

Figure 63III

CHA.7.546

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKKPGETVKISCKASGYTFTTYGMSWVKQAPGKGLKWMGWINTYS GVSTYADDFEGRFASFLETSVSTAYLQINNKNEDTATYFCARLGRGSTTGAGYLDV WGTGTTVTVSS	1714
vhCDR1	GYTFTTYG	1715
vhCDR2	INTYSGVS	1716
vhCDR3	ARLGRGSTTGAGYLDV	1717
Variable light (vl) domain	DIVLTQSPAIMASAPGEKVSMTCSASSSVSSWYLHWYQQKSGASPKLWIYGTSLA SGVPARFSGSGSGTSYSLTISVVEAEDAATYYCQQYHSDPYTFGSGTKLEIK	1718
vlCDR1	SSVSSWY	1719
vlCDR2	GTS	1720
vlCDR3	QQYHSDPYT	1721

Figure 63JJJ

CHA.7.547

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYS GVSTFPDDFKGRFAFSLETSASTAYLQINNLKNEDSATYFCARLGMGSTTGAGYFDV WGTGTTVTVSS	1722
vhCDR1	GYTFTTYG	1723
vhCDR2	INTYSGVS	1724
vhCDR3	ARLGMGSTTGAGYFDV	1725
Variable light (vl) domain	ENVLTQSPAIMASASLGEKVTLSKRASSSVNYMYWYQQKSDASPKLWIYYTSNLAGP VPAFSGSGSGNSYSLTISSEVEDAATYYCQQFTSSPWTFGGGTKLEIK	1726
vlCDR1	SSVNY	1727
vlCDR2	YTS	1728
vlCDR3	QQFTSSPWT	1729

Figure 63KKK

CHA.7.548

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYSMNWVKQSHGKSLEWIGDITPNNG SPNYNQKFKDKATLTVDKSSSTVYMELRSLTSEDSAVYYC <u>ASLFFDY</u> WGHGTTLVSS	1730
vhCDR1	GYTFTDYS	1731
vhCDR2	ITPNNGSP	1732
vhCDR3	ASLFFDY	1733
Variable light (vl) domain	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYG ASTRDSGVPDRFTGSGSGTDFTLTITSVQAEDLAVYYC <u>QNDHTYPYT</u> FGGGTKLEIK	1734
vlCDR1	QSLNLSGNQKNY	1735
vlCDR2	GAS	1736
vlCDR3	QNDHTYPYT	1737

Figure 63LLL

CHA.7.549

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELVKPGASVKLSCKASGFTFTTHWMHWVRQRPQGGLWIGNIYPS NGGSNYNEKFKTKATLTVDSSSTAYMHLSSLTSEDSAVYYCARRVNWDGYYFDYW GQGTTLTVSS	1738
vhCDR1	GFTFTTHW	1739
vhCDR2	IYPSNGGS	1740
vhCDR3	ARRVNWDGYYFDY	1741
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQKPGQSPKLLIYSASYRY SGVPDRFTGSGSGTDFLTISNVQSEDLADYFCQQYNSYPLTFGGGTKLEIK	1742
vlCDR1	QNVGTN	1743
vlCDR2	SAS	1744
vlCDR3	QQYNSYPLT	1745

Figure 63MMM

CHA.7.550

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWIHWVKQRPGQGLEWIGNINPSN GGTINYNEKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVYYCARRGLPYFFDYWGQG TTLTVSS	1746
vhCDR1	GYTFTSYW	1747
vhCDR2	INPSNGGT	1748
vhCDR3	ARRGLPYFFDY	1749
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKGSQNVGYNVAWYQQKPGQSPKALVYSASDR HSGVPDRFAGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGAGTKLELK	1750
vlCDR1	QNVGYN	1751
vlCDR2	SAS	1752
vlCDR3	QQYNSYPLT	1753

Figure 63NNN
Humanized sequences of CHA.7.518 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)

IGHV1-46*01 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYHHVVRQAPGQGLEWMGLINPSGGSTSYAQKFGQGRVTMTTRDTSTSTVYMEISLRSSEDTAVYYCAR
 (SEQ ID NO: 1754)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTVSS (SEQ ID NO: 1755)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p p b b	b b b	b i i	i i b b	b i b	b b b x	b b b	b i b i b b
518	EVQLQQSGPELVKPGASVKISCKAS	GYTFTDYNIN	WVKQSHGKSLEWIG	YIIPYIGGSG	YNQKPKSKATLSADNPSS	STAYMEISLRSSEDTAVYYCAR			
	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTSYHH	WVRQAPGQGLEWMG	IINPSGGSTS	YAQKFGQGRVTMTTRDTSTSTVYMEISLRSSEDTAVYYCAR				
h518H1	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWMG	YIIPYIGGSG	YAQKFGQGRVTMTTRDTSTSTVYMEISLRSSEDTAVYYCAR				
h518H2	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIIPYIGGSG	YAQKFGQGRVTMTADTSTSTVYMEISLRSSEDTAVYYCAR				
h518H3	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIIPYIGGSG	YAQKFGQGRATLTADTSTSTAYMEISLRSSEDTAVYYCAR				
h518H4	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIIPYIGGSG	YAQKFGQGRATLTADNSTSTAYMEISLRSSEDTAVYYCAR				

seq	100	110	120
AbM		i b b b	

518 EDKTARNAMDY WCQGTPLTVTVSS (SEQ ID NO: 1756)
 ("1-46*01" sequence is disclosed as SEQ ID NO: 1757)

h518H1	EDKTARNAMDY	WCQGTPLTVTVSS	(SEQ ID NO: 1758)
h518H2	EDKTARNAMDY	WCQGTPLTVTVSS	(SEQ ID NO: 1759)
h518H3	EDKTARNAMDY	WCQGTPLTVTVSS	(SEQ ID NO: 1760)
h518H4	EDKTARNAMDY	WCQGTPLTVTVSS	(SEQ ID NO: 1761)

deamination substitutions: Q/S/A

Figure 63PPP
Humanized sequences of CHA.7.538_1 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework
 IGHV1-46*01
 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVROAPGQGLEWMGIINPSSGGSTSYAOKFQGRVTMTDSTSTVYMEISSLRSEDYAVYCAR (SEQ ID NO: 1769)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTVSS (SEQ ID NO: 1770)

seq	10	20	30	40	50	60	70	80	90
ADM	10	20	30	40	50	60	70	80	90
	b b b	p p b b b	b b b	b i i	i i b b b	i b b b x	b b b	b b b	b i b b b
538_1	QVQLVQSGAEVKKPGASVKVSCKTS	GYAFTNYLIE	WVKQRPQGQLEWIG	VINPSSGGIY	YNDKPKVKITLTADKSSSTAYMQLSLTSDDSAVYFCAR	**	***	*	*
1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYIMH	WVROAPGQGLEWMG	IINPSSGGST	YAKFQGRVTMTDSTSTVYMEISSLRSEDYAVYCAR				
h5381H1	QVQLVQSGAEVKKPGASVKVSCKAS	GYAFTNYLIE	WVROAPGQGLEWMG	VINPSSGGIY	YAKFQGRVTMTDSTSTVYMEISSLRSEDYAVYCAR				
h5381H2	QVQLVQSGAEVKKPGASVKVSCKAS	GYAFTNYLIE	WVROAPGQGLEWIG	VINPSSGGIY	YAKFQGRVTMTDSTSTVYMEISSLRSEDYAVYCAR				
h5381H3	QVQLVQSGAEVKKPGASVKVSCKTS	GYAFTNYLIE	WVROAPGQGLEWIG	VINPSSGGIY	YAKFQGRVLTADKSTSTAYMEISSLRSEDYAVYCAR				
h5381H4	QVQLVQSGAEVKKPGASVKVSCKTS	GYAFTNYLIE	WVROAPGQGLEWIG	VINPSSGGIY	YAKFQGRVLTADKSTSTAYMEISSLRSEDYAVYCAR				

F

T

N

#

V

seq

ADM

100

110

i

b

b

b

seq

ADM

538_1

SETHDTWFAY

WGQGLTVTVSA

(SEQ ID NO: 1771)

*

("1-46*01" sequence is disclosed as SEQ ID NO: 1772)

h5381H1

SETHDTWFAY

WGQGLTVTVSS

(SEQ ID NO: 1773)

h5381H2

SETHDTWFAY

WGQGLTVTVSS

(SEQ ID NO: 1774)

h5381H3

SETHDTWFAY

WGQGLTVTVSS

(SEQ ID NO: 1775)

h5381H4

SETHDTWFAY

WGQGLTVTVSS

(SEQ ID NO: 1776)

Q

deamidation substitutions: Q/S/A

@ tryptophan oxidation substitutions: Y/F/H

Figure 63000
humanized sequences of CHA.7.538_1 antibody VL

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework
IGKV1-39*01
DIQMTQSPSSLSASVGRVTITCRASQSISSYINWYQKFGKAPKLLIYAASSLQSGVPSRFGSGGTDFLTITSSLPQEDFATYYCQQSYSTPP (SEQ ID NO: 1777)

Joining region IMGT J00242|IGKJ2*01|YTFQGTGLEIK (SEQ ID NO: 1778)

IGKV1-17*02
DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKFGKAPKLLIYAASSLQSGVPSRFGSGGTDFLTITSSLPQEDFATYYCQHNSTPP (SEQ ID NO: 1779)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
538	b b b	p p	p b b	b b i b i	i i i b b i	i b b	b b b	b b b i b b i b
	DIQMTQSPSSLSASVGRVTITCRASQSVRIAVA	WYQKFGKAPKLLIY	LASTRHT	GVPSRFGSGGTDFLTITSSLPQEDFATYYC	***	***	***	***

IGKV1-39 DIQMTQSPSSLSASVGRVTITCRASQSISSYINWYQKFGKAPKLLIYAASSLQSGVPSRFGSGGTDFLTITSSLPQEDFATYYC
h38L1 DIQMTQSPSSLSASVGRVTITCRASQSVRIAVA WYQKFGKAPKLLIY LASTRHT GVPSRFGSGGTDFLTITSSLPQEDFATYYC
h38L2 DIQMTQSPSSLSASVGRVTITCRASQSVRIAVA WYQKFGKAPKLLIY LASTRHT GVPSRFGSGGTDFLTITSSLPQEDFATYYC

seq	90	100
AbM	90	100
538	i b i i b i b b b	LQHNYPYT
	PGGTGLEIK (SEQ ID NO: 1780)	*

IGKV1-39 QQSYSTPP (SEQ ID NO: 1781)
h38L1 LQHNYPYT FQGTGLEIK (SEQ ID NO: 1782)
h38L2 LQHNYPYT FQGTGLEIK (SEQ ID NO: 1783)

@#

deamidation substitutions: Q/S/A/D
@ tryptophan oxidation substitutions: Y/F/H

Figure 63RRR
humanized sequences of CHA.7.538_2 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework
IGHV1-46*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYMHVRQAPGQGLEWMGIINPSGGSTSYAQKFGQGRVTMRDTSSTVYMELSLRSSEDTAVYYCAR (SEQ ID NO: 1784)
Joining region
IMGT J00256IGHJ4*01YEDYWGQGLTVTVSS (SEQ ID NO: 1785)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
538_2	b b b	p p b b	b b b	b l i	i i b b	i b	b b x	b b b	b i b b b
...	QVQLVQSGAEVKKPGASVKVSCKAA	GYTFSTNYWIG	WVKQRPGHGLEWIG	DIYPGGGYTN	YNEKPKGKATLTADTSSSTAYMQISLTSSEDSATVYYCAS	**	**	**	**
1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFSTNYWIG	WVKQRPGHGLEWIG	DIYPGGGYTN	YNEKPKGKATLTADTSSSTAYMQISLTSSEDSATVYYCAS	**	**	**	**
h5382H1	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFSTNYWIG	WVKQRPGHGLEWIG	DIYPGGGYTN	YNEKPKGKATLTADTSSSTAYMQISLTSSEDSATVYYCAR	**	**	**	**
h5382H2	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFSTNYWIG	WVKQRPGHGLEWIG	DIYPGGGYTN	YNEKPKGKATLTADTSSSTAYMQISLTSSEDSATVYYCAS	**	**	**	**
h5382H3	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFSTNYWIG	WVKQRPGHGLEWIG	DIYPGGGYTN	YNEKPKGKATLTADTSSSTAYMQISLTSSEDSATVYYCAS	**	**	**	**

seq	100	110
AbM	100	110
538_2	PYYGSSYGFAP	WCQGLTVTVSSA
h5382H1	PYYGSSYGFAP	WCQGLTVTVSS
h5382H2	PYYGSSYGFAP	WCQGLTVTVSS
h5382H3	PYYGSSYGFAP	WCQGLTVTVSS

deamidation substitutions: Q/S/A
@ tryptophan oxidation substitutions: Y/F/H

Figure 63SSS

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYHHWVRQAPGQGLEWMGIINPSSGGSTSYAQKFGQGRVTMTTRDTSSTVYMELSSLSRSED¹⁷⁹¹TAVYYCAR
(SEQ ID NO: 1791)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS (SEQ ID NO: 1792)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p p b b b	b b b	b i i	i i b b b	i b b b x	b b b	b b b	b i b b b

524 QVQLQQSGPEVVRPCVSVKISCKGS **GYNFPDYYNH** WYKQSHAKSLEWIG **IISIYSGNTN** YNKFPGKATMTVDKSSSTAYMELARLTSED¹⁷⁹²SAIYYCAR
* * * * *
1-46*01 QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYVNH WVRQAPGQGLEWMG IINPSSGGSTS YAQKFGQGRVTMTTRDTSSTVYMELSSLSRSED¹⁷⁹³TAVYYCAR
h524H1 QVQLVQSGAEVKKPGASVKVSCKAS **GYNFPDYYNH** WVRQAPGQGLEWMG **IISIYSGNTN** YAQKFGQGRVTMTTRDTSSTVYMELSSLSRSED¹⁷⁹⁴TAVYYCAR
h524H2 QVQLVQSGAEVKKPGASVKVSCKAS **GYNFPDYYNH** WVRQAPGQGLEWMG **IISIYSGNTN** YAQKFGQGRVTMTTRDTSSTVYMELSSLSRSED¹⁷⁹⁵TAVYYCAR
h524H3 QVQLVQSGAEVKKPGASVKISCKGS **GYNFPDYYNH** WVRQAPGQGLEWIG **IISIYSGNTN** YAQKFGQGRATMTVDTSSTAYMELSSLSRSED¹⁷⁹⁶TAVYYCAR
h524H4 QVQLVQSGAEVKKPGASVKISCKGS **GYNFPDYYNH** WVRQAPGQGLEWIG **IISIYSGNTN** YAQKFGQGRATMTVDKSTSTAYMELSSLSRSED¹⁷⁹⁷TAVYYCAR
V # N I

seq	100	110
AbM	110	
	i b b b	

524 **EGDLPNFAY** WGQGLTVTVSA (SEQ ID NO: 1793)
* ("1-46*01" sequence disclosed as SEQ ID NO: 1794)
h524H1 **EGDLPNFAY** WGQGLTVTVSS (SEQ ID NO: 1795)
h524H2 **EGDLPNFAY** WGQGLTVTVSS (SEQ ID NO: 1796)
h524H3 **EGDLPNFAY** WGQGLTVTVSS (SEQ ID NO: 1797)
h524H4 **EGDLPNFAY** WGQGLTVTVSS (SEQ ID NO: 1798)
ø

deamidation substitutions: Q/S/A
ø methionine oxidation substitutions: L/F/A

Figure 63TTT

Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework (AbM CDR definition)
IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRSNWPP
(SEQ ID NO: 1793)

Joining region IMGT J00242|IGKJ2*01|YTFGGQTKLEIK (SEQ ID NO: 1800)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
	b b b	p p	b b b	b b i	i i i b b i	i b b	b b b	b b b
524	QIVLTQSPAIMSASPGEKVTMTC	NASSSVS-IMY	WYQQKPGQAPRLIIY	DTSNLA	GVPRFSGSGSGTDYTLTISSELEPEDFAVYYC			
	*	***	***	***	***	***	***	***
IGKV3-11	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLIIY	DASNRAT	GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC			
h524L1	EIVLTQSPATLSLSPGERATLSC	NASSSVS-IMY	WYQQKPGQAPRLIIY	DTSNLA	GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC			
h524L2	EIVLTQSPATLSLSPGERATLSC	NASSSVS-IMY	WYQQKPGQAPRLIIY	DTSNLA	GIPARFSGSGSGTDYTLTISSELEPEDFAVYYC			
h524L3	EIVLTQSPATLSLSPGERVTMTC	NASSSVS-IMY	WYQQKPGQAPRLIIY	DTSNLA	GVPRFSGSGSGTDYTLTISSELEPEDFAVYYC			
	M A	#	S	#	A			

seq	90	100
AbM	90	100
	i b i	i b b
524	QQWSSYPLT	FGAGTKVEIK (SEQ ID NO: 1801)
	*	*
IGKV3-11	QQRSNWPP	(SEQ ID NO: 1802)
h524L1	QQWSSYPLT	FGQGTKLEIK (SEQ ID NO: 1803)
h524L2	QQWSSYPLT	FGQGTKLEIK (SEQ ID NO: 1804)
h524L3	QQWSSYPLT	FGQGTKVEIK (SEQ ID NO: 1805)
	q	V

deamidation substitutions: Q/S/A/D
@ tryptophan oxidation substitutions: Y/F/H

Figure 63UUU

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYMMHWVRQAPGQGLEWMGIINPSSGGSSTSYAQKFGQGRVTMTTRDTSSTVYMELSSLSRSEDVAVYYCAR
(SEQ ID NO: 1806)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTIVSS (SEQ ID NO: 1807)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p p b b b	b b b	b i i	i i b b b	i b b b x	b b b	b b b	b i b b b

530 QVQLVQSGAEVKKPGASVKVSCKAS **GYAFTNHLIE** WIKRPGQGLEWIG **VINPGSDSTD** YNEKPKDKATLTADKSSSTAYMQLSSLTSDSDSAVYYCAR
 * * * * *
 1-46*01 QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYNMH WVRQAPGQGLEWIG IINPSSGGSSTSYAQKFGQGRVTMTTRDTSSTVYMELSSLSRSEDVAVYYCAR
 h530H1 QVQLVQSGAEVKKPGASVKVSCKAS **GYAFTNHLIE** WVRQAPGQGLEWIG **VINPGSDSTD** YAQKFGQGRVTMTTRDTSSTVYMELSSLSRSEDVAVYYCAR
 h530H2 QVQLVQSGAEVKKPGASVKVSCKAS **GYAFTNHLIE** WVRQAPGQGLEWIG **VINPGSDSTD** YAQKFGQGRVTMTTRDTSSTVYMELSSLSRSEDVAVYYCAR
 h530H3 QVQLVQSGAEVKKPGASVKVSCKAS **GYAFTNHLIE** WVRQAPGQGLEWIG **VINPGSDSTD** YAQKFGQGRATLTADTSTSTAYMELSSLSRSEDVAVYYCAR
 h530H4 QVQLVQSGAEVKKPGASVKVSCKAS **GYAFTNHLIE** WVRQAPGQGLEWIG **VINPGSDSTD** YAQKFGQGRATLTADKSTSTAYMELSSLSRSEDVAVYYCAR
 # M N F

seq	100	110
AbM		110
	i b b b	

530 **SLYNSMFVY** WGQGLTVTVSA (SEQ ID NO: 1808) * ("1-46*01" sequence disclosed as SEQ ID NO: 1809)
 h530H1 **SLYNSMFVY** WGQGLTVTVSS (SEQ ID NO: 1810)
 h530H2 **SLYNSMFVY** WGQGLTVTVSS (SEQ ID NO: 1811)
 h530H3 **SLYNSMFVY** WGQGLTVTVSS (SEQ ID NO: 1812)
 h530H4 **SLYNSMFVY** WGQGLTVTVSS (SEQ ID NO: 1813)
 # e

deamidation substitutions: Q/S/A
 @ tryptophan oxidation substitutions: Y/F/H

Figure 63VVV

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework (AbM CDR definition)
IGKV1-39*01 DIQMTQSPSSLASVGDRTVITCRASQSISSYLWYQQKPKAPKLLIYAASSLSQGVPSRFGSGSGTDFTLTISLQPEDFATYYCQOQSYSTPP (SEQ ID NO: 1814) Joining region IMGT J00242|IGKJ2*01|YTFGQGTKEIK (SEQ ID NO: 1815)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
	b b b	p p	p b b b	b i b i i i b b i	i b b	b b b	b b b	i b b i b
530	DIQMTQSPASLSASVGETVTITC	**	RASENIYSYLA	WYQQKPKAPKLLVY	NAKTLVE	GVPSRFGSGSGTDFTLTISLQPEDFGSYTC	**	
	*		*	*	*	*	*	*
IGKV1-39	DIQMTQSPSSLASVGDRTVITC	RASQSISSYLWYQQKPKAPKLLIY	AASSLSQ	GVPSRFGSGSGTDFTLTISLQPEDFATYYC				
h530L1	DIQMTQSPSSLASVGDRTVITC	RASENIYSYLA	WYQQKPKAPKLLIY	NAKTLVE	GVPSRFGSGSGTDFTLTISLQPEDFATYYC			
h530L2	DIQMTQSPSSLASVGDRTVITC	RASENIYSYLA	WYQQKPKAPKLLVY	NAKTLVE	GVPSRFGSGSGTDFTLTISLQPEDFGTYTC			
		#	S	#				

seq	90	100
AbM	90	100
	i b i	i b b b
530	QHHYGTPT	FGGQTKLEIK (SEQ ID NO: 1816)
	*	
IGKV1-39	QOQSYSTPP	(SEQ ID NO: 1817)
h530L1	QHHYGTPT	FGGQTKLEIK (SEQ ID NO: 1818)
h530L2	QHHYGTPT	FGGQTKLEIK (SEQ ID NO: 1819)

deamidation substitutions: Q/S/A/D

Figure 63WWW

What	Sequences
humanized CH _A .7.518 VH h518HH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFDYNINWVRQAPGQGLEWMGYIYPYIGSGGYAQKFKQ GRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1820)
humanized CH _A .7.518 VH h518HH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFDYNINWVRQAPGQGLEWIGYIYPYIGSGGYAQKFKQ RVTMTADTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1821)
humanized CH _A .7.518 VH h518HH3	QVQLVQSGAEVKKPGASVKISCKASGYTFDYNINWVRQAPGQGLEWIGYIYPYIGSGGYAQKFKQ RATLTADTSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1822)
humanized CH _A .7.518 VH h518HH4	QVQLVQSGAEVKKPGASVKISCKASGYTFDYNINWVRQAPGQGLEWIGYIYPYIGSGGYAQKFKQGR ATLTADNSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1823)
humanized CH _A .7.518 VL h518HL1	DIQMTQSPSSLASVGDRTVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1824)
humanized CH _A .7.518 VL h518HL2	DIQMTQSPSSLASVGDRTVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGT DYTLTISSLQPEDFATYYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1825)
humanized CH _A .7.518 VL h518HL3	DIQMTQSPSSLASVGDRTVTITCRVSENIYSNLAWYQQKPGKAPKLLVYEATNLAEGVPSRFSGSGSG TDYTLTISSLQPEDFGTYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1826)

Figure 63XXX

What	Sequences
humanized CHA.7.538_1 VH h5381HH1	QVQLVQSGAEVKKPGASVKVSCKASGYAFTN ^{YL} I ^{EW} VRQAPGQGLEWMGVINPGSGGIYYAQKFQ GRVTMT RD TSTSTVYMELSSLRSEDTAVYYC ^{AR} SETHDTWFAYWGQGT ^{LV} TVSS (SEQ ID NO: 1827)
humanized CHA.7.538_1 VH h5381HH2	QVQLVQSGAEVKKPGASVKVSCKASGYAFTN ^{YL} I ^{EW} VRQAPGQGLEWIGVINPGSGGIYYAQKFQ RVMTADTSTSTVYMELSSLRSEDTAVYYC ^{AR} SETHDTWFAYWGQGT ^{LV} TVSS (SEQ ID NO: 1828)
humanized CHA.7.538_1 VH h5381HH3	QVQLVQSGAEVKKPGASVKVSCKTSGYAFTN ^{YL} I ^{EW} VRQAPGQGLEWIGVINPGSGGIYYAQKFQ RVTLTADTSTSTAYMELSSLRSEDTAVYYC ^{AR} SETHDTWFAYWGQGT ^{LV} TVSS (SEQ ID NO: 1829)
humanized CHA.7.538_1 VH h5381HH4	QVQLVQSGAEVKKPGASVKVSCKTSGYAFTN ^{YL} I ^{EW} VRQAPGQGLEWIGVINPGSGGIYYAQKFQ RVTLTAD ^{KS} TSTSTAYMELSSLRSEDTAVYYC ^{AR} SETHDTWFAYWGQGT ^{LV} TVSS (SEQ ID NO: 1830)
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLASVGD ^{RV} TTTCKASQSVRIA ^V AWYQQKPGKAPKLLIY ^{LA} STRHTGVPSRFSGSGGT DFTLT ^{ISS} LQPEDFATYYC ^{LQ} HWNPYPYTFGGQGT ^{KL} EIK (SEQ ID NO: 1831)
humanized CHA.7.538_1/538_2 VL h538HL2	DIQMTQSPSSLASVGD ^{RV} TTTCKASQSVRIA ^V AWFQQKPGKAPK ^{ALI} Y ^{LA} STRHTGVPSRFSGSGGT DFTLT ^{ISS} VQPEDFATYYC ^{LQ} HWNPYPYTFGGQGT ^{KL} EIK (SEQ ID NO: 1832)

Figure 63YY

What	Sequences
humanized CHA.7.538_2 VH h5382HH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWMGDIYPGGGYTNYAQKF QGRVTMTTRDTSTSTVYMELSSLRSEDTAVVYCARPYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1833)
humanized CHA.7.538_2 VH h5382HH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQ GRVTMTADTSTSTVYMELSSLRSEDTAVVYCASPYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1834)
humanized CHA.7.538_2 VH h5382HH3	QVQLVQSGAEVKKPGASVKMSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQ GRATLTADTSTSTAYMELSSLRSEDTAVVYCASPYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1835)
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLASVGDRTTTCASQSVRIAVAWYQQKPGKAPKLLIYLASTRHTGVPSTRFSGSGGT DFTLTITSSIQPEDFATYYVCLQHWNPYPYTFGGQGTKLEIK
humanized CHA.7.538_1/538_2 VL h538HL2	(SEQ ID NO: 1836) DIQMTQSPSSLASVGDRTTTCASQSVRIAVAWYQQKPGKAPKALIIYLASTRHTGVPSTRFSGSGGT DFTLTITSSVQPEDFATYYVCLQHWNPYPYTFGGQGTKLEIK (SEQ ID NO: 1837)

Figure 63ZZZ

What	Sequences
humanized CHA.7.524 VH h524H1	QVQLVQSGAEVKKPGASVKVCKASGYKFPDYYMIIWVVRQAPGQGLEWMGIIISYSGNTN YAQKFQGRV TMTRDTSTSTVYMEISSLRSED TA VYYCAREGDL PMFAYWGQGT LVTVSS (SEQ ID NO: 1838)
humanized CHA.7.524 VH h524H2	QVQLVQSGAEVKKPGASVKVCKASGYKFPDYYMHWVVRQAPGQGLEWIGIIISYSGNTN YAQKFQGRVT MTVDTSTSTVYMEISSLRSED TA VYYCAREGDL PMFAYWGQGT LVTVSS (SEQ ID NO: 1839)
humanized CHA.7.524 VH h524H3	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYYMIIWVVRQAPGQGLEWIGIIISYSGNTN YAQKFQGRAT MTVDTSTSTAYMEISSLRSED TA VYYCAREGDL PMFAYWGQGT LVTVSS (SEQ ID NO: 1840)
humanized CHA.7.524 VH h524H4	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYYMHWVVRQAPGQGLEWIGIIISYSGNTN YAQKFQGRAT MTVDTSTSTAYMEISSLRSED TA VYYCAREGDL PMFAYWGQGT LVTVSS (SEQ ID NO: 1841)
humanized CHA.7.524 VL h524L1	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGIPARFSGSGGTDFTLT ISSLEPEDFAVYYCQWSSYPLTIFGQGTKLEIK (SEQ ID NO: 1842)
humanized CHA.7.524 VI h524L2	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGIPARFSGSGGTIDYTL TISSLEPEDFAVYYCQWSSYPLTIFGQGTKLEIK (SEQ ID NO: 1843)
humanized CHA.7.524 VI h524L3	EIVLTQSPATLSLSPGERV TM SCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGV VPARFSGSGGTIDYT LTISSMEPEDFAVYYCQWSSYPLTIFGQGTKVEIK (SEQ ID NO: 1844)

Figure 63AAAA

What	Sequences
humanized CHA.7.530 VH h530H1	QVQLVQSGAEVKKPGASVKVCKASGYAFTNHLIEWVRQAPGQGLEWMGVINPGSDSDTDYAQKFQGRV TMTRDTSTSTVYME LS SLRSEDTAVYYCARSLYYNSWFFVYWGQGT L VTVSS (SEQ ID NO: 1845)
humanized CHA.7.530 VH h530H2	QVQLVQSGAEVKKPGASVKVCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRVT MTADTSTSTVYME LS SLRSEDTAVYYCARSLYYNSWFFVYWGQGT L VTVSS (SEQ ID NO: 1846)
humanized CHA.7.530 VH 530H3	hQVQLVQSGAEVKKPGASVKVCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRAT LTADTSTSTAYME LS SLRSEDTAVYYCARSLYYNSWFFVYWGQGT L VTVSS (SEQ ID NO: 1847)
humanized CHA.7.530 VH h530H4	QVQLVQSGAEVKKPGASVKVCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRATL TADKSTSTAYME LS SLRSEDTAVYYCARSLYYNSWFFVYWGQGT L VTVSS (SEQ ID NO: 1848)
humanized CHA.7.530 VL h530L1	DIQMTQSPSSLSASVGDRTTTCRASENIYSYLAWYQQKPGKAPKLLIYN AK TLVEGVPSRFSGSGSGTDFT LTIS SL QPEDFATYYCQH HY GPYTFGQGT K LEIK (SEQ ID NO: 1849)
humanized CHA.7.530 VL h530L2	DIQMTQSPSSLSASVGDRTTTCRASENIYSYLAWYQQKPGKAPKLLIYN AK TLVEGVPSRFSGSGSGTD F TLTIS SL QPEDF G TYCYCQH HY GPYTFGQGT K LEIK (SEQ ID NO: 1850)