

Figure 1A

Human IgG1 constant region
 ASTKGPSVFPFLAPSSKSTSGCTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVD
 KKVEPKSCDKTHITCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVL
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 1)

Human IgG1 D265A constant region
 ASTKGPSVFPFLAPSSKSTSGCTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVD
 KKVEPKSCDKTHITCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVL
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2)

Human IgG1 N297A constant region
 ASTKGPSVFPFLAPSSKSTSGCTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVD
 KKVEPKSCDKTHITCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVL
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 3)

Human IgG2 constant region
 ASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSNFGTQTYICNVNDHKPSNTKVD
 KITVERKCCVECPCPAPPVAGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQNFSTFRVSVLTW
 HQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDG
 SFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 4)

Human IgG3 constant region
 ASTKGPSVFPFLAPCSRSTSGCTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVD
 KRVELKTPLGDTHTTCPRCPPEPKSCDTPPCPRCPPEPKSCDTPPCPRCPPEPKSCDTPPCPRCPPEPKSCDTPPCPRCPPEPKSCDTPPCPRCPPEPKSCD
 VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQYNSTFRVSVLTWVILHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPS
 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNRYTQKSLSLSPGK
 (SEQ ID NO: 5)

Figure 1B

Human IgG4 constant region (Wild Type)

ASTKGPVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTIYTCNVDHDKPSNTKVDKRVESKYGPPCP[CPAPEFLGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6)

Human IgG4 constant region (S241P hinge mutant)

ASTKGPVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTIYTCNVDHDKPSNTKVDKRVESKYGPPCP[CPAPEFLGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSRLTVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 7)

Human kappa light chain

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 8)

Human lambda light chain

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPTSKQSNKYAAASSVLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 9)

Figure 2

Human TIGIT extra-cellular domain

MMTGITETTNISAEKGSILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPKDRVAPGPGGLGLTLQSLTMNDTGEYFCIYHTYPD
CTYTGRIFLEVLSSVAEHGARFQIP (SEQ ID NO: 10)

Cynomolgus macaque TIGIT extra-cellular domain

MMTGITETTNISAKKCCSVILQCHLSSDMAQVTQVNWEQHDHSLLAIRNAELGWHIYPATKDRVAPGPGGLGLTLQSLTMNDTGEYFCYHT
YPDCTYGRIFLEVLSSVAEHSARFQIP (SEQ ID NO: 11)

Human PVRIg extra-cellular domain

TPEVWVQVRMEATELSSFTIRCGFLGCSISLVTWSGGPAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTECK
EASFEGSWEACGSLPPSSDPGLSAPPTAPILRAD (SEQ ID NO: 12)

Cynomolgus macaque PVRIg extra-cellular domain

TPEVWVQVQMEATELSSFTVHCGFLGPGSISLVTWSGGPDGAGGTKLAVLHPELGTQWAPARQARWETQSSISLALEDGASSPFANTTFC
CKFAFPEGSWESCGSLPPSSDPGLSAPPTVPILRAD (SEQ ID NO: 13)

Human PD-1 extra-cellular domain

PGWFLDSPDRPWNPPTFSPALLVVTGEDNATFTCSFSNTSEFVLNWYRMSPSNQTDKLAAPEDRSQPGQDCRFRVTQLPNGRDFHMSVVR
ARRNDSGTYLCCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPRPAGQFQTLV (SEQ ID NO: 14)

Cynomolgus PD-1 extra-cellular domain

PGWFLDSPDRPWNPPTFSPALLVVTGEDNATFTCSFSNASSEFVLNWYRMSPSNQTDKLAAPEDRSQPGQDCRFRVTQLPNGRDFHMSVVR
ARRNDSGTYLCCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPRPAGQFQALV (SEQ ID NO: 15)

Figure 3A: CPA.9.018

What	sequence	SEQ ID NO:
Variable heavy (vn) domain	QVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKEMILVQDYYMDVWGQGTITVTVSS	16
VhCDR1	GFTSSYG	17
VhCDR2	IRYDGSNK	18
VhCDR3	AKEMILVQDYYMDV	19
Full length HC (IgG4(S241P); CPA.9.018.H4(S241P))	QVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKEMILVQDYYMDVWGQGTITVTVSSASTKGPSVFPLA PCRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTCTYTCNVDRHPSNTKVDKRVESKYGPPCPAPAFELGGPSVFLPPKPKDTLMISRTPEVTCWVDVSDQEDPEVFQFNWYVDGVEV HNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	20
Variable light (vl) domain	DVVMTQSPSLSPVSPGEPASISCRSSQNLHHRNGINYNWYLOKPGQSPQLLIYWGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GLQIPPTFGQGTQVDIKR	21
VlCDR1	QNLHHRNGINYN	22
VlCDR2	WGS	23
VlCDR3	MQGLQIPPT	24
Full length light chain ((CPA.9.018.H4(S241P))	DVVMTQSPSLSPVSPGEPASISCRSSQNLHHRNGINYNWYLOKPGQSPQLLIYWGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GLQIPPTFGQGTQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	25

Figure 3B : CPA.9.027

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRSLSCAASGFTFSYAMHWVRAQPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGGGTTVTSS	26
vhCDR1	GFTFSYA	27
vhCDR2	ISYDGSNK	28
vhCDR3	ARDPLPLHYGMDV	29
Full length HC (IgG4(S241P); CPA.9.027.H4(S241P))	EVQLVETGGGLIQPGRSLRSLSCAASGFTFSYAMHWVRAQPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGGGTTVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTITCTNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSEQEDPEVQFNWYVDGVEVHNAKTKPREEQNFSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCVMHEALHINHYTKLSLSPGK	30
Variable light (vl) domain	QSALTQPRASGNPGRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLSLQLGGGTQLAVLG	31
vlCDR1	SSNMGRRP	32
vlCDR2	SQN	33
vlCDR3	AYWDDSLSLQ	34
Full length light chain (CPA.9.027.H4(S241P))	QSALTQPRASGNPGRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDSLSLQLGGGTQLAVLGQPKAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWIKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	35

Figure 3C: CPA.9.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRSLSCAASGFTSSYAMHWVROAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGGGTTVTSS	36
vhCDR1	GFTSSYA	37
vhCDR2	ISYDGSNK	38
vhCDR3	ARDPLPLHYGMDV	39
Full length HC (IgG4(S241P); CPA.9.049.H4(S241P))	EVQLVETGGGLIQPGRSLRSLSCAASGFTSSYAMHWVROAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGGGTTVTSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPAPEFLGGPSVFLFPpK PKDTLMISRTPEVTCVWDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENINVKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSMHEALHINHYTKLSLSPGK	40
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCVWDDSLFSLLLGGGTQLAVLG	41
vlCDR1	SSNMGRRP	42
vlCDR2	SQN	43
vlCDR3	AVWDDSLFSL	44
Full length light chain (CPA.9.049.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCVWDDSLFSLLLGGGTQLAVLGQPKAAPSVTLPFSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	45

Figure 3D: CPA.9.057

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWIQPPGKGLEWIGSIYSGSTYYNP SLKSRVTISVDTSKNQFS KLKLS SVTAADTAUVYCARQGAAAGNPFDI WGQGTMTVT VSS	46
vhCDR1	GGSISSSSYY	47
vhCDR2	IYSGST	48
vhCDR3	ARQGAAAGNPFDI	49
Full length HC (IgG4(S241P); CPA.9.057.H4(S241P))	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWIQPPGKGLEWIGSIYSGSTYYNP SLKSRVTISVDTSKNQFS KLKLS SVTAADTAUVYCARQGAAAGNPFDI WGQGTMTVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTKTYTCNV DHKPSN TKVDKRVESKYGPPCP CPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLT V LHQDWLNGKEYKCKVSNKGLPIS SIEKTIKAKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TT PPVLDSDGGSFFLYSRITVDK SRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK	50
Variable light (vl) domain	QSVLTQPPSVSGTPGQRVTISCGSSNIGSNEVYWHQQLTGTAPKLLIYRNTQRP SGV PD RFSGSKSGT SASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLG	51
vlCDR1	SSNIGSNF	52
vlCDR2	RNT	53
vlCDR3	ATWDDSLSAWV	54
Full length light chain (CPA.9.057.H4(S241P))	QSVLTQPPSVSGTPGQRVTISCGSSNIGSNEVYWHQQLTGTAPKLLIYRNTQRP SGV PD RFSGSKSGT SASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET TTPSKQSNKYYAASSYSLTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	55

Figure 3E: CPA.9.059

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARGARYSYGQYPWGGQGLTVTVSS	56
vhCDR1	GFTVSSNY	57
vhCDR2	IYSGGST	58
vhCDR3	ARGARYSYGQYPY	59
Full length HC (IgG4(S241P); CPA.9.059.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARGARYSYGQYPWGGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTPPSSSLGTTKTCNVDPHKPSNTKVDKRVESKYGPCCPAPAEFLGGPSVFLPPKP KDTLMISRTPETVTCVVDVDSQEDPEVQFNWVYDGEVHNAKTPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLT VDKSRWQEGNVPFSCVMHEALHNHYTQKSLSLSPGK	60
Variable light (vl) domain	DIQLTQSPSFLASVGDRTITCRASHDISLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFSGSASGTEFTLTISLQPEDFATY YCLQLDSEPTWTfGQGTKEIKR	61
vlCDR1	HDISL	62
vlCDR2	AAS	63
vlCDR3	LQLDSEPTWT	64
Full length light chain (CPA.9.059.H4(S241P))	DIQLTQSPSFLASVGDRTITCRASHDISLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFSGSASGTEFTLTISLQPEDFATY YCLQLDSEPTWTfGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	65

Figure 3F: CPA.9.083

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRSLSCAASGETFSSAMHWVRAQPGKLEWVAVISYDGTPTVYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCCARDPLPLHYGMDVWGGGTTVTSS	66
vhCDR1	GFTFSSYA	67
vhCDR2	ISYDGTPTV	68
vhCDR3	ARDPLPLHYGMDV	69
Full length HC (IgG4(S241P); CPA.9.083.H4(S241P))	EVQLVETGGGLIQPGRSLRSLSCAASGETFSSAMHWVRAQPGKLEWVAVISYDGTPTVYADSVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCCARDPLPLHYGMDVWGGGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVIVTPSSSLGKTKYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSEQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCSMHEALHINHYTQKLSLSPGK	70
Variable light (vl) domain	QSALTQPRASGNPQGRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDGDRRLQLGGGTQLAVLG	71
vlCDR1	SSNMGRRP	72
vlCDR2	SQN	73
vlCDR3	AVWDGDRRLQ	74
Full length light chain (CPA.9.083.H4(S241P))	QSALTQPRASGNPQGRVTISCSGSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDGDRRLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANIKATLVCLISDFYPGAVTVAMKADSSPVKAGV ETTPSKGQSNKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	75

Figure 3G: CPA.9.086

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVISVAGEVKYYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYCCARDPLPLHYGMDVWGQGTTVTVSS	76
vhCDR1	GFTFSSYA	77
vhCDR2	ISYAGEVK	78
vhCDR3	ARDPLPLHYGMDV	79
Full length HC (IgG4(S241P); CPA.9.086.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVISVAGEVKYYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYCCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGKTKYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSYQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCSMHEALHINHYTKLSLSPGK	80
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLYSONQRPSPGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDIGRVLQIGGGTQLAVLG	81
vlCDR1	SSNMGRRP	82
vlCDR2	SQN	83
vlCDR3	AYWDDIGRVLQ	84
Full length light chain (CPA.9.086.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLYSONQRPSPGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAYWDDIGRVLQIGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	85

Figure 3H: CPA.9.089

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSAMHWVROAPGKGLEWVAVISYDRTPVYVADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYCARDPLPLHYGMDVWGQGTTVTVSS	86
vHCDR1	GFTSSYA	87
vHCDR2	ISYDRTPV	88
vHCDR3	ARDPLPLHYGMDV	89
Full length HC (IgG4(S241P); CPA.9.089.H4(S241P))	EVQLVETGGGLIQGRSLRLSCAASGFTSSAMHWVROAPGKGLEWVAVISYDRTPVYVADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGKTKYTCNVDRHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSEQEDPEVDQFNWYVDGVEVHNAKTKPREEQNFSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSMHEALHNHYTQKSLSLSPGK	90
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLG	91
vLCDR1	SSNMGRRP	92
vLCDR2	SQN	93
vLCDR3	ATWDDSLPRLN	94
Full length light chain (CPA.9.089.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLIYSONQRPSPGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	95

Figure 3i: CPA.9.093

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVROAPGKGLEWVAVISYEGDRKYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGQGTTVTVSS	96
vhCDR1	GFTSSYA	97
vhCDR2	ISYEGDRK	98
vhCDR3	ARDPLPLHYGMDV	99
Full length HC (IgG4(S241P); CPA.9.093.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVROAPGKGLEWVAVISYEGDRKYADSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYVCARDPLPLHYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVIVTPSSSLGKTKYTCNV/DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSEQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLT/LHQDWLNGKEYCKVSNK GLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGSFFLYSRL TVDKSRWQEGNVPFSCSMHEALHINHYTQKLSLSPGK	100
Variable light (vl) domain	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFEGGGTKLAVLG	101
vlCDR1	SSNMGRRP	102
vlCDR2	SQN	103
vlCDR3	ATWDDSTPHGV	104
Full length light chain (CPA.9.093.H4(S241P))	QSALTQPRASGNPGQRTVISCSSSNMGRRPVNWYQQIPGTAPKLLYSONQRPSPGVDPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFEGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVE TTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	105

Figure 3i: CPA.9.101

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLWVSVIYSGGSTYADSVKGRFTISRDNKNTLYLQ MNSLR AEDTAVYVCARGAPLEGQYPYWGQGTLVTVSS	106
vHCDR1	GFTVSSNY	107
vHCDR2	IYSGGST	108
vHCDR3	ARGAPLEGQYPY	109
Full length HC (IgG4(S241P); CPA.9.101.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLWVSVIYSGGSTYADSVKGRFTISRDNKNTLYLQ MNSLR AEDTAVYVCARGAPLEGQYPYWGQGTLVTVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTYKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEELGGPSVFLPPKPK DTLMISRTPETCVVVDVSDQEDPEVQFNWVVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKCKVSNKGL PSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGFFLYSRLTV DKSRWQEGNVFSCSVMHREALHNYTKQSLSLSPGK	110
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASHAIASLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFGSGSASGTFTLTISSLQPEDFAT YYCLQLDSFPTWTFGGQTKVEIKR	111
vLCDR1	HAIASL	112
vLCDR2	AAS	113
vLCDR3	LQLDSFPTWT	114
Full length light chain (CPA.9.101.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASHAIASLFSWYQQKPGKAPKLLIYAASLTQTGVPSPRFGSGSASGTFTLTISSLQPEDFAT YYCLQLDSFPTWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYREAKVQWVKVDNALQSGNSQESVTEQ DSKDSYSTSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	115

Figure 3K: CPA.9.103

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLR AEDTAVYVCARGARPNQPYWGGGTLVTVSS	116
vhCDR1	GFTVSSNY	117
vhCDR2	IYSGGST	118
vhCDR3	ARGARPNQPY	119
Full length HC (IgG4(S241P); CPA.9.103.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNKNTLYLQ MNSLR AEDTAVYVCARGARPNQPYWGGGTLVTVSSASTKPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGLHTFPAVLQSSGLYSLSSVTVTPSSSLGTYKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPK DTLMISRTPETCVAVDVDSQEDPEVQFNWVVDGVEVHNAKTPREEQFNSTYRVSVLTVLHQDWLNGKEYCKCKVSNKGL PSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGFFLYSRLTV DKSRWQEGNVFSCSVMIHEALHNHYTQKSLSLSPGK	120
Variable light (vl) domain	DIQLTQSPSFLSASVGDRTITCRASHGKSLFSWYQQKPGKAPKLLIYAASLTQTGVPSTRFSGSASGTEFTLTISLQPEDFATY YCLQLDSEPTWTFGGQGTKVEIKR	121
vlCDR1	HGKLSL	122
vlCDR2	AAS	123
vlCDR3	LQLDSFPTWT	124
Full length light chain (CPA.9.103.H4(S241P))	DIQLTQSPSFLSASVGDRTITCRASHGKSLFSWYQQKPGKAPKLLIYAASLTQTGVPSTRFSGSASGTEFTLTISLQPEDFATY YCLQLDSEPTWTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYLSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	125

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

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVMHWVKQPGQGLEWIGVDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTTVSS	126
vHCDR1	GYTFSSYV	127
vHCDR2	IDPYNDGA	128
vHCDR3	ARGGPYGWYFDV	129
Full length HC (lgG4(S241P))	EVQLQQSGPELVKPGSSVKMSCKASGYTSSVMHWVKQPGQGLEWIGVDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTTVSSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTGKTYTCNVDPHKPSNTKVDKRVESKYGPPCPAPFELGGPSVFLPPKP KDTLMISRTPETCVWVDVSDQEDPEVQFNWVWDGVEVHNATKPREEQFNSTYRWVSVLTVLHQDWLNGKEYCKVSNKG LPSSIEKTIKAKAQPREPQVYTLPPSQEEMITKNQSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT VDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	130
Variable light (vl) domain	DIQMTQSPASLSASVGETVITTCRASEHIYSLSWYQQKQKGKSPQLLVYNNAKTLAEGVPSRFSGSGGTQFSKINSLSQPEDFG TYCQHFGSPLTFGAGTTIELK	131
vLCDR1	EHYSY	132
vLCDR2	NAK	133
vLCDR3	QHFGSPLT	134
Full length light chain	DIQMTQSPASLSASVGETVITTCRASEHIYSLSWYQQKQKGKSPQLLVYNNAKTLAEGVPSRFSGSGGTQFSKINSLSQPEDFG TYCQHFGSPLTFGAGTTIELKRTVAAPSVFIFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	135

Figure 3M:
BM29 hlgG4 (BM29-H4) [US2016/0176963A1, Clone 22G2]

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLWIGYIYSGSTNYP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNDYFEGVDVWGQGT TVTVSS	136
vhCDR1	GGSVSSGIYY	137
vhCDR2	IYSGST	138
vhCDR3	ARDYYVSGNYYNDYFEGVDV	139
Full length HC (lgG4(S241P))	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLWIGYIYSGSTNYP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNDYFEGVDVWGQGT TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYT CNV DHKPSNTKVDKRVESKYGPPCPAPEFLGGPSV FLFPPK DTLMISRTPEVTCVAWVDV SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVASVLT V LHQDWLNGKEYK KVSNIKGLPSIEK TISKAIGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSE FLYSRLTVDKSRWQEGNIVFSCSV MHEALHNHYTQKSLSLSPGK	140
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDAS NRATGIPARFSGSGGTDFTLTIS LEPEDFAVY YCCQRSNWPPLE TFGPGTKVDIK	141
vlCDR1	QSVSSY	142
vlCDR2	DAS	143
vlCDR3	QQRSNWPPLE T	144
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDAS NRATGIPARFSGSGGTDFTLTIS LEPEDFAVY YCCQRSNWPPLE TFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVYCLLNNFYPREAKVQWVYD NALQSGNSQESVTE QDSK STYSLSSTLTLSKADYEKHKVACEVTHQGLSSPVTKSFNRGEC	145

Figure 3N: CHA.9.536.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTEYTLHWVRQAPGGLEWMGGINPNNGGTSYAQKFQGRVTMTTRDTSTSTVYMEISLRS EDTAVVYCARSGYDYSFAYWGQGLTVTVSS	146
vhCDR1	GYTFEYTLH	147
vhCDR2	GINPNNGGTS	148
vhCDR3	SGYDYSFAY	149
Full length HC (IgG4(S241P); CHA.9.536.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTEYTLHWVRQAPGGLEWMGGINPNNGGTSYAQKFQGRVTMTTRDTSTSTVYMEISLRS EDTAVVYCARSGYDYSFAYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQF NWWYDGGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMITKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFELYSLRTVDIKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	150
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWVWYQQKPGKAPKLLINSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYS TPETFGQGTKLEIK	151
vlCDR1	RASQDVKNAAV	152
vlCDR2	SPSYRYT	153
vlCDR3	QQHYSTPFT	154
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWVWYQQKPGKAPKLLINSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYS TPETFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYE KHKVVACEVTHQGLSSPVTKSFNRGEC	155

Figure 30: CHA.9.536.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGTFTETLHWVRQAPGQGLEWIGGINPNNGGTSYAQFKGRVTMTVDTS TVYMEISSLRSEDTAVYYCAGSGYYDYSAFYWGQGLTVYSS	156
vhCDR1	GYTFTETLH	157
vhCDR2	GINPNNGGTS	158
vhCDR3	SGYYDYSAFY	159
Full length HC (IgG4(S241P) CHA.9.536.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGTFTETLHWVRQAPGQGLEWIGGINPNNGGTSYAQFKGRVTMTVDTS TVYMEISSLRSEDTAVYYCAGSGYYDYSAFYWGQGLTVYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNV/DHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT/LHQDW/LNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNVPFSCSV/MHEALHNHYTQKSLSLSPGK	160
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGGKLEIK	161
vlCDR1	RASQDVKNAAV	162
vlCDR2	SPSYRYT	163
vlCDR3	QQHYSTPFT	164
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLINFFPREAKYQWVKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHQGLSSPVTKSFNRGEC	165

Figure 3P: CHA.9.536.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQFQGRVTMTVDTS TVYMEISSLRSEDTAVYYCAGSGYYDYSAFYWGQGLTVYSS	166
vhCDR1	GYTFEYTLH	167
vhCDR2	GINPNNGGTS	168
vhCDR3	SGYYDYSAFY	169
Full length HC (IgG4(S241P); CHA.9.536.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKTSGYTFEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQFQGRVTMTVDTS TVYMEISSLRSEDTAVYYCAGSGYYDYSAFYWGQGLTVYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNV/DHKPSNTKV/DKRVESKYGPPCPAPAEFLGSGPSVFLPPP KPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGSGFFLYSR LTVDKSRW/QEGNVFSCVMHEALHNHYTQKSLSLSPGK	170
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYVYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQTKLEIK	171
vlCDR1	RASQDVKNAAV	172
vlCDR2	SPSYRYT	173
vlCDR3	QQHYSTPFT	174
Full length light chain (CHA.9.536.4.H4(S241P))	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYVYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPETFQGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPRKAVQWVKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYKEHKVYACEVTHQGLSPVTKSFNRGEC	175

Figure 30: CHA.9.536.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKFFQGRATLTVDTS TAYMELSSLRSEDTAVYYCAGSGYYDYSAFWGQGTLTVSS	176
vhCDR1	GYTFTETLH	177
vhCDR2	GINPNNGGTS	178
vhCDR3	SGYYDYSAF	179
Full length HC (IgG4(S241P); CHA.9.536.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKFFQGRATLTVDTS TAYMELSSLRSEDTAVYYCAGSGYYDYSAFWGQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQYTCNVDRHPSNTKVDKRVESKYGPPCPAPPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK	180
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	181
vlCDR1	RASQDVKNAAV	182
vlCDR2	SPSYRYT	183
vlCDR3	QQHYSTPFT	184
Full length light chain (CHA.9.536.5.H4(S241P))	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSFIIPPSDEQLKSGTASVVCLLINFPYREAKYQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	185

Figure 3R: CHA.9.536.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFGGRATLTVDTS TAYMELSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSS	186
vhCDR1	GYTFEYTLH	187
vhCDR2	GINPNNGGTS	188
vhCDR3	SGYYDSFAY	189
Full length HC (IgG4(S241P); CHA.9.536.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGINPNNGGTSYAQKFGGRATLTVDTS TAYMELSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGKTTCNV/DHKPSNTKV/DKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNV/FSCSV/MHEALHNHYTQKSLSLSPGK	190
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSDTFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	191
vlCDR1	RASQDVKNAAV	192
vlCDR2	SPSYRYT	193
vlCDR3	QQHYSTPFT	194
Full length light chain (CHA.9.536.6.H4(S241P))	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSDTFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	195

Figure 35: CHA.9.536.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKFFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSS	196
vhCDR1	GYTFTETLH	197
vhCDR2	GINPNNGGTS	198
vhCDR3	SGYYDYSFAY	199
Full length HC (IgG4(S241P); CHA.9.536.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKFFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNVDHKPSNTKVDRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTPPVLDSDGSGFFLYSR LTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK	200
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGGTKLEIK	201
vlCDR1	RASQDVKNAAV	202
vlCDR2	SPSYRYT	203
vlCDR3	QQHYSTPFT	204
Full length light chain (CHA.9.536.7.H4(S241P))	DIQMTQSPSSLSASVGRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGGTKLEIKRTVAAPSFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	205

Figure 3T: CHA.9.536.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKQFGRATLTVDKSTS TAYMELSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSS	206
vhCDR1	GYTFTETLH	207
vhCDR2	GINPNNGGTS	208
vhCDR3	SGYYDYSFAY	209
Full length HC (IgG4(S241P); CHA.9.536.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTETLHWVRQAPGQGLEWIGINPNNGGTSYAQKQFGRATLTVDKSTS TAYMELSLRSEDTAVYYCAGSGYYDYSFAYWGQGLTVVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNV/DHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNVPFSCSVMEALHNHYTQKSLSLSPGK	210
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDTFT TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	211
vlCDR1	RASQDVKNAAV	212
vlCDR2	SPSYRYT	213
vlCDR3	QQHYSTPFT	214
Full length light chain (CHA.9.536.8.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAAVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGTDTFT TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	215

Figure 3U: CHA.9.560.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGPTTYAQFQGRVTMTTRDTSTSTVYMEELSLRSEDTAVYYCARGNGYVGMIDYWGQGTLTVSS	216
vhCDR1	GYTFITNYGMN	217
vhCDR2	WINTYTGPT	218
vhCDR3	NGYVGMIDY	219
Full length HC (IgG4(S241P); CHA.9.560.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYTGPTTYAQFQGRVTMTTRDTSTSTVYMEELSLRSEDTAVYYCARGNGYVGMIDYWGQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTKTYTCNVDHKPSNKKVDRKVESKYGPPCPAPFEFLGGPSVFLFPPKPKDTLMISRTPEVTCVWVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	220
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTCSRSTGAVTTSNHNWVFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFQGGTKLTVL	221
vlCDR1	RSSTGAVTTSNHN	222
vlCDR2	GTNGRG	223
vlCDR3	ALWFSNHWV	224
Full length light chain (CHA.9.560.1.H4(S241P))	QAWVTQEPSTVSPGGTVTLTCSRSTGAVTTSNHNWVFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFQGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	225

Figure 3V: CHA.9.560.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYIGEPTYAQFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGNGYYVGMIDYWGQGTLTVYSS	226
vhCDR1	GYTFITNYGMN	227
vhCDR2	WINTYIGEPT	228
vhCDR3	GNGYYVGMIDY	229
Full length HC (IgG4(S241P); CHA.9.560.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYIGEPTYAQFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRNGNGYYVGMIDYWGQGTLTVYSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTV/S WNSGALTSGVHTFPAIVLQSSGLYSLSSVWTPVPSSSLGKTKYTCNVDHKPSNKTVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	230
Variable light (vl) domain	QAWTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNHNANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	231
vlCDR1	GSSTGAVTTSNHNAN	232
vlCDR2	GTNGRGS	233
vlCDR3	ALWFSNHWV	234
Full length light chain (CHA.9.560.3.H4(S241P))	QAWTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNHNANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSVLSLTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	235

Figure 3W: CHA.9.560.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYIGEPTYAQKFGGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNNGYVGMIDYWGQGTLTVYSS	236
vhCDR1	GYTFITNYGMN	237
vhCDR2	WINTYIGEPT	238
vhCDR3	GNNGYVGMIDY	239
Full length HC (IgG4(S241P); CHA.9.560.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTFITNYGMNWRQAPGGLEWMGWINTYIGEPTYAQKFGGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNNGYVGMIDYWGQGTLTVYSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLGTKYTCNVDHKPSNTKVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWDVVSQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	240
Variable light (vl) domain	QAWTQEPSTVSPGGTVTLTCGSSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVVPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	241
vlCDR1	GSSTGAVTTSNHNAN	242
vlCDR2	GTNGRGS	243
vlCDR3	ALWFSNHWV	244
Full length light chain (CHA.9.560.4.H4(S241P))	QAWTQEPSTVSPGGTVTLTCGSSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVVPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSVLSLTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	245

Figure 3X: CHA.9.560.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYFTFTNNGMNWVRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDTS TAYLEISSURSEDNAVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW	246
vhCDR1	GYFTNNGMIN	247
vhCDR2	WINTYGEPT	248
vhCDR3	GNNGYVGMDDY	249
Full length HC (IgG4(S241P); CHA.9.560.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYFTFTNNGMNWVRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDTS TAYLEISSURSEDNAVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGKTTCNV/DHKPSNTKV/DKRVESKYGPPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTYRVVSVLTVLHQDWWLNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHREALHNYTQKSLSPGK QAWTQEPSTVSPGGTVTLTQGSSTGAVTTSNHANWVQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	250
Variable light (vl) domain	QAWTQEPSTVSPGGTVTLTQGSSTGAVTTSNHANWVQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	251
vlCDR1	GSSTGAVTTSNHAN	252
vlCDR2	GTNGRG	253
vlCDR3	ALWFSNHWV	254
Full length light chain (CHA.9.560.5.H4(S241P))	QAWTQEPSTVSPGGTVTLTQGSSTGAVTTSNHANWVQKPGQAFRGLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPSKQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	255

Figure 3Y: CHA.9.560.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYFTFTNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDTS TAYLEISSLRSEDNAVYCSRGNNGYVGMMDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW	256
vhCDR1	GYFTFTNYGMN	257
vhCDR2	WINTYGEPT	258
vhCDR3	GNNGYVGMMDY	259
Full length HC (IgG4(S241P); CHA.9.560.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYFTFTNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDTS TAYLEISSLRSEDNAVYCSRGNNGYVGMMDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGKTTCNV/DHKPSNTKV/DKRVESKYGPCCPAPAEFLGSPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNVFSCSVMEALHNHYTQKSLSLSPGK	260
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRLGRTNGRSGVPAFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	261
vlCDR1	GSSTGAVTTSNHNAN	262
vlCDR2	GTNGRGS	263
vlCDR3	ALWFSNHWV	264
Full length light chain (CHA.9.560.6.H4(S241P))	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRLGRTNGRSGVPAFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	265

Figure 3Z: CHA.9.560.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYFTFTNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDASTS TAYLEISSLRSEDNAVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSW	266
vhCDR1	GYFTFTNYGMN	267
vhCDR2	WINTYGEPT	268
vhCDR3	GNNGYVGMDDY	269
Full length HC (IgG4(S241P); CHA.9.560.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYFTFTNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDSTST TAYLEISSLRSEDNAVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTITYTCNV/DHKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK	270
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	271
vlCDR1	GSSTGAVTTSNHNAN	272
vlCDR2	GTNGRGS	273
vlCDR3	ALWFSNHWV	274
Full length light chain (CHA.9.560.7.H4(S241P))	QAWVTQEPSTVSPGGTVTLTGSSSTGAVTTSNHNANWVQKPGQAFRLIRGTNGRGSWTPARFSGSLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNHNKYAAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	275

Figure 3AA: CHA.9.560.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNVMNWVRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDASTS TAYLEISSLRSEDTAVVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSW	276
vhCDR1	GYTFTNYGMN	277
vhCDR2	WINTYGEPT	278
vhCDR3	GNNGYVGMDDY	279
Full length HC (IgG4(S241P); CHA.9.560.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNVMNWVRQAPGGLEWMGWINTYGEPTYAQKFQGRFTTLDASTS TAYLEISSLRSEDTAVVYCSRGNNGYVGMDDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTITYTCNV/DHKPSNTKV/DKRVESKYGPPCPAPAEFLGPGPSVFLFPP KPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRW/QEGNV/FSCSV/MHEALHNHYTQKSLSLSPGK	280
Variable light (vl) domain	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPAFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	281
vlCDR1	GSSTGAVTTSNHNAN	282
vlCDR2	GTNGRGS	283
vlCDR3	ALWFSNHWV	284
Full length light chain (CHA.9.560.8.H4(S241P))	QAWVTQEPSTVSPGGTVTLTQGSSTGAVTTSNHNANWVQKPGQAFRGLIRGTNGRSGVPAFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLPFSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTPPSKQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	285

Figure 3B: CHA.9.546.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARWLLSYAMDYWGQGTLVTVSS	286
vhCDR1	GFTSSYIMS	287
vhCDR2	TISGGGTNTY	288
vhCDR3	WLLSYAMDY	289
Full length HC (IgG4(S241P); CHA.9.546.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARWLLSYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGKTITCNVDHKPSN TKVDKRVESKYGPPCPAPPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWDVVSQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLY SRLTVDKSRWQEGNVFSCVMHEALHNYHTQKSLSPGK	290
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTIS LPEDFATYYCQGGQSYPTFGGQTKLEIK	291
vlCDR1	RASQININVWLT	292
vlCDR2	KASNLHT	293
vlCDR3	QGGQSYPT	294
Full length light chain (CHA.9.546.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTIS LPEDFATYYCQGGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	295

Figure 3CC: CHA.9.547.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u>	296
vhCDR1	GFTSSYIMS	297
vhCDR2	TISGGGTNTY	298
vhCDR3	WLLSYAMDY	299
Full length HC (IgG4(S241P); CHA.9.547.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTKTYTCNVVDHKPSN TKVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYCKKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	300
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTIS LPEDFATYYCQQGQSPYTFGGGTKLEIK	301
vlCDR1	RASQININVWLT	302
vlCDR2	KASNLHT	303
vlCDR3	QQGQSPYPT	304
Full length light chain (CHA.9.547.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTIS LPEDFATYYCQQGQSPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	305

Figure 3DD: CHA.9.547.2

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAKWLLSYAMDYWGQGTLVTVSS	306
vhCDR1	GFTSSYIMS	307
vhCDR2	TISGGGTNTY	308
vhCDR3	WLLSYAMDY	309
Full length HC (IgG4(S241P); CHA.9.547.2.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAKWLLSYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGKTKYTCNVDHKPSN TKVDKRVESKYGPPCPPAPEFLGGPSVFLFPPKPDITLMISRTPETCVWVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	310
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSPYTFGGGTKLEIK	311
vlCDR1	RASQININWLT	312
vlCDR2	KASNLHT	313
vlCDR3	QQGQSPYPT	314
Full length light chain (CHA.9.547.2.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLINNYPREAKYQWVKVDNALQSGNSQESVTEQDSKDSYISLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	315

Figure 3EE: CHA.9.547.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVVSS</u>	316
vhCDR1	GFTSSYIMS	317
vhCDR2	TISGGGTNTY	318
vhCDR3	WLLSYAMDY	319
Full length HC (lgG4(S241P); CHA.9.547.3.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	320
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFLTIS LPEDFATYYCQQGQSYPTFGGQTKLEIK	321
vlCDR1	RASQININWLT	322
vlCDR2	KASNLHT	323
vlCDR3	QQGQSYPT	324
Full length light chain (CHA.9.547.3.H4(S241P))	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFLTIS LPEDFATYYCQQGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	325

Figure 3FF: CHA.9.547.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	326
vhCDR1	GFTSSYIMS	327
vhCDR2	TISGGGTNTY	328
vhCDR3	WLLSYAMDY	329
Full length HC (lgG4(S241P); CHA.9.547.4.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTKTYTCNVVDHKPSN TKVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWDVSEQDEPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCVMHEALHNYTKQSLSLSPGK	330
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGSGSGTDFLTIS LPEDFATYYCQQGQSYPTFGGQTKLEIK	331
vlCDR1	RASQININWLT	332
vlCDR2	KASNLHT	333
vlCDR3	QQGQSYPT	334
Full length light chain (CHA.9.547.4.H4(S241P))	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIKASNLHTGVPSRFSGSGSGTDFLTIS LPEDFATYYCQQGQSYPTFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSYISLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	335

Figure 3GG: CHA.9.547.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNLSRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	336
vhCDR1	GFTSSYIMS	337
vhCDR2	TISGGGTNTY	338
vhCDR3	WLLSYAMDY	339
Full length HC (IgG4(S241P); CHA.9.547.6.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNLSRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTKTYTCNVVDHKPSN TKVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	340
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISS LPEDFATYYCQQGQSPYTFGGGTGLEIK	341
vlCDR1	RASQININVWLT	342
vlCDR2	KASKSH	343
vlCDR3	QQGQSPYPT	344
Full length light chain (CHA.9.547.6.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININVWL TWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISS LPEDFATYYCQQGQSPYTFGGGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	345

Figure 3HH: CHA.9.547.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u>	346
vhCDR1	GFTSSYIMS	347
vhCDR2	TISGGGTNTY	348
vhCDR3	WLLSYAMDY	349
Full length HC (IgG4(S241P) for CHA.9.547.7.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTTKTYTCNVDRKPSNTKVDKRVESKYGPPCPAPFELFGGPSVFLFPPKPDITLMISRTPEVTCVWDVVSQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYTKQSLSLSPGK	350
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININVWLITWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYC <u>QQGQSYPTFGQGTKLEIK</u>	351
vlCDR1	RASQININVWLT	352
vlCDR2	KASKSHT	353
vlCDR3	QQGQSYPT	354
Full length light chain for CHA.9.547.7.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRASQININVWLITWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYC <u>QQGQSYPTFGQGTKLEIK</u> RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKYQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355

Figure 3II: CHA.9.547.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	356
vhCDR1	GFTSSYIMS	357
vhCDR2	TISGGGTNTY	358
vhCDR3	WLLSYAMDY	359
Full length HC (lgG4(S241P); CHA.9.547.8.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSPSSSLGTKTYTCNVVDHKPSN TKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTV LHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	360
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIKASKSHITGVP SRFSGSGSGTDFLTLS LPEDFATYYCQQGQSYPTFGQGTKLEIK	361
vlCDR1	RASQININWLT	362
vlCDR2	KASKSH	363
vlCDR3	QQGQSYPT	364
Full length light chain (CHA.9.547.8.H4(S241P))	DIQMTQSPSSLSASVGDRITTCRASQININWLTWYQQKPGKAPKLLIKASKSHITGVP SRFSGSGSGTDFLTLS LPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365

Figure 3J: CHA.9.547.9

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	366
vhCDR1	GFTSSYIMS	367
vhCDR2	TISGGGTNTY	368
vhCDR3	WLLSYAMDY	369
Full length HC (lgG4(S241P); CHA.9.547.9.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVDQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYHTQKSLSPGK	370
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWVLTWYQQKPKAPKLLIKASKSHITGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYC <u>QQGQSYPTFGG</u> GTKLEIK	371
vlCDR1	RASQININWVLT	372
vlCDR2	KASKSH	373
vlCDR3	QQGQSYPT	374
Full length light chain (CHA.9.547.9.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWVLTWYQQKPKAPKLLIKASKSHITGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSYPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKYQWVKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375

Figure 3KK: CHA.9.541.1

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLLTVSS	376
vhCDR1	GYTITNYGMN	377
vhCDR2	WINTYGEPT	378
vhCDR3	GNGNPLGMDY	379
Full length HC (IgG4(S241P); CHA.9.541.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFQGRVTMTTRDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGKTKYTCNVDHKPSNKTVDKRVESKYGPPCPPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVWDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNHYTQKSLSLSPGK	380
Variable light (vl) domain	EVLVTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDFTLTISSL EPEDFAVYYCFQGGSGYPLIFGQGTKEIK	381
vlCDR1	GNGNPLGMDY	382
vlCDR2	DTSKLAS	383
vlCDR3	FQGGSYPLT	384
Full length light chain (CHA.9.541.1.H4(S241P))	EVLVTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDFTLTISSL EPEDFAVYYCFQGGSGYPLIFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKVQWVKVDNALQSGNSQ ESVTEQDSKDSITYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	385

Figure 3L: CHA.9.541.3

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMELSLRSEDTAVYYCARGNGNPLGMDYWGQGTLLTVSS	386
vhCDR1	GYTITNYGMN	387
vhCDR2	WINTYGEPT	388
vhCDR3	GNGNPLGMDY	389
Full length HC (IgG4(S241P); CHA.9.541.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFGGRFTMTLDTSTS TVYMELSLRSEDTAVYYCARGNGNPLGMDYWGQGTLLTVSSASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSLTKTYTCNVDRKPSNTKVDKRVESKYGPPCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVWVDVSEQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVPFSCVMHEALHNHYTQKSLSLSPGK	390
Variable light (vl) domain	EVLVTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGQGTKLEIK	391
vlCDR1	GNGNPLGMDY	392
vlCDR2	DTSKLAS	393
vlCDR3	FQGGSGYPLT	394
Full length light chain (CHA.9.541.3.H4(S241P))	EVLVTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISL EPEDFAVYYCFQGGSGYPLTFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKVQWVKVDNALQSGNSQ ESVTEQDSKDSITYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	395

Figure 3NN: CHA.9.541.4

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPT ³⁹⁶ Y ³⁹⁶ AQK ³⁹⁶ FQGRFTMT ³⁹⁶ LDTSTS ³⁹⁶ TVYME ³⁹⁶ LSLRSEDTAVYYCARGNGNPLGMDYWGQGT ³⁹⁶ LVTVSS ³⁹⁶	396
v _H CDR1	GYTITNYGMN	397
v _H CDR2	WINTYGEPT	398
v _H CDR3	GNGNPLGMDY	399
Full length HC (IgG4(S241P); CHA.9.541.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPT ⁴⁰⁰ Y ⁴⁰⁰ AQK ⁴⁰⁰ FQGRFTMT ⁴⁰⁰ LDTSTS ⁴⁰⁰ TVYME ⁴⁰⁰ LSLRSEDTAVYYCARGNGNPLGMDYWGQGT ⁴⁰⁰ LVTVSS ⁴⁰⁰ ASTKGPSV ⁴⁰⁰ EPLAC ⁴⁰⁰ SRSTSE ⁴⁰⁰ TAALGCLVKDY ⁴⁰⁰ PERVTVS ⁴⁰⁰ WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPS ⁴⁰⁰ SLG ⁴⁰⁰ TKY ⁴⁰⁰ TCNVD ⁴⁰⁰ HKPSN ⁴⁰⁰ TKVD ⁴⁰⁰ KRVESKY ⁴⁰⁰ GPPCP ⁴⁰⁰ PAPEFLGGPSVFLF ⁴⁰⁰ PPKPKD ⁴⁰⁰ TLMI ⁴⁰⁰ SRTP ⁴⁰⁰ ETCV ⁴⁰⁰ WVDV ⁴⁰⁰ SQEDPE ⁴⁰⁰ VQFNWYVDG ⁴⁰⁰ VEV ⁴⁰⁰ HNAK ⁴⁰⁰ TPREE ⁴⁰⁰ QFNSTY ⁴⁰⁰ RVSV ⁴⁰⁰ LV ⁴⁰⁰ LHQDW ⁴⁰⁰ LNGKEY ⁴⁰⁰ KCKV ⁴⁰⁰ SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK ⁴⁰⁰ TTTPPVLDSDGSFELY ⁴⁰⁰ SRLTV ⁴⁰⁰ DKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK ⁴⁰⁰	400
Variable light (vl) domain	EVLVLTQSPATLSLSPGERATLSCGNGLGMDY ⁴⁰¹ WYQQKPGQAPRLWIYDTSKLASGVPARFSGSGGT ⁴⁰¹ DYTLTISSL ⁴⁰¹ EPEDFAVYYCFQGGSGYPLIFGQGT ⁴⁰¹ KLEIK ⁴⁰¹	401
v _L CDR1	GNGNPLGMDY	402
v _L CDR2	DTSKLAS	403
v _L CDR3	FQGGSGYPLT	404
Full length light chain (CHA.9.541.4.H4(S241P))	EVLVLTQSPATLSLSPGERATLSCGNGLGMDY ⁴⁰⁵ WYQQKPGQAPRLWIYDTSKLASGVPARFSGSGGT ⁴⁰⁵ DYTLTISSL ⁴⁰⁵ EPEDFAVYYCFQGGSGYPLIFGQGT ⁴⁰⁵ KLEIK ⁴⁰⁵ RTVAAPSVFIFPPSDEQLKSGTASV ⁴⁰⁵ CLNNI ⁴⁰⁵ FPY ⁴⁰⁵ PREAKVQW ⁴⁰⁵ KKVDNALQSGNSQ ⁴⁰⁵ ESVTEQDSKDS ⁴⁰⁵ TSYSLSTLTLSKADY ⁴⁰⁵ EKHKVYACEV ⁴⁰⁵ THQGLSPVTKSENRGEC ⁴⁰⁵	405

Figure 300 CHA.9.541.5

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFQGRFTMTLDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	406
vhCDR1	GYTITNYGMN	407
vhCDR2	WINTYGEPT	408
vhCDR3	GNGNPLGMDY	409
Full length HC (lgG4(S241P); CHA.9.541.5.H4(S241P))	QVQLVQSGAEVKKPGASVKVCKASGYTITNYGMNWRQAPGGGLEWMGWINTYGEPTYAQKFQGRFTMTLDTSTS TVYMEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTYTCNVDHKPSNKTVDKRVESKYGPPCPAPEFLGGPSVFLF PPKPDITLMISRTPETVTCVWDVSEQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELY SRLTVDKSRWQEGNVFSCVMHEALHNYHTQKSLSPGK	410
Variable light (vl) domain	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGGSGYPLIFGGQTKLEIK	411
vlCDR1	GNGNPLGMDY	412
vlCDR2	DTSKLAS	413
vlCDR3	FQGGYPLT	414
Full length light chain (CHA.9.541.5.H4(S241P))	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGGSGYPLIFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415

Figure 3PP: CHA.9.541.6

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTITLDTSTSTVYLEISSLRSEDAVYYCARGNGNPLGMDYWGQGTIVTVSS	416
vhCDR1	GYTITNYGMN	417
vhCDR2	WINTYGEPT	418
vhCDR3	GNGNPLGMDY	419
Full length HC (IgG4(S241P); CHA.9.541.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTITLDTSTSTVYLEISSLRSEDAVYYCARGNGNPLGMDYWGQGTIVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGKTTCNV/DHKPSNTKV/DKRVESKYGPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPPVLDSDGSGFFLYSR LTVDKSRW/QEGNV/FSCVM/HEALHNHYTQKSLSLSPGK	420
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISSEPEDFAVYYCFQGGSGYPLIFGGQGTKLEIK	421
vlCDR1	GNGNPLGMDY	422
vlCDR2	DTSKLAS	423
vlCDR3	FQGGYPLT	424
Full length light chain (CHA.9.541.6.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNPLGMDYWYQQKPGQAPRLIYDTSKLASGIPARFSGSGGTDTYLTISSEPEDFAVYYCFQGGSGYPLIFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425

Figure 300: CHA.9.541.7

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTITLDTSTSTVYLEISSLRSEDAVYYCARGNGNPLGMDYWGQGLTVTVSS	426
vhCDR1	GYTITNYGMN	427
vhCDR2	WINTYGEPT	428
vhCDR3	GNGNPLGMDY	429
Full length HC (IgG4(S241P) CHA.9.541.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGGLEWMGWINTYGEPTYAQKFQGRFTITLDTSTSTVYLEISSLRSEDAVYYCARGNGNPLGMDYWGQGLTVTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNV/DHKPSNTKV/DKRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKAQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPPVLDSDGSEFFLYSR LTVDKSRW/QEGNIVFSCSV/MHEALHNHYTQKSLSLSPGK	430
Variable light (vl) domain	EVLVTQSPATLSLSPGERATLSCGNGLGMDYVYQQKPGQAPRLWIYDTSKSLASGVPARFSGSGGTDTYLTISLLEPEDFAVYYCFQGGSGYPLIFGGQTKLEIK	431
vlCDR1	GNGNPLGMDY	432
vlCDR2	DTSKSLAS	433
vlCDR3	FQGGSGYPLT	434
Full length light chain (CHA.9.541.7.H4(S241P))	EVLVTQSPATLSLSPGERATLSCGNGLGMDYVYQQKPGQAPRLWIYDTSKSLASGVPARFSGSGGTDTYLTISLLEPEDFAVYYCFQGGSGYPLIFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPPVTKSENRGEC	435

Figure 3RR: CHA.9.541.8

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGGLEWMGWINTYTGPTYAQKFQGRFTITLDTSTS TVYLEISSLRSED AVYYCARGNGNPLGMDYWGQGLTVTVSS	436
vhCDR1	GYTITNYGMN	437
vhCDR2	WINTYTGPT	438
vhCDR3	GNGNPLGMDY	439
Full length HC (IgG4(S241P); CHA.9.541.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISKASGYTITNYGMNWRQAPGGLEWMGWINTYTGPTYAQKFQGRFTITLDTSTS TVYLEISSLRSED AVYYCARGNGNPLGMDYWGQGLTVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVATVPSSSLGTQTYTCNV/DHKPSNTKV/DKRVESKYGPPCPAPPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSVQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT/LHQDW/LNGKEYCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPPVLDSDGSEFFLYSR LTVDKSRW/QEGNVPFSCVMHEALHNHYTQKSLSLSPGK	440
Variable light (vl) domain	EVLVLTQSPATLSLSPGERVTMSCGNGNPLGMDY WYQQKPGQAPRLWYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGGSGYPLIFGGQGTKLEIK	441
vlCDR1	GNGNPLGMDY	442
vlCDR2	DTSKLAS	443
vlCDR3	FQGGSYPLT	444
Full length light chain (CHA.9.541.8.H4(S241P))	EVLVLTQSPATLSLSPGERVTMSCGNGNPLGMDY WYQQKPGQAPRLWYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGGSGYPLIFGGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCCLINNFYPREAKVQWVKVDNALQSGNSQ ESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	445

Figure 35S: CHA.9.547.10

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u>	446
vhCDR1	GFTSSYIMS	447
vhCDR2	TISGGGTNTY	448
vhCDR3	WLLSYAMDY	449
Full length HC for CHA.9.547.10.H4 (S241P)	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTKTYTCNVVDHKPSN TKVDKRVESKYGPCCPPAPFELGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLSPGK	450
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWVLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LPEDFATYYCQQGQSPYTFGGGTKLEIK	451
vlCDR1	RASQININWLS	452
vlCDR2	KASKSHT	453
vlCDR3	QQGQSPYPT	454
Full length light chain For CHA.9.547.10.H4 (S241P)	DIQMTQSPSSLSASVGDRVTITCRASQININWVLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTIS S LPEDFATYYCQQGQSPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLINNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455

Figure 3TT: CHA.9.547.11

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u>	456
vhCDR1	GFTSSYIMS	457
vhCDR2	TISGGGTNTY	458
vhCDR3	WLLSYAMDY	459
Full length HC for CHA.9.547.11.H4 (S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVSTISGGTNTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGTLVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYS WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGKTITTCNVVDHKPSN TKVDKRVESKYGPCCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTV LHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCVMHEALHNYHTQKSLSPGK	460
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWVLSWYQQKPKAPKLLIYKASKSHITGVP SRFSGSGSGTDFTLTIS LPEDFATYYCQGGQSPYTFGGGTKLEIK	461
vlCDR1	RASQININWVLS	462
vlCDR2	KASKSH	463
vlCDR3	QGGQSPYTF	464
Full length light chain For CHA.9.547.11.H4 (S241P))	DIQMTQSPSSLSASVGDRITITCRASQININWVLSWYQQKPKAPKLLIYKASKSHITGVP SRFSGSGSGTDFTLTIS LPEDFATYYCQGGQSPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKYQWVKVDNALQSGNS QESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	465

Figure 3UU: CHA.9.547.12

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u>	466
vhCDR1	GFTSSYIMS	467
vhCDR2	TISGGGTNTY	468
vhCDR3	WLLSYAMDY	469
Full length HC For CHA.9.547.12.H4 (S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAIVLQSSGLYSLSSVTVPSSSLGTKTYTCNVDRKPSNTKVDKRVESKYGPCCPAPFELFGGPSVFLFPPKPKDITLMISRTPEVTCVWDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYTKQKLSLSPGK	470
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQININWVLSWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSPYTFGGGTKLEIK	471
vlCDR1	RASQININWLS	472
vlCDR2	KASKSHT	473
vlCDR3	QQGQSPYPT	474
Full length light chain for CHA.9.547.12.H4 (S241P))	DIQMTQSPSSLSASVGDRVTITCRASQININWVLSWYQQKPGKAPKLLIYKASKSHTGVPSTRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWVKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	475

Figure 3VV: CHA.9.547.13

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u>	476
vhCDR1	GFTSSYIMS	477
vhCDR2	TISGGGTNTY	478
vhCDR3	WLLSYAMDY	479
Full length HC for CHA.9.547.13.H4 (S241P)	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYIMSVVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK <u>WLLSYAMDYWGQGLTVTVSS</u> ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDPKPSNKKVDKRVESKYGPPCPAPFELFGGPSVFLFPPKPDITLMISRTPEVTCVWDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVPFSCVMHEALHNYTKQKLSLSPGK	480
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQININWVLSWYQQKPKAPKLLIYKASKSHTIGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSYPTFGQGTKLEIK	481
vlCDR1	RASQININWVLS	482
vlCDR2	KASKSHT	483
vlCDR3	QQGQSYPT	484
Full length light chain for CHA.9.547.13.H4 (S241P)	DIQMTQSPSSLSASVGDRITITCRASQININWVLSWYQQKPKAPKLLIYKASKSHTIGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQSYPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKYQWVKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	485

Figure 3WW: CHA.9.543

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASMKISKASGYSTGYTMNWRQSHGKNLEWLGIIIPYNGGTSYNQNFKGKATLTVDTSSTAY MELLSITSDSAVYYCARGVRFALDYWGQGTSVSVSS	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	DVWMTQTPLSLPVSFQDQVSISSQSLANSYGNLYLSWYLNKPGSQPLLIEISNRFSGVDRFSGSGGTDFTLNISTIKP EDLGMYYCLOGTHQHPWTFGGGTKLEIK	490
vlCDR1	RSSQSLANSYGNLYLS	491
vlCDR2	EISNRF	492
vlCDR3	LOGTHQHPWT	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)

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQDSGPGLVKPSSVKMSCKASGYTSSV MHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSLTSED SAVYVCARGGPGWYFDVW GAGTTVTSS	494
vhCDR1	GYTFSSV	495
vhCDR2	IDPYNDGA	496
vhCDR3	ARGGPGWYFDV	497
Full length HC	EVQLQDSGPGLVKPSSVKMSCKASGYTSSV MHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSLTSED SAVYVCARGGPGWYFDVW GAGTTVTSSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTPFAVLOSDLYTLSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPKPKD VLTITLTPKVT CVVWDISKDDPEVQFSW FVDDVEVHTAQTPREEQFNSTERSVSELPI MHQDWLNGKEFKCRVNSAAFPAP IEKTSKTKGRPKAPQVYTI PPKEQMAKD KVSLTCM ITDFF EDITVEWQWNGOPAENYKNTQPI MDTDG SYFYSKLNV QKSNWEAGNTTCSVLHEGLHNHHTEKSLSHSPGK	498
Variable light (vl) domain	DIQMTQSPASLSASVGETVITTCRASEHIYS LSWYQCQKQKQKSPQLLVYN NAKTLAEGVPSRFSGSGSGTQFSLKINS LQPEDFG TYQCQHHFGSPLTFGAGTTLELK	499
vlCDR1	EHYSY	500
vlCDR2	NAK	501
vlCDR3	QHHFGSPLT	502
Full length light chain	DIQMTQSPASLSASVGETVITTCRASEHIYS LSWYQCQKQKQKSPQLLVYN NAKTLAEGVPSRFSGSGSGTQFSLKINS LQPEDFG TYQCQHHFGSPLTFGAGTTLELKRA DAAPT VSIFPPPSSEQLTSGGASV CF LNNIPYK DI NVKWKIDGSE RQNGV INSWTDQ DSKSDTYSMSSTLT LTKDEYERHNSY TCEAT HK TSTSPV KSF NRNEC	503

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSETLSLTCTVSGSVSSGIYYWSWIRQPPGKGLWIGIYYSGSTNYP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYFFGV DVWVGQGTITVSS	504
vhCDR1	GGSVSSGIW	505
vhCDR2	IYVSGST	506
vhCDR3	ARDYYVSGNYYNVDYFFGV DV	507
Full length HC	QVHLQESGPGLVKPSETLSLTCTVSGSVSSGIYYWSWIRQPPGKGLWIGIYYSGSTNYP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYFFGV DVWVGQGTITVSSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEP VTVWNSSGSLSGVHTFPAVLQSDLYTLSSVTVPSSTWVPSETVTCNVAHPASSTKVDKIVPRDCGCKPCICTVPEVSSVFI PPKPKDVLTLTPKVTQCVVDISKDDPEVQFSWVFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS AAFPAPIEKTISKGRPKAPQVYTI PPRKEQMAKDVKSLT CMITDFFPEDITVEWQWNGQPAENYKNTQPI MDTDG SVFVY SKLNVQKSNWEAGNTFTCSVLHEGLHNHHT EKSL SPGK	508
Variable light (vl) domain	EVLITQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPARFSGSGSDFTLTIS SL EPDFAVY YCCQQRSNWPP PLFT FGPGTKVDIK	509
vlCDR1	QSVSSY	510
vlCDR2	DAS	511
vlCDR3	QQRSNWPP PLFT	512
Full length light chain	EVLITQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPARFSGSGSDFTLTIS SL EPDFAVY YCCQQRSNWPP PLFT FGPGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVCF LNNFY PKDINVKWKIDGSE RQ NGVLNSWTD QDSKDS TVSN MSSTLTITKDEYERHNSYTC EATH TKTSTSPIVKSFNRNEC	513

Figure 3AAA

From US20170281764 (JN Biosciences) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:10 from US2017281764)	DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMIWVRQAPKGLWVAFISSGSS SIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCARMRLDYYAMDYWGQ GTSVTVSS	514
vHCDR1 (SEQ ID NO:11 from US2017281764)	NTFGMH	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)	DVQITQSPSYLAASPGETITINCRASKSISKYLAWYQEKPKTNKLLIYSGSTLQSGIPS RFSGSGSGTDFTLTISLSEPEDEAMYYCQQHNEYPWTFGGGTKLEIK	518
vLCDR1 (SEQ ID NO:15 from US2017281764)	RASKSISKYLA	519
vLCDR2 (SEQ ID NO:16 from US2017281764)	SGSTLQS	520
vLCDR3 (SEQ ID NO:17 from US2017281764)	QQHNEYPWTF	521

Figure 3BBB

From US20170281764 (JN Biosciences) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:18 from US2017281764) vHCDR1	EVQLQSSGPELVKPGASVKISKCKTSGYTFTEYTMHWVKQSHGKNLEWIGGINPNNNG GTSYNQKFKGRATLTVDKSSSTAYMELRSLTSDDSA VYYCARPCGWYNYAMDYWG	522
(SEQ ID NO:19 from US2017281764) vHCDR2	QGTSVTVSS EYTMH	523
(SEQ ID NO:20 from US2017281764) vHCDR3	GINPNNGGTSYNQKFKG	524
(SEQ ID NO:21 from US2017281764) Light chain	PGWYNYAMDY	525
(SEQ ID NO:22 from US2017281764) vLCDR1	DIVMTQSHKFMSTSVGDRVNITCKASQGVSTAVAWYQQKPGQSPKLLIYSASYRYT GVPRFTGSGSGTDFITISSVQAEDLAVYHCQQHYITPWTGGGTKLEIK	526
(SEQ ID NO:23 from US2017281764) vLCDR2	KASQGVSTAVA	527
(SEQ ID NO:24 from US2017281764) vLCDR3	SASYRYT	528
(SEQ ID NO:25 from US2017281764)	QQHYITPWT	529

Figure 3CCC

From US20170281764 (JN Biosciences) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:26 from US2017281764)	EVQLVESGGGLVKPGGSLKLSCAASGFAFSDYDMSWVRQTPEKRLIEWVAYISDGGY NTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAIYYCARQJILLRYYFDYWGQGT TLTVSS	530
vhCDR1 (SEQ ID NO:27 from US2017281764)	DYDMS	531
vhCDR2 (SEQ ID NO:28 from US2017281764)	YISDGGYNTYYPDTVKG	532
vhCDR3 (SEQ ID NO:29 from US2017281764)	QILLRYYFDY	533
Light chain (SEQ ID NO:30 from US2017281764)	DIVMSQSPSSLAVSVGEKVTMTCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYW ASTRESGVPDFRFTGSGGTDFTLTISSVKAEDLAVYYCQQYHSYPWTFGGGKLEIK	534
vCDR1 (SEQ ID NO:31 from US2017281764)	KSSQSLLYSSNQKNYLA	535
vCDR2 (SEQ ID NO:32 from US2017281764)	WASTRES	536
vCDR3 (SEQ ID NO:33 from US2017281764)	QQYHSYPWT	537

Figure 3DD'D

From US20170281764 (JN Biosciences)			
What	sequence		SEQ ID NO:
Heavy chain			538
(SEQ ID NO:35 from US2017281764)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMIWVRQAPGKGLEWVAFISSGSSSIYVADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRLDYYAMDYWGQGTMVTVSS		
Light chain			539
(SEQ ID NO:37 from US2017281764)	DIQMTQSPSSLSASVGDRVTITCRASKSISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPWITGGGTKVEIK		
From US20170281764 (JN Biosciences)			
What	sequence		SEQ ID NO:
Heavy chain			540
(SEQ ID NO:34 from US2017281764)	MDSRLNLVFLVLLKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMIHWV RQAPGKGLEWVAFISSGSSSIYVADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARMRLDYYAMDYWGQGTMVTVSS		
Light chain			541
(SEQ ID NO:36 from US2017281764)	MRFQVQVLGLLLLWISGAQCIDIQMIQSPSSLASVGDRTVTITCRASKSISKYLAWYQ QKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYP WTFGGGTKVEIK		

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)	EVQLVESGGGLTQPGKSLKLSCEASGFTFSFTMIWVRQSPGKGLEWVAFIRSGSIVF YADAVRGRFTISRDNAKNLLFLQMNDLKSEDTAMY YCARRPLGHINTFDSWGQGTLVT VSS	542
vhCDR1 (SEQ ID NO:4 from WO2015009856)	GFTFSFTMH	543
vhCDR2 (SEQ ID NO:5 from WO2015009856)	FIRSGSIVFYADAVRG	544
vhCDR3 (SEQ ID NO:6 from WO2015009856)	RPLGHNTFDS	545
Light chain (SEQ ID NO:13 from WO2015009856)	DIVMTQSPSSLA VSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASI RFTGVDPDRFTGSGSGTDYTLTITSVQAEDMGQYFCQQGINNPLTFGDGFKLEIKR	546
vCDR1 (SEQ ID NO:1 from WO2015009856)	KSSQSLYYSGVKENLLA	547
vCDR2 (SEQ ID NO:2 from WO2015009856)	ASIRFT	548
vCDR3 (SEQ ID NO:3 from WO2015009856)	QQGINNPLT	549

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)	550
	EVQLQQSGPELVKPGTSMKISKASGYSTGHLMNWKQSHGKNLEWIGLIIPYNGGTS YNQKFKGKATLTVDKSSSTAYMELLSLTSDDSAVYFCRGLRGFYAMDYWGQGTSTVT VSS
vhCDR1 (SEQ ID NO:10 from WO2015009856)	551
	GYSTGHLMN
vhCDR2 (SEQ ID NO:11 from WO2015009856)	552
	LIIPYNGGTSYNQKFKG
vhCDR3 (SEQ ID NO:12 from WO2015009856)	553
	GLRGFYAMDY
Light chain (SEQ ID NO:14 from WO2015009856)	554
	DVVLTTQPLSLSVSGDQVSISCRSSQSLVNSYGNTELSWYHLHKPGQSPQLLIFGISNRFS GVPDFRFGSGSGTDFTLKISTIKPEDLGMYCYCLQGTHQPPPTFGPGTKLEVK
vCDR1 (SEQ ID NO:7 from WO2015009856)	555
	RSSQSLVNSYGNTELS
vCDR2 (SEQ ID NO:8 from WO2015009856)	556
	GISNRFS
vCDR3 (SEQ ID NO:9 from WO2015009856)	557
	LQGTHQPPPT

Figure 3GGG

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

Sequences and germlines (GL) of IGHV ABPs									
Ab	GL	CDR- H1 ¹ (SEQ ID NOs 538- 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 578- 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	VH 4- 39	GSISSS YYWG (SEQ ID NO 48)	SIYSG ATFYN PSLKS (SEQ ID NO 36)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VK3- II	RASQS V8SYL A(SEQ ID NO 70)	DASNRA T(SEQ ID NO 67)	QQHFN PT(SEQ ID NO 63)	EVLTSQSPATLSLSPGERATLSKRAQSQSVSSYLAWYQOK PGQAPRLIYDASNRATGIPARFSGSGGTDFTLTSSLEP EDFAVYYCQQHFNLPITGGGKVEIK (SEQ ID NO 25)
MAE2 -IgG4	VH 4- 39	GSISSS YYWG (SEQ ID NO 49)	SIYSG STFYN PSLKS (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VK3- II	RASQS V8SYL A(SEQ ID NO 70)	DASNRA T(SEQ ID NO 67)	QQHFN PT(SEQ ID NO 63)	EVLTSQSPATLSLSPGERATLSKRAQSQSVSSYLAWYQOK PGQAPRLIYDASNRATGIPARFSGSGGTDFTLTSSLEP EDFAVYYCQQHFNLPITGGGKVEIK (SEQ ID NO 25)
MAB3 -IgG4	VH 4- 39	GSISST ITVWG (SEQ ID NO 30)	SIYSG STFNP SLKS (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VK3- II	RANQS V8SYL A(SEQ ID NO 70)	DASNRA T(SEQ ID NO 67)	QQHFN PT(SEQ ID NO 63)	EVLTSQSPATLSLSPGERATLSKRAQSQSVSSYLAWYQOK PGQAPRLIYDASNRATGIPARFSGSGGTDFTLTSSLEP EDFAVYYCQQHFNLPITGGGKVEIK (SEQ ID NO 25)
MAP4 -IgG4	VH 4- 39	GSISST YWG(SEQ ID NO 30)	SIYSG STFNP SLKS (SEQ ID NO 37)	ARDAN YVGS WAFDP (SEQ ID NO 30)	VK3- II	RASQS V8SYL A(SEQ ID NO 70)	DASNRA T(SEQ ID NO 67)	QQHFN PT(SEQ ID NO 63)	EVLTSQSPATLSLSPGERATLSKRAQSQSVSSYLAWYQOK PGQAPRLIYDASNRATGIPARFSGSGGTDFTLTSSLEP EDFAVYYCQQHFNLPITGGGKVEIK (SEQ ID NO 25)
MARS -IgG4	VH 4- 39	GSISST YWG(SEQ ID NO 30)	SIYSG STFYN PSLKG (SEQ ID NO 38)	ARDAN YVGS WAFDP (SEQ ID NO 29)	VK3- II	RASQS V8SYL A(SEQ ID NO 70)	DASNRA T(SEQ ID NO 67)	QQHFN PT(SEQ ID NO 63)	EVLTSQSPATLSLSPGERATLSKRAQSQSVSSYLAWYQOK PGQAPRLIYDASNRATGIPARFSGSGGTDFTLTSSLEP EDFAVYYCQQHFNLPITGGGKVEIK (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 IMGT numbering system.⁴ According to the Kabat and Chothia numbering systems.⁵ According to the Kabat and Chothia numbering systems.⁶ According to the Kabat, Chothia, and IMGT numbering systems.

Figure 3HHH

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

		Sequences and germlines (GL) of IGHV ABPs									
Ab	MAb	CDR-III ⁷		CDR-II ⁸		CDR-III ⁹		CDR-IV		CDR-III	
		SEQ ID NO 598-602	SEQ ID NO 603-607	SEQ ID NO 608-612	SEQ ID NO 613-617	SEQ ID NO 618-622	SEQ ID NO 623-627	SEQ ID NO 628-632	SEQ ID NO 633-637	SEQ ID NO 638-642	SEQ ID NO 643-647
Ab	MAb6	VH	4	GSIKGS	SIYSGGT	ARDGV	LTLNKR	VH Protein (SEQ ID NO 613-617)	VL Protein (SEQ ID NO 633-637)	GASSRA	QOHTV
Ab	MAb7	VH	4	GSIKGS	SIYSGGT	ARDGV	LTLNKR	VH Protein (SEQ ID NO 613-617)	VL Protein (SEQ ID NO 633-637)	GASSRA	QOHTV
Ab	MAb8	VH	4	GSIKGS	SIYSGGT	ARDGV	LTLNKR	VH Protein (SEQ ID NO 613-617)	VL Protein (SEQ ID NO 633-637)	GASSRA	QOHTV
Ab	MAb9	VH	4	GSIKGS	SIYSGGT	ARDGV	LTLNKR	VH Protein (SEQ ID NO 613-617)	VL Protein (SEQ ID NO 633-637)	GASSRA	QOHTV
Ab	MAb1	VH	4	GSIKGS	SIYSGGT	ARDGV	LTLNKR	VH Protein (SEQ ID NO 613-617)	VL Protein (SEQ ID NO 633-637)	GASSRA	QOHTV

⁷ Includes CDR-III 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 Kabat and Chothia numbering systems.

¹⁰ According to the Kabat and Chothia numbering systems.

¹¹ 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 ABPs									
Ab	GL	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)
MAB1 1-IgG4	4- 31	GHSELY 4- YMG(SKQ TND)54)	STVYSG STVYNP 81ES (SEQ ID NO 40)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGPGLVKPSQSLSTCTAS GGSESGLYVVGWIRQPPKGGHEW GSIYSGSTVYVNPISLKRVTISVDIS KNQPSLKLSSVTADTAVYVCARD GVLALNKRSPDWGGGTMTVYSS (SEQ ID NO 14)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QGHIVR PPLT (SEQ ID NO 64)	EVLTQSGTILSELSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGGASSRATGPIPRFSGSGGTFDFTLSRIE PEDEAVYVCQQHIVRPPLTFGGGKVEIK (SEQ ID NO 26)
MAB1 2-IgG4	4- 31	GHSELY 4- YMG(SKQ DND)54)	STVYSG STVYNP 81ES (SEQ ID NO 40)	ARDGVL ALNKR FDI (SEQ ID NO 32)	QVQLQESGPGLVKPSQSLSTCTAS GGSESGLYVVGWIRQPPKGGHEW GSIYSGSTVYVNPISLKRVTISVDIS KNQPSLKLSSVTADTAVYVCARD GVLALNKRSPDWGGGTMTVYSS (SEQ ID NO 15)	RASQS VSSSY LA (SEQ ID NO 71)	GASSRA T (SEQ ID NO 68)	QGHIVR PPLT (SEQ ID NO 64)	EVLTQSGTILSELSPGERATILSCRASQSVSSSYLAWYQQ KPGQAPRLIYGGASSRATGPIPRFSGSGGTFDFTLSRIE PEDEAVYVCQQHIVRPPLTFGGGKVEIK (SEQ ID NO 26)
MAB1 3-IgG4	1- 46	YTHGNY 4- YMH (SEQ ID NO 38)	INPSLG LTSYAQ KPGQ (SEQ ID NO 42)	ARGGRT TWIGAF DI (SEQ ID NO 35)	QVQLVQSGAEVKKGASVKVCKA SGYTRGYTHGNYVQAPGQGLEW MGINPSLGLTSTYAKPQGRVTMTIR DTSTSTVYVMEISLRSIEDTAVYVCA RGGRTTWIGAFDIWGQGTMTVYSS (SEQ ID NO 16)	RASQS VSSSY A (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QGYVV WPPLT (SEQ ID NO 66)	EVMTQSPATISVSIKTERATILSCRASQSVSSSYLAWYQQ PGQAPRLIYGGASTRATGPIPRFSGSGGTFDFTLSRIE EDFAVYVCQQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 4-IgG4	1- 46	YTHGNY 4- YMH (SEQ ID NO 39)	INPSLG LTSYAQ KPGQ (SEQ ID NO 42)	ARGGRT TWIGAF DI (SEQ ID NO 35)	QVQLVQSGAEVKKGASVKVCKA SGYTRGYTHGNYVQAPGQGLEW MGINPSLGLTSTYAKPQGRVTMTIR DTSTSTVYVMEISLRSIEDTAVYVCA RGGRTTWIGAFDIWGQGTMTVYSS (SEQ ID NO 17)	RASQS VSSSY A (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QGYVV WPPLT (SEQ ID NO 66)	EVMTQSPATISVSIKTERATILSCRASQSVSSSYLAWYQQ PGQAPRLIYGGASTRATGPIPRFSGSGGTFDFTLSRIE EDFAVYVCQQYVYVWVWPLTFGGGKVEIK (SEQ ID NO 27)
MAB1 5-IgG4	1- 46	YTHGNY 4- YMH (SEQ ID NO 40)	INPSLG LTSYAQ KPGQ (SEQ ID NO 42)	ARGGRT TWIGAF DI (SEQ ID NO 35)	QVQLVQSGAEVKKGASVKVCKA SGYTRGYTHGNYVQAPGQGLEW MGINPSLGLTSTYAKPQGRVTMTIR DTSTSTVYVMEISLRSIEDTAVYVCA RGGRTTWIGAFDIWGQGTMTVYSS (SEQ ID NO 18)	RASQS VSSSY A (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QGYVV WPPLT (SEQ ID NO 66)	EVMTQSPATISVSIKTERATILSCRASQSVSSSYLAWYQQ PGQAPRLIYGGASTRATGPIPRFSGSGGTFDFTLSRIE EDFAVYVCQQYVYVWVWPLTFGGGKVEIK (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 3KKK

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:7 from WO2016028656)	EVQLQESGPGLVKPSQSLSLTCSVTGSSIASDYWGWIWKFPGNKMEWMGFITYSGSTSY NPSLKSRISITRDTSKNQFFLQLHLSVTITDDTATYSCARMPSTITLASLSTWEGYFDWGP GTMVTVSS	726
vhCDR1 (SEQ ID NO:1 from WO2016028656)	SDYWG	727
vhCDR2 (SEQ ID NO:2 from WO2016028656)	FTYSGSTSYNPSLK	728
vhCDR3 (SEQ ID NO:3 from WO2016028656)	MPSFITLASLSTWEGYFDF	729
Light chain (SEQ ID NO:8 from WO2016028656)	DIQMTQSPSLLSASVGDRTVLNCKASQSIHKNLAWYQQKLGEAPKFLIYYANSLQTGIPS RPSGSGGTDFTLTISGLQPEDVATYFCQQYYSGWTFGGGTVKVELK	730
vCDR1 (SEQ ID NO:4 from WO2016028656)	KASQSIHKNL	731
vCDR2 (SEQ ID NO:5 from WO2016028656)	YANSLQT	732
vCDR3 (SEQ ID NO:6 from WO2016028656)	QQYYSGWT	733

Figure 3LLL

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

Figure 3MMM

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

Figure 3000

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:13 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLSLHSTAAADTAVYYCARMPSFITLASLSTWEGYFDFWGGQG TMVTVSS	750
vhCDR1 (from WO2016028656)	SDYWG	751
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	752
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	753
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:14 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGGSISSDYWGWIQQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLSLHSTAAADTAVYYCARMPSFITLASLSTWEGYFDFWGGQG MVTVSS	754
vhCDR1 (from WO2016028656)	SDYWG	755
vhCDR2 (from WO2016028656)	GFITYSGSTSYNPSLKS	756
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	757

Figure 3PPP

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

Figure 3QQQ

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:17 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSSSDYWGWIQQPGKGLEWIGFITYSGTSYN PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARMPSFI ⁷⁶⁶ TLASLSTWEGYFD ⁷⁶⁶ FWGQ	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 TYSGSTSYNPSLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCARMPSFI TLASLSTWEGYFD ⁷⁷⁰ FWGQGMVTVSS	770
vhCDR1 (from WO2016028656)	SDYWG	771
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	772
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	773

Figure 3RRR

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:19 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSISSDYWGWIQQPGKGLEWIGFI TYSGSTSYNPSLKSRTITISRDTSKNQFSLKLSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMTVTVSS	774
vhCDR1 (from WO2016028656)	SDYWG	775
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	776
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	777
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:20 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGYSISSDYWGWIQQPGKGLEW'MGFI TYSGSTSYNPSLKSRTITISRDTSKNQFSLKLSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMTVTVSS	778
vhCDR1 (from WO2016028656)	SDYWG	779
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	780
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	781

Figure 3SSS

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

Figure 3TTT

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

Figure 3UUU

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

Figure 3VVV

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

Figure 3WWW

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:43 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLSSTVTAADTAVYYCARMPSFTLASLSTWEGYFDWGGQ TMVTVSS	814
vhCDR1 (from WO2016028656)	SDYWG	815
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	816
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	817
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:44 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCTVSGSSIASDYWGWIQPPGKMEWIGFITYSGSTSYN PSLKSRTVTISVDTSKNQSLKLSSTVTAADTAVYYCARMPSFTLASLSTWEGYFDWGGQ GTMVTVSS	818
vhCDR1 (from WO2016028656)	SDYWG	819
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	820
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	821

Figure 3XXX

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:45 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCSVTGSSIASDYWGWIQQPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQSLKLSVTAADTAVYYCARMPSFTLASLSTWEGYDFWGQG TMVTVSS	822
vhCDR1 (from WO2016028656)	SDYWG	823
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	824
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	825
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	Sequence	
Heavy chain (SEQ ID NO:46 from WO2016028656)	EVQLQQSGAGLLKPSSETLSLTCSVTGSSIASDYWGWIQQPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQISLKLSVTAADTAVYYCARMPSFTLASLSTWEGYDFWGQ GTMVTVSS	826
vhCDR1 (from WO2016028656)	SDYWG	827
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	828
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYDF	829

Figure 3YY

From WO2016028656 (Table 4, reproduced herein) What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:47 from WO2016028656)	EVQLQESGPGLVKPPGTLSLICSVTGSSIASDYWGWVRQPPGKGLEWIGFITYSGSTSYN PSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFJTLASLSTWEGYFDYWGQ GTMVTVSS	830
vhCDR1 (from WO2016028656)	SDYWG	831
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	832
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	833

Figure 3ZZZ

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGSSISDYWGWRQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLIHSVTAADTAVYYCARMPSFITLASLSTWEGYFDfWGGQT MVTVSS	834
vhCDR1 (SEQ ID NO: from WO2016028656)	SDYWG	835
vhCDR2 (SEQ ID NO: from WO2016028656)	FITYSGSTSYNP SLKS	836
vhCDR3 (SEQ ID NO: from WO2016028656)	MPSFITLASLSTWEGYFDf	837

Figure 3AAAA			
From WO2016028656 (Table 4, reproduced herein)			
What	sequence	SEQ ID NO:	
Heavy chain (SEQ ID NO:24 from WO2016028656)	EVQLQESGPGLVKPSSETLSLTCAVSGSSISDYWGWIQQPPGKGLEWWMGFITYSGSTSYN PSLKSRIITISRDTSKNQFSLKLSLHVSITAADTAVYYCARMPSFITLASLSTWEGYFDFWGGQ TMVTVSS	838	
vhCDR1 (from WO2016028656)	SDYWG	839	
vhCDR2 (WO2016028656)	FITYSGSTSYNPSLKS	840	
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDF	841	
From WO2016028656 (Table 4, reproduced herein)			
What	sequence	SEQ ID NO:	
Light chain (SEQ ID NO:25 from WO2016028656)	DIQMTQSPSSLASVGDRTVTITCKASQSIHKNLAWYQQKPKGKAPKLLIYYANSLQTGVP SRFSGSGGTDFTLTISSI.QPEDFATYYCQQYYSGWTFGGGTKVEIK	842	
vCDR1 (from WO2016028656)	KASQSIHKNLAW	843	
vCDR2 (from WO2016028656)	YANSLQT	844	
vCDR3 (from WO2016028656)	QQYYSGWT	845	

Figure 3BBB

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:26 from WO2016028656)	DIQMTQSPSSLASVGDRTVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGKVEIK	846
vCDR1 (from WO2016028656)	KASQSIHKNLAW	847
vCDR2 (from WO2016028656)	YANSLQT	848
vCDR3 (from WO2016028656)	QQYYSGWT	849
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:27 from WO2016028656)	DIQMTQSPSSLASVGDRTVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGKVEIK	850
vCDR1 (from WO2016028656)	KASQSIHKNLAW	851
vCDR2 (from WO2016028656)	YANSLQT	852
vCDR3 (from WO2016028656)	QQYYSGWT	853

Figure 3CCCC

From WO2016028656 (Table 4, reproduced herein)			
What	sequence		SEQ ID NO:
Light chain (SEQ ID NO:28 from WO2016028656)	DIQMTQSPSSLASVGDRTVTITCKASQSIHKNLAWYQQKPGKVPKLLIYYANSLQITGVP SRFSGSGGTDFLTITSLQPEDVATYYCQQYYSGWTFGGGTKVEIK		854
vCDR1 (from WO2016028656)	KASQSIHKNLAW		855
vCDR2 (from WO2016028656)	YANSLQT		856
vCDR3 (from WO2016028656)	QQYYSGWT		857
From WO2016028656 (Table 4, reproduced herein)			
What	sequence		SEQ ID NO:
Light chain (SEQ ID NO:29 from WO2016028656)	DIQMTQSPSSLASVGDRTVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQITGVPS RFSGSGGTDFLTITSLQPEDVATYYCQQYYSGWTFGGGTKVEIK		858
vCDR1 (from WO2016028656)	KASQSIHKNLAW		859
vCDR2 (from WO2016028656)	YANSLQT		860
vCDR3 (from WO2016028656)	QQYYSGWT		861

From WO2016028656 (Table 4, reproduced herein)

From WO2016028656 (Table 4, reproduced herein)

What sequence	SEQ ID NO.
Light chain (SEQ ID NO:48 from WO2016028656)	866
DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTTGVP SRFSGSGGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	
vICDR1 (from WO2016028656)	867
KASQSIHKNLAW	
vICDR2 (WO2016028656)	868
YANSLQT	
vICDR3 (WO2016028656)	869
QQYYSGWT	

Figure 3EEEE

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:49 from WO2016028656)	DIQMTQSPSSLASVGDRAVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQYYSGWTFGGGTKVEIK	870
vCDR1 (from WO2016028656)	KASQSIHKNLAW	871
vCDR2 (WO2016028656)	YANSLQT	872
vCDR3 (WO2016028656)	QQYYSGWT	873
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:50 from WO2016028656)	DIQMTQSPSSLASVGDRAVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS SRFSGSGSGTDFTLTISLQPEDFATYYCQQYYSGWTFGGGTKVEIK	874
vCDR1 (from WO2016028656)	KASQSIHKNLAW	875
vCDR2 (WO2016028656)	YANSLQT	876
vCDR3 (WO2016028656)	QQYYSGWT	877

From WO2016028656 (Table 4, reproduced herein)

sequence

DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS

DIQMTQSPSSLSASVGDRVTITCKAQSIIKLNLAWYQQKPKGKAPKFLIYYANSLQTGVPS 878
RFRSGSGSGTDFTLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK

KASQSIHKNLAW

879

YANSLQT

880

OOYYSCWT

188

sequence

DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQKPKAPKLLIYYANSLQTGIPS

DIQMTQSPSSLSASVGRDVITTCASQSIHKNLAWYQQKPKGAPKLLIYYANSLQGTIPSS
REFSGSGSGTDFTLTISSLQPEDIAITYYCOQYYSGWTFGGGIKVEIK

KASQSIHKNLAW

883

YANSLQT

884

QOYYSGWT

885

Figure 3GGGG

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWRQFPGNKLEWVMGYISNSGSAS YNPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCATLIYYDYGGAMNFWGQGTSVT VSS	886
vhCDR1 (from WO2016028656)	GYSITSDYAWN	887
vhCDR2 (WO2016028656)	YISNSGSA SYNPSLKS	888
vhCDR3 (WO2016028656)	LIYYDYGGAMNF	889

Figure 3HHHH

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO: 62 from WO2016028656)	DIVMTQSHKFMSTSVGDDRVSTCKASQGVSTTVAWYQQKPGQSPKLLIN'SASYRYTGVDPDRFTG SCSGTDFTFITSSVQSEDLAVYYCQHYYS'IPWTFGGG'KLEIK	890
vCDR1 (from WO2016028656)	KASQGVSTTV A	891
vCDR2 (WO2016028656)	SASYRYT	892
vCDR3 (WO2016028656)	QHYYSTPWWT	893
vCDR2 variant (WO2016028656)	YASNLT	894
vCDR2 variant (WO2016028656)	YASSLT	895
vCDR2 variant (WO2016028656)	YASTLT	896
vCDR2 variant (WO2016028656)	YATLT	897
vCDR2 variant (WO2016028656)	YASYLT	898
vCDR2 variant (WO2016028656)	YANQLT	899
vCDR2 variant (WO2016028656)	YAGSLT	900
vCDR2 variant (WO2016028656)	YASQLT	901
vCDR2 variant (WO2016028656)	YADSLT	902

Figure 3IIII

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO: 62 from WO2016028656)	DIVMTQSHKFMSTSVGDDRVSITCKASQGVSTTVAWYQQKPGQSPKLLIN'SASYRYTGVDPDRFTG SCSGTDFTFIISVQSEDLAVYYCQHYVSTPWTFGGGKLEIK	903
vCDR1 (from WO2016028656)	KASQGVSTTV A	904
vCDR2 (WO2016028656)	SASYRYT	905
vCDR3 (WO2016028656)	QHYYSTPWWT	906
vCDR3 variant (WO2016028656)	QQYYSGFT	907
vCDR3 variant (WO2016028656)	QQYYSGYT	908
vCDR3 variant (WO2016028656)	QQYYSGIT	909
vCDR3 variant (WO2016028656)	QQYYSGVT	910
vCDR3 variant (WO2016028656)	QQYYSGLT	911

Figure 3]]]]

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSTCTVTGYSITSDYAWNWRQFPGNKLEWMGYISNSGSAS YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYCATLIYYDYGGAMNFWGQGTSVT VSS	912
vHCDR1 (from WO2016028656)	GYSITSDYAWN	913
vHCDR2 (WO2016028656)	YISNSGSASYNPSLKS	914
vHCDR3 (WO2016028656)	LIYYDYGGAMNF	915
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	916
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	917
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	918
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	919
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	920

Figure 3KKKK

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:94 from WO2016028656)	EVQLQSGPELVKPGSSVKMSCKASGYTFSYVYMHVVKQKPGQGLEWIGYIDPYNDGAKYNEK FKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTIVYSS	921
vHCDR1 (from WO2016028656)	SYVMH	922
vHCDR2 (WO2016028656)	YIDPYNDGAKYNEKFK	923
vHCDR3 (WO2016028656)	GPYGWYFDV	924
vHCDR2 variant (WO2016028656)	YIDPYNtGAKYNEKFG	925
vHCDR2 variant (WO2016028656)	YIDPYNIGAKYNEKFG	926
vHCDR2 variant (WO2016028656)	YIDPYNKGAKYNEKFG	927
vHCDR2 variant (WO2016028656)	YIDPYNtGAKYNEKFG	928
vHCDR2 variant (WO2016028656)	YIDPYNsGAKYNEKFG	929
vHCDR2 variant (WO2016028656)	YIDPYNvGAKYNEKFG	930
vHCDR2 variant (WO2016028656)	YIDPYNwGAKYNEKFG	931
vHCDR2 variant (WO2016028656)	YIDPYNDrAKYNEKFG	932
vHCDR2 variant (WO2016028656)	YIDPYNDnAKYNEKFG	933
vHCDR2 variant (WO2016028656)	YIDPYNDqAKYNEKFG	934
vHCDR2 variant (WO2016028656)	YIDPYNdeAKYNEKFG	935
vHCDR2 variant (WO2016028656)	YIDPYNDiAKYNEKFG	936
vHCDR2 variant (WO2016028656)	YIDPYNDkAKYNEKFG	937
vHCDR2 variant (WO2016028656)	YIDPYNDsAKYNEKFG	938
vHCDR2 variant (WO2016028656)	YIDPYNDyAKYNEKFG	939
vHCDR2 variant (WO2016028656)	YIDPYNDvAKYNEKFG	940

Figure 3LLLL

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:94 from WO2016028656)	DIQMTQSPASLSASVGETVITTRASEHIYSYLSWYQQKQKSPQLLVYNAKTLAEGVPSRFSGS	941
vLCDR1	SGTQFSLKINSIQPEDFGTYTCQHIFGSLITFGAGTILELK	
(from WO2016028656)	RASEHIYSYLS	942
vLCDR2	NAKTLAE	943
(WO2016028656)		
vLCDR3	QHIFGSPLT	944
(WO2016028656)		
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)	NTKTLAE	955
vLCDR2 variant (WO2016028656)	NVKTLAE	956

Figure 3MIMMM

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

Figure 3NNNN

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:126 from WO2016028656)	EVQLVQSCAEVKKPGASVKVSCKASCYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTRDTSTSTVYMELSSLRSEDTAVYYCARGGPGYGWYFDVWGQGTTITVSS	965
vhCDR1 (from WO2016028656)	SYVMH	966
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAAQ	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)	EVQLVQSCAEVKKPGASVKVSCKASCYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSTSTVYMELSSLRSEDTAVYYCARGGPGYGWYFDVWGQGTTITVSS	969
vhCDR1 (from WO2016028656)	SYVMH	970
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAAQKFQ	971
vhCDR3 (from WO2016028656)	GGPYGWYFDV	972

Figure 30000

From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:128 from WO2016028656)	EVQLVQSCAEVKKPGSSVKVSCKASGYTFSSVMHWVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVTLTSDKSTSTAYMELSSLRSEDTAVYYCARGGPGYGWYFDVWGQGTTITVSS	973
vhCDR1 (from WO2016028656)	SYVMH	974
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	975
vhCDR3 (from WO2016028656)	GGPYGWYFDV	976
From WO2016028656 (Table 4, reproduced herein)		SEQ ID NO:
What	sequence	
Heavy chain (SEQ ID NO:129 from WO2016028656)	EVQLVQSCAEVKKPGASVKVSCKASGYTFSSVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSTSTAYMELSLRSDDTVYYCARGGPGYGWYFDVWGQGTTITVSS	977
vhCDR1 (from WO2016028656)	SYVMH	978
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	979
vhCDR3 (from WO2016028656)	GGPYGWYFDV	980

Figure 3PPPP

From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:130 from WO2016028656)	DIQMTQSPSSLSASVGDRAVITTCRASEHIYSYLSWYQQKPKAPKLLIYNNAKTLAEQVPSRFSG SCSGTDFTLTISSLQPEDFATYYCQHHFGSPLTFGGQTRLEIK	981
vCDR1 (from WO2016028656)	RASEHIYSYLS	982
vCDR2 (from WO2016028656)	NAKTLAE	983
vCDR3 (from WO2016028656)	QHHFGSPLT	984
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:131 from WO2016028656)	DIQMTQSPSSLSASVGDRAVITTCRASEHIYSYLSWYQQKPKAPKLLIYNNAKTLAE GVPSRFSGSGGTQFTLTISSLQPEDFATYYCQHHFGSPLTFGGQTRLEIK	985
vCDR1 (from WO2016028656)	RASEHIYSYLS	986
vCDR2 (from WO2016028656)	NAKTLAE	987
vCDR3 (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)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAECVPSRFSG SCSGTDFTLTISLQPEDVATYYCQHHFGSPLTFGGQTRLEIK	989
vCDR1 (from WO2016028656)	RASEHIYSYLS	990
vCDR2 (from WO2016028656)	NAKTLAE	991
vCDR3 (from WO2016028656)	QHHFGSPLT	992
From WO2016028656 (Table 4, reproduced herein) What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:133 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAECVPSRFSG SCSGTQFTLTISLQPEDVATYYCQHHFGSPLTFGGQTRLEIK	993
vCDR1 (from WO2016028656)	RASEHIYSYLS	994
vCDR2 (from WO2016028656)	NAKTLAE	995
vCDR3 (from WO2016028656)	QHHFGSPLT	996

Figure 3RRRR

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:129 from WO2016028656)	EVQLVQSGAEVKKPGASVKVCKASGYTSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVTLTSDKKSISTAYMELSLRSDDTIVVYVCARGGPYGWYFDVWVGQGITTVTVSS	997
vhCDR2 variant (from WO2016028656)	YIDPYNDGAKYAQKFQG	998
vhCDR2 variant (from WO2016028656)	YIDPYNDGAKYSQKFQG	999

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:129 from WO2016028656)	EVQLVQSGAEVKKPGASVKVCKASGYTSSVVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQ KFQGRVTLTSDKKSISTAYMELSLRSDDTIVVYVCARGGPYGWYFDVWVGQGITTVTVSS	1000
vhCDR3 variant (from WO2016028656)	GGPYGAYFDV	1001
vhCDR3 variant (from WO2016028656)	GGPYGDYFDV	1002
vhCDR3 variant (from WO2016028656)	GGPYGEYFDV	1003
vhCDR3 variant (from WO2016028656)	GGPYGFYFDV	1004
vhCDR3 variant (from WO2016028656)	GGPYGGYFDV	1005
vhCDR3 variant (from WO2016028656)	GGPYGNYFDV	1006
vhCDR3 variant (from WO2016028656)	GGPYGKYFDV	1007
vhCDR3 variant (from WO2016028656)	GGPYGNYFDV	1008
vhCDR3 variant (from WO2016028656)	GGPYGQYFDV	1009
vhCDR3 variant (from WO2016028656)	GGPYGRYFDV	1010
vhCDR3 variant (from WO2016028656)	GGPYGSYFDV	1011
vhCDR3 variant (from WO2016028656)	GGPYGTIYFDV	1012
vhCDR3 variant (from WO2016028656)	GGPYGVYFDV	1013
vhCDR3 variant (from WO2016028656)	GGPYGYIYFDV	1014

Figure 3SSSS

From WO2016028656 (Table 4, reproduced herein)			SEQ ID NO:
What	sequence		
VH 18G10	QVQLMESGPGLVQPSQTLSTCTVSGFPLTSYTVHWVRQPPGKGLFWGAIWSSGSTDYNSA		1015
(SEQ ID NO:136 from WO2016028656)	LKSRLLNINRDSKSKQVFLKMNSLQTEDTAIFYCTKSCWAFFDYWGQGVMTVSS		
VL 18G10	DIQMTQSPSLLASVCDRVTLNCLASQNIYKSLAWYQLKLGAPKLLIYNANSLQAGIPSRFSG		1016
(SEQ ID NO:137 from WO2016028656)	SCSGTDFALTISGLQPEDVATYFCQQYSGGYTFGAGTKLELK		
From WO2016028656 (Table 4, reproduced herein)			SEQ ID NO:
What	sequence		
VH 11A11	EVQLVESGGDLVQPGRSILKISCVASGFTESDYMAWVRLAPQKGLEWVASISYEGSKRTHYGD		1017
(SEQ ID NO:138 from WO2016028656)	SVRGRFIISRDNPKNILYLQMNSLGSEDTATYFCARHTGTLDWLWYWGQGTLLVIVSS		
VL 11A11	NIVMAQSPKSMISAGDRVMTMNCCKASQNVDDNNIAWYQQKPGQSPKLLIFYASNRYSGVPDR		1018
(SEQ ID NO:139 from WO2016028656)	FTGGGYCIDFTLTIKSVQAEDAAFYQCRIYNFPTFCGKLEIK		

Figure 4A

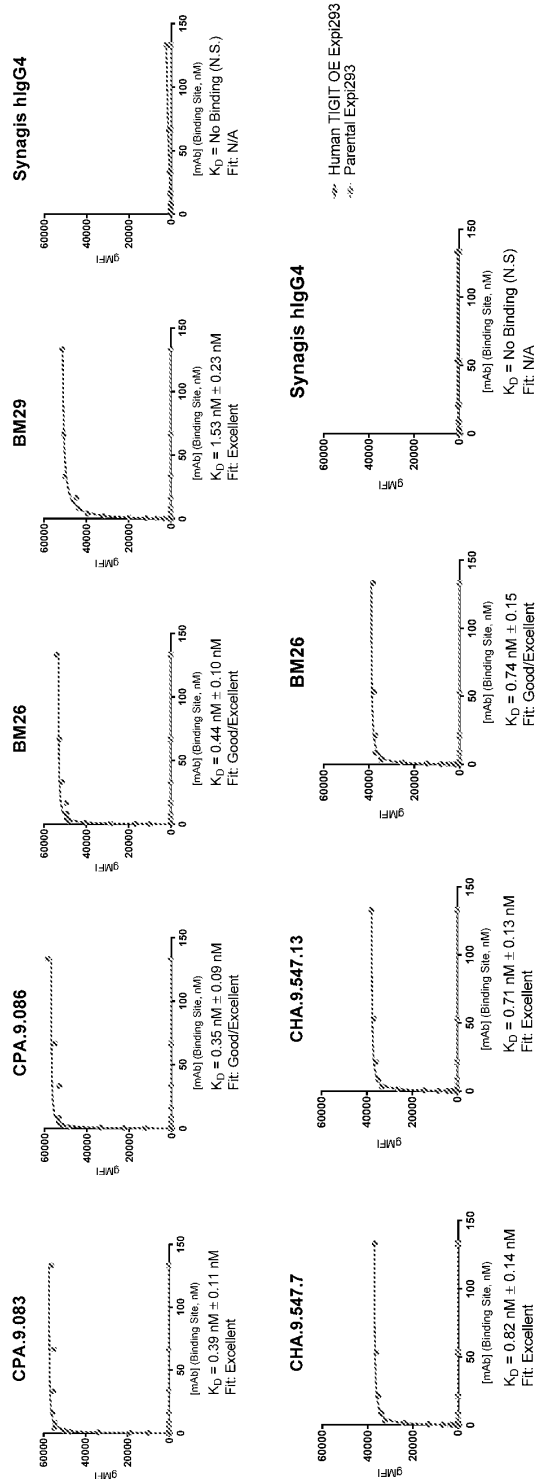


Figure 4B

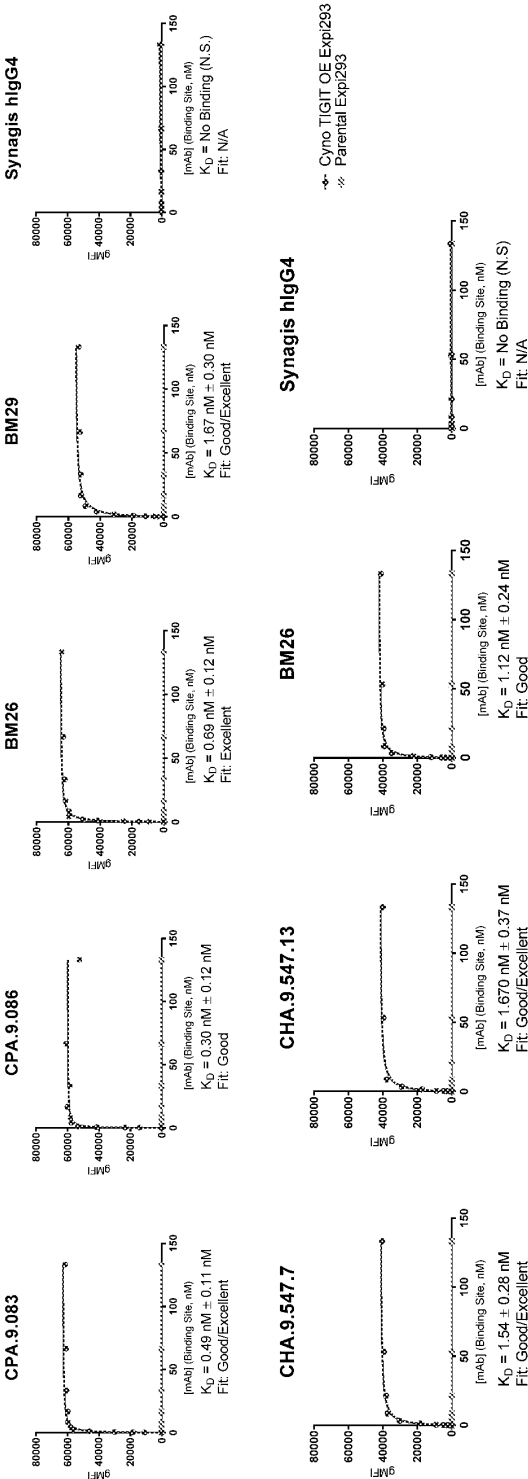


Figure 4C

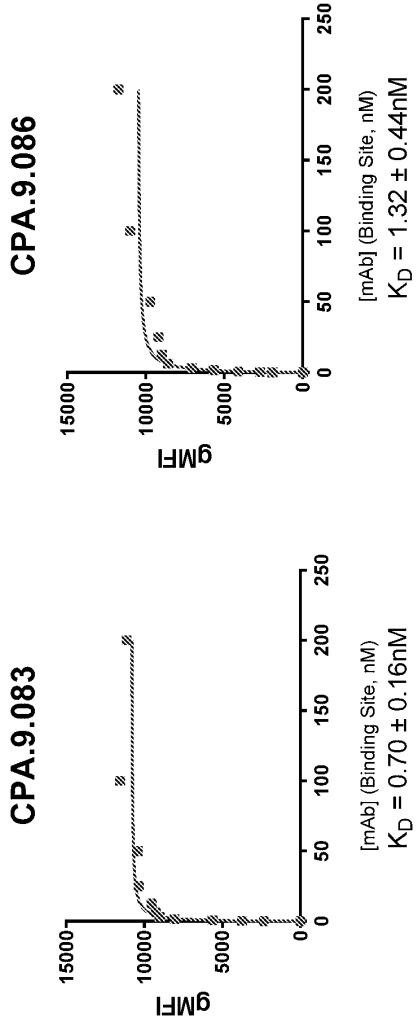


Figure 5A
CHA.7.518.1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPCASVKVSKASGYTFDYNINWVRQAPGQGLEWMGCIYIPYIGSGYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS	1019
vhCDR1	GYTFDYN	1020
vhCDR2	IYPYIGGS	1021
vhCDR3	AREDKTARNAMDY	1022
Full length HC (IgG4(S241P))	QVQLVQSGAEVKKPCASVKVSKASGYTFDYNINWVRQAPGQGLEWMGCIYIPYIGSGYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYICNVDHKPSNTKVDKRVESKYGPCTPCAPLFL	1023
Full length HC for CHA.7.518.1.H4(S241P)	GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQD WLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSLSLSPGK	
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGGTDFTLTISLQPEDFATYYCQHFHWGTPYTTFGGQGTKLEIK	1024
vlCDR1	ENIYSN	1025
vlCDR2	EAT	1026
vlCDR3	QHFHWGTPYT	1027
Full length light chain for CHA.7.518.1.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGGTDFTLTISLQPEDFATYYCQHFHWGTPYTTFGGQGTKLEIKRTVAAPSVEHPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1028

Figure 5B
CHA.7.538.1.2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYAFINYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFGQGRVTMTADTSTVY MELSSLRSEDTAVYYCARSETHDTWFAFYWGQGTLVTVSS	1029
vhCDR1	GYAFINYL	1030
vhCDR2	INPGSGGI	1031
vhCDR3	ARSETHDTWFAFY	1032
Full length HC (IgG4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYAFINYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFGQGRVTMTADTSTVY	1033
Full length HC for CHA.7.538.1.2.H4(S241P)	MELSSLRSEDTAVYYCARSETHDTWFAFYWGQGTLVTVSSASTKGPSVFPPLPCSRSTSESTAAAGCLVKDYFPEPTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTITITCNVDHKNPTKVDKRVESKYGPCCPAPEFLGGPSVLEFPK PKDITLMISKTPETCVVVDVVSQEDPEVQFNWYVDGVEVHNAAKTTPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYS RLTVDKSRWQEAGNVEFSCSMHEALHNHYTQKSLSLSPGK	1033
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCKASQSVRIA VAWFQQKPGKAPKALIVLASTRIHTCVPSRFSGSGTDFTLTISSVQPEDFA TYYCLOHWNYPTFTFGQGTKLEIK	1034
vlCDR1	QSVRIA	1035
vlCDR2	LAS	1036
vlCDR3	LQHWNYPT	1037
Full length light chain for CHA.7.518.1.H4(S241P)	DIQMTQSPSSLSASVGRVTITCKASQSVRIA VAWFQQKPGKAPKALIVLASTRIHTCVPSRFSGSGTDFTLTISSVQPEDFA TYYCLOHWNYPTFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSITYSLSSITLJLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1038

Figure 5C

From Zhu (WO 2017/041004)			
What	sequence		SEQ ID NO:
Heavy chain			
(SEQ ID NO:5 from WO	EVQLQQSGAELVRSGASVKMSCKVNDYTFTNYNMHWLRQTPGQGLIEWIGYIYPGNGDTNY		1039
2017/041004)	NQKFKGKATLTADTSSSTAYMQIISLTSEDPAVYFCARQGIHYIYIDVWGAGTTVTVSSG		
vhCDR1			
(SEQ ID NO:6 from WO	DYTFNYNMH		1040
2017/041004)			
vhCDR2			
(SEQ ID NO:7 from WO	YIYPGNGDTNYNQ		1041
2017/041004)			
vhCDR3			
(SEQ ID NO:8 from WO	QGIHYIYIDV		1042
2017/041004)			
Light chain			
(SEQ ID NO:3 from WO	DIEMTQSPATLSVTPGDRVSLSCRASQSIRDYLHWYQQKSHESPRLLIKYVVSQISGIPS		1043
2017/041004)	RFSGSGSGSEFTLSINSVPEPEDVGVVYVCQNGHSLPLTFGSGTKLEIKRTV		
vLCDR1			
(SEQ ID NO:9 from WO	RASQSIRDYLLH		1044
2017/041004)			
vLCDR2			
(SEQ ID NO:10 from WO	YVVSQIS		1045
2017/041004)			
vLCDR3			
(SEQ ID NO:11 from WO	QNGHSLPLT		1046
2017/041004)			

Figure 5D

From Zhu (WO 2017/041004) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFISDWMHWVKQRPGQGLEWIGYINPSTIGYTEY NQKFQDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA	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)	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASNLESGVPA RFGSGSGTDFTLNIHPVEEDTATYYCQHSWEIPYTFGGGTGLEIK	1051
vlCDR1 (SEQ ID NO:37 from WO 2017/041004)	RASQSVSTSSYSYMH	1052
vlCDR2 (SEQ ID NO:38 from WO 2017/041004)	YASNLES	1053
vlCDR3 (SEQ ID NO:39 from WO 2017/041004)	QHSWEIPYT	1054

Figure 5E

From Zhu (WO 2017/041004) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQ5GAEIAKPCASVKMSCKASGYTFISDWMHVVKQRPGQGLEWIGYINPSIGYTEY NQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYVWGQGTLVTVSA	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)	DVVMVTQTPLTSLVTICQPASISCKSSQSLNSDGKTYLNWLLQRPQGQPKRLIYLVSKLD SGVTPDRFTGSCSGIDFTLKISRVEAEDLGVYYCWQGTHFPRTGCGTKLEIK	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

Figure 5F

From WO 2018/017864 (334M5 antibody) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:30 from WO 2018/017864)	EVQLQQSV AELVRPGISVTIESCKASGYFTTNVWLGWVKQRPGHGLEWIGDIFPGGDYPNY NEKFKGKATLTADTSSSTAYMQLSLTSEDSSVYFCTRGYFDVWVGAGTTVTVSS	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)	TRGYEDV	1066
Light chain (SEQ ID NO:25 from WO 2018/017864)	DIQMTQSPSSLSVSAAGEKVTMSCKSSQSLINSENQKNYLAWFQQKPGQPCKMLIYGASTR ESGVPRDFTGSGCTDFTLTISSVQAEDLAVYYCQNDHSYPFTFCSGTKLEIKR	1067
vlCDR1 (SEQ ID NO:26 from WO 2018/017864)	KSSQSLINSENQKNYLA	1068
vlCDR2 (SEQ ID NO:27 from WO 2018/017864)	GASTRES	1069
vlCDR3 (SEQ ID NO:28 from WO 2018/017864)	QNDHSYP	1070

Figure 6

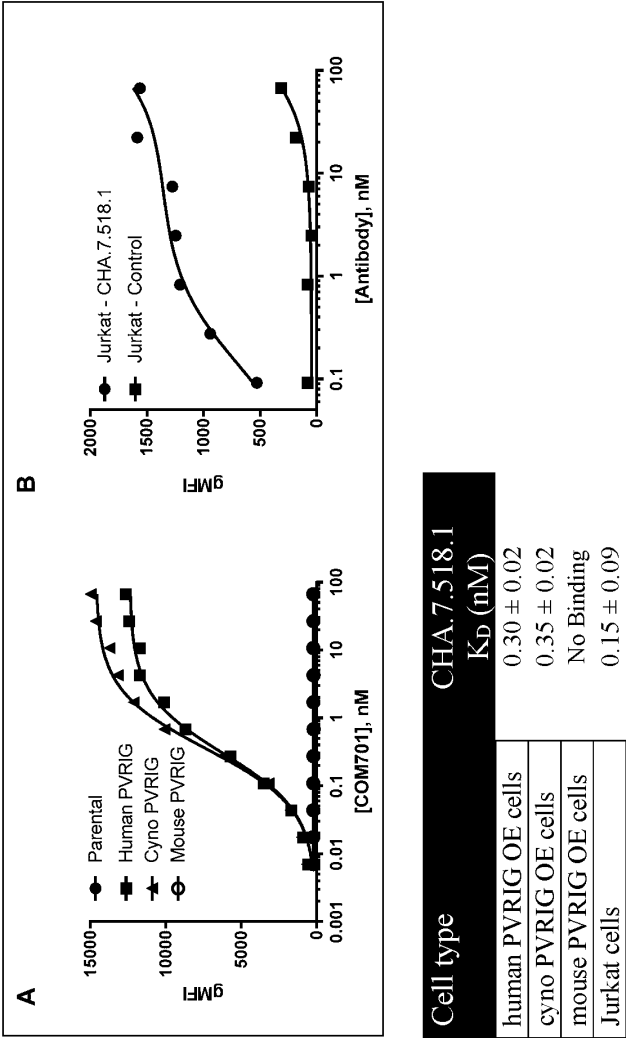


Figure 7A

Pembrolizumab (Anti-PD1 hlgG4)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVLSGGGFVQPCCSLKLSCAASGFTSSYAMSWVRQNPERRLVWVAITTCGGRNITYYPDSVKGRFTISR DNAKNILYLQMSSLRSEDITAMYYCTROGYDGYTWFAYWGQGTILVTVSS	1071
vhCDR1	GFTSSYA	1072
vhCDR2	ITGGRNT	1073
vhCDR3	TRQGYDGYTWFAY	1074
Full length HC	EVQLVLSGGGFVQPCCSLKLSCAASGFTSSYAMSWVRQNPERRLVWVAITTCGGRNITYYPDSVKGRFTISR DNAKNILYLQMSSLRSEDITAMYYCTROGYDGYTWFAYWGQGTILVTVSSASTKGPSVPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTISGVHTHPAVLQSSGLYSLSVTVTPSSSLGTTKTYTCNVVDHKPSNTKVD KRVESKYGPPCPCPAPEFLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVEFSCVMHE ALHNHYTQKSLSLSPCK	1075
Variable light (vl) domain	DIVLTQSFPTSLAVSLQQRATISCRASESVNDNSGISEFMNWFQQKPGQPPKLLIYAASNPGSGVPARFSGSGGT DFSLNIHPMEEDDTAMVFCQOSKEVPWTTCGGTELEIKR	1076
vlCDR1	ESVDNSGISF	1077
vlCDR2	AAS	1078
vlCDR3	QOSKEVPWT	1079
Full length light chain	DIVLTQSFPTSLAVSLQQRATISCRASESVNDNSGISEFMNWFQQKPGQPPKLLIYAASNPGSGVPARFSGSGGT DFSLNIHPMEEDDTAMVFCQOSKEVPWTTCGGTELEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTIISKADYEKHKVYACEVTHQGLSPVTKSFNRGE C	1080

Figure 7B	
Pembrolizumab (Anti-PD1 from WO2016028656)	
What	sequence
Full length HC (SEQ ID NO:33 from WO2016028656)	QVQLVQSGVEVKPKGASVKVCKASGYTFNYYMYWVRQPCQGLEWMGGINPSNGGTNFKNRV TLTDSSTTTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTITVTVSSASTKGPSVFLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTKITYTCNVDFHKPSNTK VDKRVESKYGPPCPCPAPELGGPSVFLPPKPKDILMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAKGQPREPQVYITLPPSQEE MTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGCNVFSCVM HEALTHNIHYTKSLSLGK
Full length light chain (SEQ ID NO:34 from WO2016028656)	EIVLTQSPATLSLSPGERATLSCRASKGVSTSGSYLHWYQQKPGQAPRLLIYLAAYLESQVPAIFSGSGGTID FTLTISSELEPEFAVYYCQHSRDPLITFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYVEKHKVYACEVTHIQGLSSPVTKSFNRGEC

Figure 7C

Nivolumab (Anti-PD1 hlgG4)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSRLRDCKASGTFSTNSGMHWVRQAPGKGLEWVA VIWYDGSKRYYADSVKGRFTI SRDNSKNTLFLQMINSIRAEDTAVYYCATINDDYWGQGITLVTS	1083
vhCDR1	GITFSNSG	1084
vhCDR2	IWYDGSKR	1085
vhCDR3	ATNDDY	1086
Full length HC	QVQLVESGGGVVQPGRSRLRDCKASGTFSTNSGMHWVRQAPGKGLEWVA VIWYDGSKRYYADSVKGRFTI SRDNSKNTLFLQMINSIRAEDTAVYYCATINDDYWGQGITLVTSASTKGPVFPAPCSRSTSESTAALGCL VKDYHPEPVTVSWNSGALISGVHTFPAVLQSSGLYSLSVVTVPSSSLGCTKTYICNVVDHKPNTKVDKRVES KYGPPCPCPAPEFLGGPSVFLPPPKPDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTITLVHQQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMIKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGFFLYSRLTVDKSRWQEGNVFSCSMHEALHN HYTQKSLSLGK	1087
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRAITGIPARFSGSGCTDFTLT SSLEPEDFAVYYCQOSSNWPRIFGGGTKVEIKR	1088
vlCDR1	QSVSSY	1089
vlCDR2	DAS	1090
vlCDR3	QOSSNWPR	1091
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRAITGIPARFSGSGCTDFTLT SSLEPEDFAVYYCQOSSNWPRIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHIQGLSSPVTKSFNRGEC	1092

Figure 7D

Nivolumab (Anti-PD1 from WO2016028656)		SEQ ID NO:
What	sequence	
Full length heavy chain	QVQLVESGGCVVQPGRSRLDCKASGITFNSGMIHWVRQAPCKGLEWVAIVYDGSKRYYADSVKGRFTI SRDNSKNTILFLQMNISLRAEDTAVYYCATNDDDYWGQGITLVTSASATKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTYTCNVDFHKPSNTKVKDRVES KYCPCPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNATKTP REEQFNSTYRVVSVLTVLIHQDWLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLTPSQEEMTKNQV SLTCLVKGFPYPSDIAVEWESNGQPENNNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHAEALHN HYTQKSLSLGK	1093
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLINVDASNRATGIPARFSGSGTDFTLT SSLEPEDFAVYYCQSSNWPRTECGQTKVEIKRTVAATPSVFIIPPSDEQLKSGTASVVCLLNINFPYREAKVQ WKVDNALQSCNSQESVTEQDSKDSITYSLSSITLTSKADYEKHKVYACEVTHQCLSSPVTKSFNRGEC	1094
from WO2016028656)		

Figure 7E

Cemiplimab (REGN2810; anti-PD1)		SEQ ID NO:
What	sequence	
Variable heavy (vh) domain (SEQ ID NO:1 from US20170174779)	EVQLLESGGVLVQPGGSLRLSCAASGFTSNFGMTWVRQAPGKGLEWVSGISGGGRDIYFADSVKGRFTISRDN SKNTLYLQMNSLKGEDTAVYCVKWGNIYFDYWGQGLVTYSS	1095
vhCDR1 (SEQ ID NO:3 from US20170174779)	GFITSNFG	1096
vhCDR2 (SEQ ID NO:4 from US20170174779)	ISGGGRDT	1097
vhCDR3 (SEQ ID NO:5 from US20170174779)	VKWGNIVFDY	1098
Variable light (vl) domain (SEQ ID NO:2 from US20170174779)	DIQMTQSPSSLSASVGDSTITTCRASISNTLNWYQQKPKAPNLLIYAASLHGGVPSREFSGSGCTDFTLTIRTLQPEDFATYYCQQSSNTPTFTFGPTVVDFR	1099
vlCDR1 (SEQ ID NO:6 from US20170174779)	LSNTF	1100
vlCDR2 (SEQ ID NO:7 from US20170174779)	AAS	1101
vlCDR3 (SEQ ID NO:8 from US20170174779)	QQSSNTPTFT	1102

Figure 7F

Cemiplimab (REGN2810; anti-PD1)		SEQ ID NO:
What	sequence	
Full length heavy chain (SEQ ID NO:9 from US20170174779)	EVQLLESGGVLVQPCCSLRLSCAASGFTTSNFGMTWVRQAPGKCLEWVSGISGGGRDITYADSVKGRFTISR DNSKNTLYLQMNSLKGEDTAVYYCVKWKGNIFYDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTCNVDEHKPSNTKVKDKRV ESKYGPPCPPCPAPEFLGGPSVLEFPPPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVEFSCVMHEALH NHYTQKSLSLSGK	1103
Full length light chain (SEQ ID NO:10 from US20170174779)	DIQMTQSPSSLSASVGDSITITCRASLSINTELNWYQQKPGKAPNLLIYAASLHCGVPSRFSGSGSGTDFTLTIT RTILQPEDFATYYCQQSSNTIPTFGPTVVDIRRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSCNSQESVTEQDSKDSITYSLSSITLILSKADYEEKHKVYACEVTHQCLSSPVTKSFNRGEC	1104

Figure 8

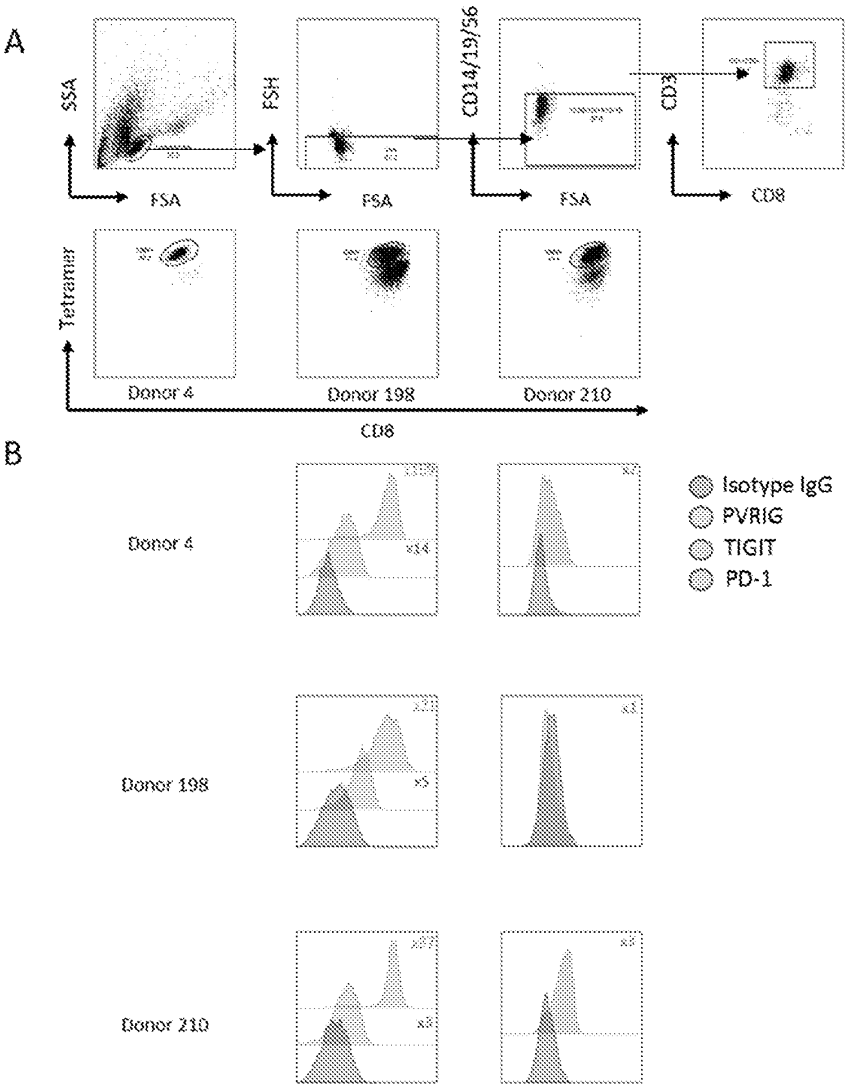


FIGURE 9

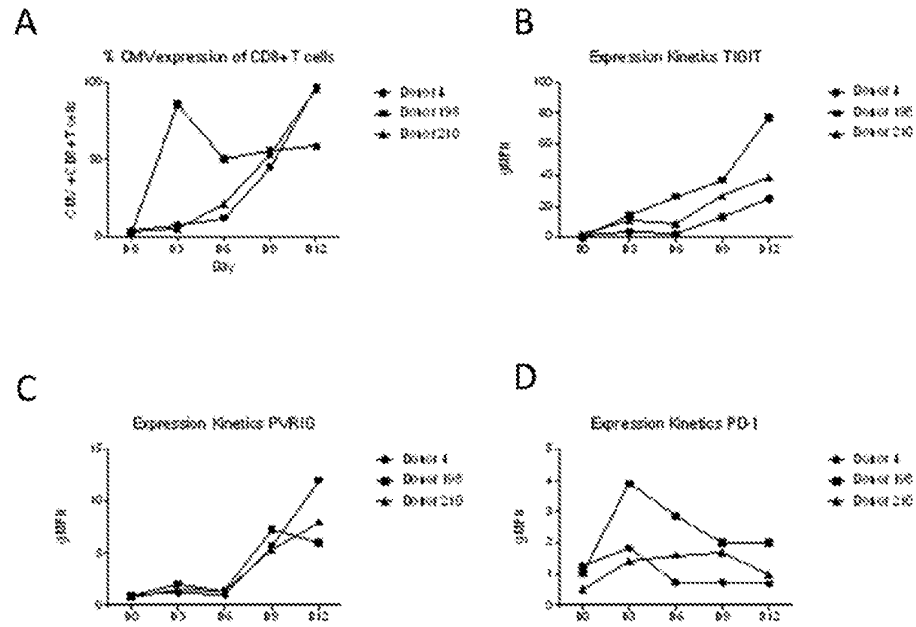


FIGURE 10

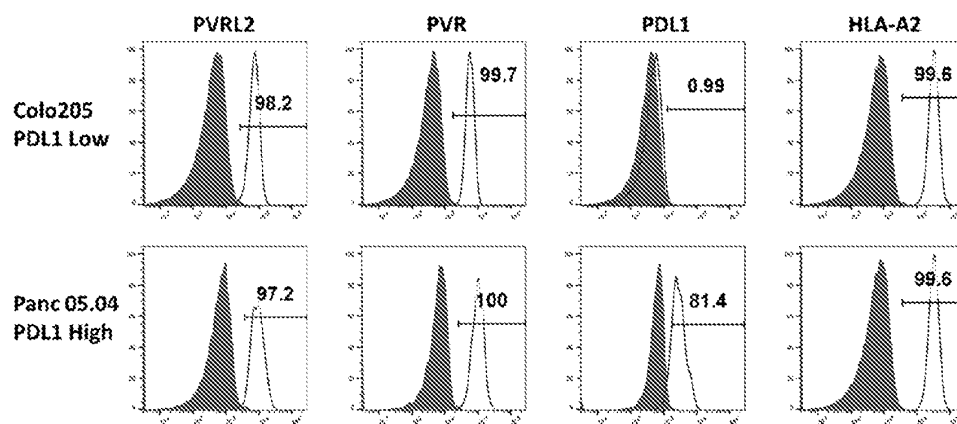


FIGURE 11A

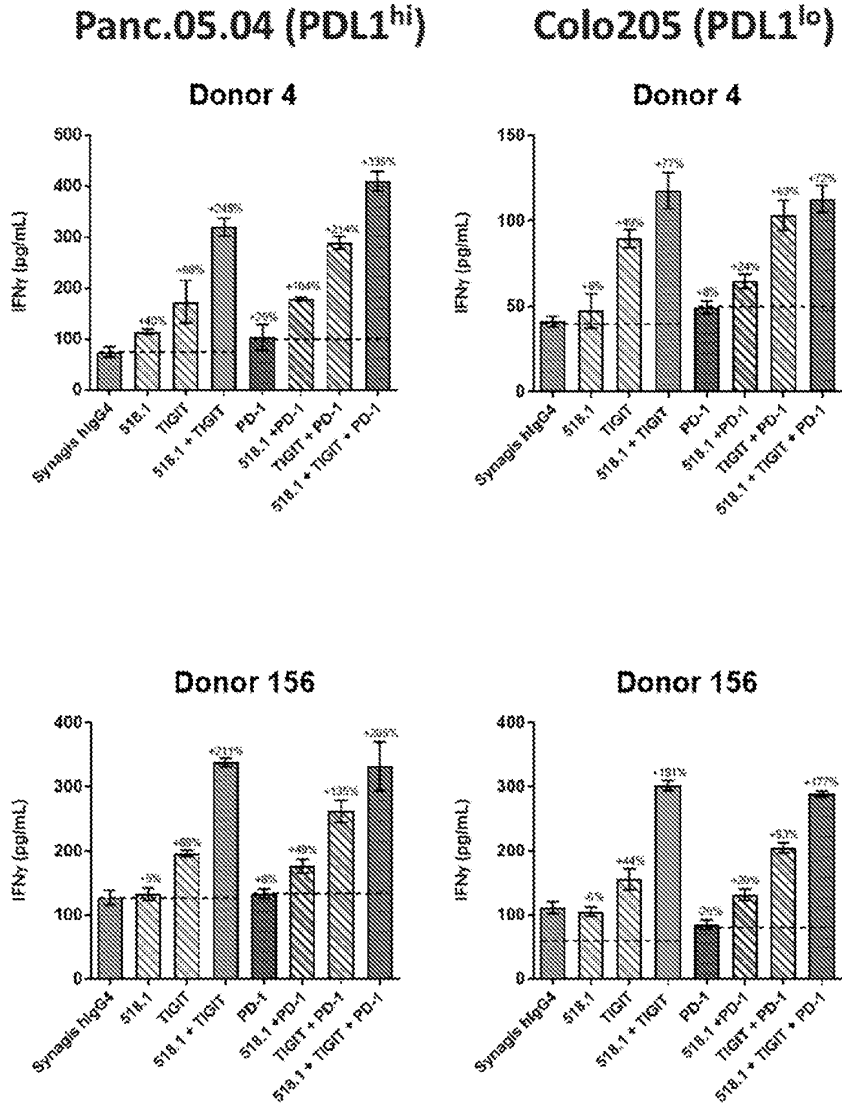


Figure 11B

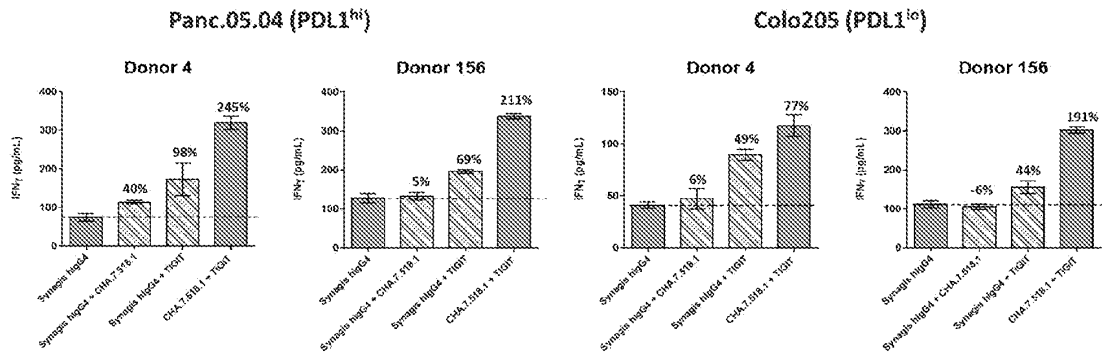


Figure 11C

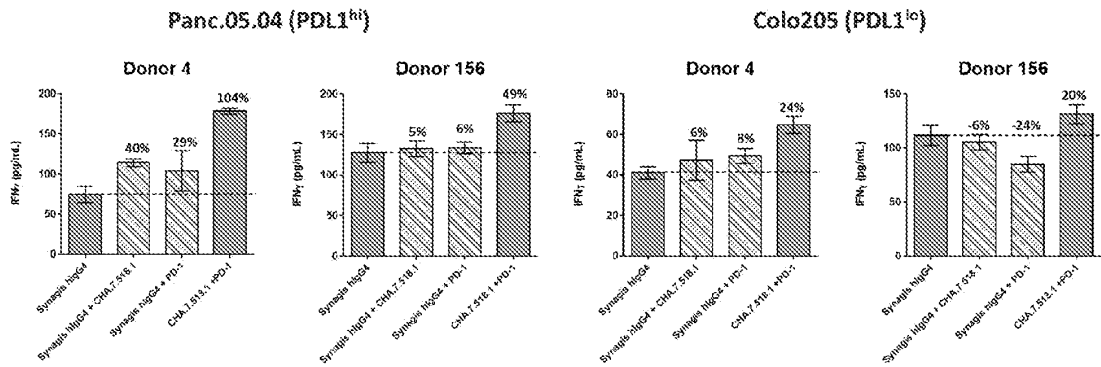


Figure 11D

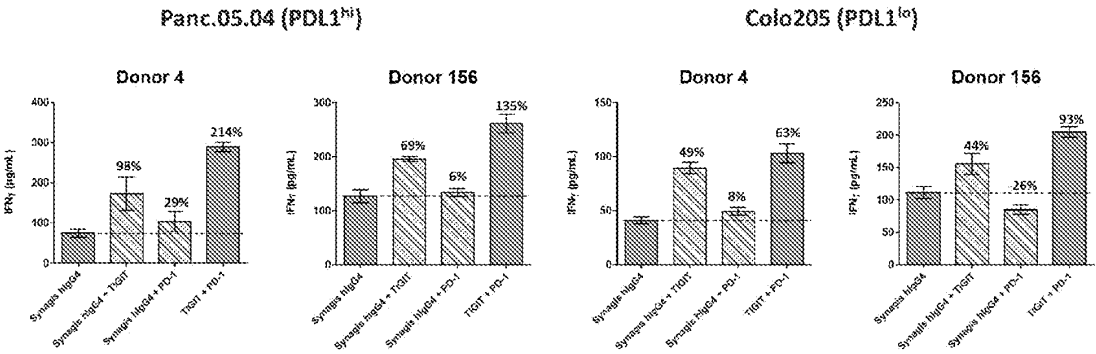


Figure 12

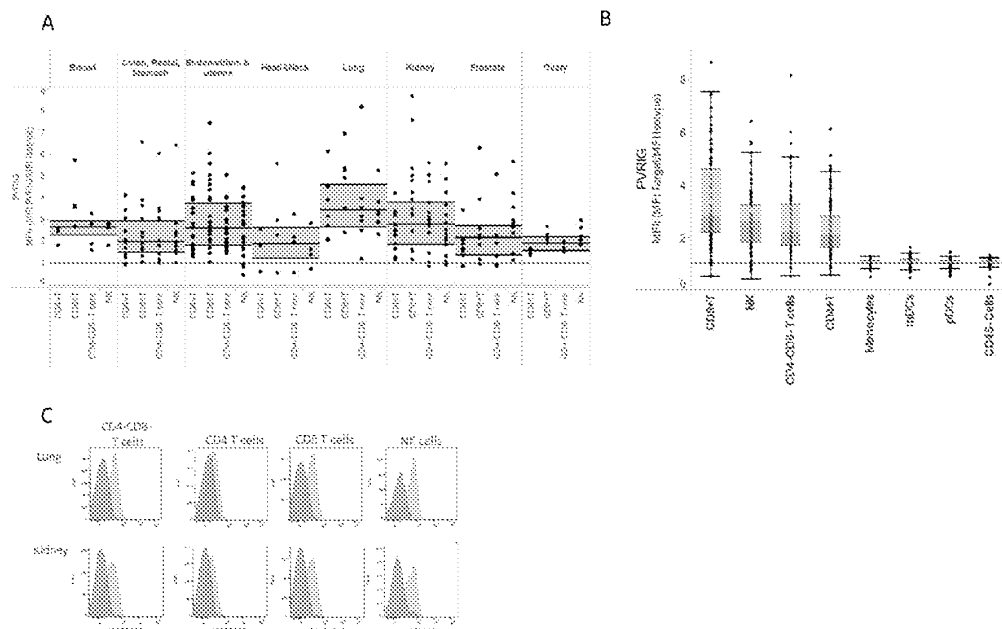


Figure 13

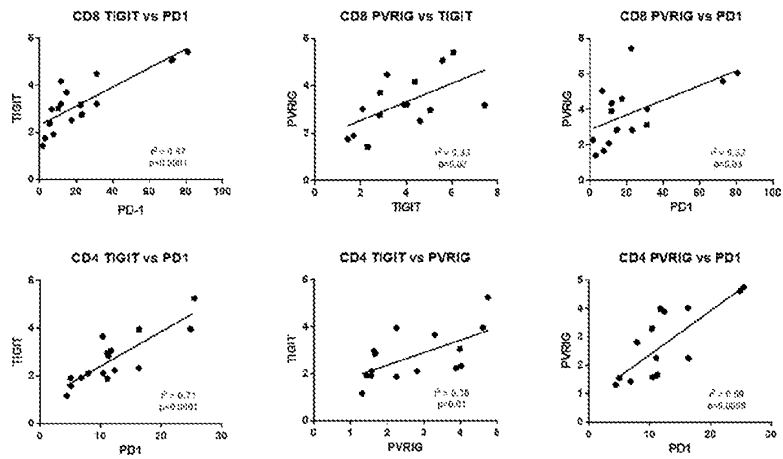


Figure 14

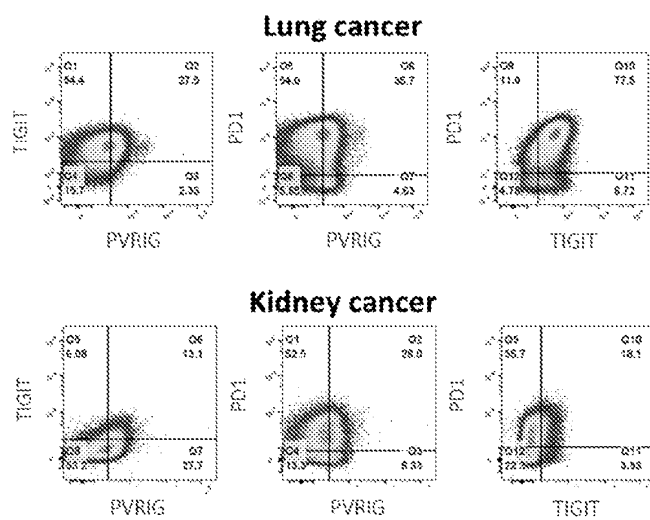


Figure 15

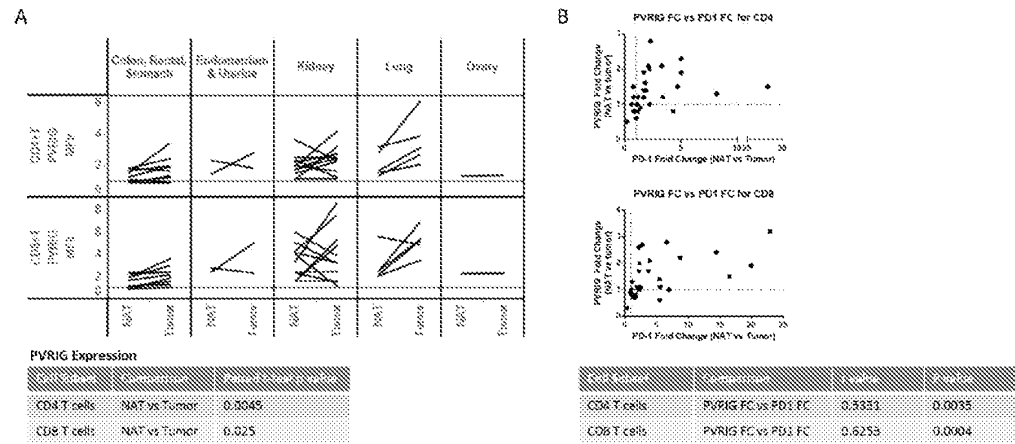


Figure 16

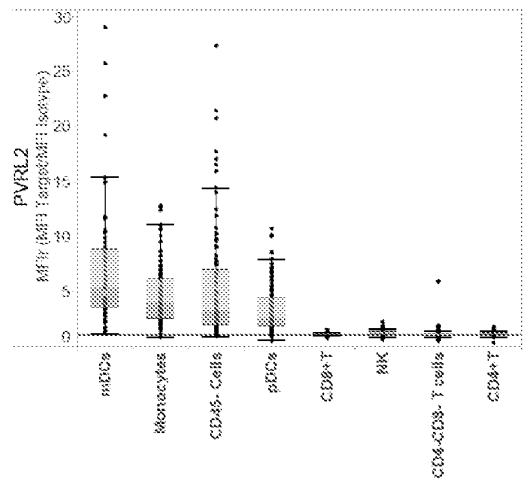


Figure 17

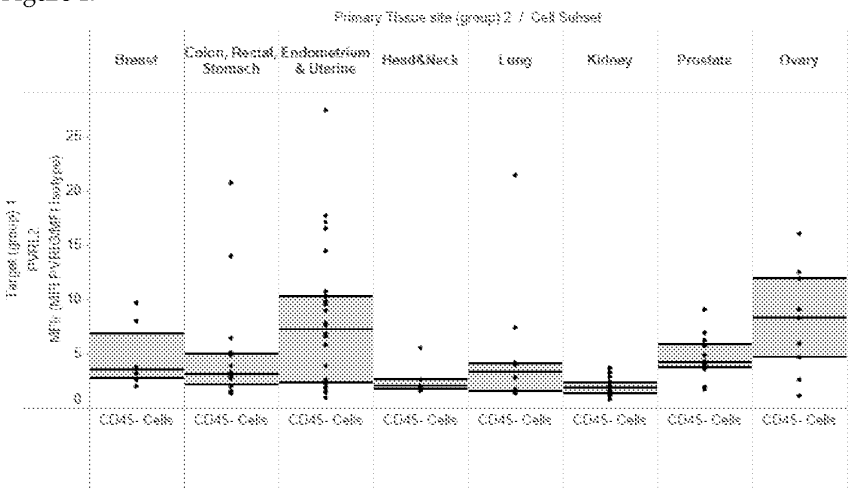


Figure 18

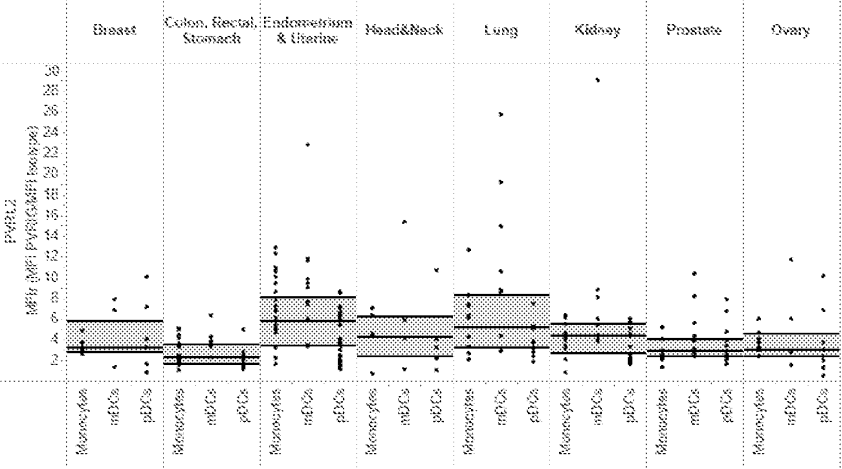


Figure 19

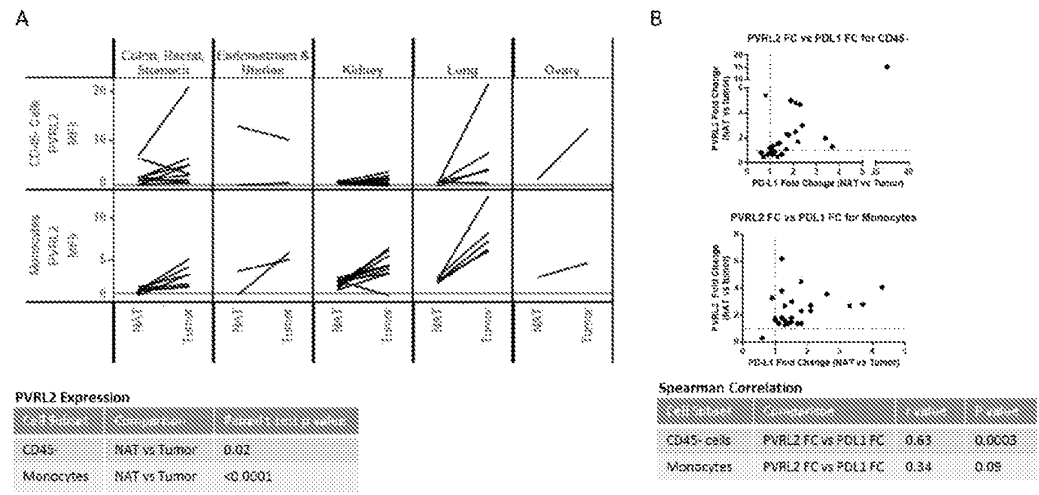


Figure 20

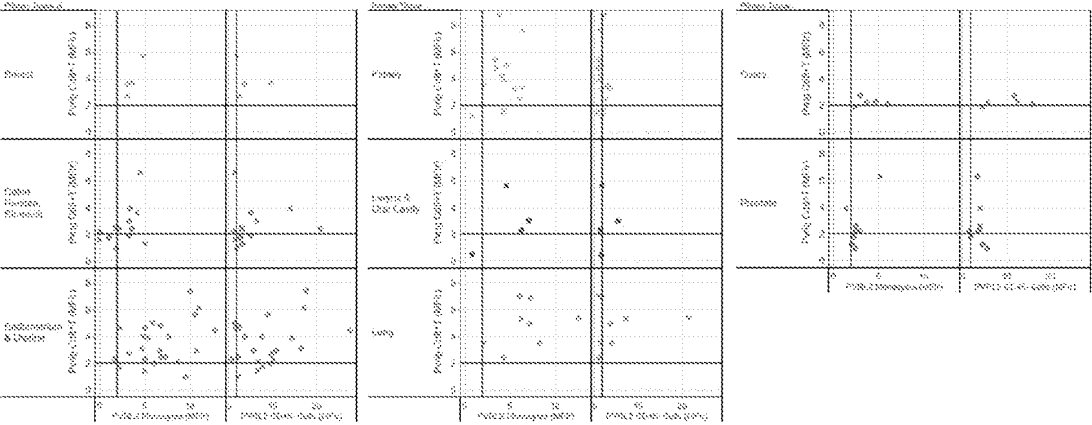


Figure 21A

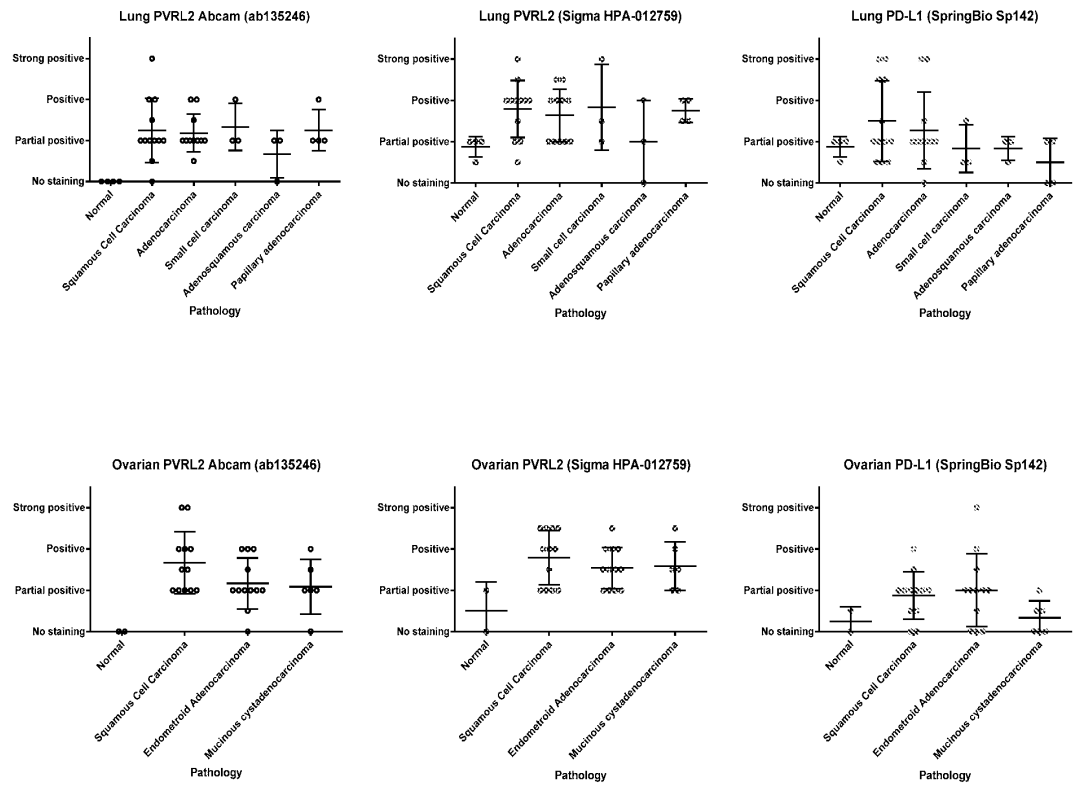


Figure 21B

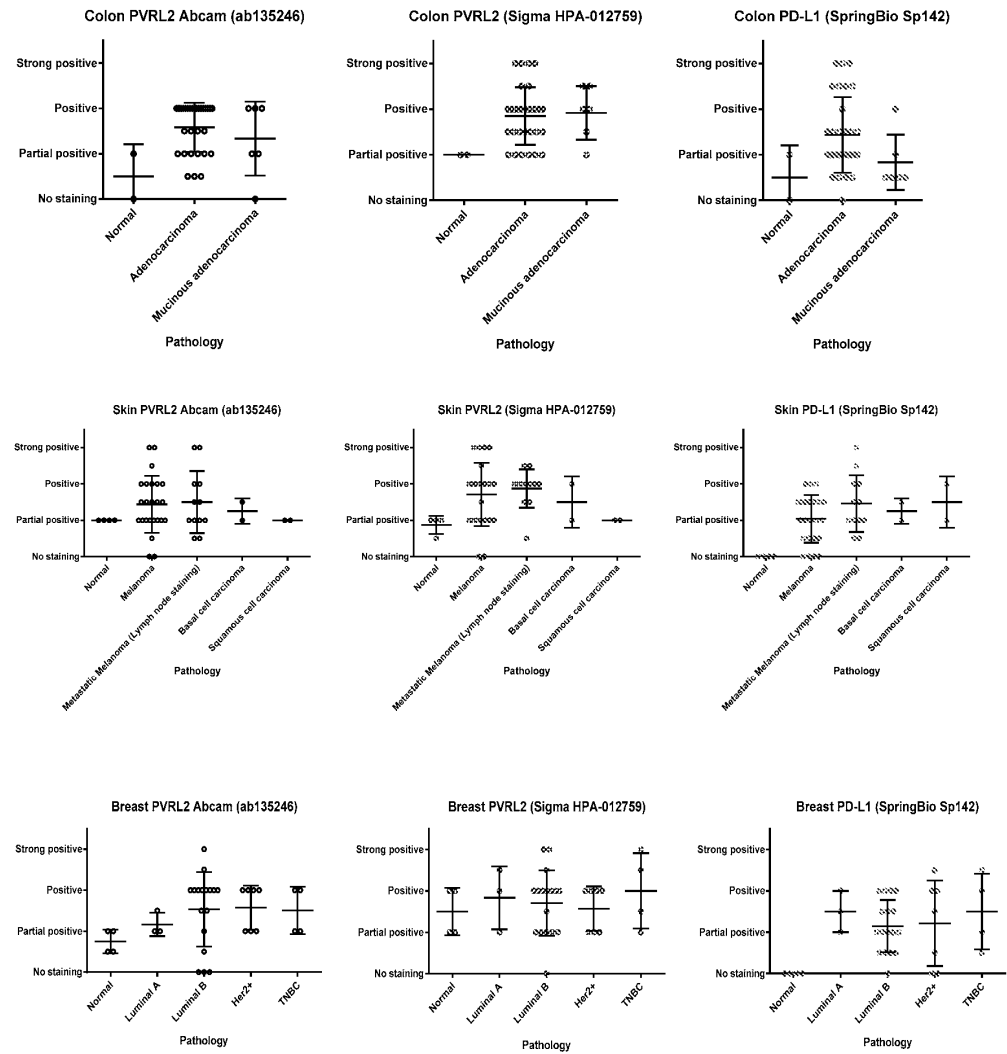


Figure 22

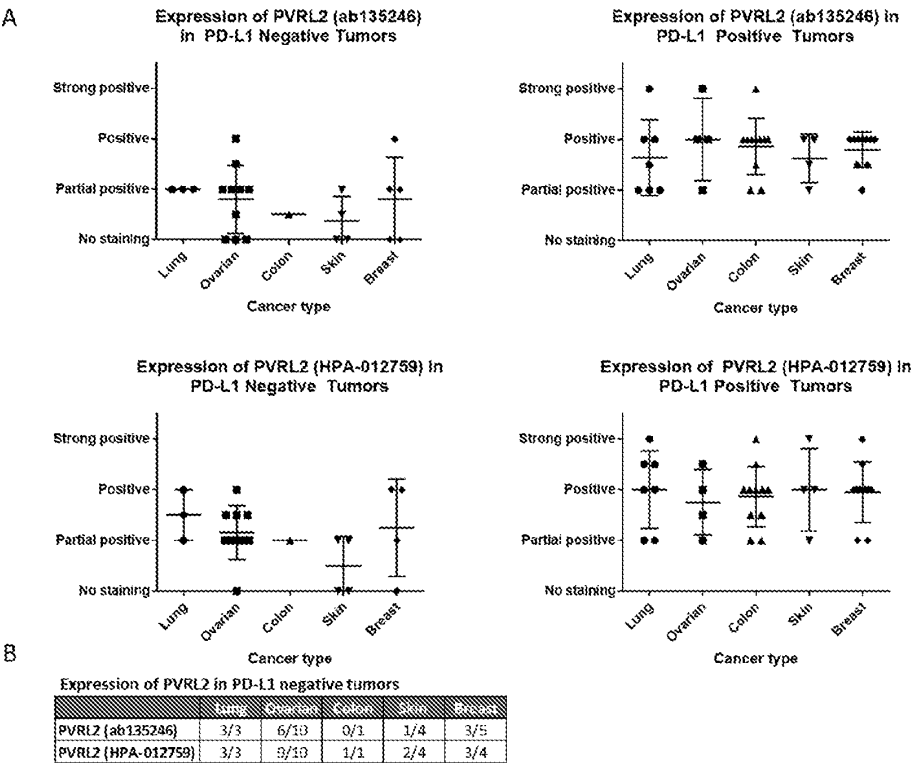


Figure 23

A. PVRL2 (HPA-012759)

B. PD-L1 (SP142)

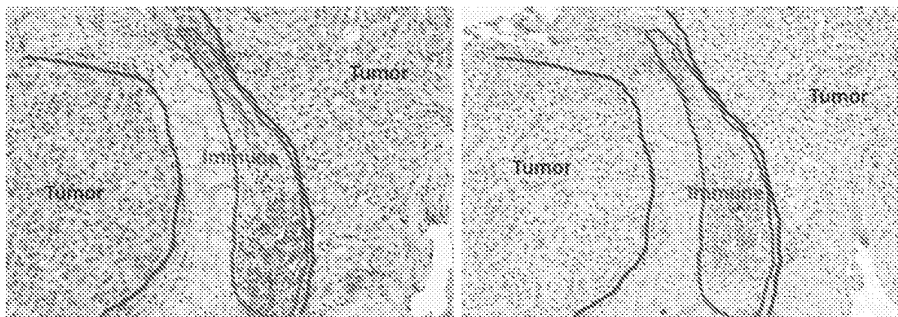


Figure 24

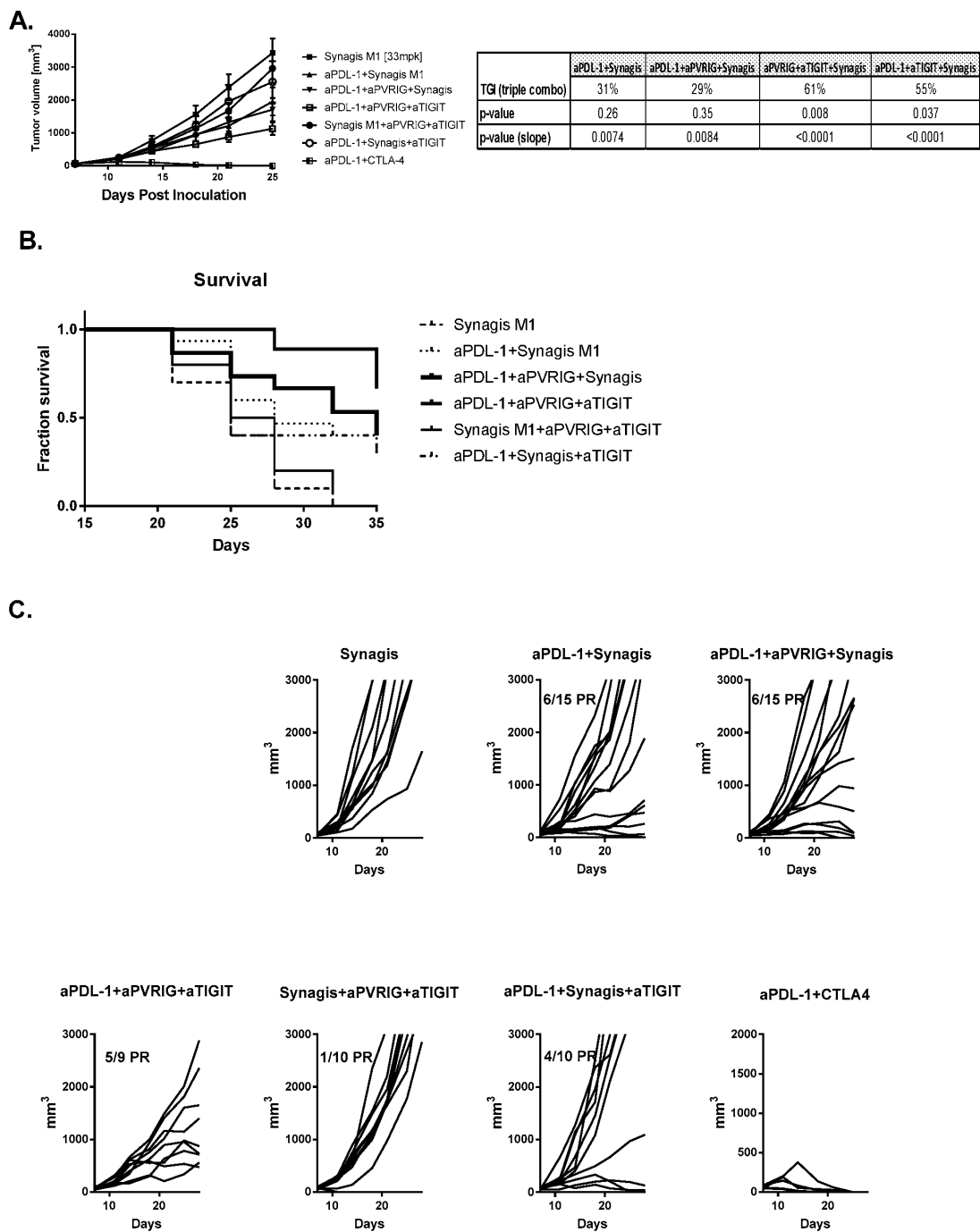


Figure 25

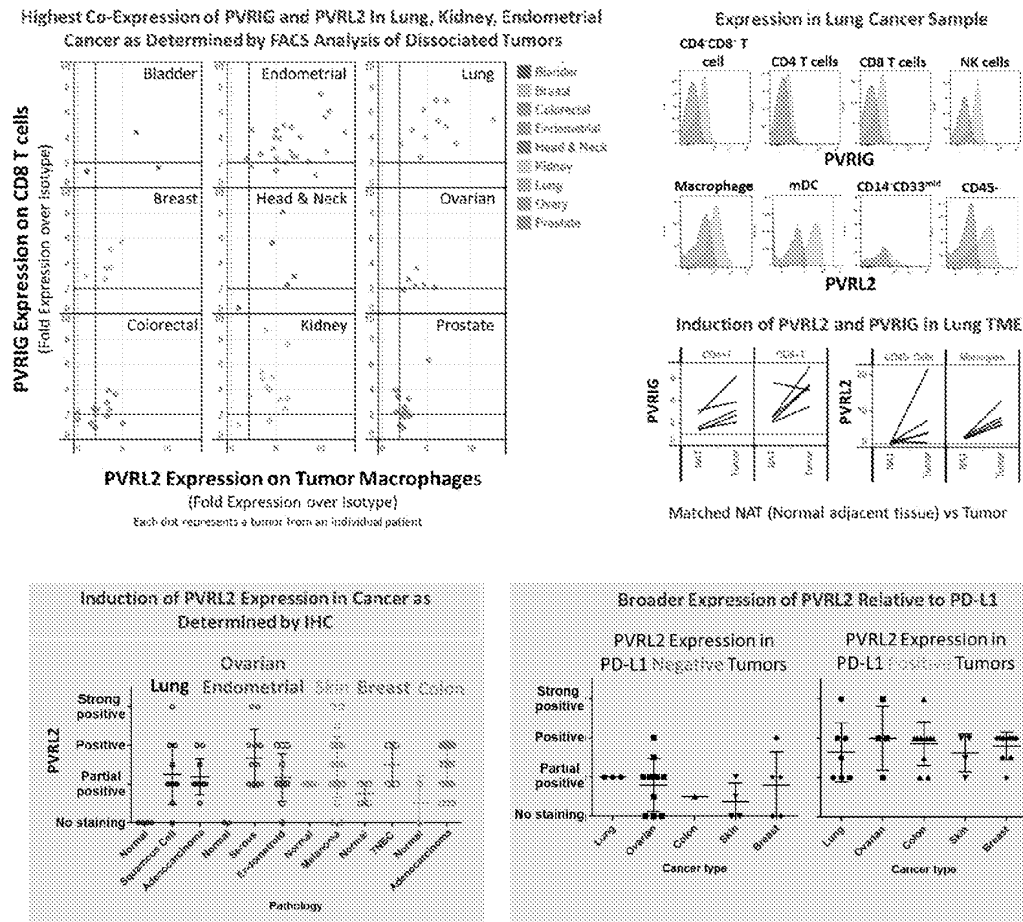


Figure 26

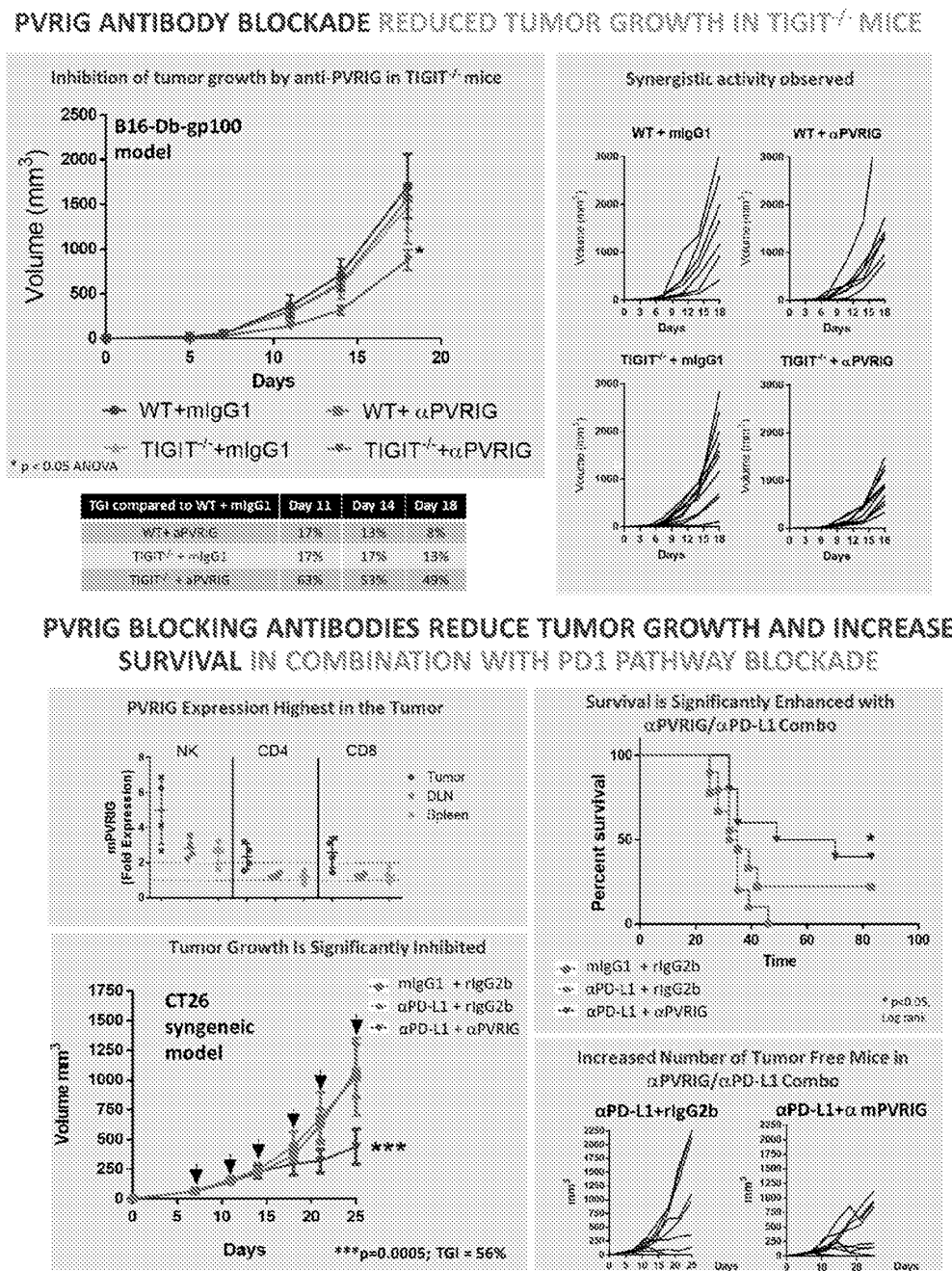


Figure 27

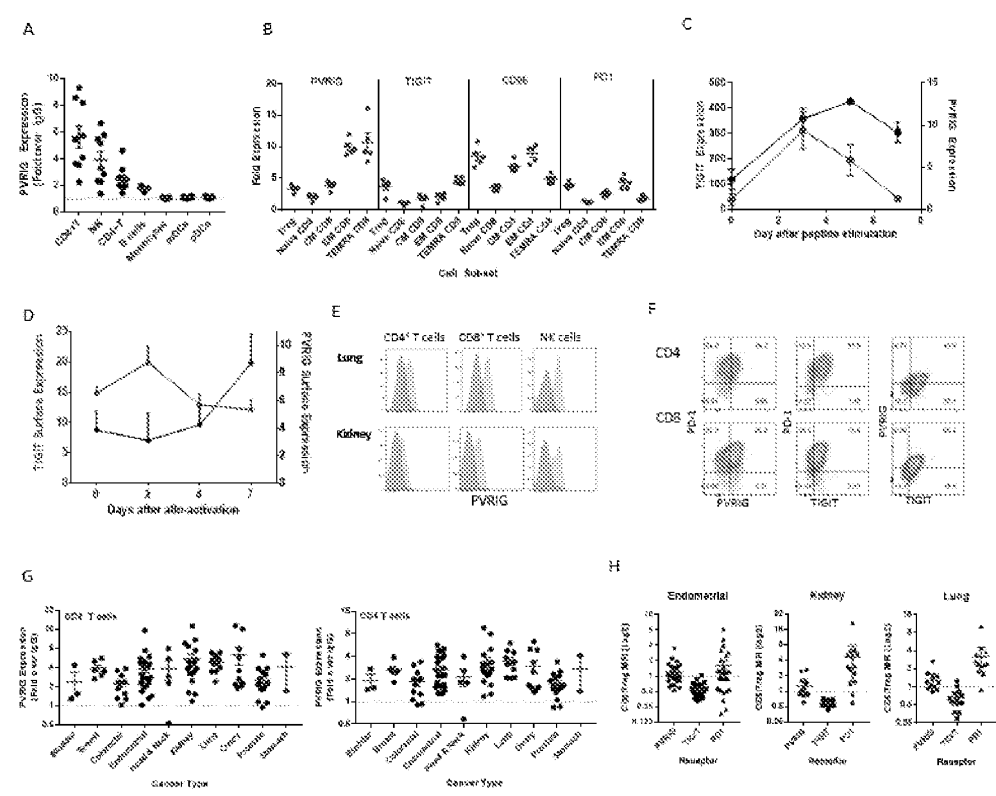


Figure 28A

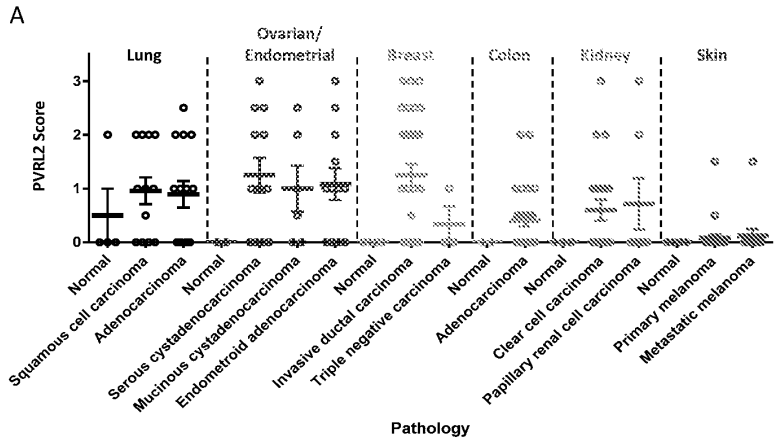


Figure 28B

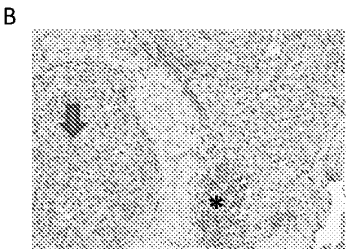


Figure 28C

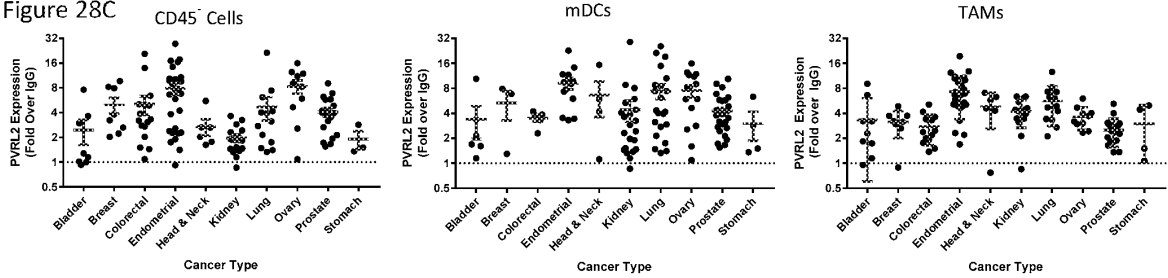


Figure 28D

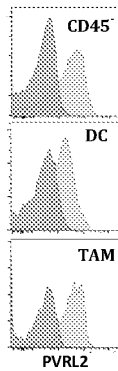


Figure 28 E

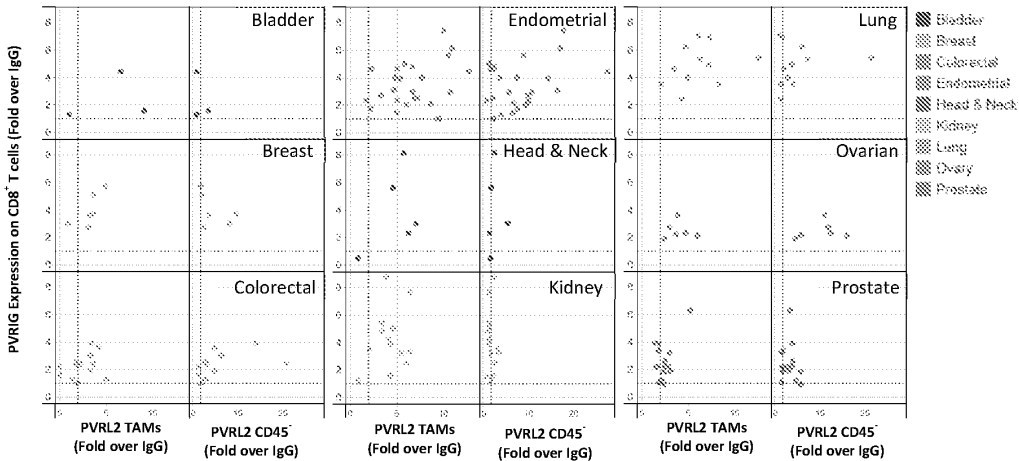


Figure 28F

	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

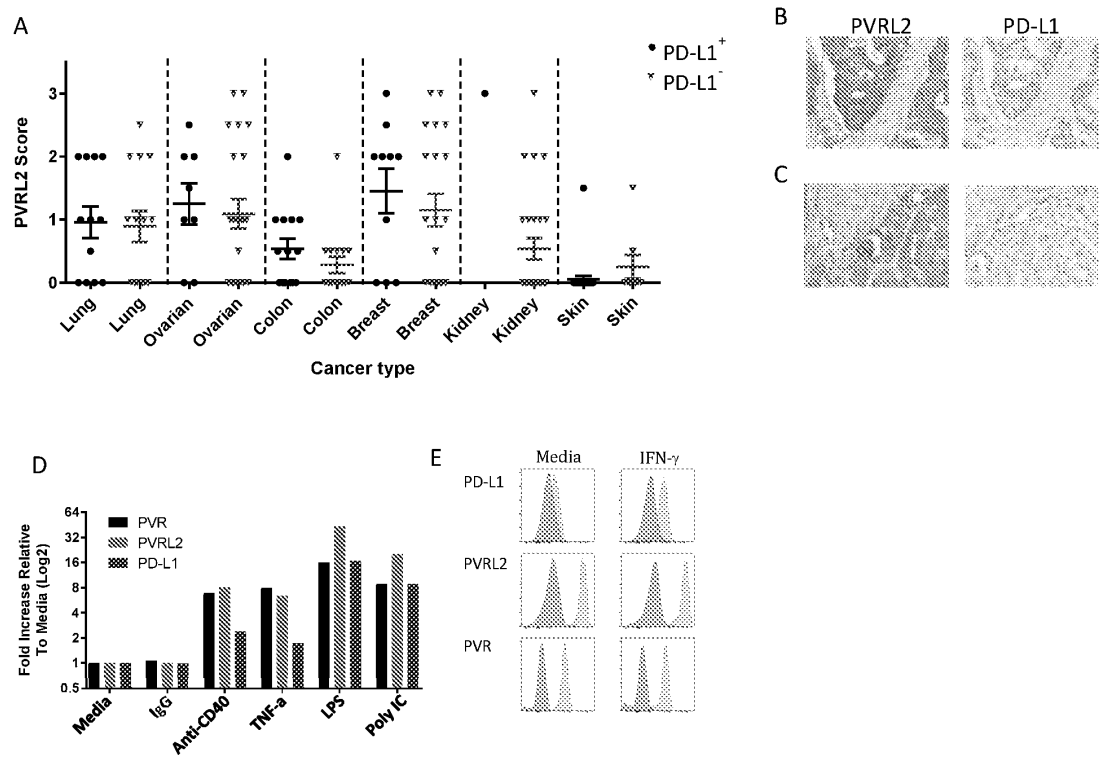


Figure 30

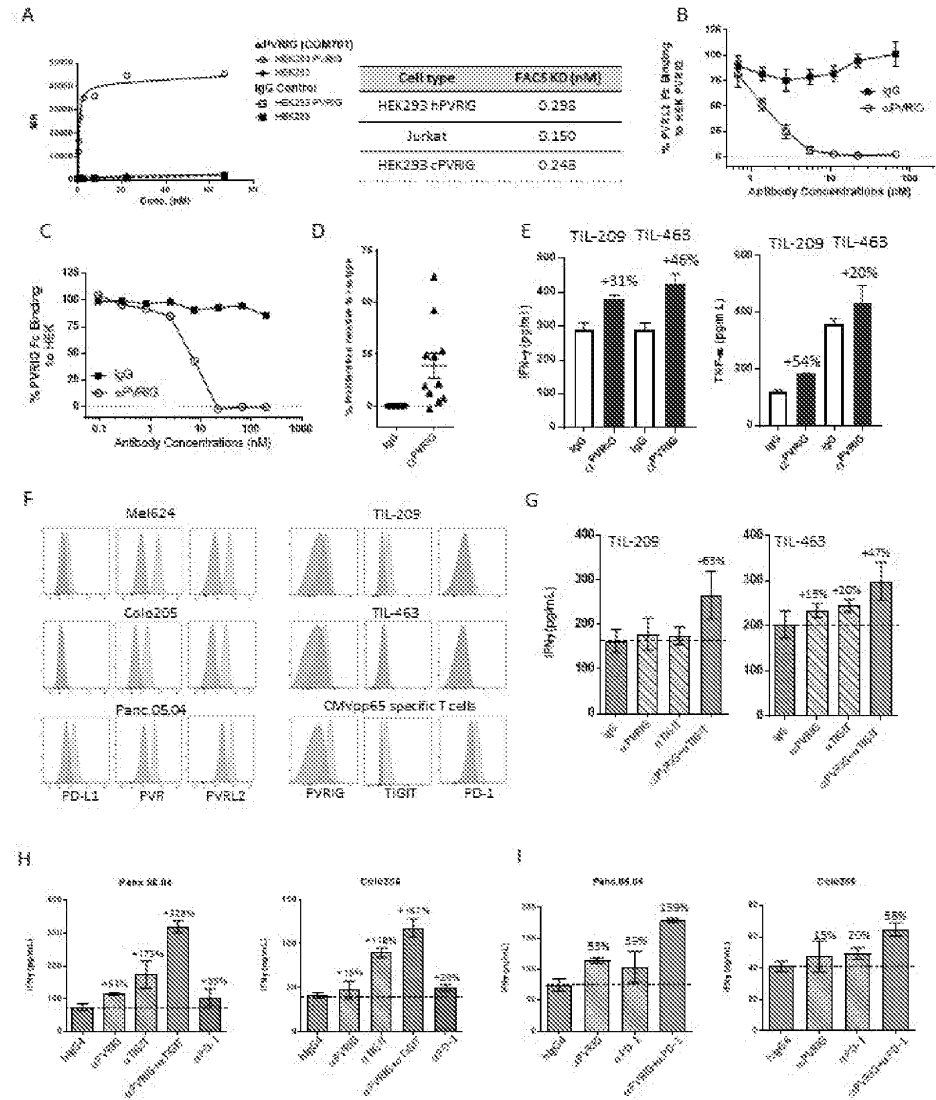


Figure 31

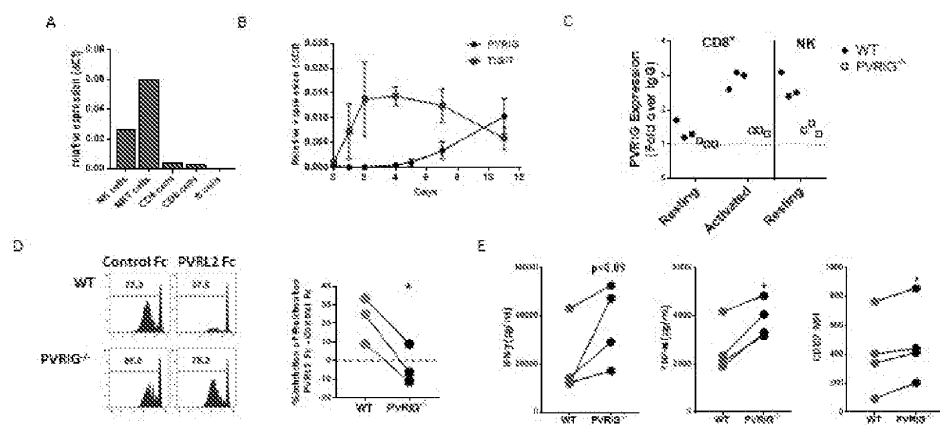


Figure 32

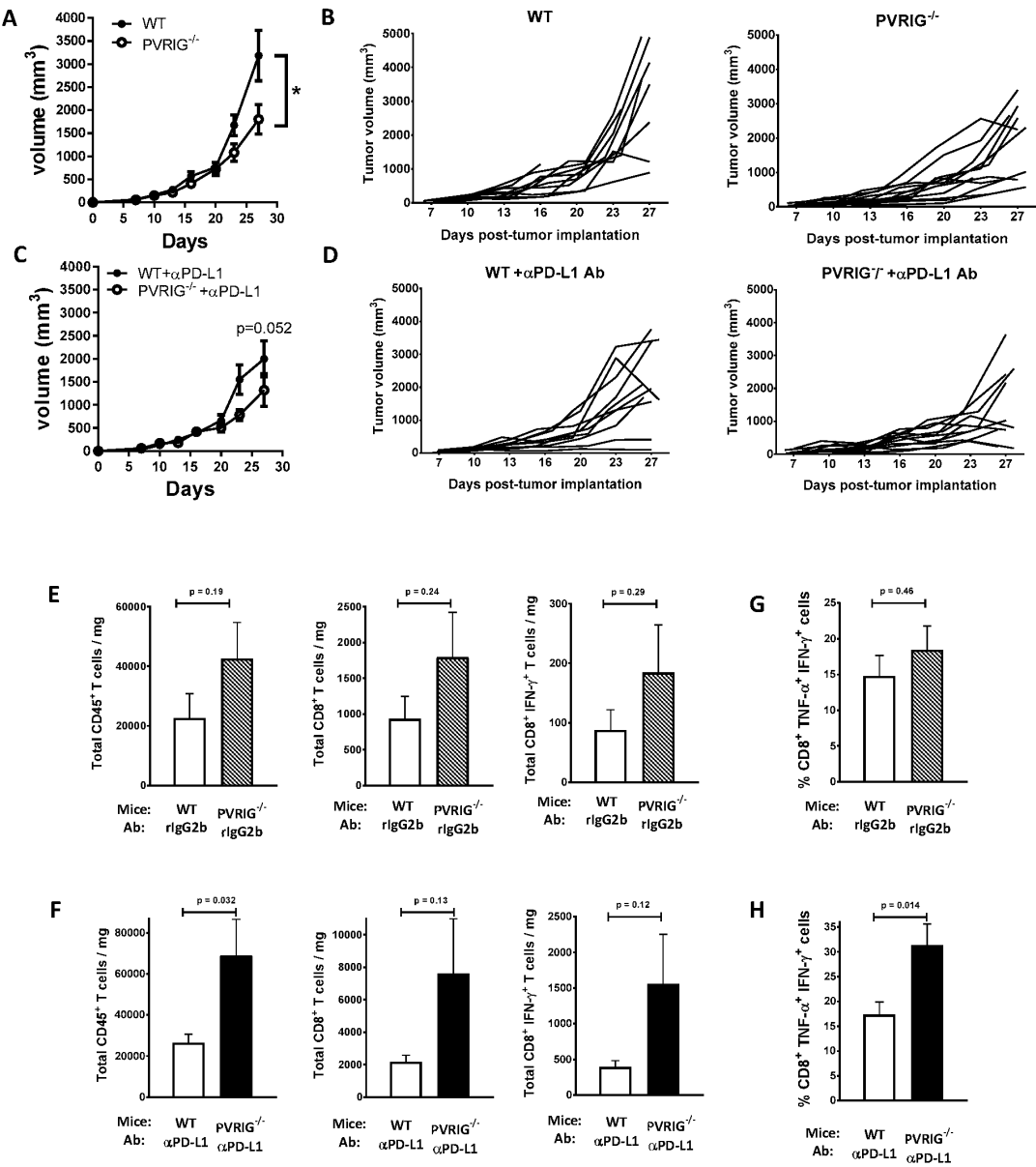


Figure 33

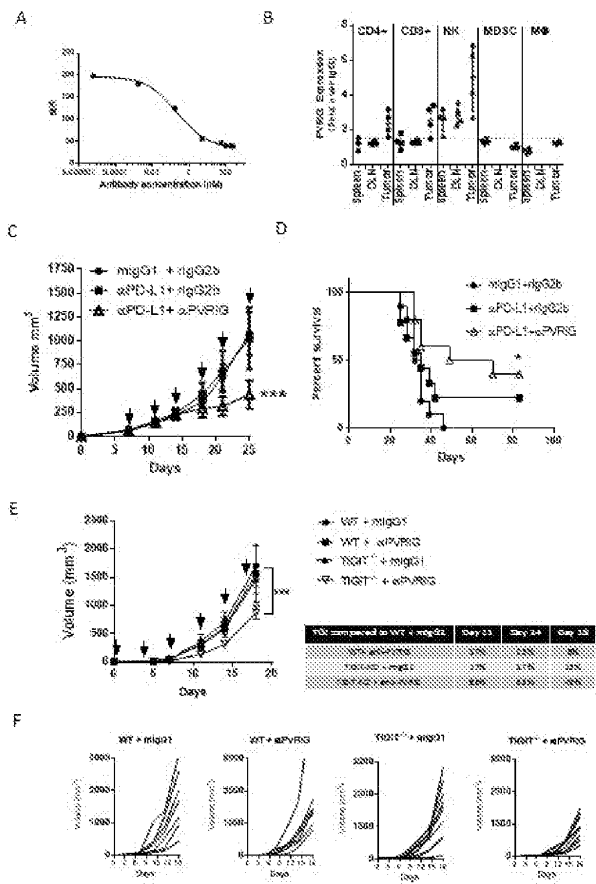


Figure 34

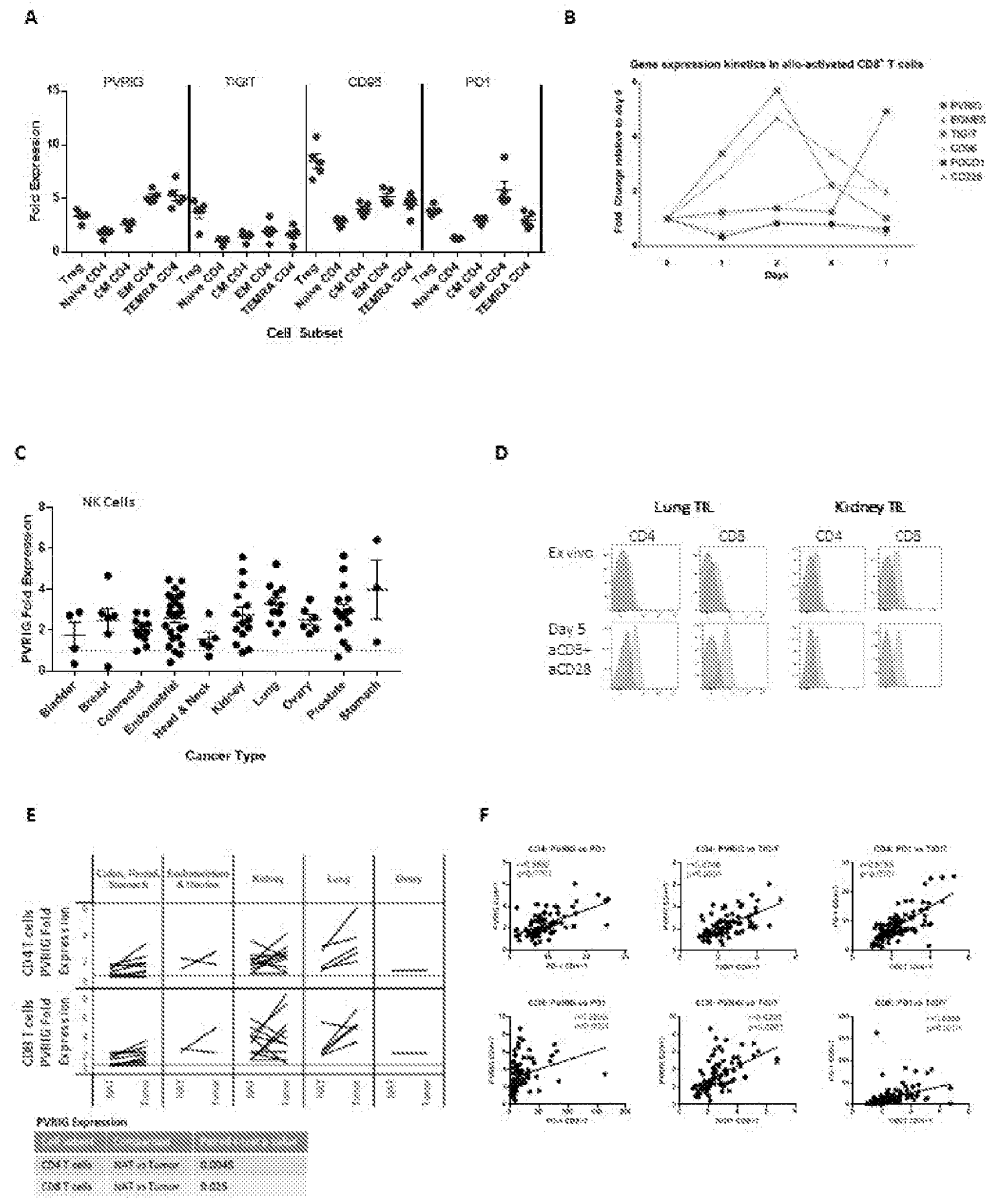


Figure 35

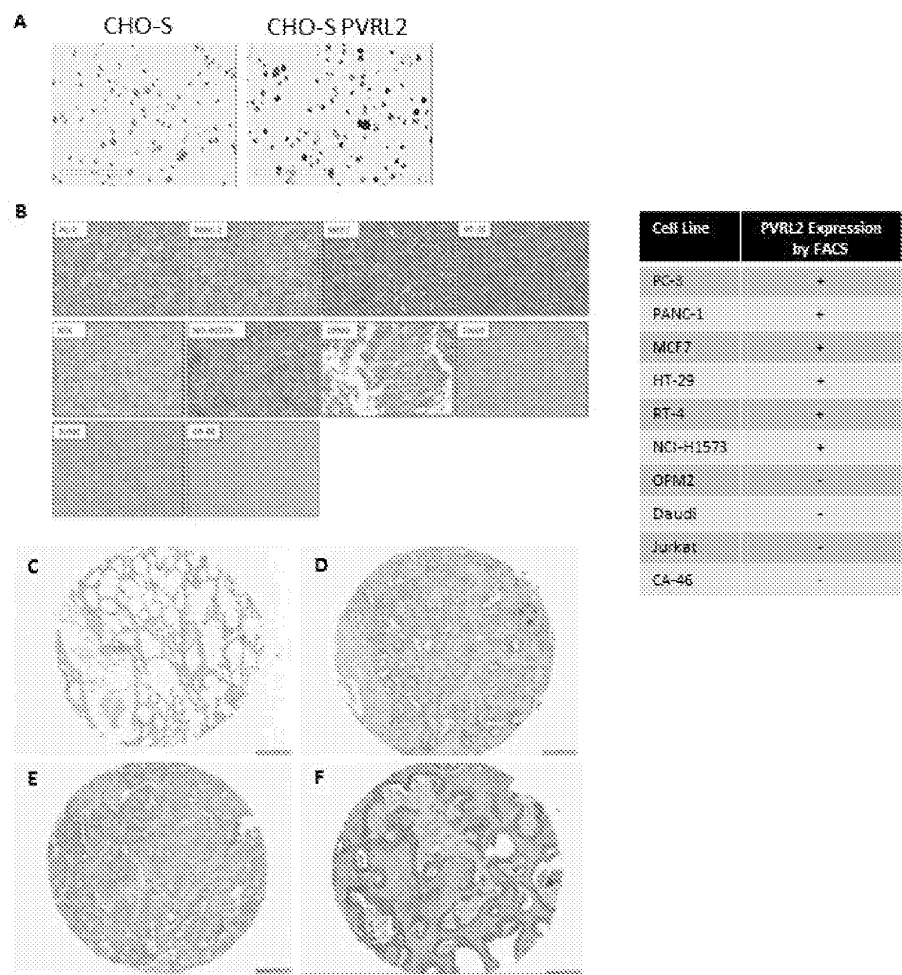


Figure 36

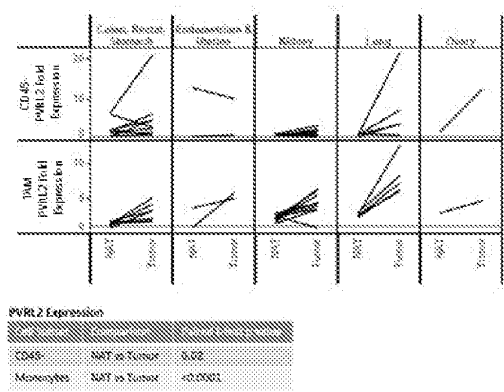


Figure 37

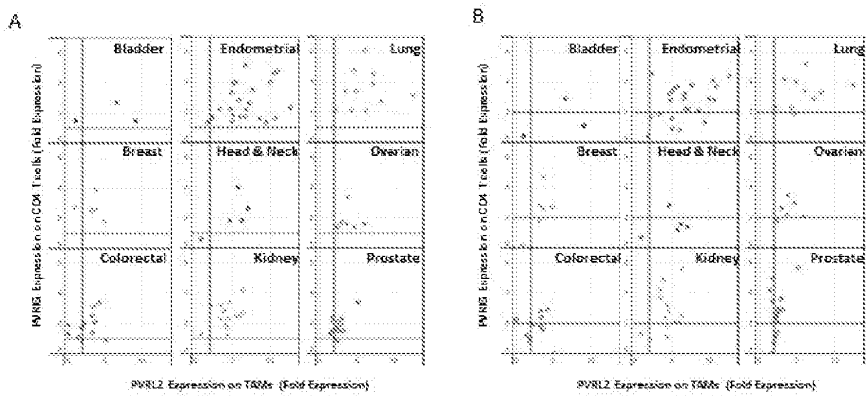


Figure 38

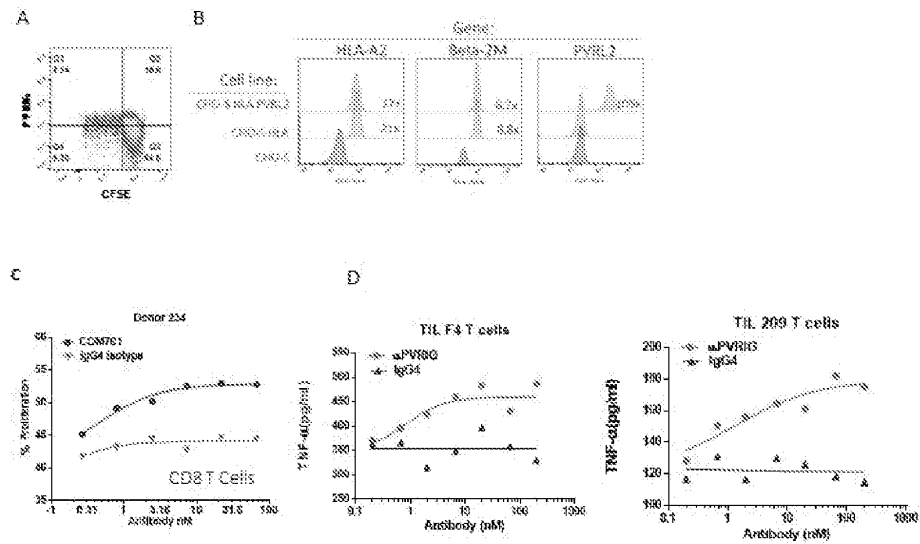


Figure 39

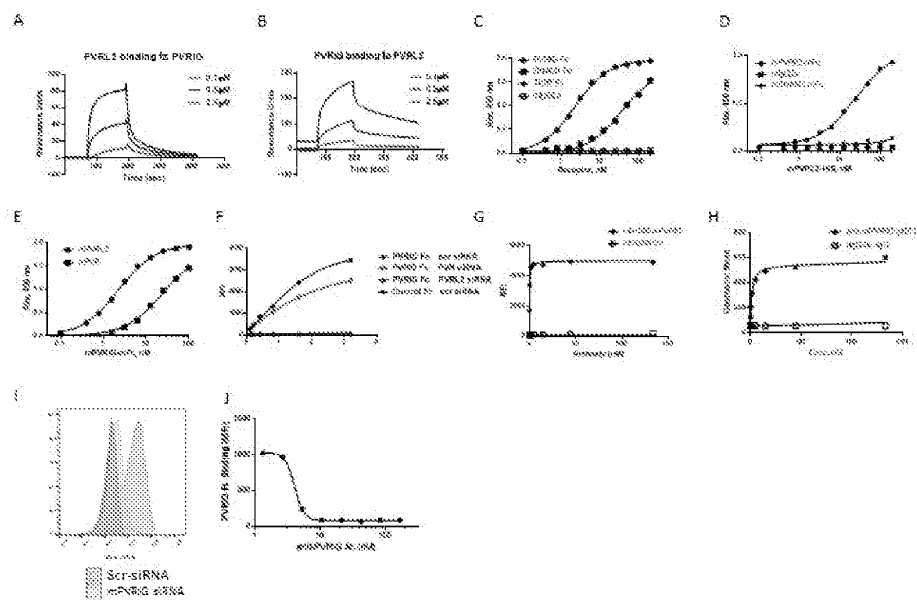


Figure 40

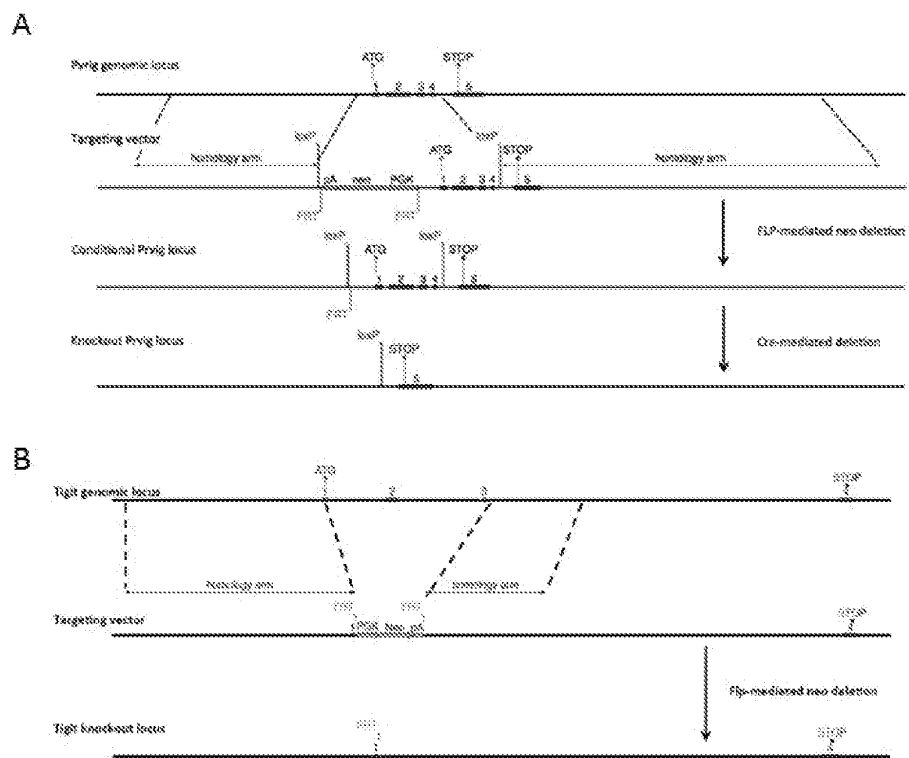


Figure 41

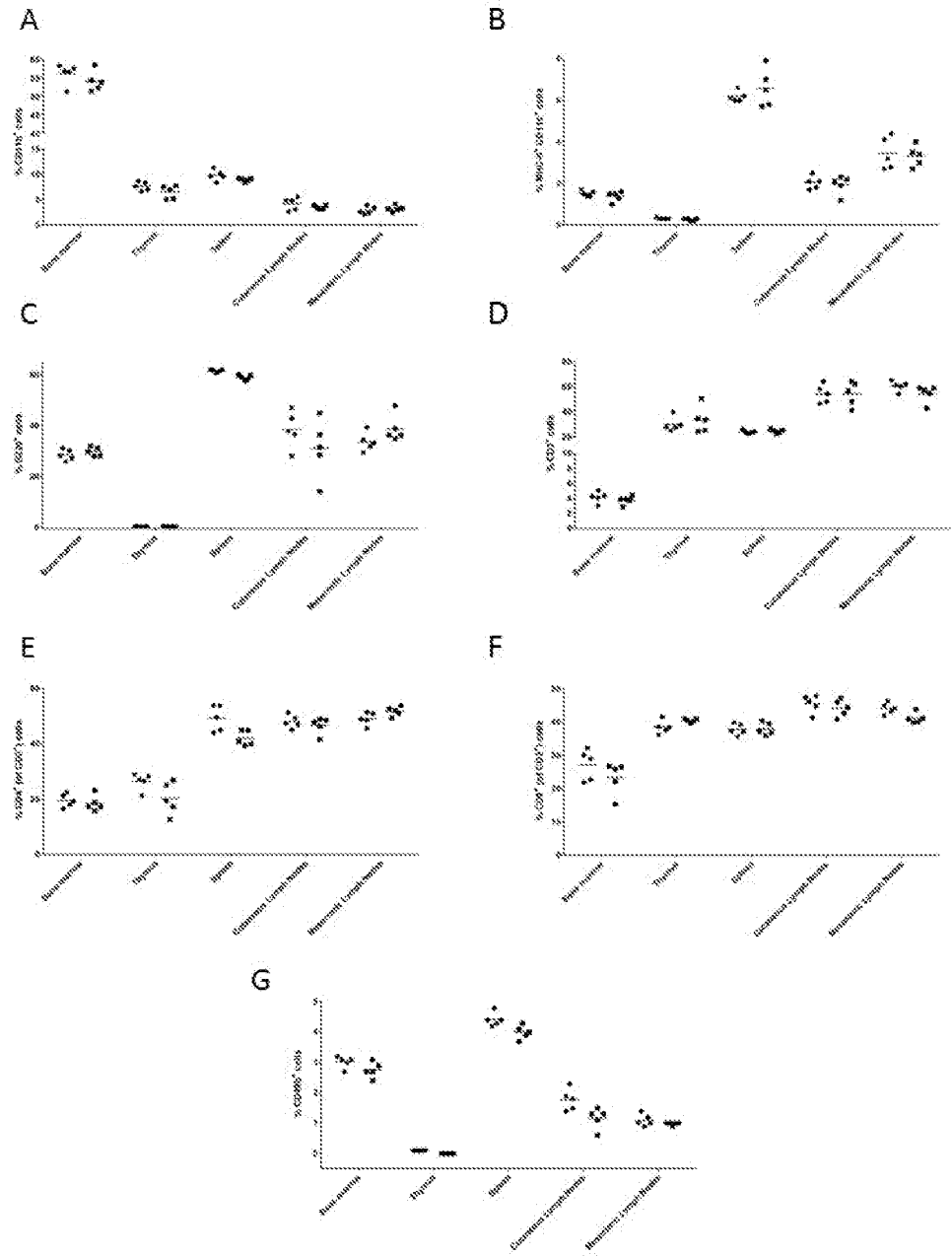


Figure 41 (cont.)

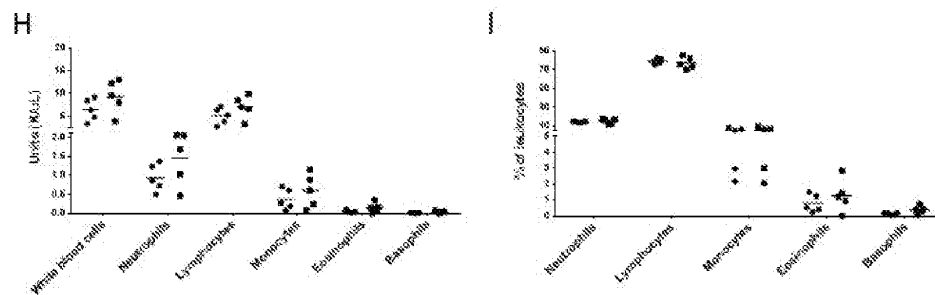


Figure 42

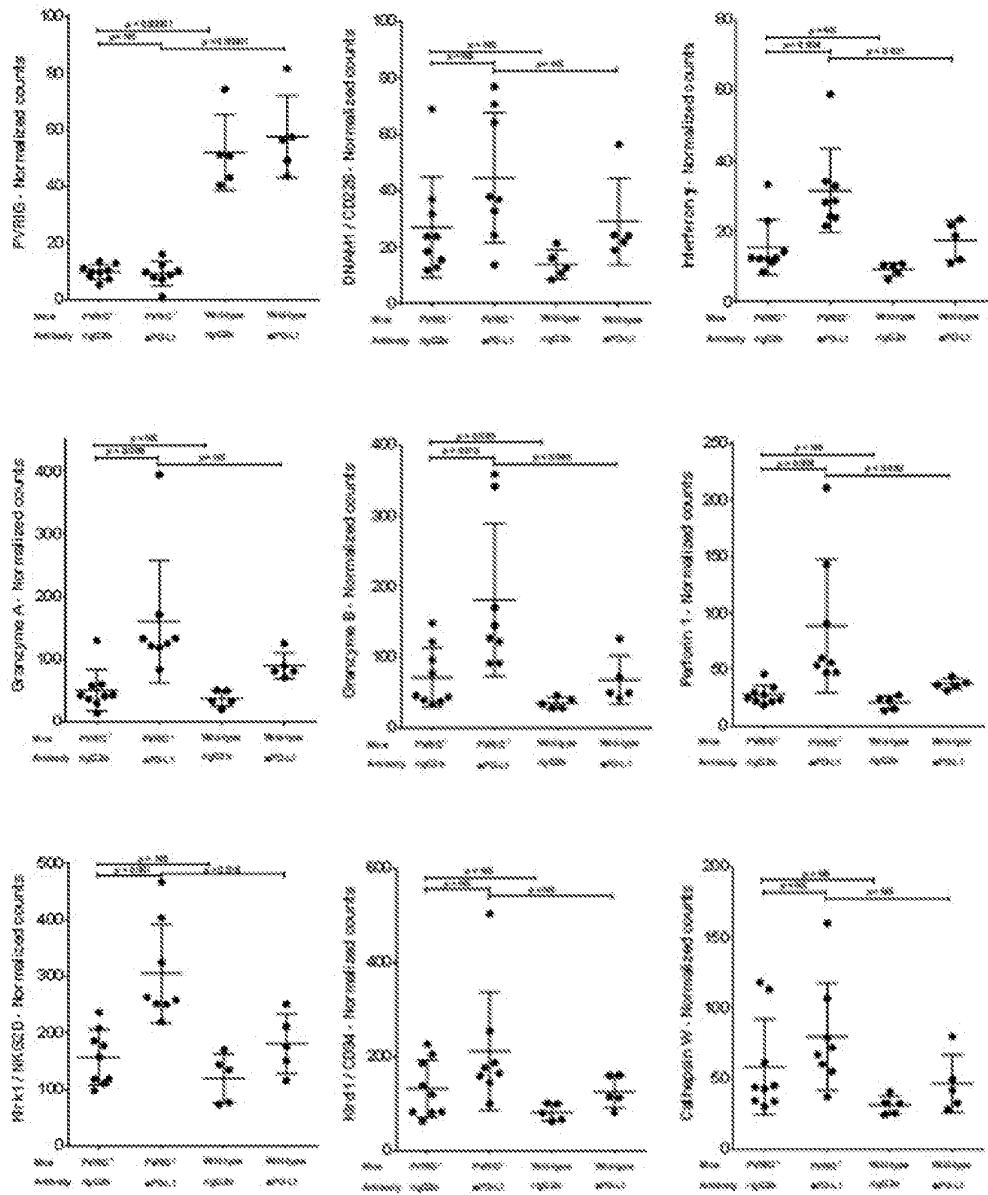


Figure 43

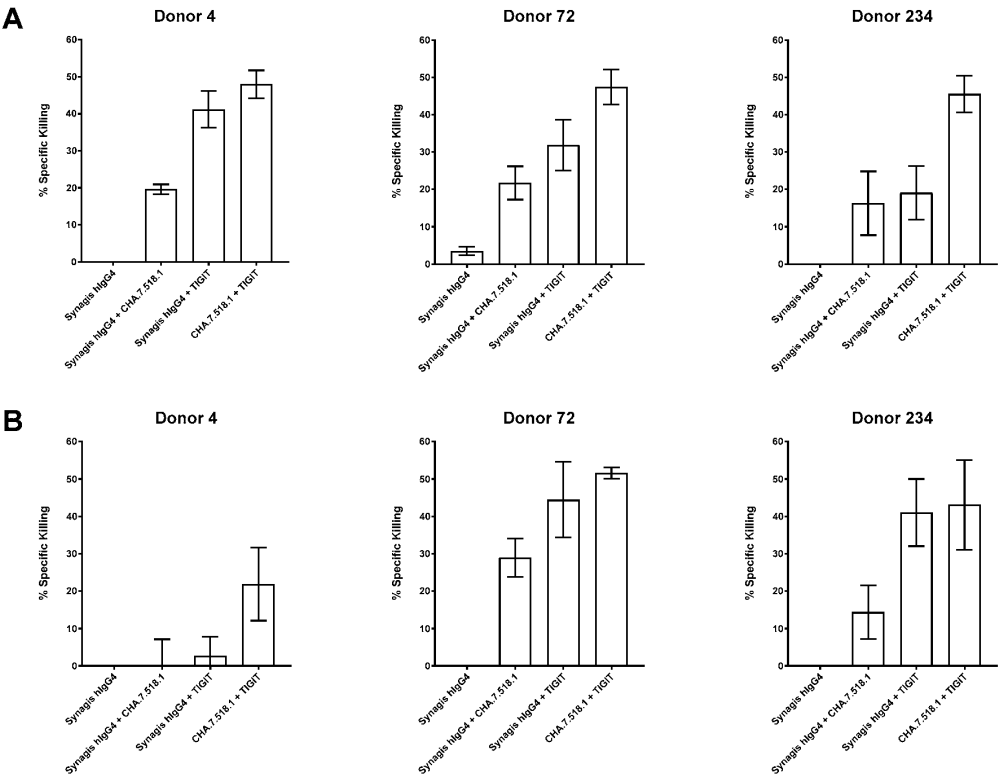


Figure 44

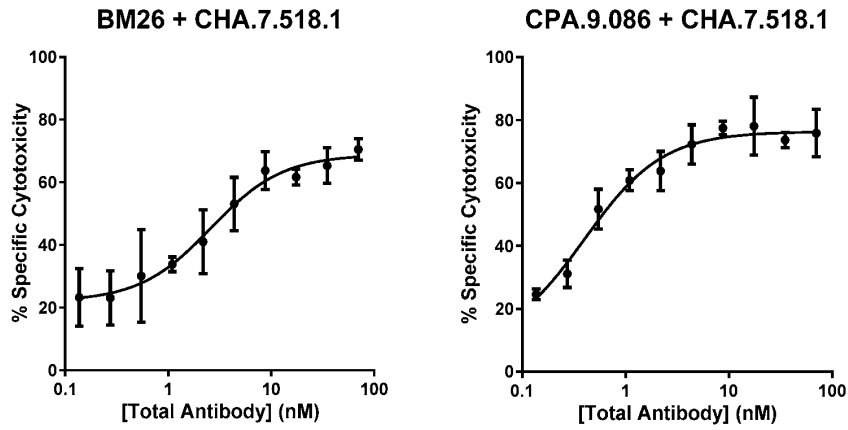
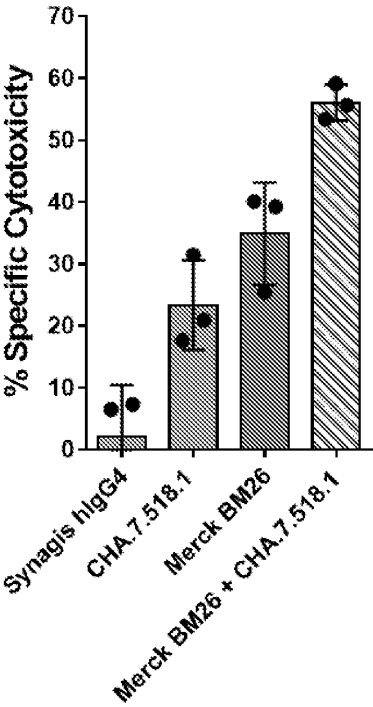


Figure 45
CPA9.086 CDR sequences

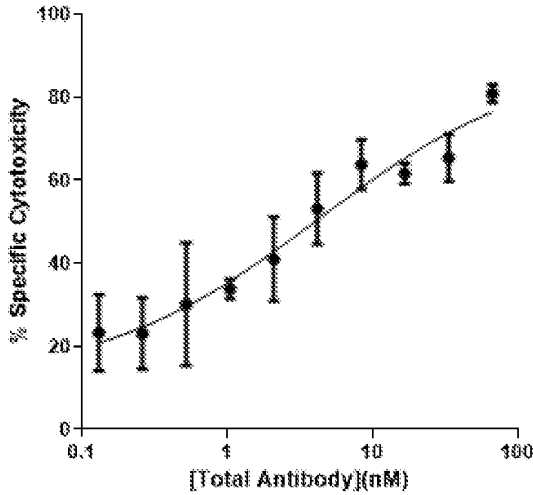
Definition		H-CDR1	H-CDR2	H-CDR3	L-CDR1	L-CDR2	L-CDR3
IMGT		GFTFSSYA (SEQ ID NO:1105)	SYAGEVK (SEQ ID NO:1107)	ARDPLPLHYGMDV (SEQ ID NO:1109)	SSNMGRRP (SEQ ID NO:1111)	SQN (SEQ ID NO:1113)	AVWDDIGRVLQ (SEQ ID NO:1115)
	Kabat	SYAMH (SEQ ID NO:1106)	VISYAGEVKYYADSVKG (SEQ ID NO:1108)	DPLPLHYGMDV (SEQ ID NO:1110)	SGSSSNM/GRRPVN (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

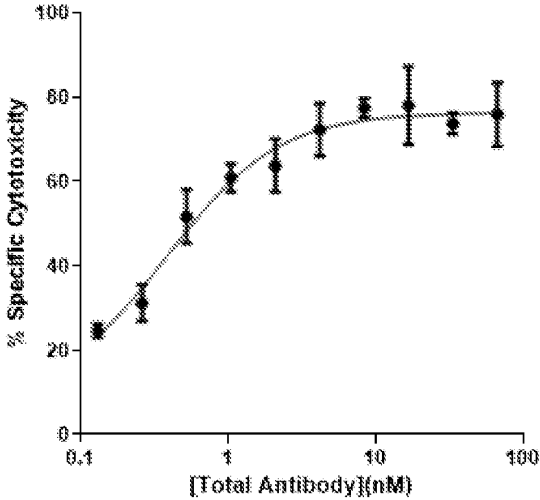


Figure 47

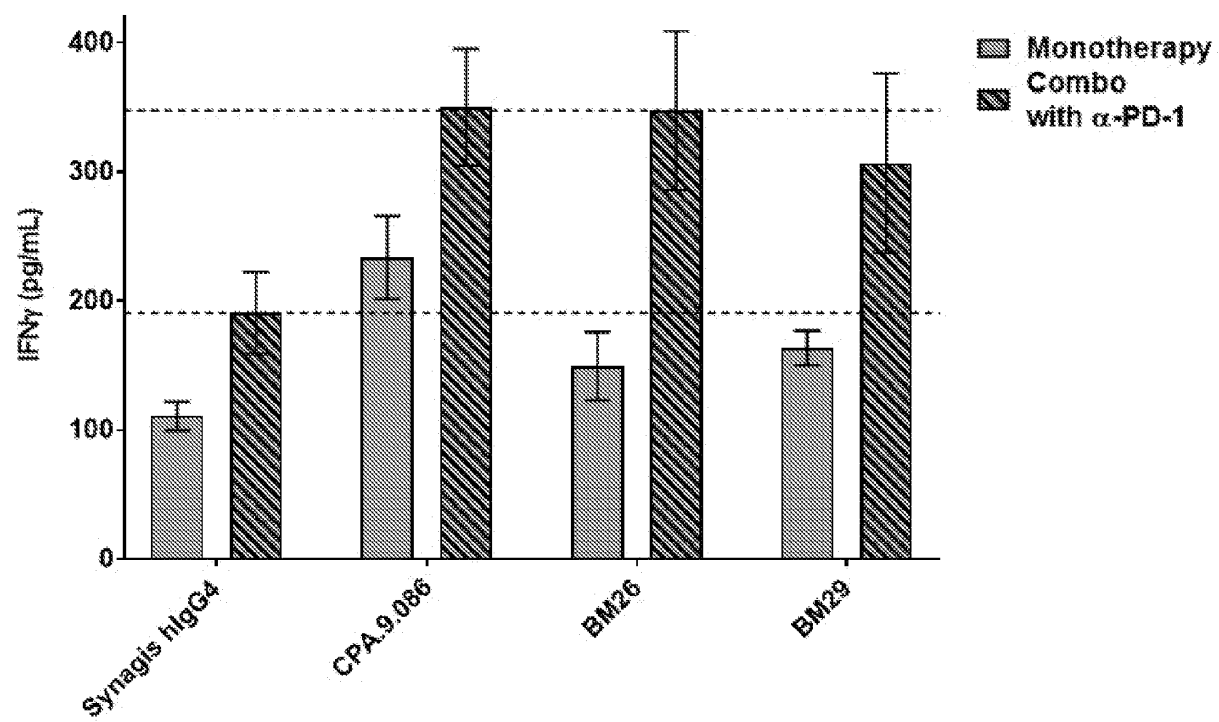


Figure 48

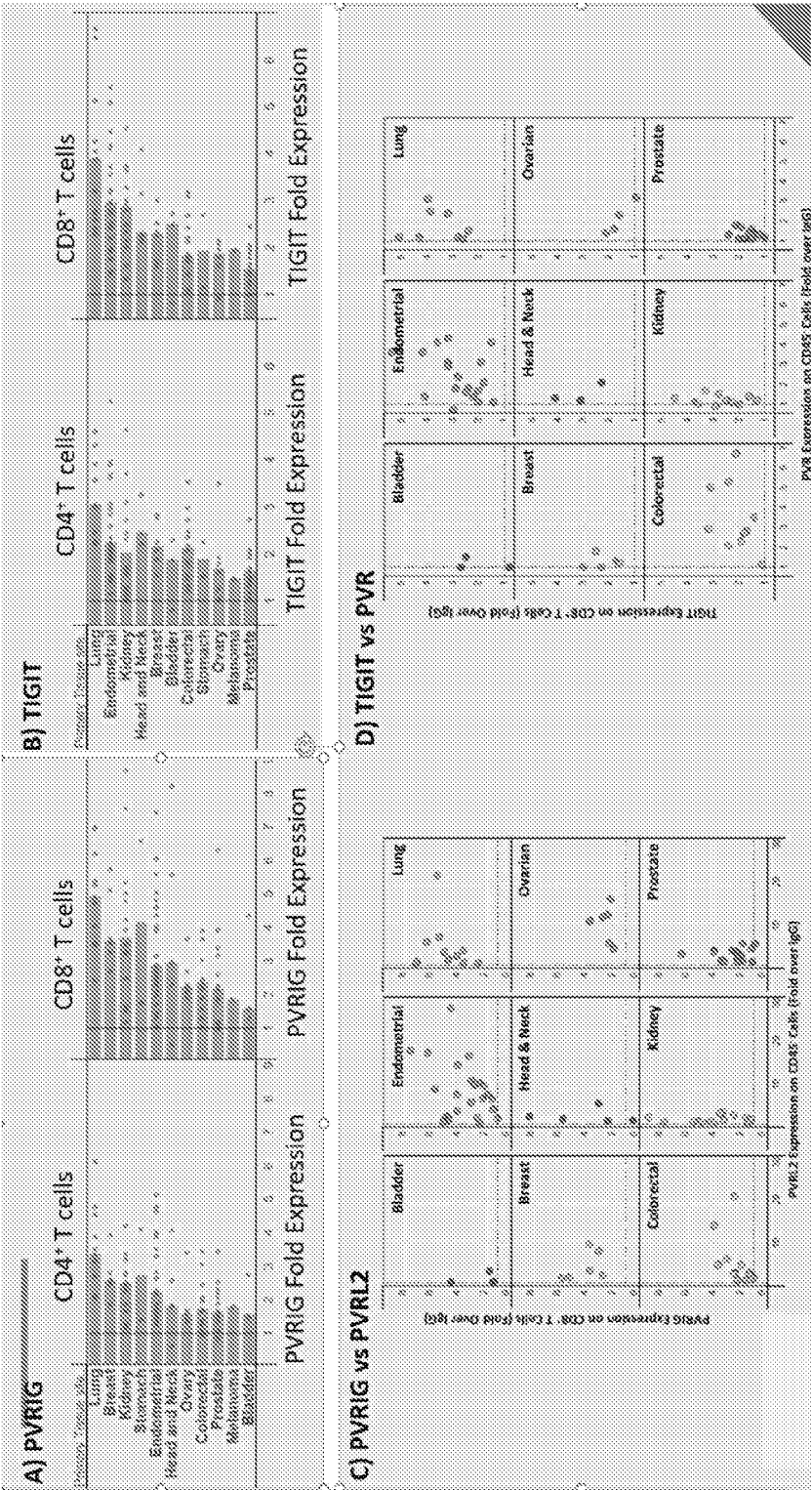


Figure 49

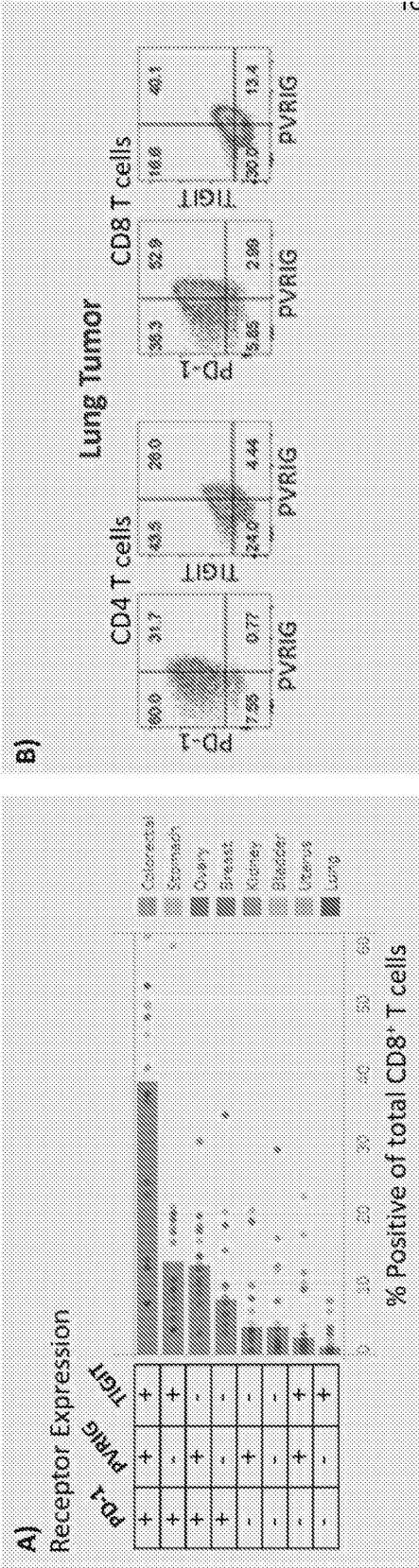
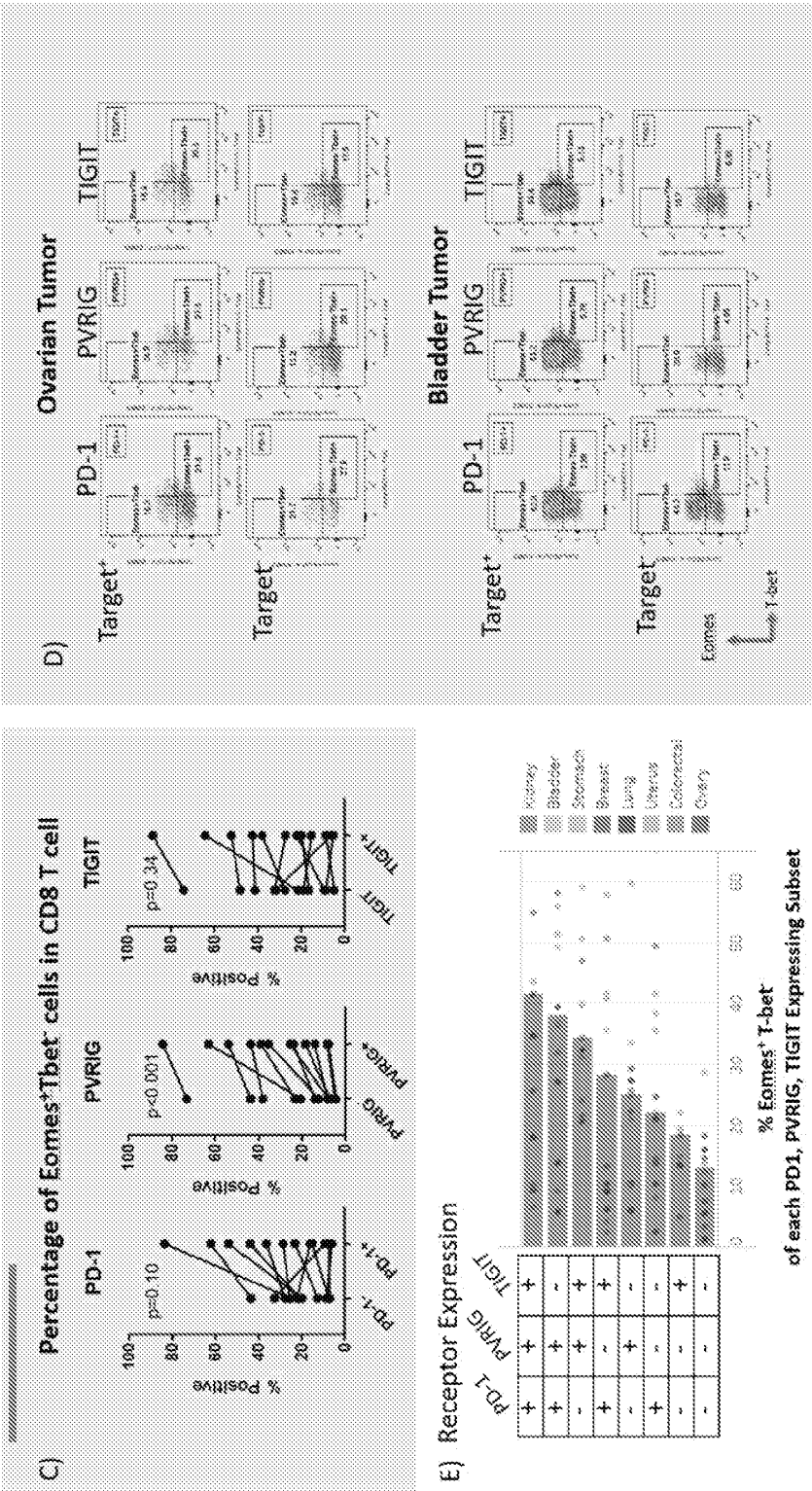


Figure 49 (cont.)



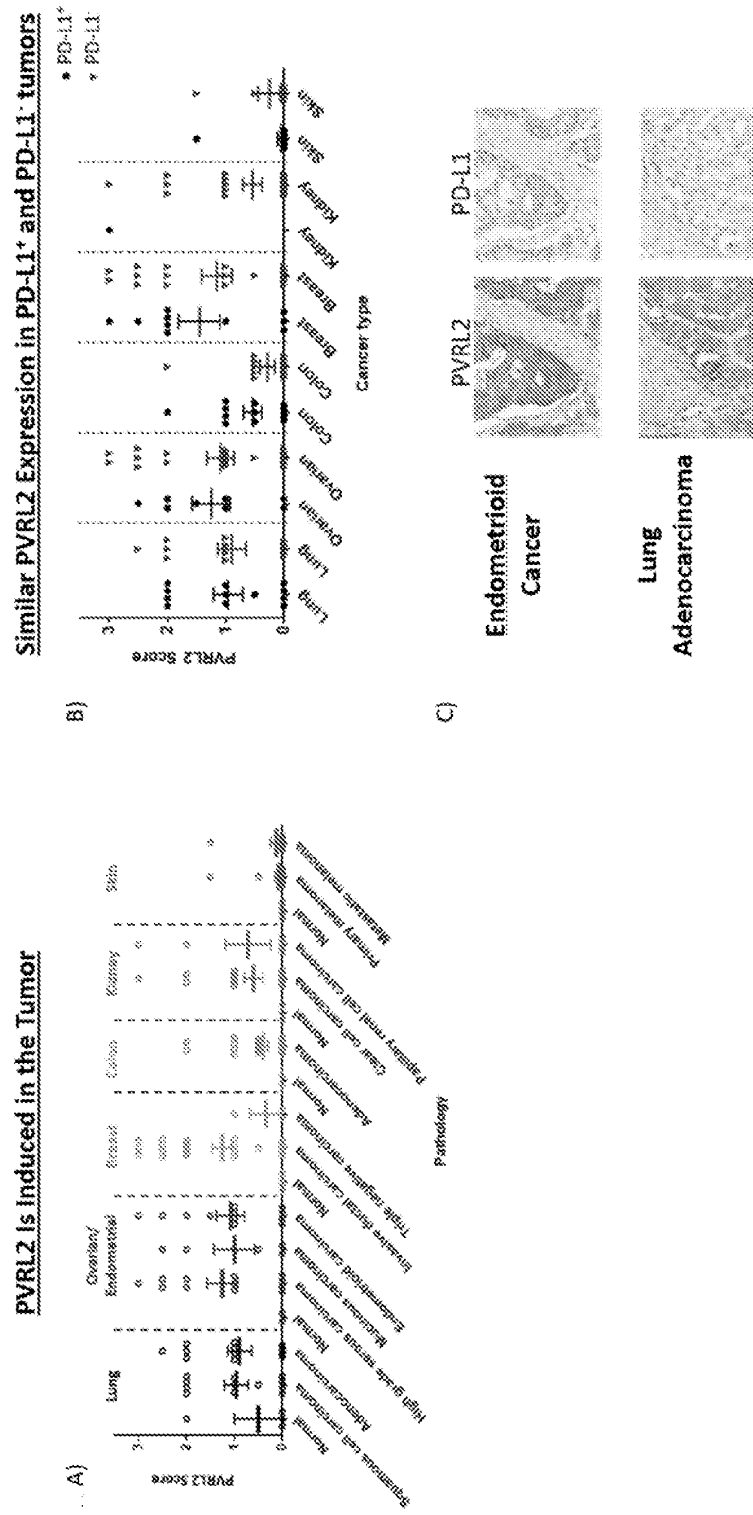


Figure 50

Figure 51

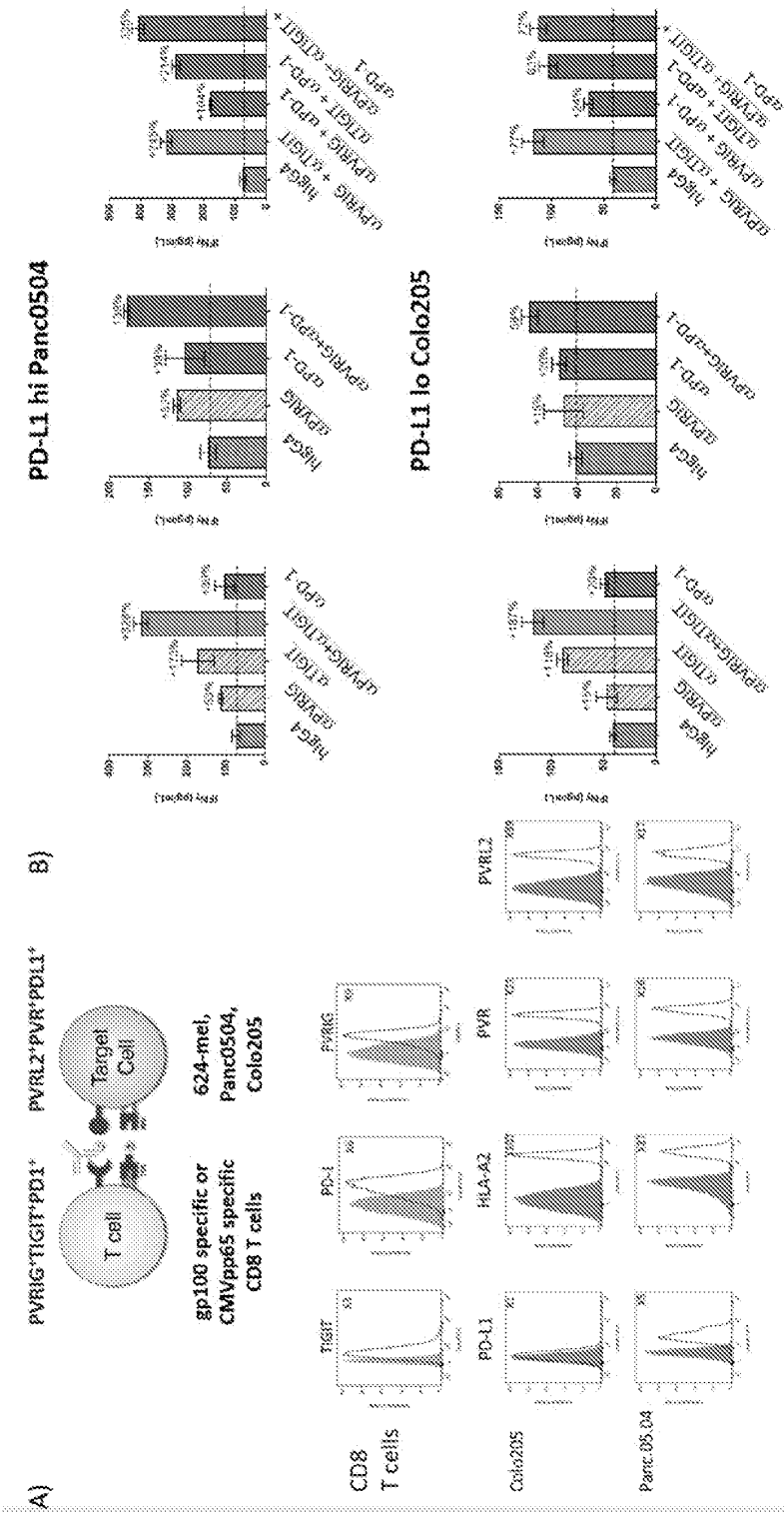
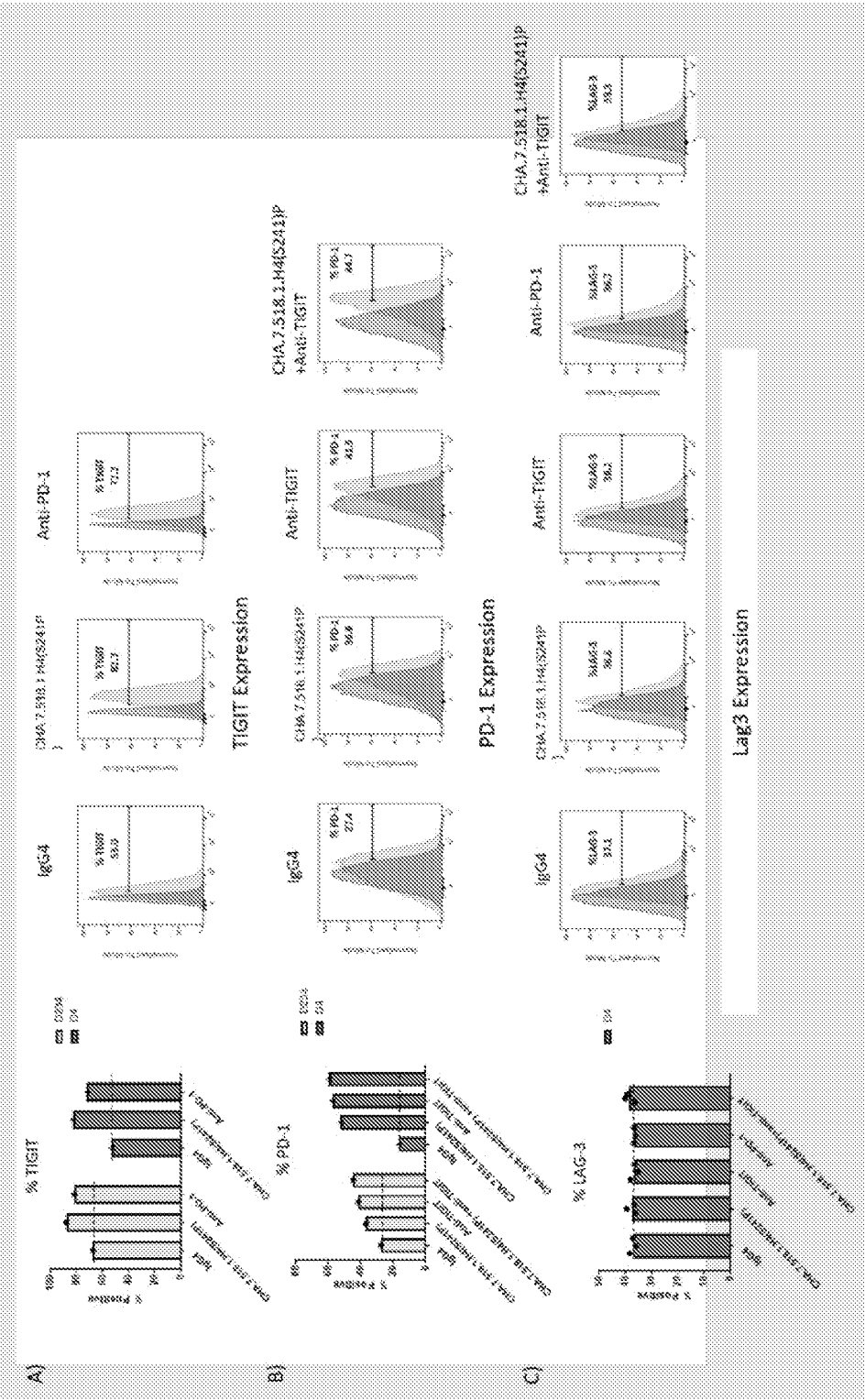


Figure 52



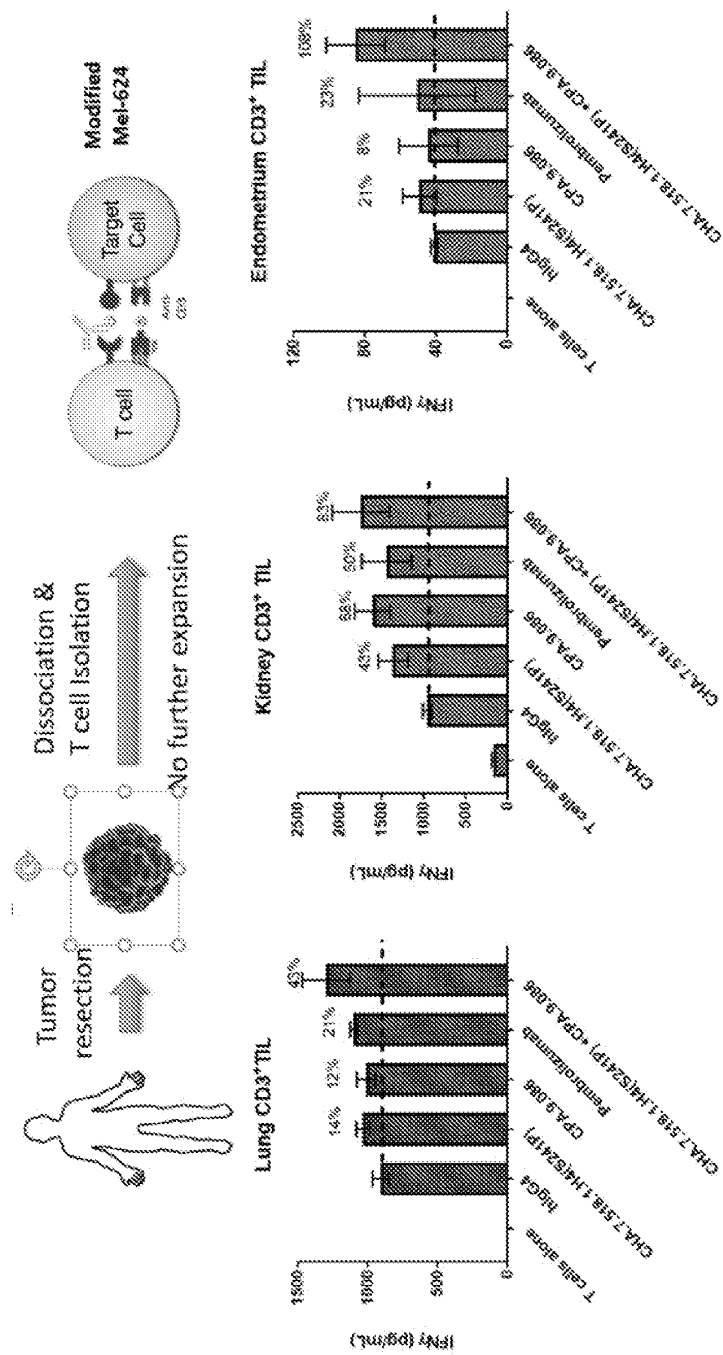
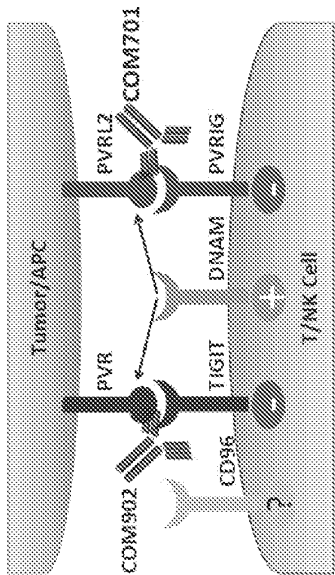
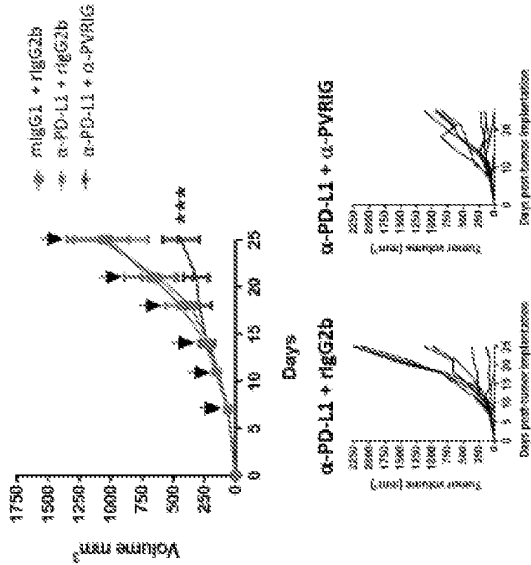


Figure 53

Figure 54



A) Reduced CT26 tumor growth in anti-PVRIG treated mice



B) Reduced MC38 tumor growth in PVRIG^{-/-} mice

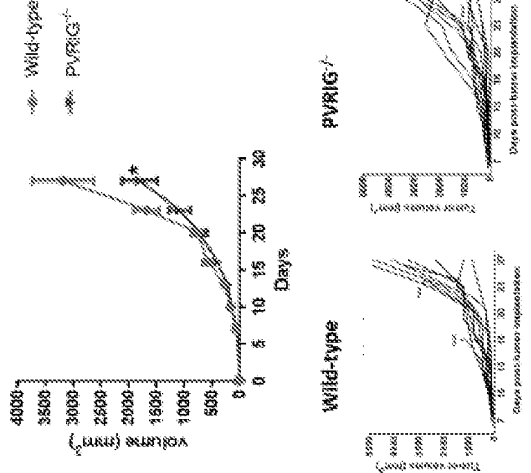


Figure 55

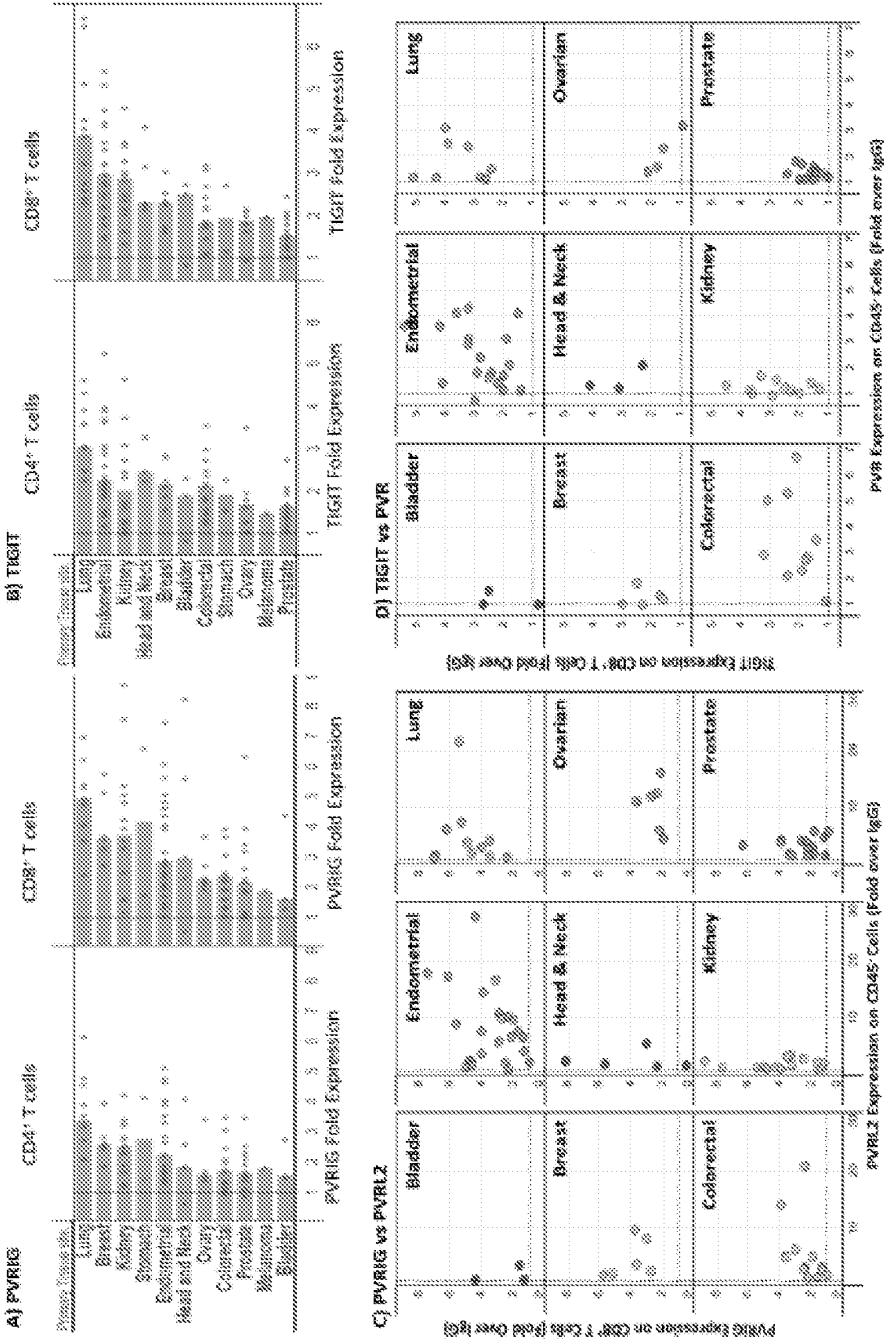


Figure 56

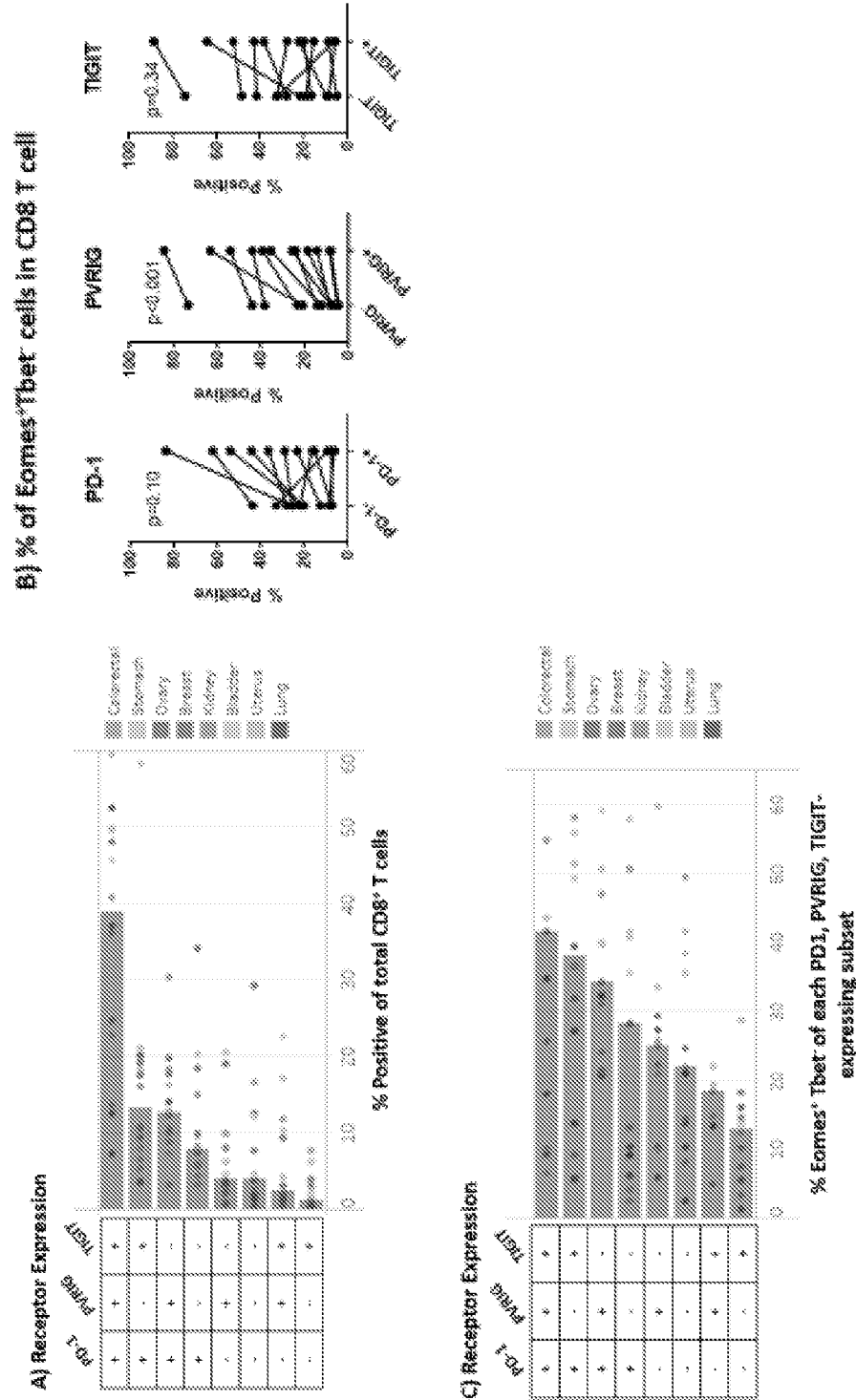
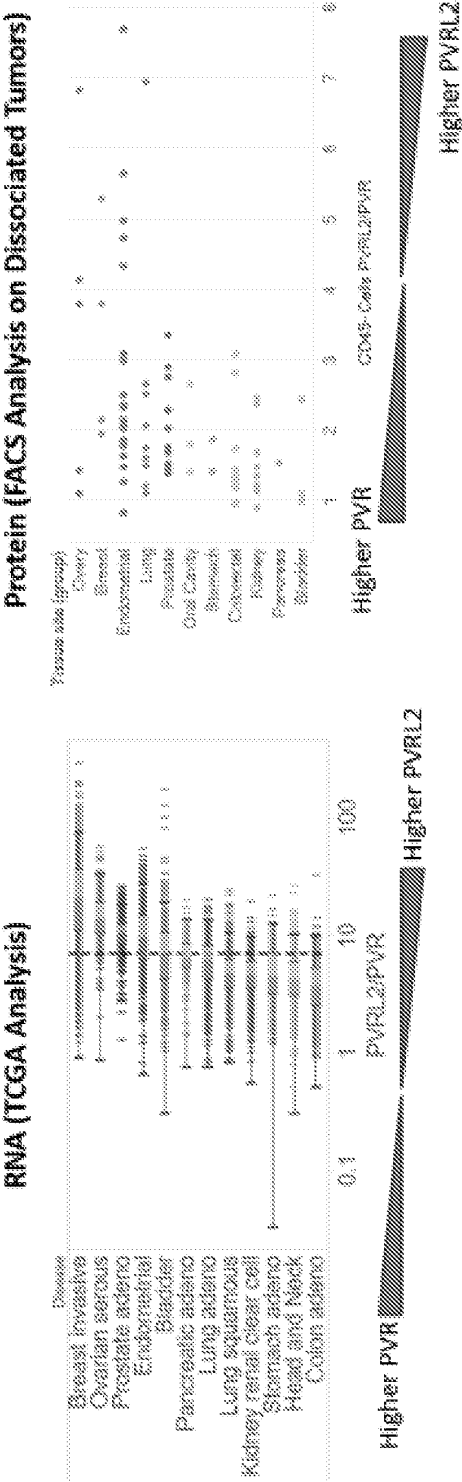


Figure 57



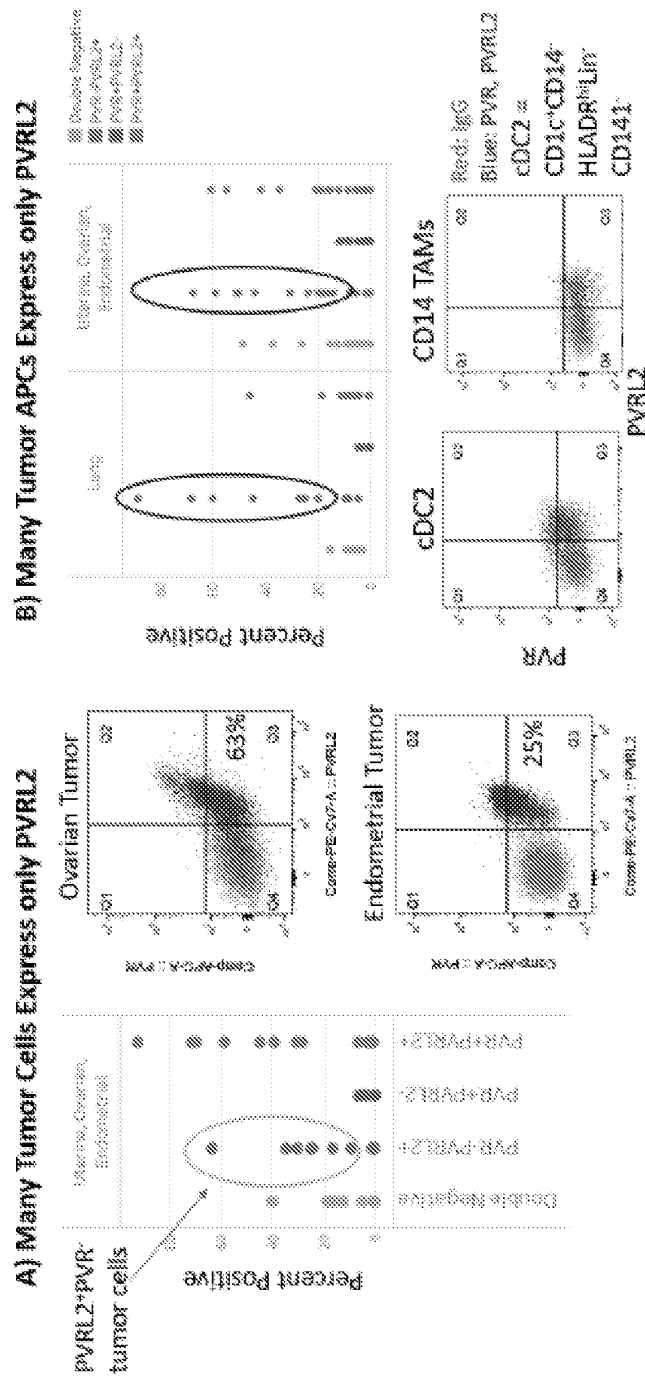


Figure 58

Figure 59

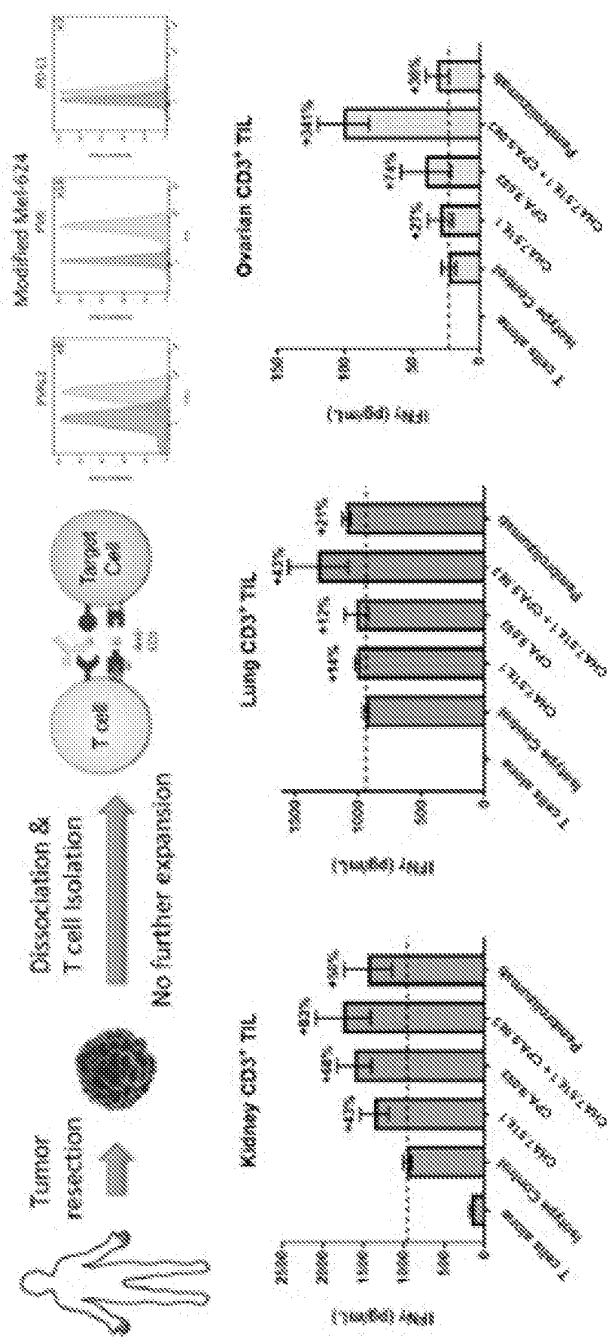


Figure 60

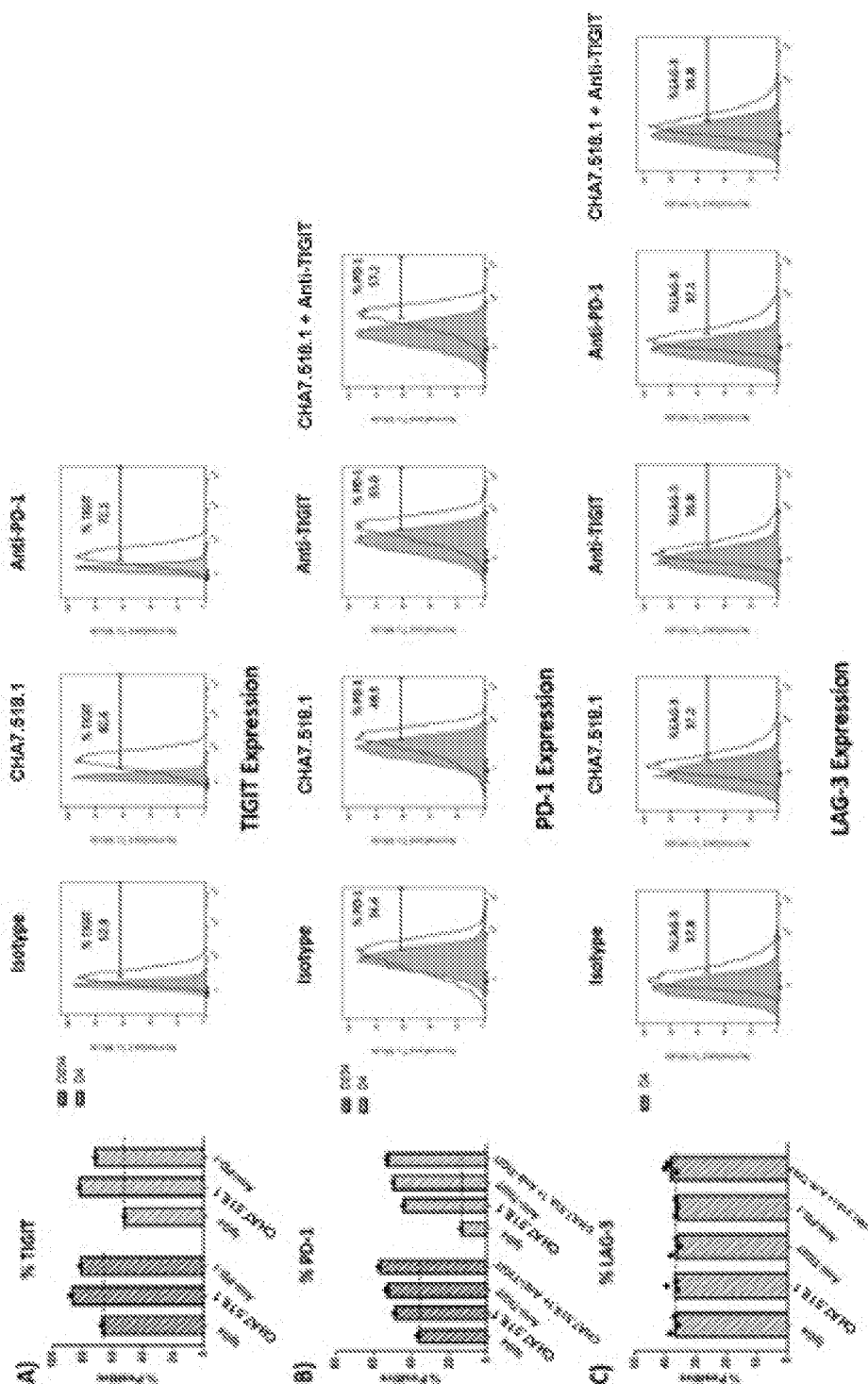
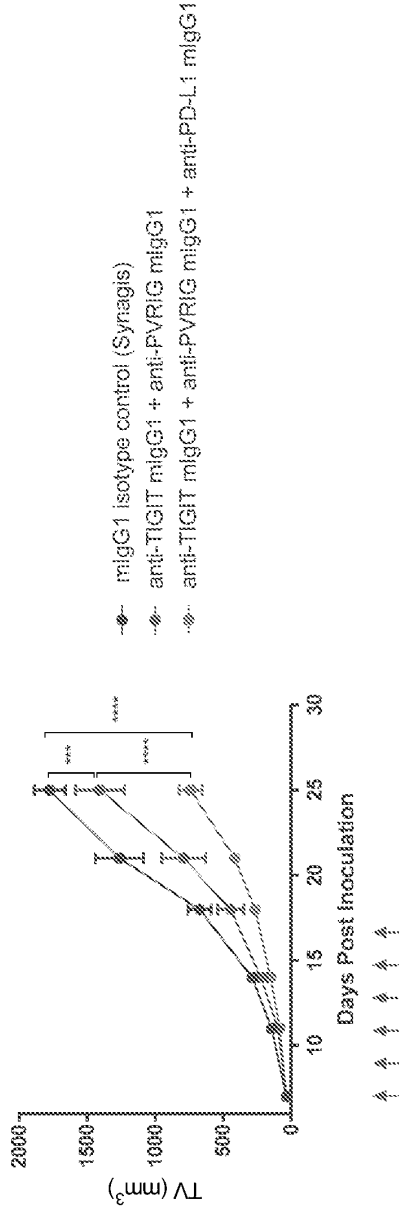


Figure 61A



TGI compared to isotype control mlgG1	Day 18	Day 21	Day 25
anti-TIGIT mlgG1 + anti-PVRIG mlgG1	34	37.3	20.7
anti-TIGIT mlgG1 + anti-PVRIG mlgG1 + anti-PD-L1 mlgG1	60.6	67.2	58.3

Figure 6IB

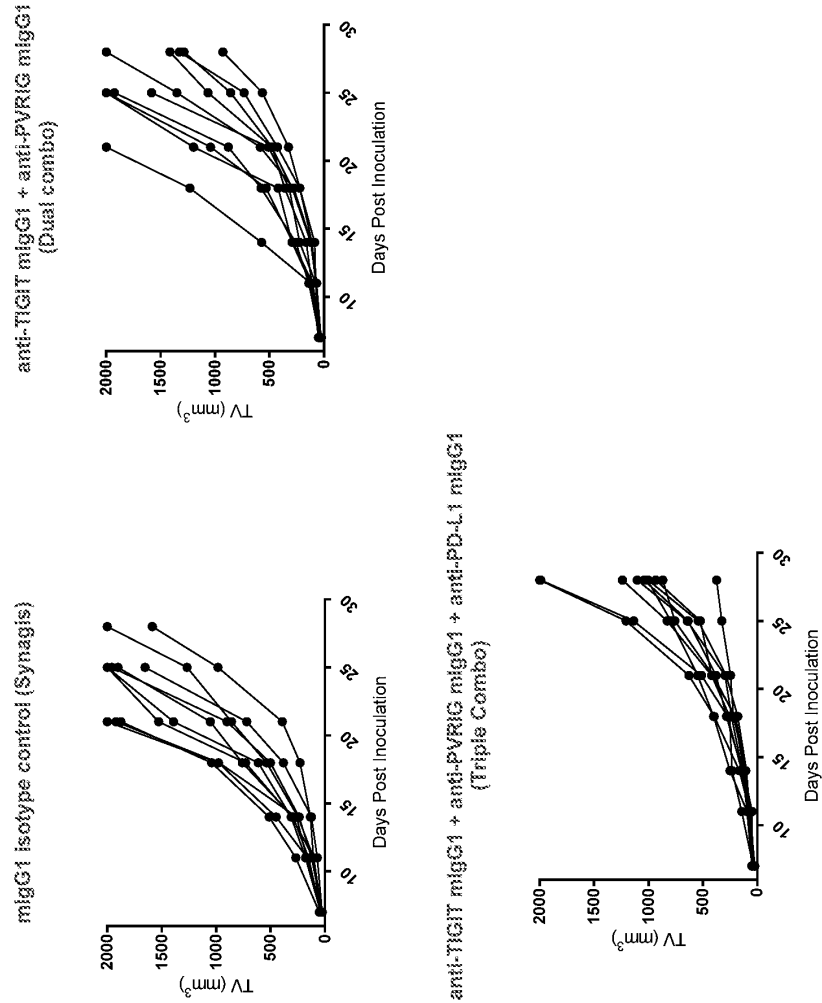


Figure 61C

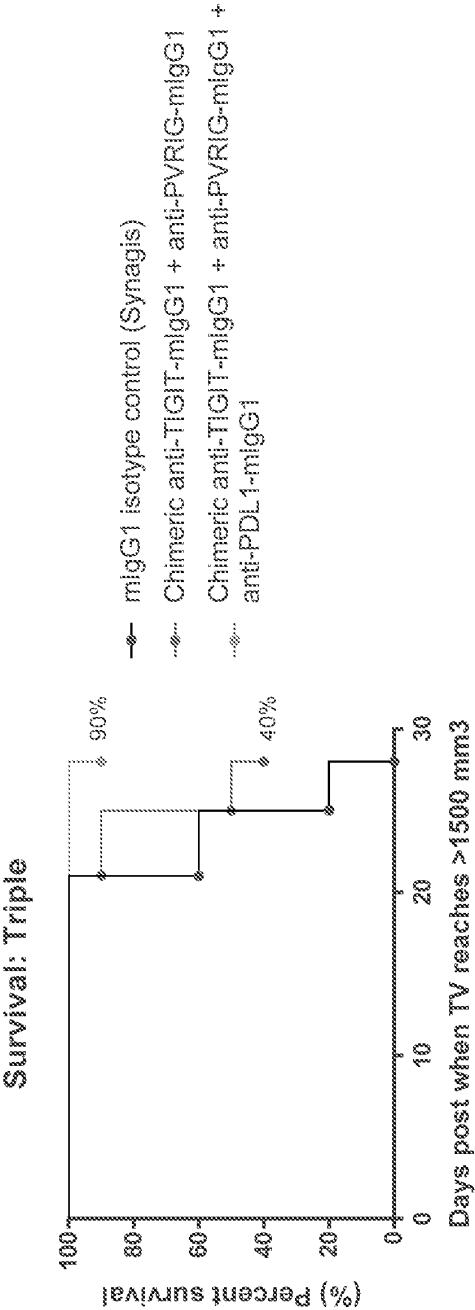


Figure 62A

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

Figure 62B

From US20170281764 (JN Biosciences)

What sequence

Heavy chain
(SEQ ID NO:34 from
US2017281764)

EVQL VESGGGLVQPGGSLRLSCAASGFTTSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADIS
VVKGRFTISADTSKNTAYLQNNSLRAEDTAVYYCARRHWPGGFDYWGGQGLTVTVAASATKGPS
VFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVP
SSSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVSVSLTVLHQDWLNGK
SYGCKVKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE
TNGKPKTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
DIQMQTSPSSLSASVGDRTTTCRASQDVSTAVAWYQQKPGKAPKLLIYASFLYSGVPSRFSGS
GGSGTDFTLTISIQLPEDFAFYQCQYLFPTPTFGQTKVEIKRTVAAPSVFIFPPSDFQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKIDSTYSLSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC

Light chain
(SEQ ID NO:36 from
US2017281764)

DIQMTSPSSLSASVGDRTTTCRASQDVSTAAWYQQKPGKAPKLLIYASFLYSGVPSRFRSGS
VTHQGLSSPVTKSFNRGEC

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)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGLVT VSA	1127
vhCDR1 (SEQ ID NO:17 from WO2015009856)	GFTFSDSWIH	1128
vhCDR2 (SEQ ID NO:18 from WO2015009856)	A WISPYGGSTYYADSVKG	1129
vhCDR3 (SEQ ID NO:19 from WO2015009856)	RHWPGGFDY	1130
Light chain (SEQ ID NO:24 from WO2015009856)	DIQMTQSPSSLSASVGDRTVTTCRASQDVSTAVAWYQKPGKAPKLLIYSASFLYSGVPS RFGSGSGTDFTLTISLQPEDFATYYCQQLYHPATFGQGTKVEIKR	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	SEQ ID NO:
Heavy chain (SEQ ID NO: 40 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWV A WISPYGG STYY ADSVKGRFTISADTSKNTA YLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSSASTK (SEQ ID NO:40), or	1135
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTA VA WYQKPGKAPKLLIYSASF YSG VPSRFGSGSGTDFLTITSLQPEDF ATYYCQQL YHPATFGQGTKVEIKR (SEQ ID NO:24)	1136
From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)		
What	sequence	SEQ ID NO
Heavy chain (SEQ ID NO: 41 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGG STYYADSVKGRFTISADTSKNTA YLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSS	1137
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTA VAWYQKPGKAPKLLIYSASF YSGVPS RFGSGSGTDFLTITSLQPEDFATYYCQQL YHPATFGQGTKVEIKR	1138

Figure 62E

From US20160222117 (GENENTECH, INC.)			SEQ ID NO:
What	sequence		
Heavy chain (SEQ ID NO:20 from US20160222117)	EVQLVESCGGLVQPGGSLRLSCAASGFTFSDSWIHVVRRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLVT VSA		1139
Heavy chain (SEQ ID NO:23 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLVT VSA		1140
Heavy chain (SEQ ID NO:24 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSGSWIHVVRRQAPGKGLEWVAWILPYGGSS YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLVT VSA		1141
From US20160222117 (GENENTECH, INC.)			SEQ ID NO
What	sequence		
Light chain (SEQ ID NO:21 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQYLYHPATFGQGGTKVEIKR		1142
Light chain (SEQ ID NO:26 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQYLYNVPWTFGQGGTKVEIKR		1143
Light chain (SEQ ID NO:27 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQYLYAPPWTFGQGGTKVEIKR		1144

Figure 62F

From US20160222117 (GENENTECH, INC.)		SEQ ID NO:
What	sequence	
Light chain (SEQ ID NO:28 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYYTVPWTFGGGTKVEIKR	1145
Light chain (SEQ ID NO:29 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQVINTFLAWYQQKPGKAPKLLIYSASTLASGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYYTVPRTFGGGTKVEIKR	1146
Light chain (SEQ ID NO:30 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYGVPRTFGGGTKVEIKR	1147
Light chain (SEQ ID NO:31 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYLLTPPTFGGGTKVEIKR	1148
Light chain (SEQ ID NO:32 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYFHTPTTFGGGTKVEIKR	1149
Light chain (SEQ ID NO:33 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQYYTPTTFGGGTKVEIKR	1150
Light chain (SEQ ID NO:34 from US20160222117)	DIQMTQSPSSLASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFL YSGVPS RFGSGSGTDFTLTISSLQPEDFATYYCQQFFYTPPTFGGGTKVEIKR	1151

Figure 62G

From US20160222117 (GENENTECH, INC.)		What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:35 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1152
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQSLFTPTTFGGQGTKVEIKR	
Light chain (SEQ ID NO:36 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1153
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQSLYTPPTTFGGQGTKVEIKR	
Light chain (SEQ ID NO:37 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1154
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQSWYHPPTTFGGQGTKVEIKR	
Light chain (SEQ ID NO:38 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1155
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQYFYIPPTTFGGQGTKVEIKR	
Light chain (SEQ ID NO:39 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1156
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQYVWYTPYTFGGQGTKVEIKR	
Light chain (SEQ ID NO:40 from US20160222117)			DIQMTQSPSSLASVGGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS	1157
			RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYFPPPTTFGGQGTKVEIKR	

Figure 62H

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

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO2013079174)	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADT VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCCARIKLGITVTITVDYWGQGTLVTVSSASTKG PSVFEPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSHFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYYTQKSLSLSPGK	1158
Light chain (SEQ ID NO: from WO2013079174)	QSAITQPASVSGSPGQSITISCTGTSSDVGGYNYSWYQQHPGKAPKLMYDVSNRPSGVSNR FSGSKSGNTASLTISGLQAEDEADYYCSYTSSTSRVFGTGKVTVLGQPKANPTVTLFPPSSEE LQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETITKPSKQSNNKYAASSYLSLTPEQW KSHRSYSCQVTHEGSTVEKTVAPTDCS	1159

Figure 62I

From US8217149 (Hoffman La Roche; Atezolizumab)		
What	sequence	SEQ ID NO:
Heavy chain (VH)		
(SEQ ID NO:20 from US8217149)	EVQLVESGGGLVQPGGSLRLSCAASGFTTSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYA	1160
Light chain (VL)	DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSA	
Light chain (VL)		
(SEQ ID NO:21 from US8217149)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKAPKWSASFLYSGVPSRFSGS	1161
	GSQTDFTLTISLQPEDFATYYC QQYL YH PATFGQGTKVEIKR	
Atezolizumab (alternate sequence))		
What	sequence	SEQ ID NO
Heavy chain		
(from IMGt database or DrugBank database)	EVQLVESGGGLVQPGGSLRLSCAASGFTTSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYA	1162
	DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSSASTK	
	GPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSQVHTFPAVLQSSGLYSLSV	
	VIVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPK	
	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTIVL	
	HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG	
	FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH	
	NHYTEQKSLSLSPGK	
Light chain		
(from IMGt database or DrugBank database)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSG	1163
	SGSGTDFTLTISLQPEDFATYYCQQYL YHPATFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT	
	ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYKEHKV	
	YACEVTHQGLSPVTKSFNRGEC	

Figure 63A

CPA.7.001

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIMQLVQSGAEVKKPGSSVKVSKCKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSS	1164
vhCDR1	GGTFSSYA	1165
vhCDR2	IIPIFGTA	1166
vhCDR3	AREEVSSPYGMDV	1167
Full length HC	QIMQLVQSGAEVKKPGSSVKVSKCKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPPKPD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVTHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTPPVLDSDGGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1168
Variable light (vl) domain	QAVVTQEPSTVSPGGTVTLTCGTSTGAVTSGHYPYWVQQKPGQAPKTLIYDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYCILLSYSGASWVFGGGTKLTVLG	1169
vlCDR1	TGAVTSGHY	1170
vlCDR2	DTG	1171
vlCDR3	LLSYSGASWV	1172
Full length light chain	QAVVTQEPSTVSPGGTVTLTCGTSTGAVTSGHYPYWVQQKPGQAPKTLIYDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYCILLSYSGASWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT PSKDSNNKYAASSYLSLTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS	1173

Figure 638
CPA.7.003

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKVSGFSLSHESMHVWRQVPGKGLEWLGGFDP EEGGTIPAKQFQGRLLTMTEDTST ETAYMELSLRSED TAVVYCATGIWYSSGWPVDYWGPGTLTVSS	1174
vhCDR1	<u>GFSLSHES</u>	1175
vhCDR2	<u>FDPEEGGT</u>	1176
vhCDR3	<u>ATGIWYSSGWPVDY</u>	1177
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGRVITADKSTST AYMELSLRSED TAVVYCARGPWYDSSGYSSAYYMDVWGQGTITVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWWLNGKEYCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1178
Variable light (vl) domain	DVVMTQSPLSLPVTPGGPASISCRSSQSLDSSGYNVDWYVLPKPGQSPQLLISLGS DRASGV PDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKR	1179
vlCDR1	<u>QSLDSSGYNV</u>	1180
vlCDR2	<u>LGS</u>	1181
vlCDR3	<u>MQALQTPIT</u>	1182
Full length light chain	DVVMTQSPLSLPVTPGGPASISCRSSQSLDSSGYNVDWYVLPKPGQSPQLLISLGS DRASGV PDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSSTYSLSLTLSKADYKEHKHYACEVTHQGLSSPVTKSFNRGEC	1183

Figure 63C
CPA.7.004

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATVSRVRGVINYYMDV WGKGTTTVTVSS	1184
vhCDR1	<u>GYTLTSL</u>	1185
vhCDR2	<u>FDPEDGET</u>	1186
vhCDR3	<u>ATVSRVRGVINYYMDV</u>	1187
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATVSRVRGVINYYMDVWGKGTTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK	1188
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDFSGSGGTDFTLKISRVEAEDVGVYCYCMQALQTPPTFGGGTKLEIKR	1189
vlCDR1	<u>QSLLYRNGNNY</u>	1190
vlCDR2	<u>LGS</u>	1191
vlCDR3	<u>MQALQTPPT</u>	1192
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDFSGSGGTDFTLKISRVEAEDVGVYCYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1193

Figure 63D
CPA.7.006

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVRRPGSSRVSCKPSGGTFTGYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDATVYYCARGFEYSDGLLDDWGGQGLTVTVSS	1194
vhCDR1	<u>GGTFTGYA</u>	1195
vhCDR2	<u>ITPISATI</u>	1196
vhCDR3	<u>ARGFEYSDGLLDD</u>	1197
Full length HC	QVQLVQSGAEVRRPGSSRVSCKPSGGTFTGYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDATVYYCARGFEYSDGLLDDWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTWSWNSGALTSGVHTFPAVLQSSGLYSLSSWTPVSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFELYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1198
Variable light (vl) domain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGGTDFTLKI SRVEAEDGVYYCMQHMEFPLTFGGGTTKVEIKR	1199
vlCDR1	<u>QSLFYSDDGNTY</u>	1200
vlCDR2	<u>RLS</u>	1201
vlCDR3	<u>MQHMEFPLI</u>	1202
Full length light chain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGGTDFTLKI SRVEAEDGVYYCMQHMEFPLTFGGGTTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVKVDN ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1203

Figure 63E
CPA.7.008

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSGTLSTLCVSSGSISSTNWWTWVRQPPGKGLEWIGEYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYWGQGTLLVTVSS	1204
vhCDR1	<u>SGSISSTNW</u>	1205
vhCDR2	<u>IYHSGST</u>	1206
vhCDR3	<u>ARVGPAAIY</u>	1207
Full length HC	QVQLQESGPGLVKPSGTLSTLCVSSGSISSTNWWTWVRQPPGKGLEWIGEYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYWGQGTLLVTVSSASTKGPVFLPSSKSTSGGTAALGCLVKDYFPEPTVYSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSLSLGTQTYICNVNHPKSNKTKVDKKVEPKCDKTHTCPPCPAPPELLGGPS VFLFPPKPKDITLMISRTEPTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1208
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNRPSGSKRFSASRSGNTASLTITG LQPEDEADYVCSAWDSSLNAWVFGGGTQLTVLG	1209
vlCDR1	<u>SNNVGYEG</u>	1210
vlCDR2	<u>RNN</u>	1211
vlCDR3	<u>SAWDSSLNAW</u>	1212
Full length light chain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNRPSGSKRFSASRSGNTASLTITG LQPEDEADYVCSAWDSSLNAWVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW/KADS SPVKAGVETITPPSKQSNINKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1213

Figure 63F
CPA.7.009

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVS GYTLTELS MHWVRQAPGKGL EW MGGFDPEDGETI Y AQFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQ NY YYYYMDVW WGK GTITVSS	1214
vhCDR1	<u>GYTLTELS</u>	1215
vhCDR2	<u>FDPEDGET</u>	1216
vhCDR3	<u>ATAKPGIAVAGQ</u> NYYYYYMDV/	1217
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVS GYTLTELS MHWVRQAPGKGL EW MGGFDPEDGETI Y AQFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQ NY YYYYMDVW WGK GTITVSSASTKGPSVFLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCD KTHITCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	1218
Variable light (vl) domain	DVVMTQSP LS LPVTPGEPASISCRSSQSL LYR NGNNYLDWY LQ KPGQSPQLLIY LGS NRASGV PD RFSGSGSGTDFTLK SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	1219
vlCDR1	<u>QSLLYRNGNNY</u>	1220
vlCDR2	<u>LGS</u>	1221
vlCDR3	<u>MQALQTPPT</u>	1222
Full length light chain	DVVMTQSP LS LPVTPGEPASISCRSSQSL LYR NGNNYLDWY LQ KPGQSPQLLIY LGS NRASGV PD RFSGSGSGTDFTLK SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1223

Figure 63G
CPA.7.010

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLR AEDTAVVYCASSPIGYSYGYWGGM DVWGQGTTVTVSS	1224
vhCDR1	<u>GFTSSYA</u>	1225
vhCDR2	<u>ISYDGSNK</u>	1226
vhCDR3	<u>ASSPIGYSYGYWGGM DV</u>	1227
Full length HC	EVQLVESGGGLVQPGRSRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLR AEDTAVVYCASSPIGYSYGYWGGM DVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	1228
Variable light (vl) domain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVQKPGSPPOHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEADYYCLIIWHTSGWVFGGGTQLTVLG	1229
vlCDR1	<u>SGIDVRTNK</u>	1230
vlCDR2	<u>FQSDSDK</u>	1231
vlCDR3	<u>LIWHTSGWV</u>	1232
Full length light chain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVQKPGSPPOHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEADYYCLIIWHTSGWVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK ADSSPVKAGVETTTPTPSKSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1233

Figure 63H
CPA.7.011

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGPAAGVGYYYMDV WGKGTTVT/SS	1234
vhCDR1	<u>GYTLTELS</u>	1235
vhCDR2	<u>FDPEDGET</u>	1236
vhCDR3	<u>ATGPAAGVGYYYMDV</u>	1237
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGPAAGVGYYYMDVWGKGTTVT/SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKHTCPGPCAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSLTYDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	1238
Variable light (vl) domain	DVVMTQSPVLSLPVTPGEPASISCRSSQSLLYRNGYNVLDWYLQKPGQSPQLLYLGSNRRASGVDPDRFSGSGGTDFTLKISRVEADVGVYYCMQALQTPPTFGQGTKEIKR	1239
vlCDR1	<u>QSLLYRNGYNV</u>	1240
vlCDR2	<u>LGS</u>	1241
vlCDR3	<u>MQALQTPPT</u>	1242
Full length light chain	DVVMTQSPVLSLPVTPGEPASISCRSSQSLLYRNGYNVLDWYLQKPGQSPQLLYLGSNRRASGVDPDRFSGSGGTDFTLKISRVEADVGVYYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1243

Figure 63I
CPA7.012

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYVCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSS	1244
vhCDR1	<u>GFTSSYA</u>	1245
vhCDR2	<u>ISYDGSNK</u>	1246
vhCDR3	<u>ARDVMVYCSSTSCYFYGMDV</u>	1247
Full length HC	EVQLVETGGGLIQPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYVCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1248
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTTCQASQDIRDYLINWYQKPGKAPKLLYNDAASNLEAGVPSRFSGSGGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTGLEIKR	1249
vlCDR1	<u>QDIRDY</u>	1250
vlCDR2	<u>DAS</u>	1251
vlCDR3	<u>QQFENLPIT</u>	1252
Full length light chain	DIQMTQSPSSLSASVGDRVTTCQASQDIRDYLINWYQKPGKAPKLLYNDAASNLEAGVPSRFSGSGGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTGLEIKRTVAAPSVPFPPSDEQLKSGTASVCLLNINFPYREAKVQWKVDNALQSGN SQESVTEQDSKDSITYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1253

Figure 63J
CPA.7.013

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLEWMGGDPEDGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYMDV WGKGTTTVTVSS	1254
vhCDR1	<u>GYTLTELS</u>	1255
vhCDR2	<u>FDPEDGET</u>	1256
vhCDR3	<u>ATGGYSSGFNYYYYMDV</u>	1257
Full length HC	QVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLEWMGGDPEDGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYMDVWGKGTTTVTVSSASTKGPVFLAPSSKSTSGGTAALGCLV KDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVWTVPSLSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTC PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVYDGVGVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1258
Variable light (vl) domain	DVVMTQSPVLSPLPTGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDFSGSGGTDFTLK SRVEAEDGVYYCMQALQTPPTFGGGTKLEIKR	1259
vlCDR1	<u>QSLLYRNGNNY</u>	1260
vlCDR2	<u>LGS</u>	1261
vlCDR3	<u>MQALQTPPT</u>	1262
Full length light chain	DVVMTQSPVLSPLPTGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDFSGSGGTDFTLK SRVEAEDGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1263

Figure 63K
CPA.7.014

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGVTTTYYYGMDVWVGQGTTVTVSS	1264
vhCDR1	<u>GYTLTELS</u>	1265
vhCDR2	<u>FDPEDGET</u>	1266
vhCDR3	<u>ATGVTTTYYYGMDV</u>	1267
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATGVTTTYYYGMDVWVGQGTTVTVSSASTKGPSVFLPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPGK	1268
Variable light (vl) domain	DVVMTQSPPLSLPTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLISLGSNRRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGGQTKVEIKR	1269
vlCDR1	<u>QSLLYSNGNNE</u>	1270
vlCDR2	<u>LGS</u>	1271
vlCDR3	<u>MQALQTPPT</u>	1272
Full length light chain	DVVMTQSPPLSLPTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLISLGSNRRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1273

Figure 63L
CPA.7.015

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QITLKESGGVVPQPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARDLDFEWWDGMDVWGQGTITVTVSS	1274
vhCDR1	<u>GFTSSYG</u>	1275
vhCDR2	<u>IRYDGSNK</u>	1276
vhCDR3	<u>ARDLDFEWWDGMDV</u>	1277
Full length HC	QITLKESGGVVPQPGGSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARDLDFEWWDGMDVWGQGTITVTVSSASTKGPSVFLPSSKTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	1278
Variable light (vl) domain	EIVLTQSPGTLSLSPGEKATLSCRVSSQSVSSMYLAWYQQKPGQAPRLIYGASYRATGIPDRFSGSGSGTDENLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTLKLEIKR	1279
vlCDR1	<u>QSVSSMY</u>	1280
vlCDR2	<u>GAS</u>	1281
vlCDR3	<u>QQYVSSPMYT</u>	1282
Full length light chain	EIVLTQSPGTLSLSPGEKATLSCRVSSQSVSSMYLAWYQQKPGQAPRLIYGASYRATGIPDRFSGSGSGTDENLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTLKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSITYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1283

Figure 63M
CPA.7.017

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFNNYGISWVRQAPGKGLEWMGQIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDMAADGMAVFDYWGQGTLLTVSS	1284
vhCDR1	<u>GGTFNNYG</u>	1285
vhCDR2	<u>IPLFGTTI</u>	1286
vhCDR3	<u>ARDRMAADGMAVFDY</u>	1287
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFNNYGISWVRQAPGKGLEWMGQIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDMAADGMAVFDYWGQGTLLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSEFELYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	1288
Variable light (vl) domain	QSVLTQPPSVSGTPGQKVIISCSGSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLG	1289
vlCDR1	<u>SSNIGRHF</u>	1290
vlCDR2	<u>KND</u>	1291
vlCDR3	<u>SSWDAALNGVV</u>	1292
Full length light chain	QSVLTQPPSVSGTPGQKVIISCSGSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKNKYAASSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1293

Figure 63N
CPA.7.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIAQKFGGRVMTEDTSTDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYMDVWGKGTTTVTVSS	1294
vhCDR1	<u>GYTLTELS</u>	1295
vhCDR2	<u>FDPEDGET</u>	1296
vhCDR3	<u>ATEVPMVRGARRYYMDV</u>	1297
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIAQKFGGRVMTEDTSTDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYMDVWGKGTTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPRPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	1298
Variable light (vl) domain	DVVMTQSPFLFVTPGEPASISCRSSQTLTYINENNYLDWVYVQKPGQSPQLLYLGSTRASGVDPDRFSGGGSGTDFTLTISRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKR	1299
vlCDR1	<u>QTLTYINENNY</u>	1300
vlCDR2	<u>LGS</u>	1301
vlCDR3	<u>MOGLQTPPT</u>	1302
Full length light chain	DVVMTQSPFLFVTPGEPASISCRSSQTLTYINENNYLDWVYVQKPGQSPQLLYLGSTRASGVDPDRFSGGGSGTDFTLTISRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1303

Figure 630
CPA.7.019

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKSETLSLTCSVSGGSINSNYWGWIRQPPGKGLEWIGGIWYSGTYNPSLESRVTISEDTSKNQIS LKLSVTAADTAVYYCARGAWELS LGDWFDPWGPGLTVTVSS	1304
vhCDR1	<u>GGISINSNY</u>	1305
vhCDR2	<u>IYSGST</u>	1306
vhCDR3	<u>ARGAWELS LGDWFDP</u>	1307
Full length HC	QVQLQESGPGLVKSETLSLTCSVSGGSINSNYWGWIRQPPGKGLEWIGGIWYSGTYNPSLESRVTISEDTSKNQIS LKLSVTAADTAVYYCARGAWELS LGDWFDPWGPGLTVTVSSASTKGPSPFLAPSSKSTSGGTAALGCLVKDYFPEP VTWSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFELYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1308
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLYGNNNRPSGVPDRFSGRSRGTASLAITGL QAEDEADYYCQSYDSSLVYVFGGGTQLTVLG	1309
vlCDR1	<u>SSNIGAGYD</u>	1310
vlCDR2	<u>GNN</u>	1311
vlCDR3	<u>QSYDSSLVYV</u>	1312
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLYGNNNRPSGVPDRFSGRSRGTASLAITGL QAEDEADYYCQSYDSSLVYVFGGGTQLTVLGQPKAAPSTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETITPSSKQSNKKNYAASSYLSLTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	1313

Figure 63P
CPA.7.021

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVKPGGSLRLSCAASGFTGTSSMINVVRQAPGKGLWVAVISFDGTEIHYADSVKGRFTISRDNKST VFLQMNSLRPDDTALYYCAKSGNIFYSGMDVWGQGTITVVS	1314
vhCDR1	<u>GFTEGTSS</u>	1315
vhCDR2	<u>ISFDGTEI</u>	1316
vhCDR3	<u>AKSGNIFYSGMDV</u>	1317
Full length HC	EVQLVESGGGVKPGGSLRLSCAASGFTGTSSMINVVRQAPGKGLWVAVISFDGTEIHYADSVKGRFTISRDNKST VFLQMNSLRPDDTALYYCAKSGNIFYSGMDVWGQGTITVVSASTGSPVFLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1318
Variable light (vl) domain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESQVPSRFSGSGGTEYTLTISSLOP DDFATYYCQQYYSYPLTFGGQGTKVEIKR	1319
vlCDR1	<u>QSISGW</u>	1320
vlCDR2	<u>ETS</u>	1321
vlCDR3	<u>QQYYSYPLT</u>	1322
Full length light chain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESQVPSRFSGSGGTEYTLTISSLOP DDFATYYCQQYYSYPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1323

Figure 63Q
CAP.7.022

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYMDVWVGKTTVTVSS	1324
vhCDR1	<u>GYTLTELS</u>	1325
vhCDR2	<u>FDPEDGET</u>	1326
vhCDR3	<u>ATGVPAAIGVYYYYYMDV</u>	1327
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVVRQAPGKGLWVGGEFDPEDGETIYAKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYMDVWVGKTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1328
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNVLDWYVLRQPGQSPQLLSLGSNRSAGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGKTKVEIKR	1329
vlCDR1	<u>QSLLYSNGYNV</u>	1330
vlCDR2	<u>LGS</u>	1331
vlCDR3	<u>MQALQSPVT</u>	1332
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNVLDWYVLRQPGQSPQLLSLGSNRSAGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1333

Figure 63R
CPA.7.023

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVS GYLTIELS MHWVRQAPGKGLWVG GDPEDGETI YAQFQGRVTMTEDTS TDTAYMELSSLRSEDTAVVYCA TDSRDGPAARGGY YMDVWVGQGTITVSS	1334
vhCDR1	<u>GYLTIELS</u>	1335
vhCDR2	<u>FDPEDGET</u>	1336
vhCDR3	<u>ATDSRDGPAARGGY</u> YMDV	1337
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVS GYLTIELS MHWVRQAPGKGLWVG GDPEDGETI YAQFQGRVTMTEDTS TDTAYMELSSLRSEDTAVVYCA TDSRDGPAARGGY YMDV WVGQGTITVSSASTKGPSVFLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VW SVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	1338
Variable light (vl) domain	DVVM TSQSP LSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLYLGSN RASGV PD R FSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKEIKR	1339
vlCDR1	<u>QSLLYINGYNY</u>	1340
vlCDR2	<u>LGS</u>	1341
vlCDR3	<u>MQALQTPPT</u>	1342
Full length light chain	DVVM TSQSP LSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLYLGSN RASGV PD R FSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASV W CLNNFYPREAKVQW/KVDNA LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1343

Figure 635
CPA.7.024

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYC <u>ARDAYYDSSGGYNNPDAFDI</u> WGQGTMTVTVSS	1344
vhCDR1	<u>GGTFFSSYA</u>	1345
vhCDR2	<u>IIPIFGTA</u>	1346
vhCDR3	<u>ARDAYYDSSGGYNNPDAFDI</u>	1347
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYC <u>ARDAYYDSSGGYNNPDAFDI</u> WGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSLSLTQTIVICNVNHPKPSNTKVDKKVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENINVKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK	1348
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVYYC <u>MOGLQTPRTFGRG</u> TKLEIKR	1349
vlCDR1	<u>QSLHNSNGYNY</u>	1350
vlCDR2	<u>LGS</u>	1351
vlCDR3	<u>MOGLQTPRT</u>	1352
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVYYC <u>MOGLQTPRTFGRG</u> TKLEIKRTVAAPSVFIFPPSDEQLKSGTASWCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1353

Figure 63T

CPA.7.033

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSS	1354
vhCDR1	<u>GGTFSSA</u>	1355
vhCDR2	<u>IPIYGIT</u>	1356
vhCDR3	<u>ARDDTARRVRGVPPYYAMDV</u>	1357
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1358
Variable light (vl) domain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEAETLVPGIPPRFSGSGFGTDFTLTKNMIES EDAAVYFCLQHDLNPLTFGGGTKVDIKR	1359
vlCDR1	<u>QDIDDD</u>	1360
vlCDR2	<u>EAS</u>	1361
vlCDR3	<u>LQHDNLIPLI</u>	1362
Full length light chain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEAETLVPGIPPRFSGSGFGTDFTLTKNMIES EDAAVYFCLQHDLNPLTFGGGTKVDIKRTVAAPSFIIPPSDEQLKSGTASVCLINNPFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSYSTSLTSLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1363

Figure 63U

CPA.7.034

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEDGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYGMDVWVGQGTITVSS	1364
vhCDR1	<u>GYTLTSL</u>	1365
vhCDR2	<u>EDPEDGET</u>	1366
vhCDR3	<u>ATEDPGPVAGPYYYGMDV</u>	1367
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEDGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYGMDVWVGQGTITVSSASTKGPSVFLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSLSLTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1368
Variable light (vl) domain	DVVMITQSPVLVPTGEPASISCRSSQSLLYINGYHYLDWVYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKR	1369
vlCDR1	<u>QSLLYINGYHY</u>	1370
vlCDR2	<u>LGS</u>	1371
vlCDR3	<u>MQALQTPPT</u>	1372
Full length light chain	DVVMITQSPVLVPTGEPASISCRSSQSLLYINGYHYLDWVYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1373

Figure 63V

CPA.7.036

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSED TAVVYCARDDTARRVRGVPPY YAMDVWGQGT TT TVSS	1374
vhCDR1	<u>GGTFSSA</u>	1375
vhCDR2	<u>IPIYGIT</u>	1376
vhCDR3	<u>ARDDTARRVRGVPPYYAMDV</u>	1377
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSED TAVVYCARDDTARRVRGVPPY YAMDVWGQGT TT TVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLT VL HQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	1378
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASISCRPSQSLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGV PD RFSGSGSGTDFTLKI SRVEAEDVGVYCYC <u>MQRLQFPLT</u> FGGGTKVEIKR	1379
vlCDR1	<u>QSLDSDDGNTY</u>	1380
vlCDR2	<u>TLS</u>	1381
vlCDR3	<u>MQRLQFPLT</u>	1382
Full length light chain	DIVMTQTPLSLPVTPGEPASISCRPSQSLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGV PD RFSGSGSGTDFTLKI SRVEAEDVGVYCYC <u>MQRLQFPLT</u> FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDNA LQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1383

Figure 63W

CPA.7.040

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLT <u>ELSMHWVRQAPGKLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS</u> TDTAYMELSSLRSEDTAVVYCATGVPAAIGVYYYYYMDVWGGGTTVTSS	1384
vhCDR1	<u>GYTLTELS</u>	1385
vhCDR2	<u>EDPEDGET</u>	1386
vhCDR3	<u>ATGVPAAIGVYYYYYMDV</u>	1387
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLT <u>ELSMHWVRQAPGKLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS</u> TDTAYMELSSLRSEDTAVVYCATGVPAAIGVYYYYYMDVWGGGTTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1388
Variable light (vl) domain	DVVMITQSPVLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSDFTLK ISRVEAEDVGVVYCMQAVQNPPITFGQGTVDIKR	1389
vlCDR1	<u>QSLLYRNGYNY</u>	1390
vlCDR2	<u>WGS</u>	1391
vlCDR3	<u>MQAVQNPPIT</u>	1392
Full length light chain	DVVMITQSPVLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSDFTLK ISRVEAEDVGVVYCMQAVQNPPITFGQGTVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWVKVDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKHVAACEVTHQGLSPVTKSFNRGEC	1393

Figure 63X

CPA.7.046

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSS	1394
vhCDR1	<u>GGTFSSA</u>	1395
vhCDR2	<u>IPIYGIT</u>	1396
vhCDR3	<u>ARDDTARRVRGVPPYYAMDV</u>	1397
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITIDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTWSWNSGALTSVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1398
Variable light (vl) domain	DVVMITQSPAFLSVTPGERVTLSCASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISV QSEDFALYCCQQYGDWLPITFGQGTREIKR	1399
vlCDR1	<u>QTMNNY</u>	1400
vlCDR2	<u>DAS</u>	1401
vlCDR3	<u>QQYGDWLPIT</u>	1402
Full length light chain	DVVMITQSPAFLSVTPGERVTLSCASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISV QSEDFALYCCQQYGDWLPITFGQGTREIKRVTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1403

Figure 63Y

CPA.7.047

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWGKGTITVSS	1404
vhCDR1	<u>GYTLTSL</u>	1405
vhCDR2	<u>FDPEGETI</u>	1406
vhCDR3	<u>ATAFPEATISYYYMDV</u>	1407
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAPGKLEWMGGFDPEGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWGKGTITVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQVTCNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNVKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSVMHEALHNHYTQKSLSLSPGK	1408
Variable light (vl) domain	DVVMITQSPISLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSDFTLKISRVEAEDVGVVYCMQAVQNPPITFGQGTKEIKR	1409
vlCDR1	<u>QSLLYRNGYNY</u>	1410
vlCDR2	<u>WGS</u>	1411
vlCDR3	<u>MQAVQNPPIT</u>	1412
Full length light chain	DVVMITQSPISLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSDFTLKISRVEAEDVGVVYCMQAVQNPPITFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1413

Figure 63Z

CPA.7.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSS	1414
vhCDR1	<u>GGTFSSA</u>	1415
vhCDR2	<u>IPIYGIT</u>	1416
vhCDR3	<u>ARDDTARRVRGVPPYYAMDV</u>	1417
Full length HC	QIMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDATVYYCARTDARRVRGVPPYYAMDVWGQGTITVTVSSASTKGPS/FPLAPSSKSTSGGTAALGC LVKDYFPEPVT/SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1418
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASMSCRSSRLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDFRFGSGSGTDFTL EISRVEAEDVGYYCMQRKEPPLTFGGGTKEIKR	1419
vlCDR1	<u>RSLLDSDDGNTH</u>	1420
vlCDR2	<u>SL</u>	1421
vlCDR3	<u>MQRKEPPLT</u>	1422
Full length light chain	DIVMTQTPLSLPVTPGEPASMSCRSSRLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDFRFGSGSGTDFTL EISRVEAEDVGYYCMQRKEPPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWVKVDM ALQSGNSQESVTEQDSKDSYSTSLTTLTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1423

Figure 63AA

CPA.7.050

What	sequence	SEQ. ID NO.:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSYAISWVRQAPGQGLEWMGGIIPFGTANYAQKFQGRVTITADKSTSTAYMELSLRSEDTAVYYCARGPWYDSSGYSSAYYMDVWGQGTTVTVSS	1424
vhCDR1	<u>GGTFFSYA</u>	1425
vhCDR2	<u>IIPFGTA</u>	1426
vhCDR3	<u>ARGPWYDSSGYSSAYYMDV</u>	1427
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFFSYAISWVRQAPGQGLEWMGGIIPFGTANYAQKFQGRVTITADKSTSTAYMELSLRSEDTAVYYCARGPWYDSSGYSSAYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1428
Variable light (vl) domain	DVVMITQSPISLPVTPGEPASISCRSSQSLHSDGYNVLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKR	1429
vlCDR1	<u>QSLHSDGYNV</u>	1430
vlCDR2	<u>LGS</u>	1431
vlCDR3	<u>MQALHTPGVI</u>	1432
Full length light chain	DVVMITQSPISLPVTPGEPASISCRSSQSLHSDGYNVLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1433

Figure 63BB
CPA.7.028

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QLQLQESGPGLVKPSSETLSLTCTVTGSSISSSYWAWIRQPPGKLEWIGGIYSGSYTYNVLSERSVTISQDTSKNQFS LKLTSVTAADTAIVYICARGAWELRLGDWFDPPWGQGTILVTSS	1434
vhCDR1	GGSISSSYW	1435
vhCDR2	IYSGST	1436
vhCDR3	ARGAWELRLGDWFDPP	1437
Full length HC	QLQLQESGPGLVKPSSETLSLTCTVTGSSISSSYWAWIRQPPGKLEWIGGIYSGSYTYNVLSERSVTISQDTSKNQFS LKLTSVTAADTAIVYICARGAWELRLGDWFDPPWGQGTILVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV/PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1438
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQQLPGTAPKLLIYGYSNRPSPGVPDFRSGSKSGTSASLAIITGL QAEDEADYYCQSYDSSLVYVVFGGGTQLTVLGGPKAA	1439
vICDR1	SSNIGAGYD	1440
vICDR2	GYS	1441
vICDR3	QSYDSSLVYVW	1442
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQQLPGTAPKLLIYGYSNRPSPGVPDFRSGSKSGTSASLAIITGL QAEDEADYYCQSYDSSLVYVVFGGGTQLTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNINNYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1443

Figure 63CC
CPA.7.030

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGGGVVQPGGSLRLSCAASRTFEDYAMHWVRQPPGKLEWVSGISWKGGINVADSVKGRFTISRDAQ NSLYLQMNSLRAEDTALYYCVKDPITLVDRAFNIVGGQTMVTVSS	1444
vhCDR1	RFTFEDYA	1445
vhCDR2	ISWKGSGI	1446
vhCDR3	VKDPTLVATDRAFNI	1447
Full length HC	QVQLQESGGGVVQPGGSLRLSCAASRTFEDYAMHWVRQPPGKLEWVSGISWKGGINVADSVKGRFTISRDAQ NSLYLQMNSLRAEDTALYYCVKDPITLVDRAFNIVGGQTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKV/DKKVEPKSCDKTHTCTPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENINVKTTTPPVLDSDGSEFLYSLKLTVDKSRW/QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1448
Variable light (vl) domain	DVVMITQSPPLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV/PDRFSGSGSGTDFTLK SRVEAEDVGYVYCMQY/LQTPDTFGQGTKEIKRAAPS	1449
vICDR1	QSLHSHNGYNY	1450
vICDR2	LGS	1451
vICDR3	MQY/LQTPDT	1452
Full length light chain	DVVMITQSPPLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV/PDRFSGSGSGTDFTLK SRVEAEDVGYVYCMQY/LQTPDTFGQGTKEIKRTVAAPSFIFPPSDEQLKSGTASVWCLLNNFYPREAKVQW/KVDNA LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1453

Figure 63DD
CPA.7.041

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFGQGRVTITTDSTST AYMELSLTSEDATVYYCARDTARRVRGVPPYYVAMDVWGQGTTVTVSS	1454
vCDR1	GGTFSSA	1455
vCDR2	IPIYGIT	1456
vCDR3	ARDDTARRVRGVPPYYVAMDV	1457
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFGQGRVTITTDSTST AYMELSLTSEDATVYYCARDTARRVRGVPPYYVAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPNTKVDKKVEPKSCDKTH TCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1458
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQNISSLLHWYQQKPKGQSPKLLINVASQSFSGVPSRFGSGSGTDFTLTIDSLPE DAATYFCHQSSSLPLTFGGGTKEIRRTVAAPS	1459
vICDR1	QNIDSS	1460
vICDR2	YAS	1461
vICDR3	HQSSSLPLT	1462
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSPVDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVFGGGTQLTLVGLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTPSKQSNKNKYAASSYLSTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	1463

Figure 63EE
CPA.7.016

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKTSGGTSSAISWVRQAPGQFEWMGGIPIYGITDYAQKFQGRVTITTTDESTSTA YMELSLTSEDTAVYVCARDDTARRVRGVPYVYVYAMDVWGQGTITVTVSS	1464
vhCDR1	GGTFSSSA	1465
vhCDR2	IPIYGIT	1466
vhCDR3	ARDDTARRVRGVPYVYVYAMDV	1467
Full length HC	EVQLVQSGAEVKKPGSSVKVCKTSGGTSSAISWVRQAPGQFEWMGGIPIYGITDYAQKFQGRVTITTTDESTSTA YMELSLTSEDTAVYVCARDDTARRVRGVPYVYVYAMDVWGQGTITVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGSPSVLEFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	1468
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRTATGIPARFSGSGGTDFLTITSSLSQSE DFAVYCCQQYDDWPQPTFGQGTIRLEIKRTVAAPS	1469
vICDR1	QSVSSY	1470
vICDR2	DAS	1471
vICDR3	QQYDDWPQT	1472
Full length light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRTATGIPARFSGSGGTDFLTITSSLSQSE DFAVYCCQQYDDWPQPTFGQGTIRLEIKRTVAAPSVPFPPSDEQLKSGTASVCLLNINFPYREAKVQWKVDNALQSGN SQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1473

Figure 63FF
CPA.7.020

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSKASGGTSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTTDES TSTAYMELSLSLTSDDTARRVGVPIYYYAMDVWGQGTITVSS	1474
vhCDR1	GGTFSSA	1475
vhCDR2	IPIYGIT	1476
vhCDR3	ARDDTARRVGVPIYYYAMDV	1477
Full length HC	QMQLVQSGAEVKKPGSSVKVSKASGGTSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTTDES TSTAYMELSLSLTSDDTARRVGVPIYYYAMDVWGQGTITVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNITKVDKKV EPKSCDKHTCPCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKP REEQYNSTYRVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREMTKNQVSLTC LVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSL SLSPGK	1478
Variable light (vl) domain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGGTDFLTISR VEPEDFAVYVCQRRDWPITFGQGTREIKRTVAAPS	1479
vlCDR1	QNVYGE	1480
vlCDR2	DTF	1481
vlCDR3	QQRDWPIT	1482
Full length light chain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGGTDFLTISR VEPEDFAVYVCQRRDWPITFGQGTREIKRTVAAPS/FIFPPSDEQLKSGTASVVCVLLINFPYPREAKVQWVKV/DN ALQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	1483

Figure 63GG
CPA.7.038

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFGQGRVTITTDSTST AYMELSLTSEDATVYYCARDTARRVRGVPPYYVYAMDVWVGQGTTVTVSS	1484
vhCDR1	GGTFSSA	1485
vhCDR2	IPIYGIT	1486
vhCDR3	ARDDTARRVRGVPPYYVYAMDV	1487
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFGQGRVTITTDSTST AYMELSLTSEDATVYYCARDTARRVRGVPPYYVYAMDVWVGQGTTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGC LVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSLSLGTQYICNVNHHKPSNTKVDDKKVEPKSCDKTH TCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSPGK	1488
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCQASRDISDSLSWYQQKPKAPKLIFDASNLKTVSSRFSGSGGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGKVEIKRTVAAPS	1489
vICDR1	RDISDS	1490
vICDR2	DAS	1491
vICDR3	HQYDNLPLT	1492
Full length light chain	DIQMTQSPSSLSASVGDRTVITCQASRDISDSLSWYQQKPKAPKLIFDASNLKTVSSRFSGSGGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGKVEIKRTVAAPSFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQQLSPVTKSFNRGEC	1493

Figure 63HH
CPA.7.044

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMLVQSGAEVKKPGSSVKVSKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDATVYCARDTARRVRGVPPYYAMDVWGQGTTVTVSS	1494
vCDR1	GGTFSSA	1495
vCDR2	IPIYGIT	1496
vCDR3	ARDDTARRVRGVPPYYAMDV	1497
Full length HC	QMLVQSGAEVKKPGSSVKVSKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDATVYCARDTARRVRGVPPYYAMDVWGQGTTVTVSSASTKGPSVFLAPSSKSTGGTAALGC LVKDYFPEPVTWSWNSGALTSVHTFPAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHHKPSNTKVDDKKVEPKSCDKTH TCPPCPAPELLGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	1498
Variable light (vl) domain	EIVMTQSPATLSLSPGERATLSCRASESVTTLAWYQQKPGQAPRLITDASNRATGIPGRFSGSGSGTDFTLTISSELEPE DFAVYYCHQHTNWPLTFGGGKLEIKRTVAAPS	1499
vICDR1	ESVTTF	1500
vICDR2	DAS	1501
vICDR3	HQHTNWPLT	1502
Full length light chain	EIVMTQSPATLSLSPGERATLSCRASESVTTLAWYQQKPGQAPRLITDASNRATGIPGRFSGSGSGTDFTLTISSELEPE DFAVYYCHQHTNWPLTFGGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1503

Figure 63II
CPA.7.045

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHVWRQAPGKGLEWMGGFDPEDGETIAQKFGGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYGMDVWGQGTTVTVSS	1504
vhCDR1	GYTLTELS	1505
vhCDR2	FDPEDGET	1506
vhCDR3	ATEVGYCSGGSCYISYYGMDV	1507
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMHVWRQAPGKGLEWMGGFDPEDGETIAQKFGGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYGMDVWGQGTTVTVSSATKGPSVFLPASPSSKTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDK THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYR VWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVWTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	1508
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLYRNGHNFLDWVYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYCMQALQTPPTFGQGTKEIKRTVAAPS	1509
vICDR1	QSLLYRNGHNF	1510
vICDR2	LGS	1511
vICDR3	MQALQTPPT	1512
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLYRNGHNFLDWVYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYFREAKVQW/KVDNA LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1513

Figure 63JJ

CHA.7.502

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLVESGGDLVQPGGSRKLSCTASGFTFSNFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVKGRFTISRDNPENTLFLQMTSLRSEDAMYYCTRLDYYTNSYSMDHWGQGTSTVTVSS	1514
vhCDR1	GFTFSNFG	1515
vhCDR2	ISSGSSTI	1516
vhCDR3	TRLDYYTNSYSMDH	1517
Variable light (vl) domain	QIVLTQSPALMSASPGEKVTLTCSASSLPYIYWYQQKPGSSPKPWYLTSLNLSGVPARFSGSRSGTSYSLTISSVEAEDAATYYCQQWSSNPFTFGSGTKLEIK	1518
vlCDR1	SSLPY	1519
vlCDR2	LTS	1520
vlCDR3	QQWSSNPFT	1521

Figure 63KK

CHA.7.503

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELAKPGASVKMSCKASGYTFTSNWMHWVKQRPGQGLEWIGYINP SNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTADSAVYYCALMISAWLPYWG QGTLVTVSA	1522
vhCDR1	GYTFTSNW	1523
vhCDR2	INPSNGYT	1524
vhCDR3	ALMISAWLPY	1525
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRASQSVSASSYSYVHWYQQKPGQPPKLLIKYASSLE SGVPARFSGSGSGTDFTLNHPVEEEDTATYYCLHTWEIPYTFGGGTKLEIK	1526
vlCDR1	QSVSASSYSY	1527
vlCDR2	YAS	1528
vlCDR3	LHTWEIPYT	1529

Figure 63LL

CHA.7.506

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

Figure 63MM

CHA.7.508

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPDLVKPGASMKISCKASGYTFIDYNIHWVKQSQGKSLDWIGYIYPYNG GTGYNQKFKNKATLTVDSSSSTAYMEVRSLTFEDSAVYFCAREADYYGNRGQFDYW GQGTLVTVSA	1538
vhCDR1	GYTFIDYN	1539
vhCDR2	IYPYNGGT	1540
vhCDR3	AREADYYGNRGQFDY	1541
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASENIFSNLAWYQQKQKGKSPQLLVYGEANLAD GVPSRFSGSGSGTQYSLKINSLSQSEDFGNYYCQHFWGTPYTFGGGTLEIK	1542
vlCDR1	ENIFSN	1543
vlCDR2	GEA	1544
vlCDR3	QHFWGTPYT	1545

Figure 63NN

CHA.7.510

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPGILQPSQTLSTCSFSG <u>GFSLNTSGTG</u> VGWIRQPSGKGLEWLTHI <u>IWWNDNK</u> FYNTFLKSRLTISKETSNNQVFLKIASVDTADAATYYC <u>ARMAYGNLWFVNWGQ</u> GTLVAVST	1546
vhCDR1	GFSLNTSGTG	1547
vhCDR2	IWWNDNK	1548
vhCDR3	ARMAYGNLWFVN	1549
Variable light (vl) domain	DIVLTQSPASLAVSLGQRASISCRASRSVTISGYSYMYWYQQKPGQPPRLLFY <u>LASNL</u> ASGVPARFSGSGSGTDFTLNHPVEEEDAAIYYC <u>QHSREL</u> PYTFGGGKLEIK	1550
vlCDR1	RSVTISGYSY	1551
vlCDR2	LAS	1552
vlCDR3	QHSREL	1553

Figure 6300

CHA.7.512

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKPPRETVKISCKASGYTFTDYS SMHWVKQAPGKGLKWMGW <u>INTETGEPTYADDFKGRFAFSLEASASSAYLQINILKDEDTATYFCARSRGGYYEDYYALDYW</u> GQGTSTVTSS	1554
vhCDR1	GYTFTDYS	1555
vhCDR2	INTETGEP	1556
vhCDR3	ARSRGGYYEDYYALDY	1557
Variable light (vl) domain	DIQMTQSPASLSASVSGESVTITCRASGNIHYYLAWYQQKQKGKSPQLLVYNAK NLAD <u>GVPSRFSGSGGTQFSLKINSIQPEDFGSYQCQHFWISPPTFGGGTKLEIK</u>	1558
vlCDR1	GNIHYY	1559
vlCDR2	NAK	1560
vlCDR3	QHFWISPPT	1561

Figure 63PP

CHA.7.514

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLRQSGADLVKPGASVKLSCTASGFNIKDTYIDWVKQRPEQGLDWIGRIDPANGNTKYDPKFQGKATIIITDSSNTAYLQLSNLTSEDTAVYYCARYGSYPYFDYWGRGTTLAVSS	1562
vhCDR1	GFNIKDTY	1563
vhCDR2	IDPANGNT	1564
vhCDR3	ARYGSYPYFDY	1565
Variable light (vl) domain	SIVMTQTPKFLLISAGDRVITICKASQSVRNDVAWYQQKPGQSPKLLMYYASNRYTGVPDRFTGSGYGTDFITISTVQAEDLAVYFCQQDYSSPPTFGGGTKLEIK	1566
vlCDR1	QSVRND	1567
vlCDR2	YAS	1568
vlCDR3	QQDYSSPPT	1569

Figure 63QQ

CHA.7.516

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVRPGVSVKISCKVSGYTFTDYVMHWVKQSHAKSLEWIGIIISPYS GNTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDSAIYYCAREGDLPMFAYWGQG TLVTVSA	1570
vhCDR1	GYTFTDYV	1571
vhCDR2	ISPYSNT	1572
vhCDR3	AREGDLPMFAY	1573
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVSYIYWYQQNPGSSPRLLIYDTSILASGVPF RFSGSGSGTSYSLTISRMEAEDAATYYCQQWTSYPLTFGSGTKLELK	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 GYNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVYYCAREDKTARNAMDYWGQG TPVTVSS	1578
vhCDR1	GYTFTDYN	1579
vhCDR2	IYPYIGGS	1580
vhCDR3	AREDKTARNAMDY	1581
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTIIICRVSENIYSNLAWYQQKQKGKSPQLLVYEATNLAEG VPSRFSGSGSGTQYSLKINSLSQSEDFGSYYCQHFHWGTPYTFGGGTKLEIK	1582
vlCDR1	ENIYSN	1583
vlCDR2	EAT	1584
vlCDR3	QHFHWGTPYT	1585

Figure 6355

CHA.7.520_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLSLTCTVT <u>GYSITSDYA</u> WNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYC <u>ARHYRYPYAMDY</u> WGQGTSVTVSS	1586
vhCDR1	GYSITSDYA	1587
vhCDR2	ISYSGST	1588
vhCDR3	ARHYRYPYAMDY	1589
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVYFAS T RESGV P DRFIGSGSGTDFTLTITSVQAEDLADYFC QQHYSTPFT FGSGTKLEIK	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	QVQLKQSGPGLVQPSSITCTVSGFSLTSFGVHWVRQSPGKGLEWLGVIWSGGT TVYDAAFISRLISKDNSKSQVFFKMNSLQTNDTAIYYCARKRGNFYVMDYWGQGT SVTVSS	1594
vhCDR1	GFSLTSG	1595
vhCDR2	IWSGGTT	1596
vhCDR3	ARKRGNFYVMDY	1597
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVY FASTRESGVDPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	1598
vlCDR1	QSLNSSNQKNY	1599
vlCDR2	FAS	1600
vlCDR3	QQHYSTPFT	1601

Figure 63UU

CHA.7.522

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGSELVVRPGTSVKLSCKASGYTFTSYWVHWVRQRHGQGLEWIGNVYPG SGSTNYDEKFKSKGTLTVDTSSTAYMHLSSLTSEDSAVYYCTRGVLRFPDLYWGQG TTLTVSS	1602
vhCDR1	GYTFTSYW	1603
vhCDR2	VYPGSGST	1604
vhCDR3	TRGVLRFPDLY	1605
Variable light (vl) domain	DIVMTQAAPSVPTPGESVSISCRSSKSLHNSNGNTYLYWFLQRPQGSPHLLIYRMS NLASGVDPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK	1606
vlCDR1	KSLHNSNGNTY	1607
vlCDR2	RMS	1608
vlCDR3	MQHLEYPLT	1609

Figure 63VV

CHA.7.524

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPEVVRPGVSVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGI <u>ISIYSG</u> <u>NTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAREGDLPMFAYWGQG</u> TLVTVSA	1610
vhCDR1	GYKFPDYV	1611
vhCDR2	ISIYSGNT	1612
vhCDR3	AREGDLPMFAY	1613
Variable light (vl) domain	QIVLTQSPAIMASAPGEKVTMTCNASSSVSYMYWYQQKPISSPRLLIY <u>DTS</u> NLASGV PVRFSGSGSGTSYSLTIGRMEAEDAATYYC <u>QQWSSYPLT</u> FGAGTKVEVK	1614
vlCDR1	SSVS	1615
vlCDR2	DTS	1616
vlCDR3	QQWSSYPLT	1617

Figure 63WW

CHA.7.526

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSG <u>FSLTAYN</u> INWVRQPPGKGLEWLGMIWGDGNTDYN SPLKSRITISKDNSKQVFLKMDSLQTD TARYYCA <u>RD LKVR RDSPY TMDY</u> WGQGTSVTVSS	1618
vhCDR1	GFSLTAYN	1619
vhCDR2	IWGDGNT	1620
vhCDR3	ARDLKVR RDSPY TMDY	1621
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASNRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCHQYLSSYTFGGGTKLEIK	1622
vlCDR1	QSVLYSSNQKNY	1623
vlCDR2	WAS	1624
vlCDR3	HQYLSSYT	1625

Figure 63XX

CHA.7.527

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGGLVKPSQSLSLTCTVT <u>GYSLTSDYA</u> WNWIRQFPGNKLEWMGYI <u>ITYSG</u> <u>GTTYNPSLKS</u> RISITRDTSKNQFFLQLTSVTTEDTATYYC <u>ARRGSGTTVVGDWYFDV</u> WGAGTTTVTVSS	1626
vhCDR1	GYSLTSDYA	1627
vhCDR2	ITYSGGT	1628
vhCDR3	ARRGSGTTVVGDWYFDV	1629
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKYYLAWYQQKPGQSPKLLIYW <u>ASTRESGV</u> PDRFTGSGSGTDFTPTISSVTAEDLAVYYC <u>QQFYTPYPT</u> FGGGTKLEMK	1630
vlCDR1	QSLLYSFNQKYY	1631
vlCDR2	WAS	1632
vlCDR3	QQFYTPYPT	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	DIQMTQSPASLSVSVGETVTITCRASDNIFSNLAWYHQKGKSPHLLVYGATNLAD GVPSRFSGSGSGTQYSLKINSLSQSEDFGDYYCQHFWGTPYTFGGGKLEIK	1638
vlCDR1	DNIFSN	1639
vlCDR2	GAT	1640
vlCDR3	QHFWGTPYT	1641

Figure 63ZZ

CHA.7.530

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELMRPGTSVKVSCKASGYAFTNHLIEWIKQRPQGQGLEWIGVINPGSDSTDYNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSLYYNSWFVYWGQGTLLTVSA	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>GFSIRDTY</u> IHWVKQRPEQGLDWIGKIDPANG KSEYDPKFQGRATMTTDTSSNTAYLQLSSLTSEDVAVYYCTRYGYYPYFDVWGAGTT VTVFS	1650
vhCDR1	GFSIRDTY	1651
vhCDR2	IDPANGKS	1652
vhCDR3	TRYGYYPYFDV	1653
Variable light (vl) domain	SIVMTQTPKFLLVSAGDRVAITCKASQSVRHDVWVYQQKPGQSPKLLIYYASSRYTG VPDRFTGSGYGTDFTFITISTVQAEDLALYFCLQDFSSPWTFGGGTKLEIK	1654
vlCDR1	QSVRHD	1655
vlCDR2	YAS	1656
vlCDR3	LQDFSSPWT	1657

Figure 63BBB

CHA.7.535

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKTS <u>GYTFTKNT</u> TMHWVRQSHGKSLEWIGGINPNSG <u>GASFNQKFMGKATLTVDKSSSTAYMELRSLTSEDSAVYYC</u> <u>ARDGYDGDWFFDVWG</u> AGTTVTVSS	1658
vhCDR1	GYTFTKNT	1659
vhCDR2	INPNSGGA	1660
vhCDR3	ARDGYDGDWFFDV	1661
Variable light (vl) domain	DIQMNQSPFSLASLGDTVTITCHAS <u>QNIYVW</u> LSWYQQKPGNIPKLLIY <u>KAS</u> DLHTGVPSRFSGSGSGTDFTLNISLQPEDATYYC <u>QQGQSYPR</u> TFGGGTKLEIK	1662
vlCDR1	QNIYVW	1663
vlCDR2	KAS	1664
vlCDR3	QQGQSYPR	1665

Figure 63CCC

CHA.7.537

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLITCTVSG <u>FLIGHG</u> VNWIRQPPGKGLEWLGV <u>IWGDGN</u> IDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDTARYFC <u>AVNSAMDY</u> WGQGTAVT VSS	1666
vhCDR1	GFLIGHG	1667
vhCDR2	IWGDGNT	1668
vhCDR3	AVNSAMDY	1669
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLNCTASENVASEVSWYQQKPEQSPKLLIY <u>GTS</u> NRYT GVPDRFTGSGSATDFTLTISVQAEDLGDYHCG <u>QSYNYPFT</u> FGSGTKLEIE	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> IEWVKQRPQGQLEWIGVINPGSG <u>GIYYNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCARSETHDTWFAY</u> WGQG TLVTVSA	1674
vhCDR1	GYAFTNYL	1675
vhCDR2	INPGSGGI	1676
vhCDR3	ARSETHDTWFAY	1677
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIY <u>LAS</u> TRHTG 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	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYPGGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCASPYYGSSYGFAFWGQGTLVTVSA	1682
vhCDR1	GYTFTNYW	1683
vhCDR2	IYPGGGYT	1684
vhCDR3	ASPYYGSSYGFAF	1685
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQHWNYPYTFGGGTKLEIKR	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 IKWVRQPPGKGLEWLG TIWGDGS IDYNSALKSRLSISKDNSKSQVFLKMTSLQTDDTARYYC ASDSLGITFGYWGQGT TVSA	1690
vhCDR1	GFSLSGYG	1691
vhCDR2	IWGDGST	1692
vhCDR3	ASDSLGITFGY	1693
Variable light (vl) domain	DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGV 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	QVQLKESGPGLVAPSQSLITCTVSG <u>FSLT</u> SYAITWVRQPPGKGLEWLGVIWP <u>GGGT</u> NYNSALKSRLSISKDNSKSHLFLKMNSLQDDTARYYC <u>VRSYDGYLDWYFDV</u> WGTV TTVTVSS	1698
vhCDR1	GFSLTSYA	1699
vhCDR2	IWP <u>GGGT</u>	1700
vhCDR3	VRSYDGYLDWYFDV	1701
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLSCKASENVGTYVSWYQQKPDQSPKLLIY <u>GAS</u> NRYT GVPDRFTGSGSATDFTLISSVQAEDLSDYHCG <u>QSYSYPYT</u> FGGGTKLEII	1702
vlCDR1	ENVGTY	1703
vlCDR2	GAS	1704
vlCDR3	GQSYSYPYT	1705

Figure 63HHH

CHA.7.545

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKKPGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYSGVSTFPDDFKGRFAFSLETSASTAYLQINNLIKNEFSATYFCARLGMGSTTGAGYFDVWGTGTTVTVS	1706
vhCDR1	GYTFTTYG	1707
vhCDR2	INTYSGVS	1708
vhCDR3	ARLGMGSTTGAGYFDV	1709
Variable light (vl) domain	DIVLTQSPAISASPGKVTMTCSASSVSSWYLHWYQQKSGASPKLWIYGTSNLA SGVPARFSGSGSGTSYSLTISVEAEDAATYYCQQYRSDPYTFGSGTKLEIK	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 GVSTYADDFEGRFASFLETSVSTAYLQINNLIKNEATATYFCARLGRGSTTGAGYLDV WGTGTTTVTVSS	1714
vhCDR1	GYTFTTYG	1715
vhCDR2	INTYSGVS	1716
vhCDR3	ARLGRGSTTGAGYLDV	1717
Variable light (vl) domain	DIVLTQSPAIMASAPGKVSMTCSASSVSSWYLHWYQQKSGASPKLWIYGTSLNLA SGVPPARFSGSGSGTSYSLTISVVEAEDAATYYCQQYHSDPYTFGSGTKLEIK	1718
vlCDR1	SSVSSWY	1719
vlCDR2	GTS	1720
vlCDR3	QQYHSDPYT	1721

Figure 63JJJ

CHA.7.547

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYSGVSTFPDDFKGRFAFSLETSASTAYLQINNLNKNEFSATYFCARLGMGSTTGAGYFDVWGTGTTVTVS	1722
vhCDR1	GYTFTTYG	1723
vhCDR2	INTYSGVS	1724
vhCDR3	ARLGMGSTTGAGYFDV	1725
Variable light (vl) domain	ENVLTQSPAIMSASLGKVTLSKRASSSVNYMYWYQQKSDASPRLWIYYTSNLAGPVPARFSGSGSGNSYSLSITSSVEGEDAATYYCQQFTSSPWTFGGGTKLEIK	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 SPNYNQKFKDKATLTVDKSSSTVYMEIRSLTSEDSAVYYCASLFFDYWGHGTTLTVSS	1730
vhCDR1	GYTFTDYS	1731
vhCDR2	ITPNNGSP	1732
vhCDR3	ASLFFDY	1733
Variable light (vl) domain	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQQKPGQPPKLLIYG ASTRDSGVPDRFTGSGSGTDFTLTITSVQAEDLAVYYCQNDHTYPYTFGGGTKLEIK	1734
vlCDR1	QSLNLSGNQKNY	1735
vlCDR2	GAS	1736
vlCDR3	QNDHTYPYT	1737

Figure 63LLL

CHA.7.549

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELVKPGASVKLSCKAS <u>GFTFTTHW</u> MHWVRQRPQGQGLEWIGNI <u>YPS</u> <u>NGGS</u> NYNEKF TKAT LTVD RS STAYMHLSSLTSEDSAVYYCARRVNWDGYYFDYW GQGTTTLTVSS	1738
vhCDR1	GFTFTTHW	1739
vhCDR2	IYPSNGGS	1740
vhCDR3	ARRVNWDGYYFDY	1741
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKLLIYS <u>S</u> ASYRY SGVPDRFTGSGSGTDFTLTISNVQSEDLADYFC <u>QQYNSYPLT</u> FGGGTKLEIK	1742
vlCDR1	QNVGTN	1743
vlCDR2	SAS	1744
vlCDR3	QQYNSYPLT	1745

Figure 63MMM

CHA.7.550

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWIHWVKRPGQGLEWIGNINPSN GGTNYNEKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVYYCARRGLPYFFDYWGQG TTLTVSS	1746
vhCDR1	GYTFTSYW	1747
vhCDR2	INPSNGGT	1748
vhCDR3	ARRGLPYFFDY	1749
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVCKGSQNVGYNVAWYQQKPGQSPKALVYSASDR 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 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYMHWRQAPGQGLEWMGIINPSGGSTSYAOKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR
 (SEQ ID NO: 1754)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS (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	b i i	i i b b b	i b b	b b b x	b b b b	b i b b b
518	EVQLQQSGPELVKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIYPYIGGSG	YNQKFKSKATLSADNPSTAYNELRSITSEDSAVYYCAR	*****	****	***	* * * *
	* * *	**	*	**	**	*			
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTSYMH	WVRQAPGQGLEWIG	IINPSGGSTS	YAKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h518H1	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIYPYIGGSG	YAKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h518H2	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIYPYIGGSG	YAKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h518H3	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIYPYIGGSG	YAKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h518H4	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWIG	YIYPYIGGSG	YAKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				

seq	100	110	120
AbM		i b b b	
518	EDKTARNAMDY	WGQGLTVTVSS	(SEQ ID NO: 1756)
	*		("1-46*01" sequence is disclosed as SEQ ID NO: 1757)
h518H1	EDKTARNAMDY	WGQGLTVTVSS	(SEQ ID NO: 1758)
h518H2	EDKTARNAMDY	WGQGLTVTVSS	(SEQ ID NO: 1759)
h518H3	EDKTARNAMDY	WGQGLTVTVSS	(SEQ ID NO: 1760)
h518H4	EDKTARNAMDY	WGQGLTVTVSS	(SEQ ID NO: 1761)

deamidation substitutions: Q/S/A

Figure 63000
Humanized sequences of CHA.7.518 antibody VL

Potential humanized sequence based on IMGT IGHV1-39*01 acceptor framework

IGHV1-39*01
DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQKPKAKPLIIYAASSLSQSGVPSRFSGSGTDTLTITSSLOPEDFATYYCQSYSTPP (SEQ ID NO: 1762)

Joining region IMGT J00242|IGHJ2*01|YTFGGTKLEIK (SEQ ID NO: 1763)

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 i i b b i	i b b	b b b	b b b
518	DIQMTQSPASLSVSGETVTITC	RVSENIYSNLA	WYQKQKSPQLIIV	EATNLAE	GVPSRFSGSGSGTQYSLKINSLQSEDFGSYYC	***	*	*

IGHV1-39	DIQMTQSPSSLSASVGDRTITC	RASQSISSYLN	WYQKPKAKPLIIY	AASSLSQ	GVPSRFSGSGSGTDTLTITSSLOPEDFATYYC
b518L1	DIQMTQSPSSLSASVGDRTITC	RVSENIYSNLA	WYQKPKAKPLIIY	EATNLAE	GVPSRFSGSGSGTDTLTITSSLOPEDFATYYC
b518L2	DIQMTQSPSSLSASVGDRTITC	RVSENIYSNLA	WYQKPKAKPLIIY	EATNLAE	GVPSRFSGSGSGTDTLTITSSLOPEDFATYYC
b518L3	DIQMTQSPSSLSASVGDRTITC	RVSENIYSNLA	WYQKPKAKPLIIY	EATNLAE	GVPSRFSGSGSGTDTLTITSSLOPEDFATYYC

seq	90	100
AbM	90	100
	i b i i b i	b b b
518	QHFWGTPYT	EGGKLEIK (SEQ ID NO: 1764)

IGHV1-39	QOSYSTPP (SEQ ID NO: 1765)
b518L1	QHFWGTPYT EGGKLEIK (SEQ ID NO: 1766)
b518L2	QHFWGTPYT EGGKLEIK (SEQ ID NO: 1767)
b518L3	QHFWGTPYT EGGKLEIK (SEQ ID NO: 1768)

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

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
QVQLVQSGAEVKKPGASVKVCKASGYTFTSYMHWRQAPGQGLEWMGIINPSSGGSTSYAQKFGQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1769)

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

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 b x	b b b b	b i b i b b
538_1	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNYLIE	WVKQRPQGQLEWIG	VINPSSGGIY	YNDKFKVKTTLTADKSSSTAYMQLSSLSRSEDTAVYYCAR				
	***	*	*	*	*	*	*	*	*
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	CYTFTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	YAKFKQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR				
h5381H1	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNYLIE	WVRQAPGQGLEWMG	VINPSSGGIY	YAKFKQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR				
h5381H2	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNYLIE	WVRQAPGQGLEWIG	VINPSSGGIY	YAKFKQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR				
h5381H3	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNYLIE	WVRQAPGQGLEWIG	VINPSSGGIY	YAKFKQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR				
h5381H4	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNYLIE	WVRQAPGQGLEWIG	VINPSSGGIY	YAKFKQGRVTMTTRDTSITVYMELSSLRSEDTAVYYCAR				
	V		#		#	N	T		F

seq	100	110
AbM	110	
	i b b b	
538_1	SETHDTWFAY	WGQGLTVTVSSA (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

RECTIFIED SHEET (RULE 91) ISA/EP

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
QVQLVQSGAEVKRPGASVKVCKASGYTFSTSYMHWRQAPGQGLEWMGIIINPSGGSTSYAQKFGQGRVTMTTRDTSTSYVMELSLRSEDYAVYYCAR (SEQ ID NO: 1784)
Joining region
IMGT J00256[IGHJ4*01]YFDYWGQGLVTVSS (SEQ ID NO: 1785)

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 b x	b b b	b i b i b b
538_2	QVQLVQSGAEVLRPGTSVKMSCKAA	GYTFNNYWG	WVRQAPGQGLEWIG	DIYPGGGYTN	YNEKFKGKATLTADTSSSTAYVQLSSLTSEDYAVYYCAS	** * * * *	** * * * *	** * * * *	** * * * *
1-46*01	QVQLVQSGAEVKRPGASVKVCKAS	GYTFSTSYMH	WVRQAPGQGLEWIG	IINPSGGST	YAKFGQGRVTMTTRDTSTSYVMELSLRSEDYAVYYCAR	** * * * *	** * * * *	** * * * *	** * * * *
h5382H1	QVQLVQSGAEVKRPGASVKVCKAS	GYTFNNYWG	WVRQAPGQGLEWIG	DIYPGGGYTN	YAKFGQGRVTMTTRDTSTSYVMELSLRSEDYAVYYCAR	** * * * *	** * * * *	** * * * *	** * * * *
h5382H2	QVQLVQSGAEVKRPGASVKVCKAS	GYTFNNYWG	WVRQAPGQGLEWIG	DIYPGGGYTN	YAKFGQGRVTMTTRDTSTSYVMELSLRSEDYAVYYCAS	** * * * *	** * * * *	** * * * *	** * * * *
h5382H3	QVQLVQSGAEVKRPGASVKMSCKAS	GYTFNNYWG	WVRQAPGQGLEWIG	DIYPGGGYTN	YAKFGQGRATLTADTSTSTAYVQLSSLTSEDYAVYYCAS	** * * * *	** * * * *	** * * * *	** * * * *

seq	100	110
AbM	100	110
	i b b b	
538_2	PYIGSSYGFAP	WQQTILVTVSA (SEQ ID NO: 1786)
	*	*(I-46*01" sequence is disclosed as SEQ ID NO: 1787)
h5382H1	PYIGSSYGFAP	WQQTILVTVSS (SEQ ID NO: 1788)
h5382H2	PYIGSSYGFAP	WQQTILVTVSS (SEQ ID NO: 1789)
h5382H3	PYIGSSYGFAP	WQQTILVTVSS (SEQ ID NO: 1790)

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 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMHVWVQAPGQGLEWNGIINPSGGSTSYAQKFQGRVTMTTRDTSTSTVYMEISLRSSEDTAVYYCAR
(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 b	b i b i b b

524 QVQLQQSGPEVVRPGVSVKISCKGS **G**YK**F**P**D**YV**M**H **W**V**K**Q**S**H**A**K**S**L**E**W**I**G **I**I**S**I**S**G**N**T**N** **Y**N**O**K**F**K**G**K**A**T**M**T**V**D**K**S**S**T**A**Y**M**E**L**S**S**L**R**S**E**D**T**A**V**Y**Y**C**A**R
 1-46*01 QVQLVQSGAEVKKPGASVKVSCKAS GYFTSYMH VWRQAPGQGLEWNG IINPSGGSTS YAQKFQGRVTMTTRDTSTSTVYMEISLRSSEDTAVYYCAR
 h524H1 QVQLVQSGAEVKKPGASVKVSCKAS **G**YK**F**P**D**YV**M**H **W**V**R**Q**A**P**G**Q**G**L**E**W**N**G **I**I**S**I**S**G**N**T**N** **Y**A**K**F**Q**G**R**V**T**M**T**R**D**T**S**T**S**T**V**Y**M**E**L**S**S**L**R**S**E**D**T**A**V**Y**Y**C**A**R
 h524H2 QVQLVQSGAEVKKPGASVKVSCKAS **G**YK**F**P**D**YV**M**H **W**V**R**Q**A**P**G**Q**G**L**E**W**I**G **I**I**S**I**S**G**N**T**N** **Y**A**K**F**Q**G**R**V**T**M**T**V**D**T**S**T**S**T**V**Y**M**E**L**S**S**L**R**S**E**D**T**A**V**Y**Y**C**A**R
 h524H3 QVQLVQSGAEVKKPGASVKISCKGS **G**YK**F**P**D**YV**M**H **W**V**R**Q**A**P**G**Q**G**L**E**W**I**G **I**I**S**I**S**G**N**T**N** **Y**A**K**F**Q**G**R**A**T**M**T**V**D**T**S**T**S**T**A**Y**M**E**L**S**S**L**R**S**E**D**T**A**V**Y**Y**C**A**R
 h524H4 QVQLVQSGAEVKKPGASVKISCKGS **G**YK**F**P**D**YV**M**H **W**V**R**Q**A**P**G**Q**G**L**E**W**I**G **I**I**S**I**S**G**N**T**N** **Y**A**K**F**Q**G**R**A**T**M**T**V**D**K**S**T**S**T**A**Y**M**E**L**S**S**L**R**S**E**D**T**A**V**Y**Y**C**A**R

V

N

I

seq	100	110
AbM		110
	i b b b	

524 **E**G**D**L**P**N**F**A**Y** **W**G**Q**G**T**L**V**T**V**S**A** (SEQ ID NO: 1793)
 * ("1-46*01" sequence disclosed as SEQ ID NO: 1794)
 h524H1 **E**G**D**L**P**N**F**A**Y** **W**G**Q**G**T**L**V**T**V**S**S** (SEQ ID NO: 1795)
 h524H2 **E**G**D**L**P**N**F**A**Y** **W**G**Q**G**T**L**V**T**V**S**S** (SEQ ID NO: 1796)
 h524H3 **E**G**D**L**P**N**F**A**Y** **W**G**Q**G**T**L**V**T**V**S**S** (SEQ ID NO: 1797)
 h524H4 **E**G**D**L**P**N**F**A**Y** **W**G**Q**G**T**L**V**T**V**S**S** (SEQ ID NO: 1798)

e

deamidation substitutions: Q/S/A

@ 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: 1799)

Joining region IMGT J00242|IGKJ2*01|YTFGGGTKLEIK (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 i b b i	i b b	b b b	b b b
524	QIVLTQSPATLSLSPGERATLSC NASSVS-YMY WYQQKPISSPRLIIY DTSNLAS GVPVRFSGSGSGTYSISLTICRMEAEADAATYYC							
	* *							
IGKV3-11	EIVLTQSPATLSLSPGERATLSC RASQSVSSYLA WYQQKPGQAPRLIIY DASNRAT GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC							
h524L1	EIVLTQSPATLSLSPGERATLSC NASSVS-YMY WYQQKPGQAPRLIIY DTSNLAS GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC							
h524L2	EIVLTQSPATLSLSPGERATLSC NASSVS-YMY WYQQKPGQAPRLIIY DTSNLAS GIPARFSGSGSGTDYTLTISSELEPEDFAVYYC							
h524L3	EIVLTQSPATLSLSPGERVTMSC NASSVS-YMY WYQQKPGQAPRLIIY DTSNLAS GVPARFSGSGSGTDYTLTISSEMEPEDFAVYYC							
	M A # S # A							

seq	90	100
AbM	90	100
	ibi iib i	b 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)	
	e 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 QVQLVQSGAEVKKPGASVKVCKASGYFTSTSYHHWVQAPGQGLEWMGIINPSGGSTSYAQKFGQGRVTMTTRDTSTSTVYMELSLRSSEDTAVYYCAR
(SEQ ID NO: 1806)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS (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 b	b i b i b b
530	QVQLQQSGAEELMRPCTSYKVSCKAS	GYFTNNHLIE	WIKRPGQGLEWIG	VINPGSDSTD	YNKFKDKATLTADKSSSTAYMQLSSLTSDSDSAVYFCAR	**	****	**	* * * *
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSGGSTS	YAQKFQGRVTMTTRDTSTSTVYMELSLRSSEDTAVYYCAR				
h530H1	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNHLIE	WVRQAPGQGLEWMG	VINPGSDSTD	YAQKFQGRVTMTTRDTSTSTVYMELSLRSSEDTAVYYCAR				
h530H2	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNHLIE	WVRQAPGQGLEWIG	VINPGSDSTD	YAQKFQGRVTMTADTSTSTVYMELSLRSSEDTAVYYCAR				
h530H3	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNHLIE	WVRQAPGQGLEWIG	VINPGSDSTD	YAQKFQGRATLTADTSTSTAYMELSLRSSEDTAVYYCAR				
h530H4	QVQLVQSGAEVKKPGASVKVCKAS	GYFTNNHLIE	WVRQAPGQGLEWIG	VINPGSDSTD	YAQKFQGRATLTADKSTSTAYMELSLRSSEDTAVYYCAR				

seq	100	110
AbM	110	
	i b b b	
530	SLYNSWFFVY	WGQGLTVTVSA (SEQ ID NO: 1808)
	*	("1-46*01" sequence disclosed as SEQ ID NO: 1809)
h530H1	SLYNSWFFVY	WGQGLTVTVSS (SEQ ID NO: 1810)
h530H2	SLYNSWFFVY	WGQGLTVTVSS (SEQ ID NO: 1811)
h530H3	SLYNSWFFVY	WGQGLTVTVSS (SEQ ID NO: 1812)
h530H4	SLYNSWFFVY	WGQGLTVTVSS (SEQ ID NO: 1813)

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 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQOKPKAPKLLIYAASSLSQGVPSRFGSGGTDFTLTISLSQPEDFATYYCQOSYSTPP (SEQ ID NO: 1814) Joining region IMGT J00242 IGKJ2*01 YTFGQGTKLEIK (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 i i b b i	i b b	b b b b	b b b	ib bib
530	DIQMTQSPASLSASVGETVTITC	**	RASENIYSYLA	WYQOKRGKSPQLIVY	NAKTLVE	GVPSRFGSGGSGTQFSLKINSIQPEDFGSYVC			**
	*		*	*	*	*	*	*	*
IGKV1-39	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQOKPKAPKLLIY	AASSLSQ	GVPSRFGSGGSGGTDFTLTISLSQPEDFATYYC				
h530L1	DIQMTQSPSSLSASVGDRVTITC	RASENIYSYLA	WYQOKPKAPKLLIY	NAKTLVE	GVPSRFGSGGSGGTDFTLTISLSQPEDFATYYC				
h530L2	DIQMTQSPSSLSASVGDRVTITC	RASENIYSYLA	WYQOKPKAPKLLIY	NAKTLVE	GVPSRFGSGGSGGTDFTLTISLSQPEDFATYYC				
		#		S	#				
seq	90	100							
AbM	90	100							
	ibi iib i	b b b							
530	QHHYGTPTYT	FGGQTKLEIK	(SEQ ID NO: 1816)						
	*								
IGKV1-39	QQSYSTPP		(SEQ ID NO: 1817)						
h530L1	QHHYGTPTYT	FGGQTKLEIK	(SEQ ID NO: 1818)						
h530L2	QHHYGTPTYT	FGGQTKLEIK	(SEQ ID NO: 1819)						
# deamidation substitutions: Q/S/A/D									

Figure 63WWW

What	Sequences
humanized CHA.7.518 VH h518HH1	QVQLVQSGAEVKKPGASVKVSKASGYTFDTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFKQ GRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1820)
humanized CHA.7.518 VH h518HH2	QVQLVQSGAEVKKPGASVKVSKASGYTFDTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFKQ RVTMTADTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1821)
humanized CHA.7.518 VH h518HH3	QVQLVQSGAEVKKPGASVKISKASGYTFDTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFKQ RATLTADTSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1822)
humanized CHA.7.518 VH h518HH4	QVQLVQSGAEVKKPGASVKISKASGYTFDTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFKQGR ATLTADNSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLLVTVSS (SEQ ID NO: 1823)
humanized CHA.7.518 VL h518HL1	DIQMTQSPSSLSASVGDRTVTITCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGGT DFTLTITSSIQPEDFATYYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1824)
humanized CHA.7.518 VL h518HL2	DIQMTQSPSSLSASVGDRTVTITCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGGT DYTLTITSSIQPEDFATYYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1825)
humanized CHA.7.518 VL h518HL3	DIQMTQSPSSLSASVGDRTVTITCRVSENIYSNLAWYQQKPKGAPKLLIYEATNLAEGVPSRFSGSGGT TDYTLTITSSIQPEDFGTYCQHFHWGTPYTFGGQGTKLEIK (SEQ ID NO: 1826)

Figure 63XXX

What	Sequences
humanized CHA.7.538_1 VH h5381HH1	QVQLVQSGAEVKKPGASVKVSCKASGYAFN ^Y LJEWVRQAPGGQLEWGMGVINPGSGGIYYAQKFQ GRVTMT ^R DTSTSTVYME ^L SSLRSEDTAVYYCAR ^S ETHDTWFAYWGQGT ^L VTVSS (SEQ ID NO: 1827)
humanized CHA.7.538_1 VH h5381HH2	QVQLVQSGAEVKKPGASVKVSCKASGYAFN ^Y LJEWVRQAPGGQLEWGMGVINPGSGGIYYAQKFQ RVTMT ^A DTSTSTVYME ^L SSLRSEDTAVYYCAR ^S ETHDTWFAYWGQGT ^L VTVSS (SEQ ID NO: 1828)
humanized CHA.7.538_1 VH h5381HH3	QVQLVQSGAEVKKPGASVKVSCKTSGYAFN ^Y LJEWVRQAPGGQLEWGMGVINPGSGGIYYAQKFQ RVTLTADTSTSTAYME ^L SSLRSEDTAVYYCAR ^S ETHDTWFAYWGQGT ^L VTVSS (SEQ ID NO: 1829)
humanized CHA.7.538_1 VH h5381HH4	QVQLVQSGAEVKKPGASVKVSCKTSGYAFN ^Y LJEWVRQAPGGQLEWGMGVINPGSGGIYYAQKFQ RVTLTAD ^K STSTAYME ^L SSLRSEDTAVYYCAR ^S ETHDTWFAYWGQGT ^L VTVSS (SEQ ID NO: 1830)
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLSASVGD ^R VTITCKASQSVRIA ^V AWYQQKPGKAPKLLIYLA ^S TRHTGVPSRFSGSGGT DFTLTIS ^S LQPEDFATYYC ^L QHWNPYTFGGQTKLEIK (SEQ ID NO: 1831)
humanized CHA.7.538_1/538_2 VL h538HL2	DIQMTQSPSSLSASVGD ^R VTITCKASQSVRIA ^V AWYQQKPGKAPKALIIYLA ^S TRHTGVPSRFSGSGGT DFTLTIS ^S VQPEDFATYYC ^L QHWNPYTFGGQTKLEIK (SEQ ID NO: 1832)

Figure 63YYY

What	Sequences
humanized CHA.7.538_2 VH h5382HH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFETNYWIGWVRQAPGQGLEWMGDIYPGGGYTN ¹ YAQKF QGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCARPYGSSYGFAFWGQGT ² LVTVSS (SEQ ID NO: 1833)
humanized CHA.7.538_2 VH h5382HH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFETNYWIGWVRQAPGQGLEWIGDIYPGGGYTN ¹ YAQKFQ GRVTMTADTSTSTFVYMELSSLRSEDTAVYYCASPYYGSSYGFAFWGQGT ² LVTVSS (SEQ ID NO: 1834)
humanized CHA.7.538_2 VH h5382HH3	QVQLVQSGAEVKKPGASVKMSCKASGYTFETNYWIGWVRQAPGQGLEWIGDIYPGGGYTN ¹ YAQKFQ GRATLTADTSTSTAYMELSSLRSEDTAVYYCASPYGSSYGFAFWGQGT ² LVTVSS (SEQ ID NO: 1835)
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLSASVGDRTVTITCKASQSVRIAVAWYQQKPGKAPKLLIYLASTRHTGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCLOHWNYPYTFGGQGTKLEIK
humanized CHA.7.538_1/538_2 VL h538HI.2	DIQMTQSPSSLSASVGDRTVTITCKASQSVRIAVAWFQQKPGKAPKALIIYLASTRHTGVPSRFSGSGSGT DFTLTISSVQPEDFATYYCLOHWNYPYTFGGQGTKLEIK (SEQ ID NO: 1837)

Figure 63ZZZ

What	Sequences
humanized CHA.7.524 VH h524H1	QVQLVQSGAEVKKPGASVKVCKASGKYKFPDYVMIIWVVRQAPGQGLEWMGIISYSGNTN YAQKFQGRV TMTRDITSTVYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLLTVSS (SEQ ID NO: 1838)
humanized CHA.7.524 VH h524H2	QVQLVQSGAEVKKPGASVKVCKASGKYKFPDYVMIIWVVRQAPGQGLEWIGIISYSGNTN YAQKFQGRVT MTVDTSTSTVYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLLTVSS (SEQ ID NO: 1839)
humanized CHA.7.524 VH h524H3	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMIIWVVRQAPGQGLEWIGIISYSGNTN YAQKFQGRAT MTVDTSTSTAYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLLTVSS (SEQ ID NO: 1840)
humanized CHA.7.524 VH h524H4	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMIIWVVRQAPGQGLEWIGIISYSGNTN YAQKFQGRAT MTVDTSTSTAYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLLTVSS (SEQ ID NO: 1841)
humanized CHA.7.524 VL h524L1	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGIPARFSGSGSGTDFTLT ISSLEPEDFAVYYCQQWSSYP LT FGQGTKLEIK (SEQ ID NO: 1842)
humanized CHA.7.524 VI h524L2	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGIPARFSGSGSGTD YTL TSSLEPEDFAVYYCQQWSSYP LT FGQGTKLEIK (SEQ ID NO: 1843)
humanized CHA.7.524 VI h524L3	EIVLTQSPATLSLSPGERV TM SCNASSSVSYMYWYQKPGQAPRLIYDTSNLSGVPARFSGSGSGTDYT LTSSMEPEDFAVYYCQQWSSYP LT FGQGTKVEIK (SEQ ID NO: 1844)

Figure 63AAAA

What	Sequences
humanized CHA.7.530 VH h530H1	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWMGVINPGSDSDTDYAQKFQGRV TMTRDTSTSTVYMELSSLRSED TA VYYCARSLYYNSWFFVYWGQGT LV TVSS (SEQ ID NO: 1845)
humanized CHA.7.530 VH h530H2	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRVT MTADTSTSTVYMELSSLRSED TA VYYCARSLYYNSWFFVYWGQGT LV TVSS (SEQ ID NO: 1846)
humanized CHA.7.530 VH 530H3	hQVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRAT LTADTSTSTAYMELSSLRSED TA VYYCARSLYYNSWFFVYWGQGT LV TVSS (SEQ ID NO: 1847)
humanized CHA.7.530 VH h530H4	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSDTDYAQKFQGRATL TADKSTSTAYMELSSLRSED TA VYYCARSLYYNSWFFVYWGQGT LV TVSS (SEQ ID NO: 1848)
humanized CHA.7.530 VL h530L1	DIQMTQSPSSLSASVGDRTTTCRASENIYSYLA W YQQKPGKAPKLLIYN AK TLVEGVPSRFSGSGGTDF LTISSLQPEDFATYYCQH HY GPYTFGGQGT KL EIK (SEQ ID NO: 1849)
humanized CHA.7.530 VL h530L2	DIQMTQSPSSLSASVGDRTTTCRASENIYSYLA W YQQKPGKAPKLLIYN AK TLVEGVPSRFSGSGGTDF TLTISSLQPEDF GT YYCQH HY GPYTFGGQGT KL EIK (SEQ ID NO: 1850)