Figure 1A

Human IgG1 constant region
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 1)
Human IgG1 D265A constant region
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2)
Human IgG1 N297A constant region
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ[A]STYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 3)
Human IgG2 constant region
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVD
KTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVV
HQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 4)
Human IgG3 constant region
ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVD
KRVELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPS
REEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK
(SEQ ID NO: 5)

Figure 1B

Human IgG4 constant region (Wild Type)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDK
RVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6)

Human IgG4 constant region (S241P hinge mutant)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDK
RVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 7)

Human kappa light chain

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC (SEQ ID NO: 8)

Human lambda light chain

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGS
TVEKTVAPTECS (SEQ ID NO: 9)

Figure 2

Human TIGIT extra-cellular domain

MMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPD GTYTGRIFLEVLESSVAEHGARFQIP (SEQ ID NO: 10)

Cynomolgus macaque TIGIT extra-cellular domain

MMTGTIETTGNISAKKGGSVILQCHLSSTMAQVTQVNWEQHDHSLLAIRNAELGWHIYPAFKDRVAPGPGLGLTLQSLTMNDTGEYFCTYHT YPDGTYRGRIFLEVLESSVAEHSARFQIP (SEQ ID NO: 11)

Human PVRIG extra-cellular domain

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCK FASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRAD (SEQ ID NO: 12)

Cynomolgus macaque PVRIG extra-cellular domain

TPEVWVQVQMEATELSSFTVHCGFLGPGSISLVTVSWGGPDGAGGTKLAVLHPELGTRQWAPARQARWETQSSISLALEDSGASSPFANTTFC CKFASFPEGSWESCGSLPPSSDPGLSAPPTPVPILRAD (SEQ ID NO: 13)

Human PD-1 extra-cellular domain

PGWFLDSPDRPWNPPTFSPALLVVTEGDNATFTCSFSNTSESFVLNWYRMSPSNQTDKLAAFPEDRSQPGQDCRFRVTQLPNGRDFHMSVVR ARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPSPRPAGQFQTLV (SEQ ID NO: 14)

Cynomolgus PD-1 extra-cellular domain

PGWFLESPDRPWNAPTFSPALLLVTEGDNATFTCSFSNASESFVLNWYRMSPSNQTDKLAAFPEDRSQPGQDCRFRVTRLPNGRDFHMSVVR ARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPSPRPAGQFQALV (SEQ ID NO: 15)

Figure 3A: CPA.9.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKEMLVQDYYYMDVWGQGTTVTVSS	16
vhCDR1	GFTFSSYG	17
vhCDR2	IRYDGSNK	18
vhCDR3	AKEMLVQDYYYMDV	19
Full length HC (IgG4(S241P); **CPA.9.018.H4(S241P)**)	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKEMLVQDYYYMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	20
Variable light (vl) domain	DVVMTQSPLSLPVSPGEPASISCRSSQNLLHRNGINYLNWYLQKPGQSPQLLIYWGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GLQIPPTFGQGTKVDIKR	21
vlCDR1	QNLLHRNGINY	22
vlCDR2	WGS	23
vlCDR3	MQGLQIPPT	24
Full length light chain ((**CPA.9.018.H4(S241P)**)	DVVMTQSPLSLPVSPGEPASISCRSSQNLLHRNGINYLNWYLQKPGQSPQLLIYWGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GLQIPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	25

Figure **3B : CPA.9.027**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	26
vhCDR1	GFTFSSYA	27
vhCDR2	ISYDGSNK	28
vhCDR3	ARDPLPLHYYGMDV	29
Full length HC (IgG4(S241P); CPA.9.027.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	30
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDSLSSLQLGGGTQLAVLG	31
vlCDR1	SSNMGRRP	32
vlCDR2	SQN	33
vlCDR3	AVWDDSLSSLQ	34
Full length light chain (CPA.9.027.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDSLSSLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	35

Figure **3C: CPA.9.049**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	36
vhCDR1	GFTFSSYA	37
vhCDR2	ISYDGSNK	38
vhCDR3	ARDPLPLHYYGMDV	39
Full length HC (IgG4(S241P); CPA.9.049.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	40
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDSLFSLLLGGGTQLAVLG	41
vlCDR1	SSNMGRRP	42
vlCDR2	SQN	43
vlCDR3	AVWDDSLFSLL	44
Full length light chain (CPA.9.049.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDSLFSLLLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	45

Figure 3D: **CPA.9.057**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARQGAAAGNPFDIWGQGTMVTVSS	46
vhCDR1	GGSISSSSYY	47
vhCDR2	IYYSGST	48
vhCDR3	ARQGAAAGNPFDi	49
Full length HC (IgG4(S241P); CPA.9.057.H4(S241P))	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARQGAAAGNPFDIWGQGTMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	50
Variable light (vl) domain	QSVLTQPPSVSGTPGQRVTISCSGSSSNIGSNFVYWHQQLTGTAPKLLIYRNTQRPSGVPDRFSGSKSGTSASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLG	51
vlCDR1	SSNIGSNF	52
vlCDR2	RNT	53
vlCDR3	ATWDDSLSAWV	54
Full length light chain (CPA.9.057.H4(S241P))	QSVLTQPPSVSGTPGQRVTISCSGSSSNIGSNFVYWHQQLTGTAPKLLIYRNTQRPSGVPDRFSGSKSGTSASLAIGGLRSEDE ADYYCATWDDSLSAWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	55

Figure 3E: **CPA.9.059**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGARYSYGQYPYWGQGTLVTVSS	56
vhCDR1	GFTVSSNY	57
vhCDR2	IYSGGST	58
vhCDR3	ARGARYSYGQYPY	59
Full length HC (IgG4(S241P); CPA.9.059.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGARYSYGQYPYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT VDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	60
Variable light (vl) domain	DIQLTQSPSFLSASVGDRVTITCRASHDISSLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFGQGTKVEIKR	61
vlCDR1	HDISSL	62
vlCDR2	AAS	63
vlCDR3	LQLDSFPTWT	64
Full length light chain (CPA.9.059.H4(S241P))	DIQLTQSPSFLSASVGDRVTITCRASHDISSLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	65

Figure **3F: CPA.9.083**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGTPVYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	**66**
vhCDR1	GFTFSSYA	67
vhCDR2	ISYDGTPV	68
vhCDR3	ARDPLPLHYYGMDV	69
Full length HC (IgG4(S241P); CPA.9.083.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGTPVYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	70
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDGDRRSLQLGGGTQLAVLG	71
vlCDR1	SSNMGRRP	72
vlCDR2	SQN	73
vlCDR3	AVWDGDRRSLQ	74
Full length light chain (CPA.9.083.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDGDRRSLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	75

Figure 3G: **CPA.9.086**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYAGEVKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	**76**
vhCDR1	GFTFSSYA	77
vhCDR2	ISYAGEVK	78
vhCDR3	ARDPLPLHYYGMDV	79
Full length HC (IgG4(S241P); CPA.9.086.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYAGEVKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	80
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDIGRVLQLGGGTQLAVLG	81
vlCDR1	SSNMGRRP	82
vlCDR2	SQN	83
vlCDR3	AVWDDIGRVLQ	84
Full length light chain (CPA.9.086.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCAVWDDIGRVLQLGGGTQLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	85

Figure **3H: CPA.9.089**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDRTPVYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	86
vhCDR1	GFTFSSYA	87
vhCDR2	ISYDRTPV	88
vhCDR3	ARDPLPLHYYGMDV	89
Full length HC (IgG4(S241P); CPA.9.089.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDRTPVYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	90
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLG	91
vlCDR1	SSNMGRRP	92
vlCDR2	SQN	93
vlCDR3	ATWDDSLPRLN	94
Full length light chain (CPA.9.089.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSLPRLNFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	95

Figure **3I: CPA.9.093**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYEGDRKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSS	96
vhCDR1	GFTFSSYA	97
vhCDR2	ISYEGDRK	98
vhCDR3	ARDPLPLHYYGMDV	99
Full length HC (IgG4(S241P); CPA.9.093.H4(S241P))	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYEGDRKYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDPLPLHYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	100
Variable light (vl) domain	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFGGGTKLAVLG	101
vlCDR1	SSNMGRRP	102
vlCDR2	SQN	103
vlCDR3	ATWDDSTPHGV	104
Full length light chain (CPA.9.093.H4(S241P))	QSALTQPRSASGNPGQRVTISCSGSSSNMGRRPVNWYQQIPGTAPKLLIYSQNQRPSGVPDRFSGSQSGTSASLTISGLQSE DEAEYFCATWDDSTPHGVFGGGTKLAVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	105

Figure 3J: **CPA.9.101**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGAPLFGQYPYWGQGTLVTVSS	106
vhCDR1	GFTVSSNY	107
vhCDR2	IYSGGST	108
vhCDR3	ARGAPLFGQYPY	109
Full length HC (IgG4(S241P); CPA.9.101.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGAPLFGQYPYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPAPEFLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	110
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASHAIASLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFAT YYCLQLDSFPTWTFGQGTKVEIKR	111
vlCDR1	HAIASL	112
vlCDR2	AAS	113
vlCDR3	LQLDSFPTWT	114
Full length light chain (CPA.9.101.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASHAIASLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFAT YYCLQLDSFPTWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	115

Figure **3K: CPA.9.103**

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGARPNGQYPYWGQGTLVTVSS	116
vhCDR1	GFTVSSNY	117
vhCDR2	IYSGGST	118
vhCDR3	ARGARPNGQYPY	119
Full length HC (IgG4(S241P); CPA.9.103.H4(S241P))	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGARPNGQYPYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	120
Variable light (vl) domain	DIQLTQSPSFLSASVGDRVTITCRASHGIKSLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFGQGTKVEIKR	121
vlCDR1	HGIKSL	122
vlCDR2	AAS	123
vlCDR3	LQLDSFPTWT	124
Full length light chain (CPA.9.103.H4(S241P))	DIQLTQSPSFLSASVGDRVTITCRASHGIKSLFSWYQQKPGKAPKLLIYAASTLQTGVPSRFSGSASGTEFTLTISSLQPEDFATY YCLQLDSFPTWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	125

Figure 3L:

BM26 hIgG4 (BM26-H4) (WO2016/028656A1, Clone 31C6)

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSS	126
vhCDR1	GYTFSSYV	127
vhCDR2	IDPYNDGA	128
vhCDR3	ARGGPYGWYFDV	129
Full length HC (IgG4(S241P))	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT VDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	130
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFG TYYCQHHFGSPLTFGAGTTLELK	131
vlCDR1	EHIYSY	132
vlCDR2	NAK	133
vlCDR3	QHHFGSPLT	134
Full length light chain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFG TYYCQHHFGSPLTFGAGTTLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	135

Figure 3M:

BM29 hIgG4 (BM29-H4) (US2016/0176963A1, Clone 22G2)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYYFFGVDVWGQGTTVTVSS	136
vhCDR1	GGSVSSGIYY	137
vhCDR2	IYYSGST	138
vhCDR3	ARDYYVSGNYYNVDYYFFGVDV	139
Full length HC (IgG4(S241P))	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYYFFGVDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	140
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVY YCQQRSNWPPLFTFGPGTKVDIK	141
vlCDR1	QSVSSY	142
vlCDR2	DAS	143
vlCDR3	QQRSNWPPLFT	144
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVY YCQQRSNWPPLFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	145

Figure 3**N: CHA.9.536.1**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTLHWVRQAPGQGLEWMGGINPNNGGTSYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARSGYYDYSFAYWGQGTLVTVSS	146
vhCDR1	GYTFTEYTLH	147
vhCDR2	GINPNNGGTS	148
vhCDR3	SGYYDYSFAY	149
Full length HC (IgG4(S241P); **CHA.9.536.1.H4(S241P)**)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTLHWVRQAPGQGLEWMGGINPNNGGTSYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	150
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYS TPFTFGQGTKLEIK	151
vlCDR1	RASQDVKNAVV	152
vlCDR2	SPSYRYT	153
vlCDR3	QQHYSTPFT	154
Full length light chain **(CHA.9.536.1.H4(S241P)**	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYS TPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	155

Figure 3**O: CHA.9.536.3**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	156
vhCDR1	GYTFTEYTLH	157
vhCDR2	GINPNNGGTS	158
vhCDR3	SGYYDYSFAY	159
Full length HC (IgG4(S241P) CHA.9.536.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	160
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	161
vlCDR1	RASQDVKNAVV	162
vlCDR2	SPSYRYT	163
vlCDR3	QQHYSTPFT	164
Full length light chain (CHA.9.536.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	165

Figure 3**P: CHA.9.536.4**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	166
vhCDR1	GYTFTEYTLH	167
vhCDR2	GINPNNGGTS	168
vhCDR3	SGYYDYSFAY	169
Full length HC (IgG4(S241P); **CHA.9.536.4.H4(S241P)**)	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRVTMTVDTSTS TVYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	170
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	171
vlCDR1	RASQDVKNAVV	172
vlCDR2	SPSYRYT	173
vlCDR3	QQHYSTPFT	174
Full length light chain (**CHA.9.536.4.H4(S241P)**)	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	175

Figure 3Q: **CHA.9.536.5**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDTSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	176
vhCDR1	GYTFTEYTLH	177
vhCDR2	GINPNNGGTS	178
vhCDR3	SGYYDYSFAY	179
Full length HC (IgG4(S241P); CHA.9.536.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDTSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	180
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	181
vlCDR1	RASQDVKNAVV	182
vlCDR2	SPSYRYT	183
vlCDR3	QQHYSTPFT	184
Full length light chain (CHA.9.536.5.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	185

Figure 3**R: CHA.9.536.6**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDTSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	186
vhCDR1	GYTFTEYTLH	187
vhCDR2	GINPNNGGTS	188
vhCDR3	SGYYDYSFAY	189
Full length HC (IgG4(S241P); CHA.9.536.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDTSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	190
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	191
vlCDR1	RASQDVKNAVV	192
vlCDR2	SPSYRYT	193
vlCDR3	QQHYSTPFT	194
Full length light chain (CHA.9.536.6.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	195

Figure 35: **CHA.9.536.7**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	196
vhCDR1	GYTFTEYTLH	197
vhCDR2	GINPNNGGTS	198
vhCDR3	SGYYDYSFAY	199
Full length HC (IgG4(S241P); CHA.9.536.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	200
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIK	201
vlCDR1	RASQDVKNAVV	202
vlCDR2	SPSYRYT	203
vlCDR3	QQHYSTPFT	204
Full length light chain (CHA.9.536.7.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	205

Figure 3T: **CHA.9.536.8**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSS	206
vhCDR1	GYTFTEYTLH	207
vhCDR2	GINPNNGGTS	208
vhCDR3	SGYYDYSFAY	209
Full length HC (IgG4(S241P); CHA.9.536.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKTSGYTFTEYTLHWVRQAPGQGLEWIGGINPNNGGTSYAQKFQGRATLTVDKSTS TAYMELSSLRSEDTAVYYCAGSGYYDYSFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	210
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIK	211
vlCDR1	RASQDVKNAVV	212
vlCDR2	SPSYRYT	213
vlCDR3	QQHYSTPFT	214
Full length light chain (CHA.9.536.8.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQDVKNAVVWYQQKPGKAPKLLIYSPSYRYTGVPSRFSGSGSGTDFTF TISSVQPEDFATYYCQQHYSTPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

Figure 3**U: CHA.9.560.1**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGYYVGMDYWGQGTLVTVSS	216
vhCDR1	GYTFTNYGMN	217
vhCDR2	WINTYTGEPT	218
vhCDR3	GNGYYVGMDY	219
Full length HC (IgG4(S241P); CHA.9.560.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	220
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCRSSTGAVTTSNHANWFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	221
vlCDR1	RSSTGAVTTSNHAN	222
vlCDR2	GTNGRGS	223
vlCDR3	ALWFSNHWV	224
Full length light chain (CHA.9.560.1.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCRSSTGAVTTSNHANWFQQKPGQAPRTLIYGTNGRGSWTPARFSGSLLGGKAALTL SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	225

Figure 3V: **CHA.9.560.3**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	226
vhCDR1	GYTFTNYGMN	227
vhCDR2	WINTYTGEPT	228
vhCDR3	GNGYYVGMDY	229
Full length HC (IgG4(S241P); CHA.9.560.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	230
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	231
vlCDR1	GSSTGAVTTSNHAN	232
vlCDR2	GTNGRGS	233
vlCDR3	ALWFSNHWV	234
Full length light chain (CHA.9.560.3.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	235

Figure 3W: **CHA.9.560.4**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	236
vhCDR1	GYTFTNYGMN	237
vhCDR2	WINTYTGEPT	238
vhCDR3	GNGYYVGMDY	239
Full length HC (IgG4(S241P); CHA.9.560.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTLDTSTS TAYMELSSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	240
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	241
vlCDR1	GSSTGAVTTSNHAN	242
vlCDR2	GTNGRGS	243
vlCDR3	ALWFSNHWV	244
Full length light chain (CHA.9.560.4.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	245

Figure **3X: CHA.9.560.5**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDTSTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	246
vhCDR1	GYTFTNYGMN	247
vhCDR2	WINTYTGEPT	248
vhCDR3	GNGYYVGMDY	249
Full length HC (IgG4(S241P); CHA.9.560.5.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDTSTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	250
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	251
vlCDR1	GSSTGAVTTSNHAN	252
vlCDR2	GTNGRGS	253
vlCDR3	ALWFSNHWV	254
Full length light chain (CHA.9.560.5.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	255

Figure **3Y: CHA.9.560.6**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDTSTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	256
vhCDR1	GYTFTNYGMN	257
vhCDR2	WINTYTGEPT	258
vhCDR3	GNGYYVGMDY	259
Full length HC (IgG4(S241P); CHA.9.560.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDTSTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	260
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	261
vlCDR1	GSSTGAVTTSNHAN	262
vlCDR2	GTNGRGS	263
vlCDR3	ALWFSNHWV	264
Full length light chain (CHA.9.560.6.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	265

Figure 3Z: **CHA.9.560.7**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDASTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	266
vhCDR1	GYTFTNYGMN	267
vhCDR2	WINTYTGEPT	268
vhCDR3	GNGYYVGMDY	269
Full length HC (IgG4(S241P); CHA.9.560.7.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDTSTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	270
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	271
vlCDR1	GSSTGAVTTSNHAN	272
vlCDR2	GTNGRGS	273
vlCDR3	ALWFSNHWV	274
Full length light chain (CHA.9.560.7.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSWTPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	275

Figure **3AA: CHA.9.560.8**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDASTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSS	276
vhCDR1	GYTFTNYGMN	277
vhCDR2	WINTYTGEPT	278
vhCDR3	GNGYYVGMDY	279
Full length HC (IgG4(S241P); CHA.9.560.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTFTLDASTS TAYLEISSLRSEDTAVYYCSRGNGYYVGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	280
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVL	281
vlCDR1	GSSTGAVTTSNHAN	282
vlCDR2	GTNGRGS	283
vlCDR3	ALWFSNHWV	284
Full length light chain (CHA.9.560.8.H4(S241P))	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNHANWVQQKPGQAFRGLIRGTNGRGSGVPARFSGSLLGGKAALTI SGAQPEDEAEYYCALWFSNHWVFGGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	285

Figure **3BB: CHA.9.546.1**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARWLLSYYAMDYWGQGTLVTVSS	286
vhCDR1	GFTFSSYIMS	287
vhCDR2	TISGGGTNTY	288
vhCDR3	WLLSYYAMDY	289
Full length HC (IgG4(S241P); CHA.9.546.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	290
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	291
vlCDR1	RASQNINVWLT	292
vlCDR2	KASNLHT	293
vlCDR3	QQGQSYPYT	294
Full length light chain (CHA.9.546.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	295

Figure **3CC: CHA.9.547.1**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	296
vhCDR1	GFTFSSYIMS	297
vhCDR2	TISGGGTNTY	298
vhCDR3	WLLSYYAMDY	299
Full length HC (IgG4(S241P); CHA.9.547.1.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	300
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	301
vlCDR1	RASQNINVWLT	302
vlCDR2	KASNLHT	303
vlCDR3	QQGQSYPYT	304
Full length light chain (CHA.9.547.1.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	305

Figure **3DD: CHA.9.547.2**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	306
vhCDR1	GFTFSSYIMS	307
vhCDR2	TISGGGTNTY	308
vhCDR3	WLLSYYAMDY	309
Full length HC (IgG4(S241P); CHA.9.547.2.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	310
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	311
vlCDR1	RASQNINVWLT	312
vlCDR2	KASNLHT	313
vlCDR3	QQGQSYPYT	314
Full length light chain (CHA.9.547.2.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	315

Figure **3EE: CHA.9.547.3**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	316
vhCDR1	GFTFSSYIMS	317
vhCDR2	TISGGGTNTY	318
vhCDR3	WLLSYYAMDY	319
Full length HC (IgG4(S241P); CHA.9.547.3.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	320
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	321
vlCDR1	RASQNINVWLT	322
vlCDR2	KASNLHT	323
vlCDR3	QQGQSYPYT	324
Full length light chain (CHA.9.547.3.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	325

Figure **3FF: CHA.9.547.4**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	326
vhCDR1	GFTFSSYIMS	327
vhCDR2	TISGGGTNTY	328
vhCDR3	WLLSYYAMDY	329
Full length HC (IgG4(S241P); **CHA.9.547.4.H4(S241P))**	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	330
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	331
vlCDR1	RASQNINVWLT	332
vlCDR2	KASNLHT	333
vlCDR3	QQGQSYPYT	334
Full length light chain **CHA.9.547.4.H4(S241P))**	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	335

Figure **3GG: CHA.9.547.6**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	336
vhCDR1	GFTFSSYIMS	337
vhCDR2	TISGGGTNTY	338
vhCDR3	WLLSYYAMDY	339
Full length HC (IgG4(S241P); CHA.9.547.6.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	340
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	341
vlCDR1	RASQNINVWLT	342
vlCDR2	KASKSHT	343
vlCDR3	QQGQSYPYT	344
Full length light chain (CHA.9.547.6.H4(S241P))	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	345

Figure **3HH: CHA.9.547.7**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	346
vhCDR1	GFTFSSYIMS	347
vhCDR2	TISGGGTNTY	348
vhCDR3	WLLSYYAMDY	349
Full length HC (IgG4(S241P) for CHA.9.547.7.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	350
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASKHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	351
vlCDR1	RASQNINVWLT	352
vlCDR2	KASKSHT	353
vlCDR3	QQGQSYPYT	354
Full length light chain for CHA.9.547.7.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLTWYQQKPGKAPKLLIYKASKHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355

Figure **3II: CHA.9.547.8**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	356
vhCDR1	GFTFSSYIMS	357
vhCDR2	TISGGGTNTY	358
vhCDR3	WLLSYYAMDY	359
Full length HC (IgG4(S241P); CHA.9.547.8.H4(S241P))	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	360
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	361
vlCDR1	RASQNINVWLT	362
vlCDR2	KASKSHT	363
vlCDR3	QQGQSYPYT	364
Full length light chain (CHA.9.547.8.H4(S241P))	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365

Figure 3JJ: **CHA.9.547.9**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	366
vhCDR1	GFTFSSYIMS	367
vhCDR2	TISGGGTNTY	368
vhCDR3	WLLSYYAMDY	369
Full length HC (IgG4(S241P); **CHA.9.547.9.H4(S241P))**	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	370
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	371
vlCDR1	RASQNINVWLT	372
vlCDR2	KASKSHT	373
vlCDR3	QQGQSYPYT	374
Full length light chain **(CHA.9.547.9.H4(S241P))**	DIQMTQSPSSLSASVGDRITITCRASQNINVWLTWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375

Figure **3KK: CHA.9.541.1**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	376
vhCDR1	GYTITNYGMN	377
vhCDR2	WINTYTGEPT	378
vhCDR3	GNGNPLGMDY	379
Full length HC (IgG4(S241P); CHA.9.541.1.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRVTMTRDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	380
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	381
vlCDR1	GNGNPLGMDY	382
vlCDR2	DTSKLAS	383
vlCDR3	FQGSGYPLT	384
Full length light chain (CHA.9.541.1.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	385

Figure **3LL: CHA.9.541.3**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	386
vhCDR1	GYTITNYGMN	387
vhCDR2	WINTYTGEPT	388
vhCDR3	GNGNPLGMDY	389
Full length HC (IgG4(S241P); CHA.9.541.3.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	390
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	391
vlCDR1	GNGNPLGMDY	392
vlCDR2	DTSKLAS	393
vlCDR3	FQGSGYPLT	394
Full length light chain (CHA.9.541.3.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	395

Figure **3NN: CHA.9.541.4**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	396
vhCDR1	GYTITNYGMN	397
vhCDR2	WINTYTGEPT	398
vhCDR3	GNGNPLGMDY	399
Full length HC (IgG4(S241P); CHA.9.541.4.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	400
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	401
vlCDR1	GNGNPLGMDY	402
vlCDR2	DTSKLAS	403
vlCDR3	FQGSGYPLT	404
Full length light chain (CHA.9.541.4.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	405

Figure **3OO CHA.9.541.5**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	406
vhCDR1	GYTITNYGMN	407
vhCDR2	WINTYTGEPT	408
vhCDR3	GNGNPLGMDY	409
Full length HC (IgG4(S241P); CHA.9.541.5.H4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTMTLDTSTS TVYMELSSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	410
Variable light (vl) domain	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	411
vlCDR1	GNGNPLGMDY	412
vlCDR2	DTSKLAS	413
vlCDR3	FQGSGYPLT	414
Full length light chain (CHA.9.541.5.H4(S241P))	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415

Figure **3PP: CHA.9.541.6**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	416
vhCDR1	GYTITNYGMN	417
vhCDR2	WINTYTGEPT	418
vhCDR3	GNGNPLGMDY	419
Full length HC (IgG4(S241P); CHA.9.541.6.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	420
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	421
vlCDR1	GNGNPLGMDY	422
vlCDR2	DTSKLAS	423
vlCDR3	FQGSGYPLT	424
Full length light chain (CHA.9.541.6.H4(S241P))	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425

Figure **3QQ: CHA.9.541.7**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	426
vhCDR1	GYTITNYGMN	427
vhCDR2	WINTYTGEPT	428
vhCDR3	GNGNPLGMDY	429
Full length HC (IgG4(S241P) **CHA.9.541.7.H4(S241P)**)	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	430
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	431
vlCDR1	GNGNPLGMDY	432
vlCDR2	DTSKLAS	433
vlCDR3	FQGSGYPLT	434
Full length light chain **(CHA.9.541.7.H4(S241P))**	EIVLTQSPATLSLSPGERATLSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSL EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	435

Figure **3RR: CHA.9.541.8**

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSS	436
vhCDR1	GYTITNYGMN	437
vhCDR2	WINTYTGEPT	438
vhCDR3	GNGNPLGMDY	439
Full length HC (IgG4(S241P); CHA.9.541.8.H4(S241P))	QVQLVQSGAEVKKPGASVKISCKASGYTITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYAQKFQGRFTITLDTSTS TVYLEISSLRSEDTAVYYCARGNGNPLGMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	440
Variable light (vl) domain	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGSGYPLTFGQGTKLEIK	441
vlCDR1	GNGNPLGMDY	442
vlCDR2	DTSKLAS	443
vlCDR3	FQGSGYPLT	444
Full length light chain (CHA.9.541.8.H4(S241P))	EIVLTQSPATLSLSPGERVTMSCGNGNPLGMDYWYQQKPGQAPRLWIYDTSKLASGVPARFSGSGSGTDYTLTISSM EPEDFAVYYCFQGSGYPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	445

Figure 35S: CHA.9.547.10

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	446
vhCDR1	GFTFSSYIMS	447
vhCDR2	TISGGGTNTY	448
vhCDR3	WLLSYYAMDY	449
Full length HC for **CHA.9.547.10.H4 (S241P)**)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	450
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	451
vlCDR1	RASQNINVWLS	452
vlCDR2	KASKSHT	453
vlCDR3	QQGQSYPYT	454
Full length light chain For **CHA.9.547.10.H4 (S241P)**	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455

Figure 3TT: CHA.9.547.11

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	456
vhCDR1	GFTFSSYIMS	457
vhCDR2	TISGGGTNTY	458
vhCDR3	WLLSYYAMDY	459
Full length HC for **CHA.9.547.11.H4 (S241P)**)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVSTISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	460
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	461
vlCDR1	RASQNINVWLS	462
vlCDR2	KASKSHT	463
vlCDR3	QQGQSYPYT	464
Full length light chain For **CHA.9.547.11.H4 (S241P)**)	DIQMTQSPSSLSASVGDRITITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	465

Figure 3UU: CHA.9.547.12

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	466
vhCDR1	GFTFSSYIMS	467
vhCDR2	TISGGGTNTY	468
vhCDR3	WLLSYYAMDY	469
Full length HC For **CHA.9.547.12.H4 (S241P)**)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	470
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	471
vlCDR1	RASQNINVWLS	472
vlCDR2	KASKSHT	473
vlCDR3	QQGQSYPYT	474
Full length light chain for **CHA.9.547.12.H4 (S241P)**)	DIQMTQSPSSLSASVGDRVTITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	475

Figure 3VV: CHA.9.547.13

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSS	476
vhCDR1	GFTFSSYIMS	477
vhCDR2	TISGGGTNTY	478
vhCDR3	WLLSYYAMDY	479
Full length HC for CHA.9.547.13.H4 (S241P)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYIMSWVRQAPGKGLEWVATISGGGTNTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKWLLSYYAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	480
Variable light (vl) domain	DIQMTQSPSSLSASVGDRITITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIK	481
vlCDR1	RASQNINVWLS	482
vlCDR2	KASKSHT	483
vlCDR3	QQGQSYPYT	484
Full length light chain for CHA.9.547.13.H4 (S241P)	DIQMTQSPSSLSASVGDRITITCRASQNINVWLSWYQQKPGKAPKLLIYKASKSHTGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQGQSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	485

Figure 3WW: CHA.9.543

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVRQSHGKNLEWLGLIFPYNGGTSYNQNFKGKATLTVDTSSSTAY MELLSLTSVDSAVYYCARGVRFALDYWGQGTSVSVSS	486
vhCDR1	GYSFTGYTMN	487
vhCDR2	LIFPYNGGTS	488
vhCDR3	GVRFALDY	489
Full length HC for **CHA.9.543.H4(S241P)**	Mouse hybridoma, sequence not available	
Variable light (vl) domain	DVVMTQTPLSLPVSFGDQVSISCRSSQSLANSYGNTYLSWYLHKPGQSPQLLIYEISNRFSGVPDRFSGSGSGTDFTLNISTKP EDLGMYYCLQGTHQPWTFGGGTKLEIK	490
vlCDR1	RSSQSLANSYGNTYLS	491
vlCDR2	EISNRFS	492
vlCDR3	LQGTHQPWT	493
Full length light chain for **CHA.9.543.H4(S241P)**	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	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSS	494
vhCDR1	GYTFSSYV	495
vhCDR2	IDPYNDGA	496
vhCDR3	ARGGPYGWYFDV	497
Full length HC	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEKFKGKATLTSDKSSSTAY MELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKD VLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAP IEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNV QKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	498
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFG TYYCQHHFGSPLTFGAGTTLELK	499
vlCDR1	EHIYSY	500
vlCDR2	NAK	501
vlCDR3	QHHFGSPLT	502
Full length light chain	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFG TYYCQHHFGSPLTFGAGTTLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	503

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYYFFGVDVWGQGTTVTVSS	504
vhCDR1	GGSVSSGIYY	505
vhCDR2	IYYSGST	506
vhCDR3	ARDYYVSGNYYNVDYYFFGVDV	507
Full length HC	QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDYYVSGNYYNVDYYFFGVDVWGQGTTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEP VTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIF PPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVY SKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK	508
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVY YCQQRSNWPPLFTFGPGTKVDIK	509
vlCDR1	QSVSSY	510
vlCDR2	DAS	511
vlCDR3	QQRSNWPPLFT	512
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVY YCQQRSNWPPLFTFGPGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	513

Figure 3AAA

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:10 from US20170281764)	DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMHWVRQAPEKGLEWVAFISSGSS SIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARMRLDYYAMDYWGQ GTSVTVSS	514
vhCDR1 (SEQ ID NO:11 from US20170281764)	NFGMH	515
vhCDR2 (SEQ ID NO:12 from US20170281764)	FISSGSSSIYYADTVKG	516
vhCDR3 (SEQ ID NO:13 from US20170281764)	MRLDYYAMDY	517
Light chain (SEQ ID NO:14 from US20170281764)	DVQITQSPSYLAASPGETITINCRASKSISKYLAWYQEKPGKTNKLLIYSGSTLQSGIPS RFSGSGSGTDFTLTISSLEPEDFAMYYCQQHNEYPWTFGGGTKLEIK	518
vlCDR1 (SEQ ID NO:15 from US20170281764)	RASKSISKYLA	519
vlCDR2 (SEQ ID NO:16 from US20170281764)	SGSTLQS	520
vlCDR3 (SEQ ID NO:17 from US20170281764)	QQHNEYPWT	521

Figure 3BBB

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:18 from US20170281764)	EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKNLEWIGGINPNNG GTSYNQKFKGRATLTVDKSSSTAYMELRSLTSDDSAVYYCARPGWYNYAMDYWG QGTSVTVSS	522
vhCDR1 (SEQ ID NO:19 from US20170281764)	EYTMH	523
vhCDR2 (SEQ ID NO:20 from US20170281764)	GINPNNGGTSYNQKFKG	524
vhCDR3 (SEQ ID NO:21 from US20170281764)	PGWYNYAMDY	525
Light chain (SEQ ID NO:22 from US20170281764)	DIVMTQSHKFMSTSVGDRVNITCKASQGVSTAVAWYQQKPGQSPKLLIYSASYRYT GVPDRFTGSGSGTDFTFTISSVQAEDLAVYHCQQHYITPWTFGGGTKLEIK	526
vlCDR1 (SEQ ID NO:23 from US20170281764)	KASQGVSTAVA	527
vlCDR2 (SEQ ID NO:24 from US20170281764)	SASYRYT	528
vlCDR3 (SEQ ID NO:25 from US20170281764)	QQHYITPWT	529

Figure 3CCC

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:26 from US20170281764)	EVQLVESGGGLVKPGGSLKLSCAASGFAFSDYDMSWVRQTPEKRLEWVAYISDGGY NTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAIYYCARQILLRYYFDYWGQGT TLTVSS	530
vhCDR1 (SEQ ID NO:27 from US20170281764)	DYDMS	531
vhCDR2 (SEQ ID NO:28 from US20170281764)	YISDGGYNTYYPDTVKG	532
vhCDR3 (SEQ ID NO:29 from US20170281764)	QILLRYYFDY	533
Light chain (SEQ ID NO:30 from US20170281764)	DIVMSQSPSSLAVSVGEKVTMTCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYW ASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYHSYPWTFGGGTKLEIK	534
vlCDR1 (SEQ ID NO:31 from US20170281764)	KSSQSLLYSSNQKNYLA	535
vlCDR2 (SEQ ID NO:32 from US20170281764)	WASTRES	536
vlCDR3 (SEQ ID NO:33 from US20170281764)	QQYHSYPWT	537

Figure 3DDD

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:35 from US20172817 64)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAFISSGSSS IYYADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRLDYYAMDYWGQ GTMVTVSS	538
Light chain (SEQ ID NO:37 from US20172817 64)	DIQMTQSPSSLSASVGDRVTITCRASKSISKYLAWYQQKPGKAPKLLIYSGSTLQSGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPWTFGGGTKVEIK	539

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:34 from US20172817 64)	MDSRLNLVFLVLILKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWV RQAPGKGLEWVAFISSGSSSIYYADTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARMRLDYYAMDYWGQGTMVTVSS	540
Light chain (SEQ ID NO:36 from US20172817 64)	MRFQVQVLGLLLLWISGAQCDIQMTQSPSSLSASVGDRVTITCRASKSISKYLAWYQ QKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYP WTFGGGTKVEIK	541

Figure 3EEE

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

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:15 from WO2015009856)	EVQLVESGGGLTQPGKSLKLSCEASGFTFSSFTMIWVRQSPGKGLEWVAFIRSGSGIVF YADAVRGRFTISRDNAKNLLFLQMNDLKSEDTAMYYCARRPLGHNTFDSWGQGTLVT VSS	542
vhCDR1 (SEQ ID NO:4 from WO2015009856)	GFTFSSFTMH	543
vhCDR2 (SEQ ID NO:5 from WO2015009856)	FIRSGSGIVFYADAVRG	544
vhCDR3 (SEQ ID NO:6 from WO2015009856)	RPLGHNTFDS	545
Light chain (SEQ ID NO:13 from WO2015009856)	DIVMTQSPSSLAVSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASI RFTGVPDRFTGSGSGTDYTLTITTVQAEDMGQYFCQQGHNNPLTFGDGTKLEIKR	546
vlCDR1 (SEQ ID NO:1 from WO2015009856)	KSSQSLYYSGVKENLLA	547
vlCDR2 (SEQ ID NO:2 from WO2015009856)	ASIRFT	548
vlCDR3 (SEQ ID NO:3 from WO2015009856)	QQGHNNPLT	549

Figure 3FFF

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

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:16 from WO2015009856)	EVQLQQSGPELVKPGTSMKISCKASGYSFTGHLMNWVKQSHGKNLEWIGLIIPYNGGTS YNQKFKGKATLTVDKSSSTAYMELLSLTSDDSAVYFCSRGLRGFYAMDYWGQGTSVT VSS	550
vhCDR1 (SEQ ID NO:10 from WO2015009856)	GYSFTGHLMN	551
vhCDR2 (SEQ ID NO:11 from WO2015009856)	LIIPYNGGTSYNQKFKG	552
vhCDR3 (SEQ ID NO:12 from WO2015009856)	GLRGFYAMDY	553
Light chain (SEQ ID NO:14 from WO2015009856)	DVVLTQTPLSLSVSFGDQVSISCRSSQSLVNSYGNTFLSWYLHKPGQSPQLLIFGISNRFS GVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPPTFGPGTKLEVK	554
vlCDR1 (SEQ ID NO:7 from WO2015009856)	RSSQSLVNSYGNTFLS	555
vlCDR2 (SEQ ID NO:8 from WO2015009856)	GISNRFS	556
vlCDR3 (SEQ ID NO:9 from WO2015009856)	LQGTHQPPT	557

Figure 3GGG
From US 9713641 (Table 5, reproduced herein; SEQ ID NOs: are from US 9713641)

						Sequences and germlines (GL) of 1IGHT ABPs					
Ab	VH GL	CDR-H1[1] (SEQ ID NOS 558-562)	CDR-H2[2] (SEQ ID NOS 563-567)	CDR-H3[3] (SEQ ID NOS 568-572)	VH Protein (SEQ ID NOS 573-577)	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	GSITSSS YYWG (SEQ ID NO 48)	SIYYSG ATFYN P5LKS (SEQ ID NO 36)	ARDAN YYGSA WAFDP (SEQ ID NO 29)	QLQLQESGPGLVKPSETLSLTCTVSG GSITSSSYYWGWIRQPPGKGLEWIGSI GSYSGATFYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARDANYY GSAWAFDPWGQGTLVTVSS (SEQ ID NO 4)	VK3-11	RASQS VSSYL A (SEQ ID NO 67) 70)	DASNRA T (SEQ ID NO 63)	QQHFNL PT (SEQ ID NOS 588-592)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEP EDFAVYYCQQHFNLPTFGGGTKVEIK (SEQ ID NO 25)
MAB2 -IgG4	VH 4-39	GSISSSK YYWG (SEQ ID NO 40)	SIYYSG STFYN P5LKS (SEQ ID NO 37)	ARDAN YYGSA WAFDP (SEQ ID NO 29)	QLQLQESGPGLVKPSETLSLTCTVS GGSISSSKYYWGWIRQPPGKGLEWI GSIYYSGSTFYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD ANYYGSAWAFDPWGQGTLVTVSS (SEQ ID NO 5)	VK3-11	RASQS VSSYL A (SEQ ID NO 67) 70)	DASNRA T (SEQ ID NO 63)	QQHFNL PT (SEQ ID NO 63)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEP EDFAVYYCQQHFNLPTFGGGTKVEIK (SEQ ID NO 25)
MAB3 -IgG4	VH 4-39	GSISSTS ITYWG (SEQ ID NO 36)	SIYYSG ATYNP SLKS (SEQ ID NO 37)	ARDAN YYGSA WAFDP (SEQ ID NO 29)	QLQLQESGPGLVKPSETLSLTCTVS GGSISSTSITYWGWTRQPPGKGLEWI GSIYYSGSTYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD ANYYGSAWAFDPWGQGTLVTVSS (SEQ ID NO 6)	VK3-11	RASQS VSSYL T (SEQ ID NO 67) 70)	DASNRA T (SEQ ID NO 63)	QQHFNL PT (SEQ ID NO 63)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEP EDFAVYYCQQHFNLPTFGGGTKVEIK (SEQ ID NO 25)
MAB4 -IgG4	VH 4-39	GSSSTSH YWG (SEQ ID NO 30)	SIYYSG SIYNP SLKS (SEQ ID NO 37)	ARDAN YYGGA WAFDP (SEQ ID NO 30)	QLQLQESGPGLVKPSETLSLTCTVS GGSISSTSHYWGWIRQPPGKGLEWI GSIYYSGSIYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD ANYYGGAWAFDPWGQGTLVTVSS (SEQ ID NO 7)	VK3-11	RASQS VSSYL T (SEQ ID NO 67) 70)	DASNRA T (SEQ ID NO 63)	QQHFNI PT (SEQ ID NO 63)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLIP EDFAVYYCQQHFNLPTFGGGTKVEIK (SEQ ID NO 25)
MAB5 -IgG4	VH 4-39	GSISSTSH YWG (SEQ ID NO 30)	SIYYSG SIYNP SLKS (SEQ ID NO 37)	ARDAN YYGSA WAFDP (SEQ ID NO 29)	QLQLQESGPGLVKPSETLSLTCTVS GGSISSTSHYWGWIRQPPGKGLEWI GSIYYSGSIYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD ANYYGSAWAFDPWGQGTLVTVSS (SEQ ID NO 8)	VK3-11	RASQS VSSYL T (SEQ ID NO 67) 70)	DASNRA T (SEQ ID NO 63)	QQHFNL PT (SEQ ID NO 63)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEP EDFAVYYCQQHFNLPTFGGGTKVEIK (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 TIGIT ABPs									
Ab	VH GL	CDR-H3[7] (SEQ ID NOS 598-612)	CDR-H2[8] (SEQ ID NOS 583-597)	CDR-H1[9] (SEQ ID NOS 568-582)	VH Protein (SEQ ID NOS 613-617)	VL GL	CDR-L1[10] (SEQ ID NOS 618-622)	CDR-L2[11] (SEQ ID NOS 623-627)	CDR-L3[12] (SEQ ID NOS 628-632)	VL Protein (SEQ ID NOS 633-637)
MAB6	VH	GSIESGSS	SIYYSGGT	ARDGV	QLQLQESGPGLVKPSETLSLTCTVSG	VK3-	RASQS	GASSRA	QQHTV	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
-IgG4	4-	YYWG	YYNPSLK	LTTLNKR	GSIESGSYYWGWIRQPPGKGLEWIG	20	VSSSY	T (SEQ	RPPLT	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL
	39	(SEQ ID	S (SEQ ID	SFDI	SIYYSGTTYYNPSLKSRVTISVDTSK		LA	ID NO 68)	(SEQ ID	EPEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO
		NO 51)	NO 39)	(SEQ ID NO 31)	NQFSLKLSSVTAADTAVYYCARDGV LTLNKRSFDWGQGTMVTVSS (SEQ ID NO 9)		(SEQ ID NO 71)		NO 64)	26)
MAB7	VH	GSIESGSV	SIYYSGST	ARDGV	QVQLQESGPGLVKPSQTLSLTCTVSG	VK3-	RASQS	GASSRA	QQHTV	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
-IgG4	4-	YYWG	YYNPSLK	LTTLNKR	GSIESGVYYWGWIRQPPGKGLEWIG	20	VSSSY	T (SEQ	RPPLT	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL
	31	(SEQ ID	S (SEQ ID	SFDI	SIYYSGSTYYNPSLKSRVTISVDTSK		LA	ID NO 68)	(SEQ ID	EPEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO
		NO 52)	NO 40)	(SEQ ID NO 31)	NQFSLKLSSVTAADTAVYYCARDGV LTLNKRSFDWGQGTMVTVSS (SEQ ID NO 10)		(SEQ ID NO 71)		NO 64)	26)
MAB8	VH	GSIASGGS	SIYYSGQT	ARDGV	QLQLQESGPGLVKPSETLSLTCTVSG	VK3-	RASQS	GASSRA	QQHTV	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
-IgG4	4-	YYWG	YYNPSLK	LTTLNKR	GSIASGSYYWGWIRQPPGKGLEWIG	20	VSSSY	T (SEQ	RPPLT	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL
	39	(SEQ ID	S (SEQ ID	SFDI	SIYYSGQTYYNPSLKSRVTISVDTSK		LA	ID NO 68)	(SEQ ID	EPEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO
		NO 53)	NO 41)	(SEQ ID NO 31)	NQFSLKLSSVTAADTAVYYCARDG VLTLNKRSFDIWGQGTMVTVSS (SEQ ID NO 11)		(SEQ ID NO 71)		NO 64)	26)
MAB9	VH	GSIESGL	SIYYSGST	ARDGV	QVQLQESGPGLVKPSQTLSLTCTVS	VK3-	RASQSV	GASSRA	QQHTV	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
-IgG1	4-	YYWG	YNPSLKS	LTTLNKR	GGSIESGLYYWGWIRQPPGKGLEWI	20	SSSYLA	T (SEQ	RPPLT	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL
	31	(SEQID NO 54)	(SEQIDNO 42)	SFDI (SEQ ID NO 31)	GSIYYSGSTYYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD GVLTLNKRSFDIWGQGTMVTVSS (SEQ ID NO 12)		(SEQID NO 71)	ID NO (68)	(SEQ ID NO 64)	EPIDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQIDNO 26)
MAB1	VH	GSIESGL	SIYYSGST	ARDGV	QVQLQESGPGLVKPSQTLSLTCTVS	VK3-	RASQS	GASSRA	QQHTV	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
0-	4-	YYWG	YNPSLKS	LALNKR	GGSIESGLYYWGWIRQPPGKGLEWI	20	VSSSY	T (SEQ	RPPLT	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL
IgG4	31	(SEQID NO 54)	(SEQIDNO 42)	SFDI (SEQ ID NO 32)	GSIYYSGSTYYNPSLKSRATISVDTS KNQFSLKLSSVTAADTAVYYCARD GVLALNKRSFDIWGQGTMVTVSS (SEQ ID NO 13)		LA (SEQ ID NO 71)	ID NO (68)	(SEQ ID NO 64)	EPEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO 26)

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

[8] According to the Kabat numbering system.

[9] According to the IMGT numbering system.

[10] According to the Kabat and Chothia numbering systems.

[11] According to the Kabat and Chothia numbering systems.

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

Figure 3III

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

Sequences and germlines (GL) of TIGIT ABPs

Ab	VH GL	CDR-H1[13] (SEQ ID NOS 638-642)	CDR-H2[14] (SEQ ID NOS 643-647)	CDR-H3[15] (SEQ ID NOS 648-652)	VH Protein (SEQ ID NOS 653-657)	VL GL	CDR-L1[16] (SEQ ID NOS 658-662)	CDR-L2[17] (SEQ ID NOS 663-667)	CDR-L3[18] (SEQ ID NOS 668-672)	VL Protein (SEQ ID NOS 673-677)
MAB1	VH	GSISSHLY	SIYYSG	ARDGVL	QVQLQESGPGLVKPSQTLSLTCTVS	VK3-20	RASQS	GASSRA	QQHTVR	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
1-IgG4	4-31	YWG(SEQ ID NO:54)	SIYYNP SLKS (SEQ ID NO:40)	ALNKRS FDI (SEQ ID NO:32)	GGSISESHLYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD GVLALNKRSPDIWGQGTMVTVSS (SEQ ID NO:14)		VSSSY LA (SEQ ID NO:71)	T (SEQ ID NO:68)	PPLT (SEQ ID NO:64)	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO:26)
MAB1	VH	GSISSGLY	SIYYSG	ARDGVL	QVQLQESGPGLVKPSQTLSLTCTAS	VK3-20	RASQS	GASSRA	QQHTVR	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ
2-IgG4	4-31	YWG(SEQ ID NO:54)	SIYYNP SLKS (SEQ ID NO:40)	ALNKRS FDI (SEQ ID NO:32)	GGSISESHLYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARD GVLALNKRSPDIWGQGTMVTVSS (SEQ ID NO:15)		VSSSY LA (SEQ ID NO:71)	T (SEQ ID NO:68)	PPLT (SEQ ID NO:64)	KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQHTVRPPLTFGGGTKVEIK (SEQ ID NO:26)
MAB1	VH	YTFPGNY	INPSLG	ARGGRT	QVQLVQSGAEVKKPGASVKVSCKA	VK3-15	RASQS	GASTRA	QQYVV	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK
3-IgG4	1-46	YMH (SEQ ID NO:58)	LTSYAQ KFQG (SEQ ID NO:42)	TWIGAF DI (SEQ ID NO:33)	SGYTFPGNYYMHWVRQAPGQGLEW MGIINPSLGLTSYAQKFQGRVTMTR DTSTSTVYMELSSLRSEDTAVYYCA RGGRTTWIGAFDIWGQGTMVTVSS (SEQ ID NO:16)		VSSNL A (SEQ ID NO:72)	T (SEQ ID NO:69)	WPPLT (SEQ ID NO:65)	PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYVVWPPLTFGGGTKVEIK (SEQ ID NO:27)
MAB1	VH	YTFPAY	INPSLG	ARGGRT	QVQLVQSGAEVKKPGASVKVSCKA	VK3-15	RASQS	GASTRA	QQYVV	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK
4-IgG4	1-46	YMH (SEQ ID NO:59)	LTSYAQ KFQG (SEQ ID NO:42)	TWIGAF DI (SEQ ID NO:33)	SGYTFPAYYMHWVRQAPGQGLEW MGIINPSLGLTSYAQKFQGRVTMTR DTSTSTVYMELSSLRSEDTAVYYCA RGGRTTWIGAFDIWGQGTMVTVSS (SEQ ID NO:17)		VSSNL A (SEQ ID NO:72)	T (SEQ ID NO:69)	WPPLT (SEQ ID NO:65)	PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYVVWPPLTFGGGTKVEIK (SEQ ID NO:27)
MAB1	VH	YTFRDY	INPSIG	ARGGRT	QVQLVQSGAEVKKPGASVKVSCKA	VK3-15	RASQS	GASTRA	QQYVV	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK
5-IgG4	1-46	YMH (SEQ ID NO:60)	LTSYA R&FQG (SEQ ID NO:46)	TWIGAF DI (SEQ ID NO:33)	SGYTFRDYYMHWVRQAPGQGLEW MGIINPSIGLTSYARKFQGRVTMTR DTSTSTVYMELSSLRSEDTAVYYCA RGGRTTWIGAFDIWGQGTMVTVSS (SEQ ID NO:18)		VSSNL A (SEQ ID NO:72)	T (SEQ ID NO:69)	WPPLT (SEQ ID NO:65)	PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFAVYYCQQYVVWPPLTFGGGTKVEIK (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 3JJJ

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

Sequences and germlines (GL) of TIGIT ABPs										
Ab	VH GL	CDR-H1[19] (SEQ ID NOS 678-683)	CDR-H2[20] (SEQ ID NOS 684-689)	CDR-H3[21] (SEQ ID NOS 690-695)	VH Protein (SEQ ID NOS 696-701)	VL GL	CDR-L1[22] (SEQ ID NOS 702-707)	CDR-L2[23] (SEQ ID NOS 708-713)	CDR-L3[24] (SEQ ID NOS 714-719)	VL Protein (SEQ ID NOS 720-725)
MAB16-IgG4	VH 1-46	YTFRE YYMH (SEQ ID NO 60)	IINPSIGL TSYARK FQG (SEQ ID NO 43)	ARGGRT TWIGAL DI (SEQ ID NO 34)	QVQLVQSGAEVKKPGASVKVSCKASGYT FREYYMHWVRQAPGQGLEWMGIINPSIGL TSYARKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARGGRTTWIGALDIWGQGT MVTVSS (SEQ ID NO 19)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYVVW PPLT (SEQ ID NO 65)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYVVWPPLTFGGGTKVEIK (SEQ ID NO 27)
MAB17-IgG4	VH 1-46	YTFPA YYIH (SEQ ID NO 61)	IINPSLG LTSYAR KFQG (SEQ ID NO 44)	ARGGRT TWIGAL DI (SEQ ID NO 34)	QVQLVQSGAEVKKPGASVKVSCKASGYT FPAYYIHWVRQAPGQGLEWMGIINPSLGL TSYARKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARGGRTTWIGALDIWGQG TMVTVSS (SEQ ID NO 20)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYVVW PPLT (SEQ ID NO 65)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYVVWPPLTFGGGTKVEIK (SEQ ID NO 27)
MAB18-IgG4	VH 1-46	YTFPA YYMH (SEQ ID NO 59)	IINPSLGL TSYARKF QG (SEQ ID NO 44)	ARGGRTT WIGAFDI (SEQ ID NO 33)	QVQLVQSGAEVKKPGASVKVSCKASGYT FPAYYMHWVRQAPGQGLEWMGIINPSLG LTSYARKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARGGRTTWIGAFDIWGQ GTMVTVSS (SEQ ID NO 21)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYVVW PPLT (SEQ ID NO 65)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYVVWPPLTFGGGTKVEIK (SEQ ID NO 27)
MAB19-IgG4	VH 1-46	YTFTS HYMG (SEQ ID NO 62)	VINPSM GATSYA QKFQG (SEQ ID NO 45)	ARLHVS GSYYPA YLDY (SEQ ID NO 35)	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSHYMGWVRQAPGQGLEWMGVINPSM GATSYAQKFQGRVTMTRDTSTLSTVYME LSSLRSEDTAVYYCARLHVSGSYYPAYLD YWGQGTMVTVSS (SEQ ID NO 22)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYIVFP WT (SEQ ID NO 66)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRHLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYIVFPWTFGGGTKVEIK (SEQ ID NO 28)
MAB20-IgG4	VH 1-46	YIFTSH YMG (SEQ ID NO 62)	IINPSMG ATSYAQ KFQG (SEQ ID NO 46)	ARLHVS GSYYPA YLDY (SEQ ID NO 35)	QVQLVQSGAEVKKPGASVKVSCKASGYTF TSHYMGWVRQAPGQGLEWVGIINPSMGAT SYAQKFQGRVTMTRDTSTSTVYMELSSLAS EDTAVYYCARLHVSGSYYPAYLDYWGQG TMVTVSS (SEQ ID NO 23)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYIVFP WT (SEQ ID NO 66)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRHLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYIVFPWTFGGGTKVEIK (SEQ ID NO 28)
MAB21-IgG4	VH 1-46	YIFTSH YMG (SEQ ID NO 62)	IINPSMG ATSYTQ KFRG (SEQ ID NO 47)	ARLHVS GSYYPA YLDY (SEQ ID NO 35)	QVQLVQSGAEVKKPGASVKVSCKASGYTF TSHYMGWVRQAPGQGLEWMGIINPSMGA TSYTQKFRGRVTMTRDTSTSTVYMELSSLA SEDTAVYYCARLHVSGSYYPAYLDYWGQ GTMVTVSS (SEQ ID NO 24)	VK3-15	RASQSV SSNLA (SEQ ID NO 72)	GASTRA T (SEQ ID NO 69)	QQYIVFP WT (SEQ ID NO 66)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRHLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYIVFPWTFGGGTKVEIK (SEQ ID NO 28)

[19] Includes CDR-H1 as defined by both the Chothia and Kabat numbering systems, inclusive of the boundaries of both numbering systems.
[20] According to the Kabat numbering system.
[21] According to the IMGT numbering system.
[22] According to the Kabat and Chothia numbering systems.
[23] According to the Kabat and Chothia numbering systems.
[24] According to the Kabat, Chothia, and IMGT numbering systems.

Figure 3KKK

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:7 from WO2016028656)	EVQLQESGPGLVKPSQSLSLTCSVTGSSIASDYWGWIRKFPGNKMEWMGFITYSGSTSY NPSLKSRISITRDTSKNQFFLQLHSVTTDDTATYSCARMPSFITLASLSTWEGYFDFWGP GTMVTVSS	726
vhCDR1 (SEQ ID NO:1 from WO2016028656)	SDYWG	727
vhCDR2 (SEQ ID NO:2 from WO2016028656)	FITYSGSTSYNPSLKS	728
vhCDR3 (SEQ ID NO:3 from WO2016028656)	MPSFITLASLSTWEGYFDF	729
Light chain (SEQ ID NO:8 from WO2016028656)	DIQMTQSPSLLSASVGDRVTLNCKASQSIHKNLAWYQQKLGEAPKFLIYYANSLQTGIPS RFSGSGSGTDFTLTISGLQPEDVATYFCQQYYSGWTFGGGTKVELK	730
vlCDR1 (SEQ ID NO:4 from WO2016028656)	KASQSIHKNLA	731
vlCDR2 (SEQ ID NO:5 from WO2016028656)	YANSLQT	732
vlCDR3 (SEQ ID NO:6 from WO2016028656)	QQYYSGWT	733

Figure 3LLL

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:9 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGGSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	734
vhCDR1 (WO2016028656)	DYWG	735
vhCDR2 (WO2016028656)	FITYSGSTSYNPSLKS	736
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDF	737

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:10 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGGSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	738
vhCDR1 (from WO2016028656)	SDYWG	739
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	740
vhCDR3 (WO2016028656)	MPSFITLASLSTWEGYFDF	741

Figure 3MMM

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:11 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGGSISSDYWGWIRQPPGKGLEWIGEITYSGSTSYNP SLKSRITISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT MVTVSS	742
vhCDR1 (from WO2016028656)	SDYWG	743
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	744
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	745

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:12 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSISSDYWGWIRQPPGKGLEWMGFITYSGSTSYN PSLKSRITISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	746
vhCDR1 (from WO2016028656)	SDYWG	747
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	748
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	749

Figure 3OOO

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:13 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGGSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	750
vhCDR1 (from WO2016028656)	SDYWG	751
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	752
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	753

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:14 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGGSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT 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)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:15 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT MVTVSS	758
vhCDR1 (from WO2016028656)	SDYWG	759
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	760
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	761

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:16 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSISSDYWGWIRQPPGKGLEWMGFITYSGSTSYN PSLKSRITISVDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG 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)	EVQLQESGPGLVKPSETLSLTCAVSGYSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ GTMVTVSS	766
vhCDR1 (from WO2016028656)	SDYWG	767
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	768
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	769

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:18 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCAVSGYSISSDYWGWIRQPPGKGLEWIGFI TYSGSTSYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMVTVSS	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)	EVQLQESGPGLVKPSETLSLTCAVSGYSISSDYWGWIRQPPGKGLEWIGFI TYSGSTSYNPSLKSRITISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMVTVSS	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)	EVQLQESGPGLVKPSETLSLTCAVSGSSISSDYWGWIRQPPGKGLEWMGFI TYSGSTSYNPSLKSRITISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFI TLASLSTWEGYFDFWGQGTMVTVSS	778
vhCDR1 (from WO2016028656)	SDYWG	779
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	780
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	781

Figure 3SS

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:21 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCAVSGYSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ GTMVTVSS	782
vhCDR1 (from WO2016028656)	SDYWG	783
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	784
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	785

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:22 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCAVSGYSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYN PSLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	786
vhCDR1 (from WO2016028656)	SDYWG	787
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	788
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	789

Figure 3TTT

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:37 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSSAS	790
vhCDR1 (from WO2016028656)	SDYWG	791
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	792
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	793

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:38 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG 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)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:39 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRKPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	798
vhCDR1 (from WO2016028656)	SDYWG	799
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	800
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	801

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:40 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRQPPGKKLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG 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)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:41 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRQPPGKGMEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ GTMVTVSS	806
vhCDR1 (from WO2016028656)	SDYWG	807
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	808
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	809

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:42 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRKPPGKKMEWIGFITYSGSTSYN PSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ 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)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:43 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRQFPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTADDTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	814
vhCDR1 (from WO2016028656)	SDYWG	815
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	816
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	817

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:44 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCTVSGSSIASDYWGWIRKPPGKKMEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ 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)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:45 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCSVTGSSIASDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG TMVTVSS	822
vhCDR1 (from WO2016028656)	SDYWG	823
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	824
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	825

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:46 from WO2016028656)	EVQLQQSGAGLLKPSETLSLTCSVTGSSIASDYWGWIRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ GTMVTVSS	826
vhCDR1 (from WO2016028656)	SDYWG	827
vhCDR2 (from WO2016028656)	FITYSGSTSYNPSLKS	828
vhCDR3 (from WO2016028656)	MPSFITLASLSTWEGYFDF	829

Figure 3YY

From WO2016028656 (Table 4, reproduced herein)

What	Sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:47 from WO2016028656)	EVQLQESGPGLVKPPGTLSLTCSVTGSSIASDYWGWVRQPPGKGLEWIGFITYSGSTSYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQ 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)	EVQLQESGPGLVKPSETLSLTCAVSGSSISSDYWGWIRQPPGKGLEWIGFITYSGSTSYNP SLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQGT MVTVSS	834
vhCDR1 (SEQ ID NO: from WO2016028656)	SDYWG	835
vhCDR2 (SEQ ID NO: from WO2016028656)	FITYSGSTSYNPSLKS	836
vhCDR3 (SEQ ID NO: from WO2016028656)	MPSFITLASLSTWEGYFDF	837

Figure 3AAAA

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:24 from WO2016028656)	EVQLQESGPGLVKPSETLSLTCAVSGSSISSDYWGWIRQPPGKGLEWMGFITYSGSTSYN PSLKSRITISRDTSKNQFSLKLHSVTAADTAVYYCARMPSFITLASLSTWEGYFDFWGQG 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)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	842
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	843
vlCDR2 (from WO2016028656)	YANSLQT	844
vlCDR3 (from WO2016028656)	QQYYSGWT	845

Figure 3BBBB

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:26 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	846
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	847
vlCDR2 (from WO2016028656)	YANSLQT	848
vlCDR3 (from WO2016028656)	QQYYSGWT	849

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:27 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGIPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	850
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	851
vlCDR2 (from WO2016028656)	YANSLQT	852
vlCDR3 (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)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKLLIYYANSLQTGVP SRFSGSGSGTDFTLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	854
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	855
vlCDR2 (from WO2016028656)	YANSLQT	856
vlCDR3 (from WO2016028656)	QQYYSGWT	857

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:29 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	858
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	859
vlCDR2 (from WO2016028656)	YANSLQT	860
vlCDR3 (from WO2016028656)	QQYYSGWT	861

Figure 3DDDD

From WO2016028656 (Table 4, reproduced herein)

What	sequences	SEQ ID NO:
Light chain (SEQ ID NO:30 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKVPKFLIYYANSLQTGIPS RFSGSGSGTDFTLTISSLQPEDVATYYCQQYYSGWTFGGGTKVEIK	862
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	863
vlCDR2 (from WO2016028656)	YANSLQT	864
vlCDR3 (from WO2016028656)	QQYYSGWT	865

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:48 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	866
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	867
vlCDR2 (WO2016028656)	YANSLQT	868
vlCDR3 (WO2016028656)	QQYYSGWT	869

Figure 3EEEE

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:49 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	870
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	871
vlCDR2 (WO2016028656)	YANSLQT	872
vlCDR3 (WO2016028656)	QQYYSGWT	873

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:50 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGVP SRFSGSGSGTDFTLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK	874
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	875
vlCDR2 (WO2016028656)	YANSLQT	876
vlCDR3 (WO2016028656)	QQYYSGWT	877

Figure 3FFFF

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:51 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKFLIYYANSLQTGVPS RFSGSGSGTDFTLTISSLQPEDFATYFCQQYYSGWTFGGGTKVEIK	878
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	879
vlCDR2 (WO2016028656)	YANSLQT	880
vlCDR3 (WO2016028656)	QQYYSGWT	881

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:52 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCKASQSIHKNLAWYQQKPGKAPKLLIYYANSLQTGIPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSGWTFGGGTKVEIK	882
vlCDR1 (from WO2016028656)	KASQSIHKNLAW	883
vlCDR2 (WO2016028656)	YANSLQT	884
vlCDR3 (WO2016028656)	QQYYSGWT	885

Figure 3GGGG

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSAS YNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCATLIYYDYGGAMNFWGQGTSVT VSS	886
vhCDR1 (from WO2016028656)	GYSITSDYAWN	887
vhCDR2 (WO2016028656)	YISNSGSASYNPSLKS	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)	DIVMTQSHKFMSTSVGDRVSITCKASQGVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPDRFTG SGSGTDFTFTISSVQSEDLAVYYCQHYYSTPWTFGGGTKLEIK	890
vlCDR1 (from WO2016028656)	KASQGVSTTVA	891
vlCDR2 (WO2016028656)	SASYRYT	892
vlCDR3 (WO2016028656)	QHYYSTPWT	893
vlCDR2 variant (WO2016028656)	YASNLQT	894
vlCDR2 variant (WO2016028656)	YASSLQT	895
vlCDR2 variant (WO2016028656)	YASTLQT	896
vlCDR2 variant (WO2016028656)	YATTLQT	897
vlCDR2 variant (WO2016028656)	YASYLQT	898
vlCDR2 variant (WO2016028656)	YANQLQT	899
vlCDR2 variant (WO2016028656)	YAGSLQT	900
vlCDR2 variant (WO2016028656)	YASQLQT	901
vlCDR2 variant (WO2016028656)	YADSLQT	902

Figure 3IIII

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:62 from WO2016028656)	DIVMTQSHKFMSTSVGDRVSITCKASQGVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPDRFTG SGSGTDFTFTISSVQSEDLAVYYCQHYYSTPWTFGGGTKLEIK	903
vlCDR1 (from WO2016028656)	KASQGVSTTVA	904
vlCDR2 (WO2016028656)	SASYRYT	905
vlCDR3 (WO2016028656)	QHYYSTPWT	906
vlCDR3 variant (WO2016028656)	QQYYSGFT	907
vlCDR3 variant (WO2016028656)	QQYYSGYT	908
vlCDR3 variant (WO2016028656)	QQYYSGIT	909
vlCDR3 variant (WO2016028656)	QQYYSGVT	910
vlCDR3 variant (WO2016028656)	QQYYSGLT	911

Figure 3JJJ

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:63 from WO2016028656)	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSAS YNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCATLIYYDYGGAMNFWGQGTSVT VSS	912
vhCDR1 (from WO2016028656)	GYSITSDYAWN	913
vhCDR2 (WO2016028656)	YISNSGSASYNPSLKS	914
vhCDR3 (WO2016028656)	LIYYDYGGAMNF	915
vHCDR3 variant (WO2016028656)	MPSFITLASLSTFEGYFDF	916
vHCDR3 variant (WO2016028656)	MPSFITLASLSTYEGYFDF	917
vHCDR3 variant (WO2016028656)	MPSFITLASLSTIEGYFDF	918
vHCDR3 variant (WO2016028656)	MPSFITLASLSTVEGYFDF	919
vHCDR3 variant (WO2016028656)	MPSFITLASLSTLEGYFDF	920

Figure 3KKKK

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:94 from WO2016028656)	EVQLQQSGPELVKPGSSVKMSCKASGYTFSSYVMHWVKQKPGQGLEWIGYIDPYNDGAKYNEK FKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGPYGWYFDVWGAGTTVTVSS	921
vhCDR1 (from WO2016028656)	SYVMH	922
vhCDR2 (WO2016028656)	YIDPYNDGAKYNEKFK	923
vhCDR3 (WO2016028656)	GPYGWYFDV	924
vHCDR2 variant (WO2016028656)	YIDPYNrGAKYNEKFG	925
vHCDR2 variant (WO2016028656)	YIDPYNlGAKYNEKFG	926
vHCDR2 variant (WO2016028656)	YIDPYNkGAKYNEKFG	927
vHCDR2 variant (WO2016028656)	YIDPYNfGAKYNEKFG	928
vHCDR2 variant (WO2016028656)	YIDPYNsGAKYNEKFG	929
vHCDR2 variant (WO2016028656)	YIDPYNyGAKYNEKFG	930
vHCDR2 variant (WO2016028656)	YIDPYNvGAKYNEKFG	931
vHCDR2 variant (WO2016028656)	YIDPYNDrAKYNEKFKG	932
vHCDR2 variant (WO2016028656)	YIDPYNDnAKYNEKFKG	933
vHCDR2 variant (WO2016028656)	YIDPYNDqAKYNEKFKG	934
vHCDR2 variant (WO2016028656)	YIDPYNDeAKYNEKFKG	935
vHCDR2 variant (WO2016028656)	YIDPYNDlAKYNEKFKG	936
vHCDR2 variant (WO2016028656)	YIDPYNDkAKYNEKFKG	937
vHCDR2 variant (WO2016028656)	YIDPYNDsAKYNEKFKG	938
vHCDR2 variant (WO2016028656)	YIDPYNDyAKYNEKFKG	939
vHCDR2 variant (WO2016028656)	YIDPYNDvAKYNEKFKG	940

Figure 3LLLL

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:94 from WO2016028656)	DIQMTQSPASLSASVGETVTITCRASEHIYSYLSWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSG SGTQFSLKINSLQPEDFGTYYCQHHFGSPLTFGAGTTLELK	941
vICDR1 (from WO2016028656)	RASEHIYSYLS	942
vICDR2 (WO2016028656)	NAKTLAE	943
vICDR3 (WO2016028656)	QHHFGSPLT	944
vLCDR2 variant (WO2016028656)	AAKTLAE	945
vLCDR2 variant (WO2016028656)	YAKTLAE	946
vLCDR2 variant (WO2016028656)	WAKTLAE	947
vLCDR2 variant (WO2016028656)	SAKTLAE	948
vLCDR2 variant (WO2016028656)	TAKTLAE	949
vLCDR2 variant (WO2016028656)	IAKTLAE	950
vLCDR2 variant (WO2016028656)	VAKTLAE	951
vLCDR2 variant (WO2016028656)	NNKTLAE	952
vLCDR2 variant (WO2016028656)	NIKTLAE	953
vLCDR2 variant (WO2016028656)	NLLTLAE	954
vLCDR2 variant (WO2016028656)	NTKTLAE	955
vLCDR2 variant (WO2016028656)	NVKTLAE	956

Figure 3MMMM

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:124 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQRLEWIGYIDPYNDGAKYS QKFQGRVTLTRDTSASTAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTTVTVSS	957
vhCDR1 (from WO2016028656)	SYVMHW	958
vhCDR2 (from WO2016028656)	YIDPYNDGAKYSQKFQ	959
vhCDR3 (from WO2016028656)	GGPYGWYFDV	960

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:125 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQRLEWIGYIDPYNDGAKYS QKFQGRVTLTSDKSASTAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTTVTVSS	961
vhCDR1 (from WO2016028656)	SYVMH	962
vhCDR2 (from WO2016028656)	YIDPYNDGAKYSQKFQ	963
vhCDR3 (from WO2016028656)	GGPYGWYFDV	964

Figure 3NNNN

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:126 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTRDTSTSTVYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTTVTVSS	965
vhCDR1 (from WO2016028656)	SYVMH	966
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQ	967
vhCDR3 (SEQ ID NO:13 from WO2016028656)	GGPYGWYFDV	968

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:127 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSTSTVYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTTVTVSS	969
vhCDR1 (from WO2016028656)	SYVMH	970
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	971
vhCDR3 (from WO2016028656)	GGPYGWYFDV	972

Figure 3OOOO

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:128 from WO2016028656)	EVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVTLTSDKSTSTAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTTVTVSS	973
vhCDR1 (from WO2016028656)	SYVMH	974
vhCDR2 (from WO2016028656)	YIDPYNDGAKYAQKFQ	975
vhCDR3 (from WO2016028656)	GGPYGWYFDV	976

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:129 from WO2016028656)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKY AQKFQGRVTLTSDKSISTAYMELSRLRSDDTVVYYCARGGPYGWYFDVWGQGTTVTVSS	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)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKAPKLLIYNAKTLAEGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQHHFGSPLTFGQGTRLEIK	981
vlCDR1 (from WO2016028656)	RASEHIYSYLS	982
vlCDR2 (from WO2016028656)	NAKTLAE	983
vlCDR3 (from WO2016028656)	QHHFGSPLT	984

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:131 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKAPKLLIYNAKTLAE GVPSRFSGSGSGTQFTLTISSLQPEDFATYYCQHHFGSPLTFGQGTRLEIK	985
vlCDR1 (from WO2016028656)	RASEHIYSYLS	986
vlCDR2 (from WO2016028656)	NAKTLAE	987
vlCDR3 (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)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSG SGSGTDFTLTISSLQPEDVATYYCQHHFGSPLTFGQGTRLEIK	989
vlCDR1 (from WO2016028656)	RASEHIYSYLS	990
vlCDR2 (from WO2016028656)	NAKTLAE	991
vlCDR3 (from WO2016028656)	QHHFGSPLT	992

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:133 from WO2016028656)	DIQMTQSPSSLSASVGDRVTITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSG SGSGTQFTLTISSLQPEDVATYYCQHHFGSPLTFGQGTRLEIK	993
vlCDR1 (from WO2016028656)	RASEHIYSYLS	994
vlCDR2 (from WO2016028656)	NAKTLAE	995
vlCDR3 (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)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYA QKFQGRVTLTSDKSISTAYMELSRLRSDDTVVYYCARGGPYGWYFDVWGQGTTVTVSS	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)	EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQ KFQGRVTLTSDKSISTAYMELSRLRSDDTVVYYCARGGPYGWYFDVWGQGTTVTVSS	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)	GGPYGIYFDV	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)	GGPYGTYFDV	1012
vhCDR3 variant (from WO2016028656)	GGPYGVYFDV	1013
vhCDR3 variant (from WO2016028656)	GGPYGYYFDV	1014

Figure 35SSS

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
VH 18G10	QVQLMESGPGLVQPSQTLSLTCTVSGFPLTSYTVHWVRQPPGKGLEWIGAIWSSGSTDYNSA	1015
(SEQ ID NO:136 from WO2016028656)	LKSRLNINRDSSKSQVFLKMNSLQTEDTAIYFCTKSGWAFFDYWGQGVMVTVSS	
VL 18G10	DIQMTQSPSLLSASVGDRVTLNCIASQNIYKSLAWYQLKLGEAPKLLIYNANSLQAGIPSRFSG	1016
(SEQ ID NO:137 from WO2016028656)	SGSGTDFALTISGLQPEDVATYFCQQYSGGYTFGAGTKLELK	

From WO2016028656 (Table 4, reproduced herein)

What	sequence	SEQ ID NO:
VH 11A11	EVQLVESGGDLVQPGRSLKISCVASGFTFSDYYMAWVRLAPQKGLEWVASISYEGSRTHYGD	1017
(SEQ ID NO:138 from WO2016028656)	SVRGRFIISRDNPKNILYLQMNSLGSEDTATYFCARHTGTLDWLVYWGQGTLVTVSS	
VL 11A11	NIVMAQSPKSMSISAGDRVTMNCKASQNVDNNIAWYQQKPGQSPKLLIFYASNRYSGVPDR	1018
(SEQ ID NO:139 from WO2016028656)	FTGGGYGTDFTLTIKSVQAEDAAFYYCQRIYNFPTFGSGTKLEIK	

Figure 4A

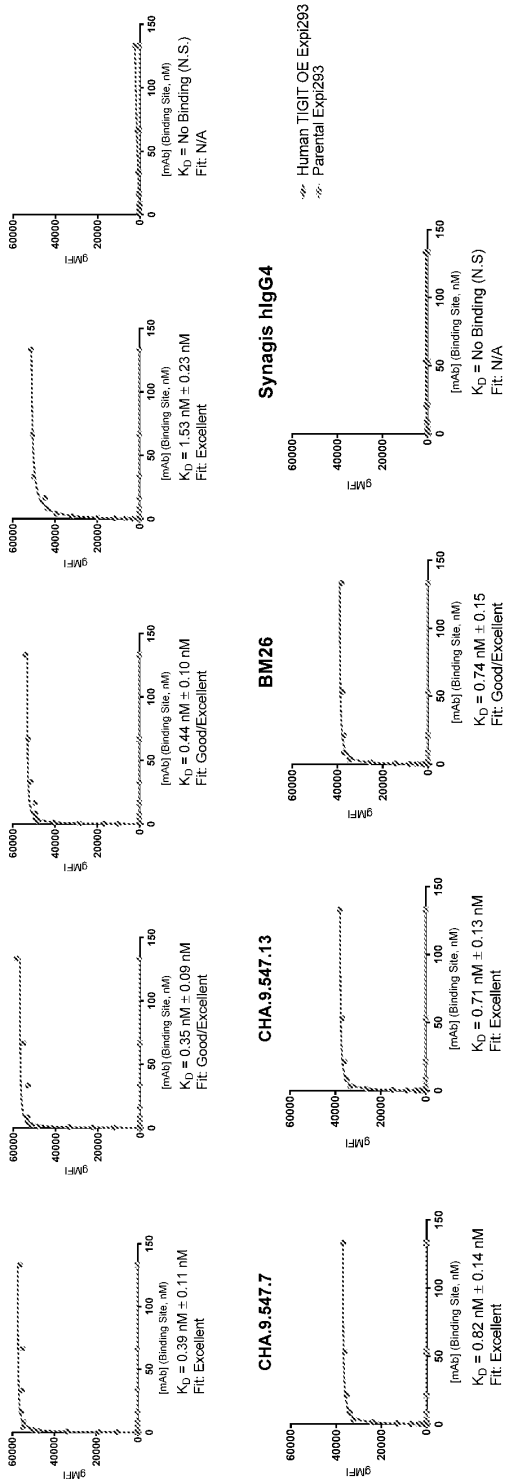

CPA.9.083
KD = 0.39 nM ± 0.11 nM
Fit: Excellent
CPA.9.086
KD = 0.35 nM ± 0.09 nM
Fit: Good/Excellent
BM26
KD = 0.44 nM ± 0.10 nM
Fit: Good/Excellent
BM29
KD = 1.53 nM ± 0.23 nM
Fit: Excellent
Synagis hIgG4
KD = No Binding (N.S.)
Fit: N/A
CHA.9.547.7
KD = 0.82 nM ± 0.14 nM
Fit: Excellent
CHA.9.547.13
KD = 0.71 nM ± 0.13 nM
Fit: Excellent
BM26
KD = 0.74 nM ± 0.15
Fit: Good/Excellent
Synagis hIgG4
KD = No Binding (N.S)
Fit: N/A
Human TIGIT OE Expi293
Parental Expi293
gMFI
[mAb] (Binding Site, nM)

Figure 4B

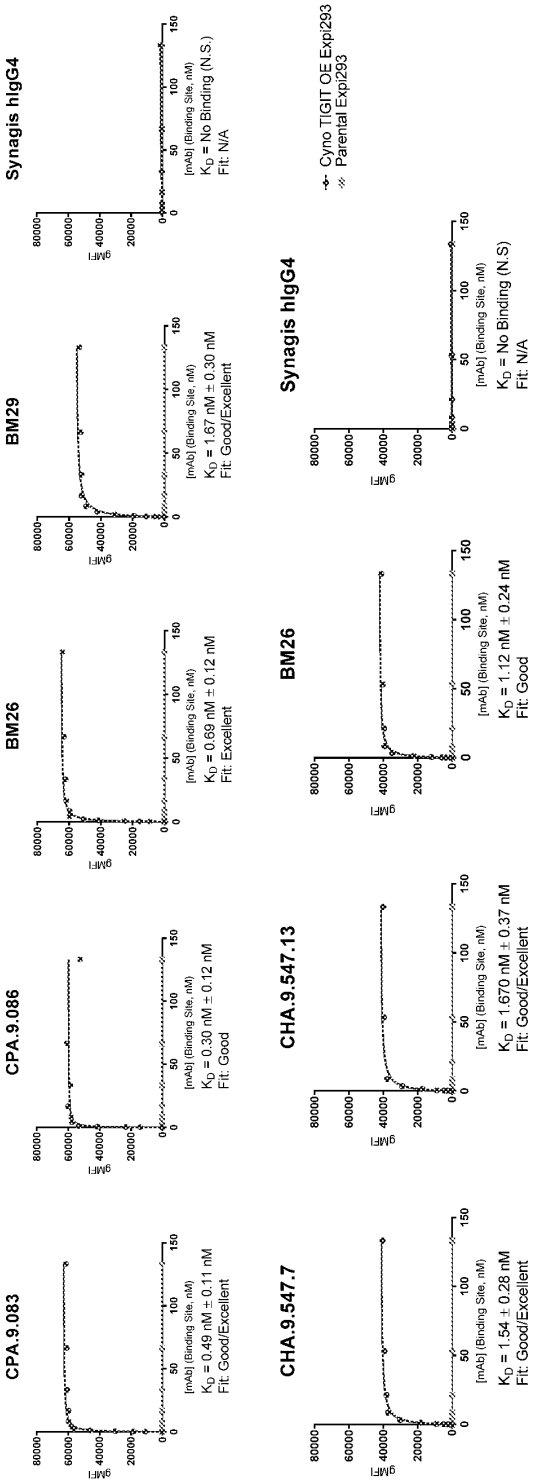

CPA.9.083
K_D = 0.49 nM ± 0.11 nM
Fit: Good/Excellent
CPA.9.086
K_D = 0.30 nM ± 0.12 nM
Fit: Good
BM26
K_D = 0.69 nM ± 0.12 nM
Fit: Excellent
BM29
K_D = 1.67 nM ± 0.30 nM
Fit: Good/Excellent
Synagis hIgG4
K_D = No Binding (N.S.)
Fit: N/A
CHA.9.547.7
K_D = 1.54 ± 0.28 nM
Fit: Good/Excellent
CHA.9.547.13
K_D = 1.670 nM ± 0.37 nM
Fit: Good/Excellent
BM26
K_D = 1.12 nM ± 0.24 nM
Fit: Good
Synagis hIgG4
K_D = No Binding (N.S)
Fit: N/A
Cyno TIGIT OE Expi293
Parental Expi293
gMFI
[mAb] (Binding Site, nM)

Figure 4C

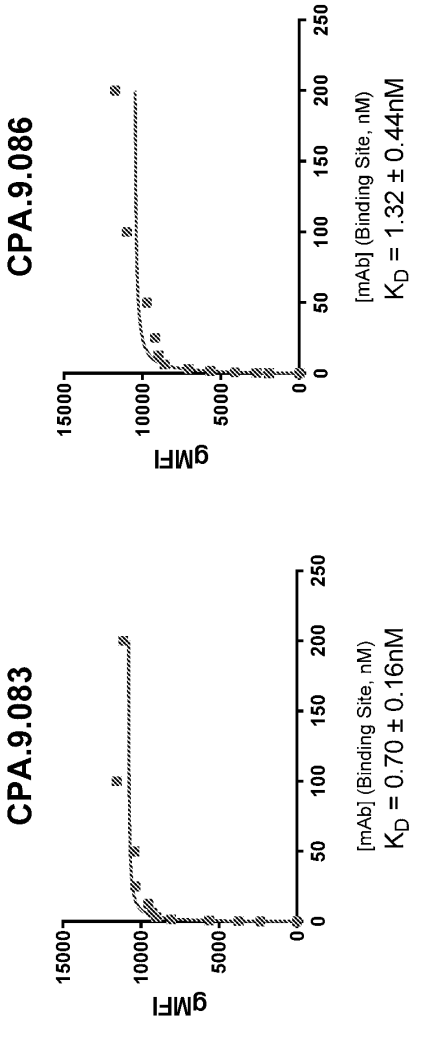

CPA.9.086
gMFI
15000
10000
5000
0
0
50
100
150
200
250
[mAb] (Binding Site, nM)
K_D = 1.32 ± 0.44nM
CPA.9.083
gMFI
15000
10000
5000
0
0
50
100
150
200
250
[mAb] (Binding Site, nM)
K_D = 0.70 ± 0.16nM

Figure 5A
CHA.7.518.1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFQGRVTMTRDTST STVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS	1019
vhCDR1	GYTFTDYN	1020
vhCDR2	IYPYIGGS	1021
vhCDR3	AREDKTARNAMDY	1022
Full length HC (IgG4(S241P))	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFQGRVTMTRDTST STVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	1023
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQHFWGTPYTFGQGTKLEIK	1024
vlCDR1	ENIYSN	1025
vlCDR2	EAT	1026
vlCDR3	QHFWGTPYT	1027
Full length light chain for CHA.7.518.1.H4(S241P)	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQHFWGTPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1028

Figure 5B
CHA.7.538.1.2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS	1029
vhCDR1	GYAFTNYL	1030
vhCDR2	INPGSGGI	1031
vhCDR3	ARSETHDTWFAY	1032
Full length HC (IgG4(S241P) Full length HC for CHA.7.538.1.2. H4(S241P)	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPGK	1033
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIYLASTRHTGVPSRFSGSGSGTDFTLTISSVQPEDFA TYYCLQHWNYPYTFGQGTKLEIK	1034
vlCDR1	QSVRIA	1035
vlCDR2	LAS	1036
vlCDR3	LQHWNYPYT	1037
Full length light chain for CHA.7.538.1.2. H4(S241P)	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIYLASTRHTGVPSRFSGSGSGTDFTLTISSVQPEDFA TYYCLQHWNYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1038

RECTIFIED SHEET (RULE 91) ISA/EP

Figure 5C

From Zhu (WO 2017/041004) What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:5 from WO 2017/041004)	EVQLQQSGAELVRSGASVKMSCKVNDYTFTNYNMHWLRQTPGQGLEWIGYIYPGNGDTNY NQKFKGKATLTADTSSSTAYMQLSSLTSEDPAVYFCARQGIHYYYIDVWGAGTTVTVSSG	1039
vhCDR1 (SEQ ID NO:6 from WO 2017/041004)	DYTFTNYNMH	1040
vhCDR2 (SEQ ID NO:7 from WO 2017/041004)	YIYPGNGDTNYNQ	1041
vhCDR3 (SEQ ID NO:8 from WO 2017/041004)	QGIHYYYIDV	1042
Light chain (SEQ ID NO:3 from WO 2017/041004)	DIEMTQSPATLSVTPGDRVSLSCRASQSIRDYLHWYQQKSHESPRLLIKYVSQSISGIPS RFSGSGSGSEFTLSINSVEPEDVGVYYCQNGHSLPLTFGSGTKLEIKRTV	1043
vlCDR1 (SEQ ID NO:9 from WO 2017/041004)	RASQSIRDYLH	1044
vlCDR2 (SEQ ID NO:10 from WO 2017/041004)	YVSQSIS	1045
vlCDR3 (SEQ ID NO:11 from WO 2017/041004)	QNGHSLPLT	1046

Figure 5D

From Zhu (WO 2017/041004)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO 2017/041004)	QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHWVKQRPGQGLEWIGYINPSTGYTEY NQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA	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 RFSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK	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)	QVQLQQSGAELAKPGASVKMSCKASGYTFTSDWMHWVKQRPGQGLEWIGYINPSTGYTEY	1055
	NQKFKDKATLTADKSSSTAYMQLRSLTSEDSAVYYCARGSSGSWFAYWGQGTLVTVSA	
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)	DVVMTQTPLTLSVTIGQPASISCKSSQSLLNSDGKTYLNWLLQRPGQSPKRLIYLVSKLD	1059
	SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK	
vlCDR1 (SEQ ID NO:41 from WO 2017/041004)	KSSQSLLNSDGKTYLN	1060
vlCDR2 (SEQ ID NO:42 from WO 2017/041004)	LVSKLDS	1061
vlCDR3 (SEQ ID NO:43 from WO 2017/041004)	WQGTHFPRT	1062

Figure 5F

From WO 2018/017864 (334M5 antibody)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:30 from WO 2018/017864)	EVQLQQSVAELVRPGTSVTISCKASGYTFTNYWLGWVKQRPGHGLEWIGDIFPGGDYPNY NEKFKGKATLTADTSSSTAYMQLSSLTSEDSSVYFCTRGYFDVWGAGTTVTVSS	1063
vhCDR1 (SEQ ID NO:31 from WO 2018/017864)	TNYWLG	1064
vhCDR2 (SEQ ID NO:32 from WO 2018/017864)	DIFPGGDYPNYNEKFKG	1065
vhCDR3 (SEQ ID NO:33 from WO 2018/017864)	TRGYFDV	1066
Light chain (SEQ ID NO:25 from WO 2018/017864)	DIQMTQSPSSLSVSAGEKVTMSCKSSQSLLNSENQKNYLAWFQQKPGQPPKMLIYGASTR ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPFTFGSGTKLEIKR	1067
vlCDR1 (SEQ ID NO:26 from WO 2018/017864)	KSSQSLLNSENQKNYLA	1068
vlCDR2 (SEQ ID NO:27 from WO 2018/017864)	GASTRES	1069
vlCDR3 (SEQ ID NO:28 from WO 2018/017864)	QNDHSYP	1070

Figure 7A

Pembrolizumab (Anti-PD1 hIgG4)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVLSGGGFVQPGGSLKLSCAASGFTFSSYAMSWVRQNPERRLVWVATITGGGRNTYYPDSVKGRFTISR DNAKNTLYLQMSSLRSEDTAMYYCTRQGYDGYTWFAYWGQGTLVTVSS	1071
vhCDR1	GFTFSSYA	1072
vhCDR2	ITGGGRNT	1073
vhCDR3	TRQGYDGYTWFAY	1074
Full length HC	EVQLVLSGGGFVQPGGSLKLSCAASGFTFSSYAMSWVRQNPERRLVWVATITGGGRNTYYPDSVKGRFTISR DNAKNTLYLQMSSLRSEDTAMYYCTRQGYDGYTWFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVD KRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSPGK	
Variable light (vl) domain	DIVLTQSPTSLAVSLGQRATISCRASESVDNSGISFMNWFQQKPGQPPKLLIYAASNPGSGVPARFSGSGSGT DFSLNIHPMEEDDTAMYFCQQSKEVPWTFGGGTELEIKR	1076
vlCDR1	ESVDNSGISF	1077
vlCDR2	AAS	1078
vlCDR3	QQSKEVPWT	1079
Full length light chain	DIVLTQSPTSLAVSLGQRATISCRASESVDNSGISFMNWFQQKPGQPPKLLIYAASNPGSGVPARFSGSGSGT DFSLNIHPMEEDDTAMYFCQQSKEVPWTFGGGTELEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C	

Figure 7B

Pembrolizumab (Anti-PD1 from WO2016028656)

What	sequence	SEQ ID NO:
Full length HC (SEQ ID NO:33 from WO2016028656)	QVQLVQSGVEVKKPGASVKVSCKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNFNEKFKNRV TLTTDSSTTTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTTVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK VDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGK	1081
Full length light chain (SEQ ID NO:34 from WO2016028656)	EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESGVPARFSGSGSGTD FTLTISSLEPEDFAVYYCQHSRDLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1082

Figure 7C

Nivolumab (Anti-PD1 hIgG4)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSS	1083
vhCDR1	GITFSNSG	1084
vhCDR2	IWYDGSKR	1085
vhCDR3	ATNDDY	1086
Full length HC	QVQLVESGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVES KYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1087
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTI SSLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKR	1088
vlCDR1	QSVSSY	1089
vlCDR2	DAS	1090
vlCDR3	QQSSNWPRT	1091
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTI SSLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1092

Figure 7D

Nivolumab (Anti-PD1 from WO2016028656)

What	sequence	SEQ ID NO:
Full length heavy chain (SEQ ID NO:35 from WO2016028656)	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVES KYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1093
Full length light chain (SEQ ID NO:36 from WO2016028656)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTI SSLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1094

Figure 7E

Cemiplimab (REGN2810; anti-PD1)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain (SEQ ID NO:1 from US20170174779)	EVQLLESGGVLVQPGGSLRLSCAASGFTFSNFGMTWVRQAPGKGLEWVSGISGGGRDTYF ADSVKGRFTISRDNSKNTLYLQMNSLKGEDTAVYYCVKWGNIYFDYWGQGTLVTVSS	1095
vhCDR1 (SEQ ID NO:3 from US20170174779)	GFTFSNFG	1096
vhCDR2 (SEQ ID NO:4 from US20170174779)	ISGGGRDT	1097
vhCDR3 (SEQ ID NO:5 from US20170174779)	VKWGNIYFDY	1098
Variable light (vl) domain (SEQ ID NO:2 from US20170174779)	DIQMTQSPSSLSASVGDSITITCRASLSINTFLNWYQQKPGKAPNLLIYAASSLHGGVPS RFSGSGSGTDFTLTIRTLQPEDFATYYCQQSSNTPFTFGPGTVVDFR	1099
vlCDR1 (SEQ ID NO:6 from US20170174779)	LSINTF	1100
vlCDR2 (SEQ ID NO:7 from US20170174779)	AAS	1101
vlCDR3 (SEQ ID NO:8 from US20170174779)	QQSSNTPFT	1102

Figure 7F

Cemiplimab (REGN2810; anti-PD1)

What	sequence	SEQ ID NO:
Full length heavy chain (SEQ ID NO:9 from US20170174779)	EVQLLESGGVLVQPGGSLRLSCAASGFTFSNFGMTWVRQAPGKGLEWVSGISGGGRDTYFADSVKGRFTISR DNSKNTLYLQMNSLKGEDTAVYYCVKWGNIYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRV ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALH NHYTQKSLSLSLGK	1103
Full length light chain (SEQ ID NO:10 from US20170174779)	DIQMTQSPSSLSASVGDSITITCRASLSINTFLNWYQQKPGKAPNLLIYAASSLHGGVPSRFSGSGSGTDFTLTI RTLQPEDFATYYCQQSSNTPTTFGPGTVVDFRRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1104

Figure 8

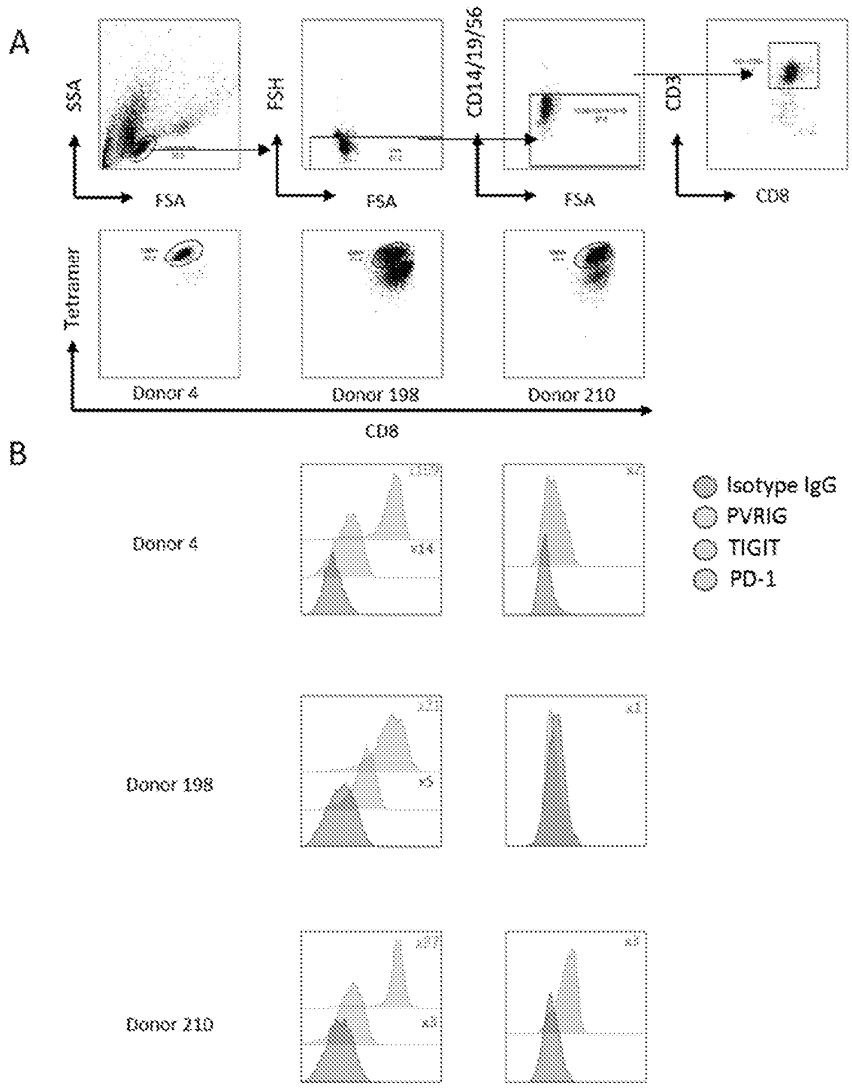

A
SSA
FSA
FSH
FSA
CD14/19/56
FSA
CD3
CD8
Tetramer
Donor 4
Donor 198
Donor 210
CD8
B
Donor 4
Donor 198
Donor 210
Isotype IgG
PVRIG
TIGIT
PD-1

FIGURE 9

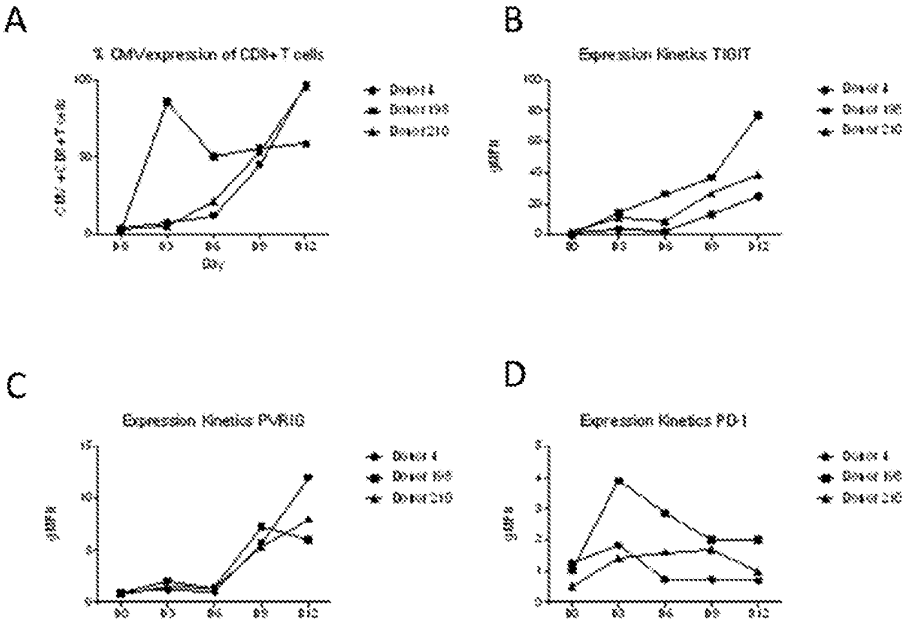

A
% CMVexpression of CD8+ T cells
B
Expression Kinetics TIGIT
C
Expression Kinetics PVRIG
D
Expression Kinetics PD-1

FIGURE 10

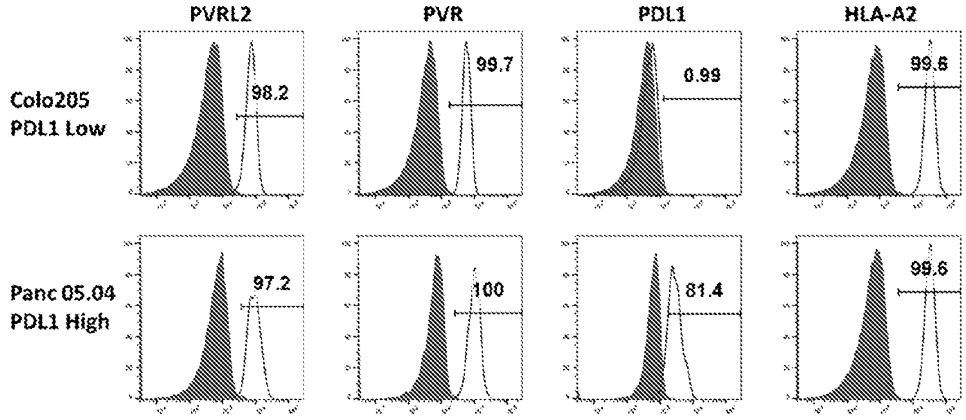

PVRL2
PVR
PDL1
HLA-A2
Colo205
PDL1 Low
98.2
99.7
0.99
99.6
Panc 05.04
PDL1 High
97.2
100
81.4
99.6

FIGURE 11A

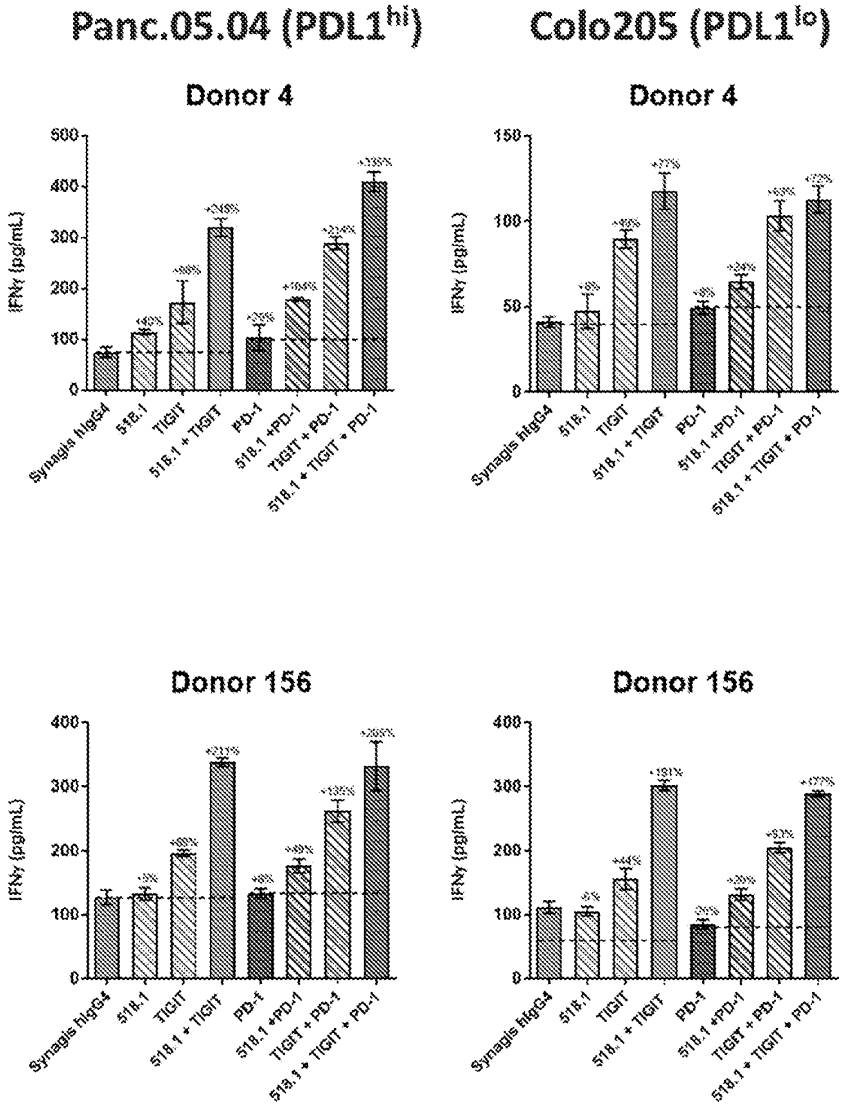

Panc.05.04 (PDL1hi)
Colo205 (PDL1lo)
Donor 4
Donor 4
Donor 156
Donor 156
IFNγ (pg/mL)
Synagis hIgG4
518.1
TIGIT
518.1 + TIGIT
PD-1
518.1 +PD-1
TIGIT + PD-1
518.1 + TIGIT + PD-1

Figure 11B

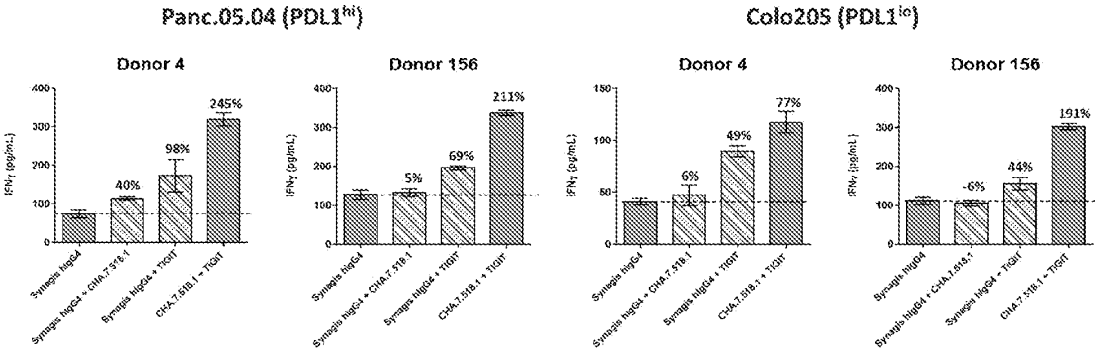

Panc.05.04 (PDL1hi)
Colo205 (PDL1lo)
Donor 4
Donor 156
Donor 4
Donor 156
40%
98%
245%
5%
69%
211%
6%
49%
77%
-6%
44%
191%
Synagis hIgG4
Synagis hIgG4 + CHA.7.518.1
Synagis hIgG4 + TIGIT
CHA.7.518.1 + TIGIT

Figure 11C

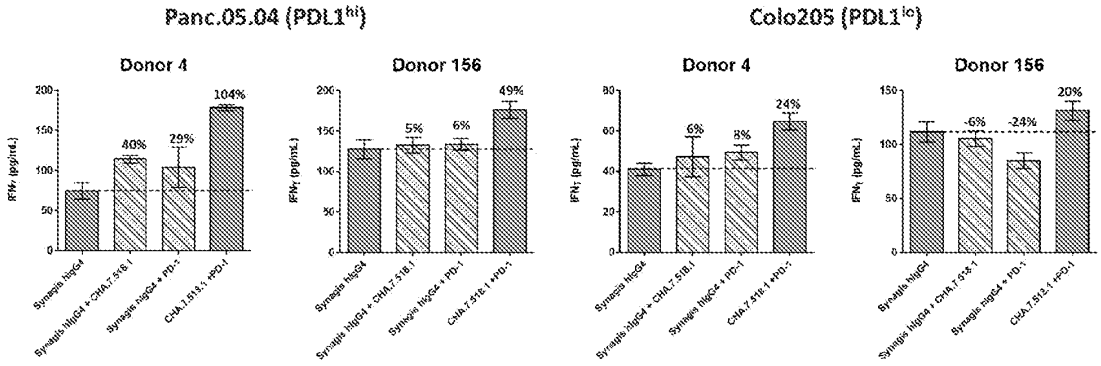

Panc.05.04 (PDL1hi)
Colo205 (PDL1lo)
Donor 4
Donor 156
Donor 4
Donor 156
IFNγ (pg/mL)
40%
29%
104%
5%
6%
49%
6%
8%
24%
-6%
-24%
20%
Synagis hIgG4
Synagis hIgG4 + CHA.7.518.1
Synagis hIgG4 + PD-1
CHA.7.518.1 +PD-1

Figure 11D

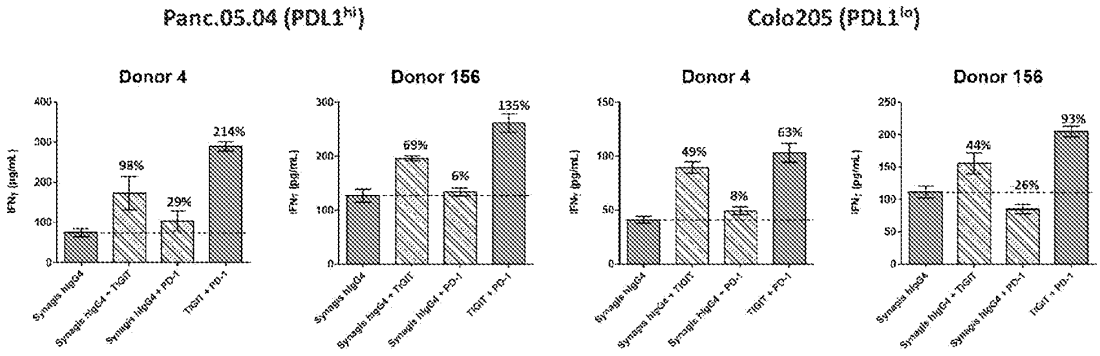

Panc.05.04 (PDL1hi)
Colo205 (PDL1lo)
Donor 4
Donor 156
Donor 4
Donor 156
98%
29%
214%
69%
6%
135%
49%
8%
63%
44%
26%
93%
Synagis hIgG4
Synagis hIgG4 + TIGIT
Synagis hIgG4 + PD-1
TIGIT + PD-1

Figure 12

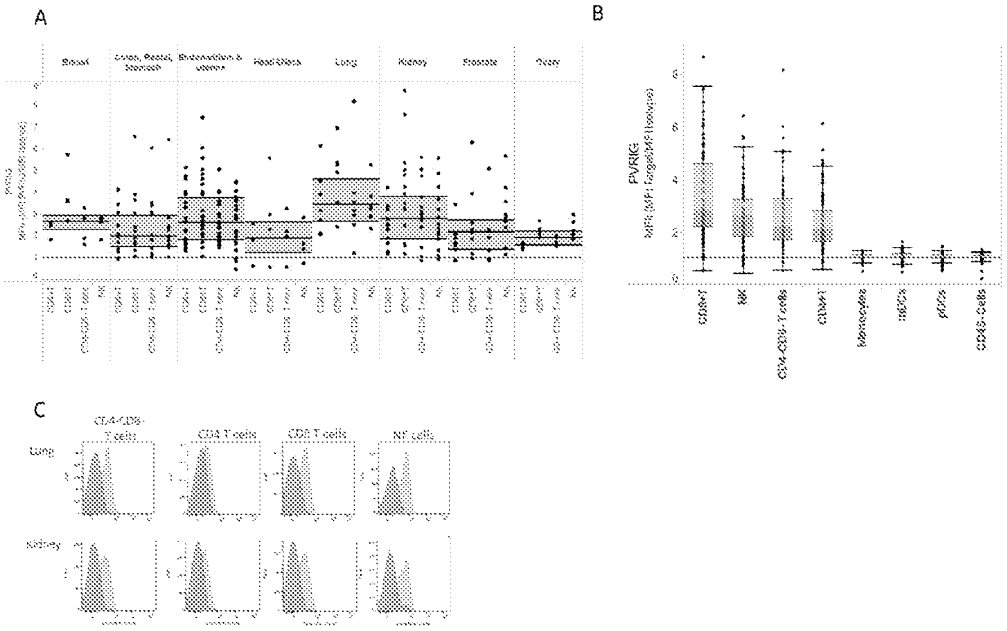

A
B
C
Breast
Kidney
Prostate
Ovary
Lung
CD4+
CD8+
NK
Monocytes
MDSCs
gMDSCs
CD45- Cells

Figure 13

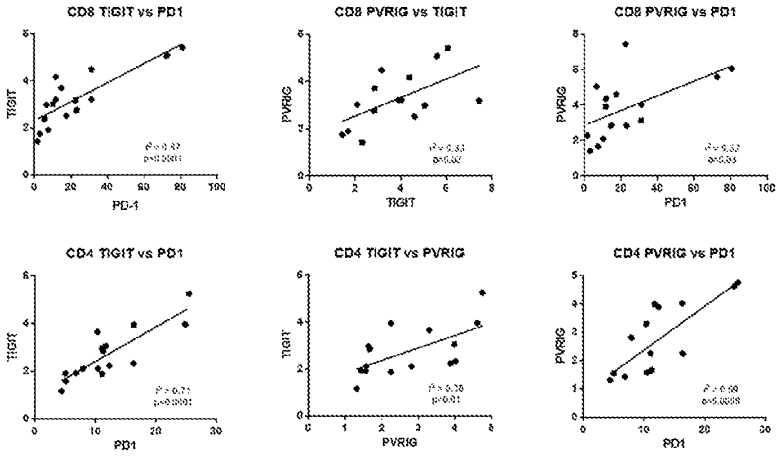

CD8 TIGIT vs PD1
TIGIT
PD-1
CD8 PVRIG vs TIGIT
PVRIG
TIGIT
CD8 PVRIG vs PD1
PVRIG
PD1
CD4 TIGIT vs PD1
TIGIT
PD1
CD4 TIGIT vs PVRIG
TIGIT
PVRIG
CD4 PVRIG vs PD1
PVRIG
PD1

Figure 14

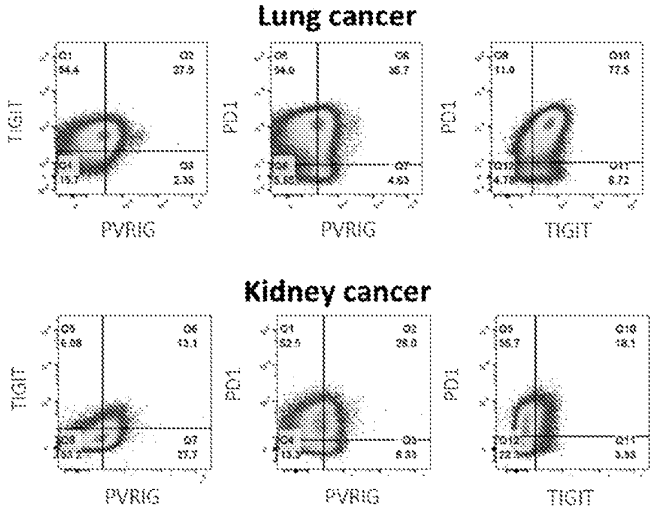
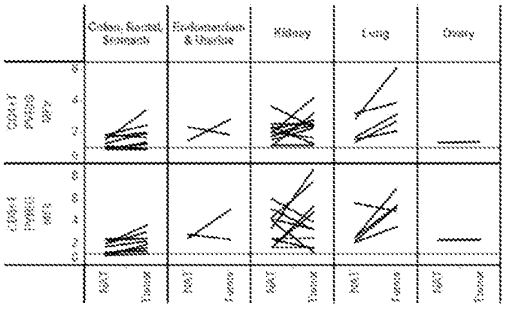

Lung cancer
TIGIT
PVRIG
PD1
PVRIG
PD1
TIGIT
Kidney cancer
TIGIT
PVRIG
PD1
PVRIG
PD1
TIGIT

Figure 15

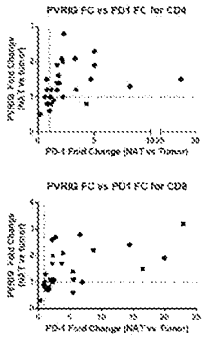
A



PVRIG Expression

CD4 T cells	NAT vs Tumor	0.0045
CD8 T cells	NAT vs Tumor	0.025

B



CD4 T cells	PVRIG FC vs PD1 FC	0.3331	0.0035
CD8 T cells	PVRIG FC vs PD1 FC	0.6253	0.0004

Figure 16

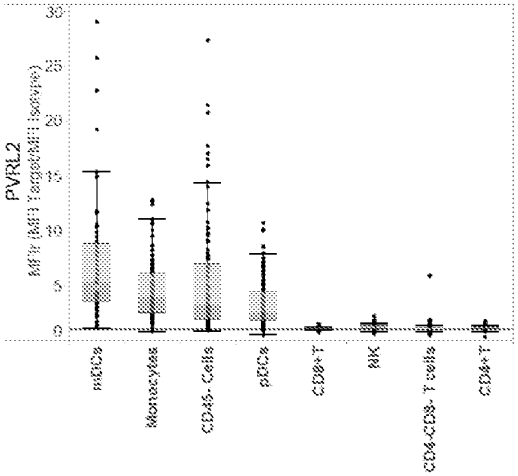

PVRL2
30
25
20
15
10
5
0
Monocytes
CD45- Cells
pDCs
CD8+ T
NK
CD4-CD8- T cells
CD4+ T

Figure 17

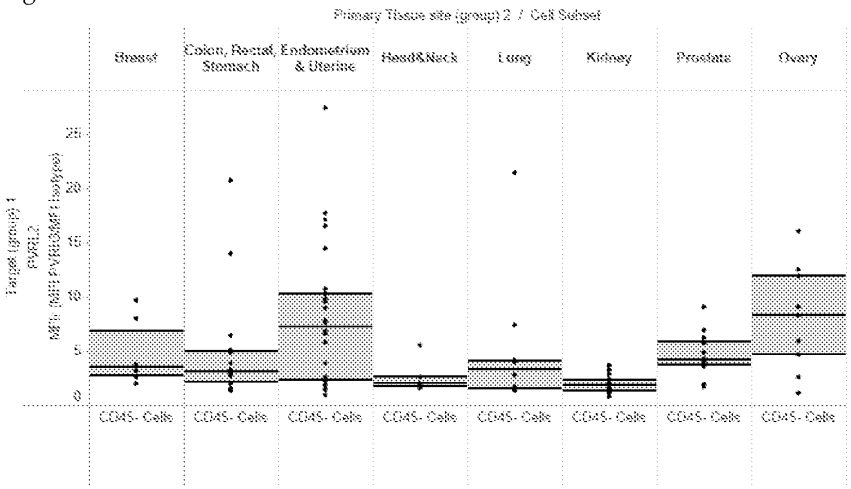

Primary Tissue site (group) 2 / Cell Subset
Breast
Colon, Rectal, Endometrium & Uterine
Stomach
Head&Neck
Lung
Kidney
Prostate
Ovary
25
20
15
10
5
0
CD45- Cells

Figure 18

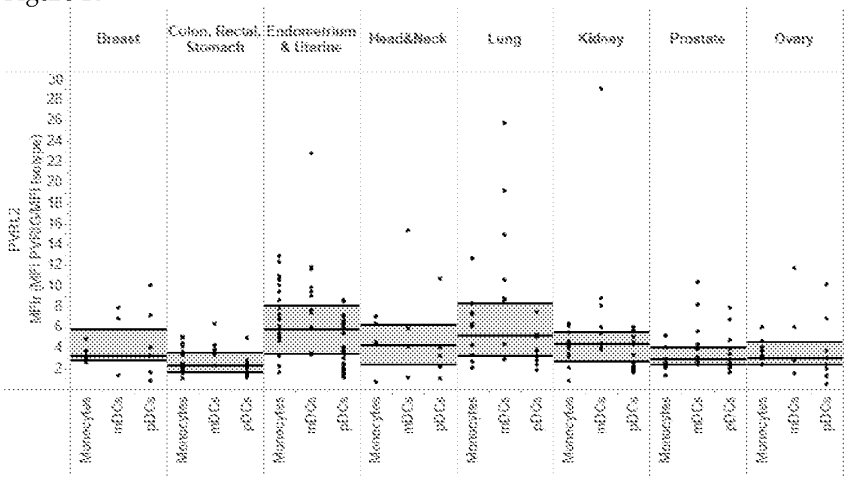
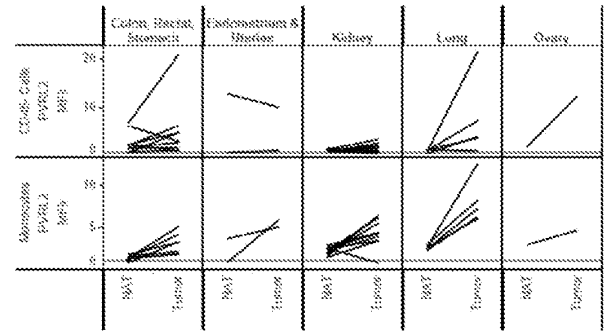

Breast
Colon, Rectal, Stomach
Endometrium & Uterine
Head&Neck
Lung
Kidney
Prostate
Ovary
PMP2
Wild-type
SCC
pSCC

Figure 19

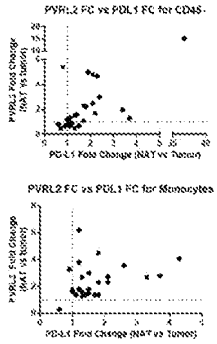
A



PVRL2 Expression

CD45-	NAT vs Tumor	0.02
Monocytes	NAT vs Tumor	<0.0001

B



Spearman Correlation

CD45- cells	PVRL2 FC vs PDL1 FC	0.63	0.0003
Monocytes	PVRL2 FC vs PDL1 FC	0.34	0.09

Figure 20

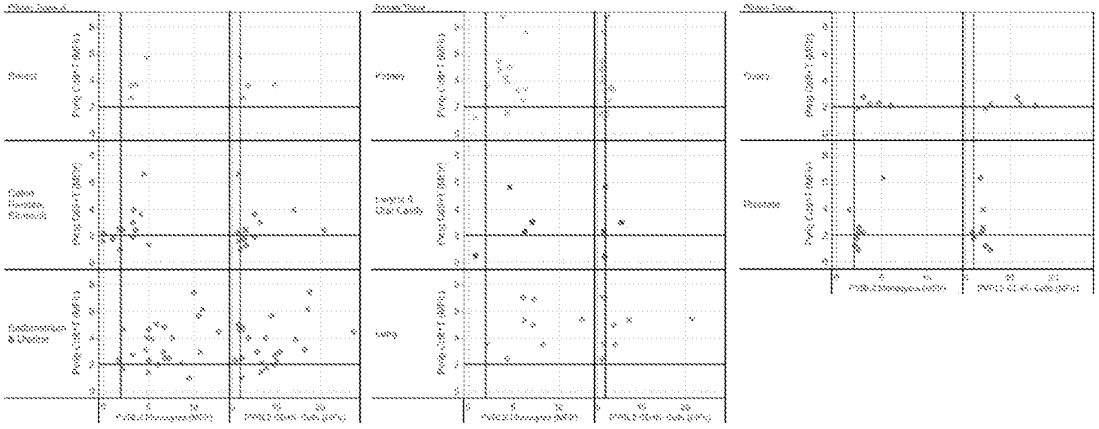


Figure 21A

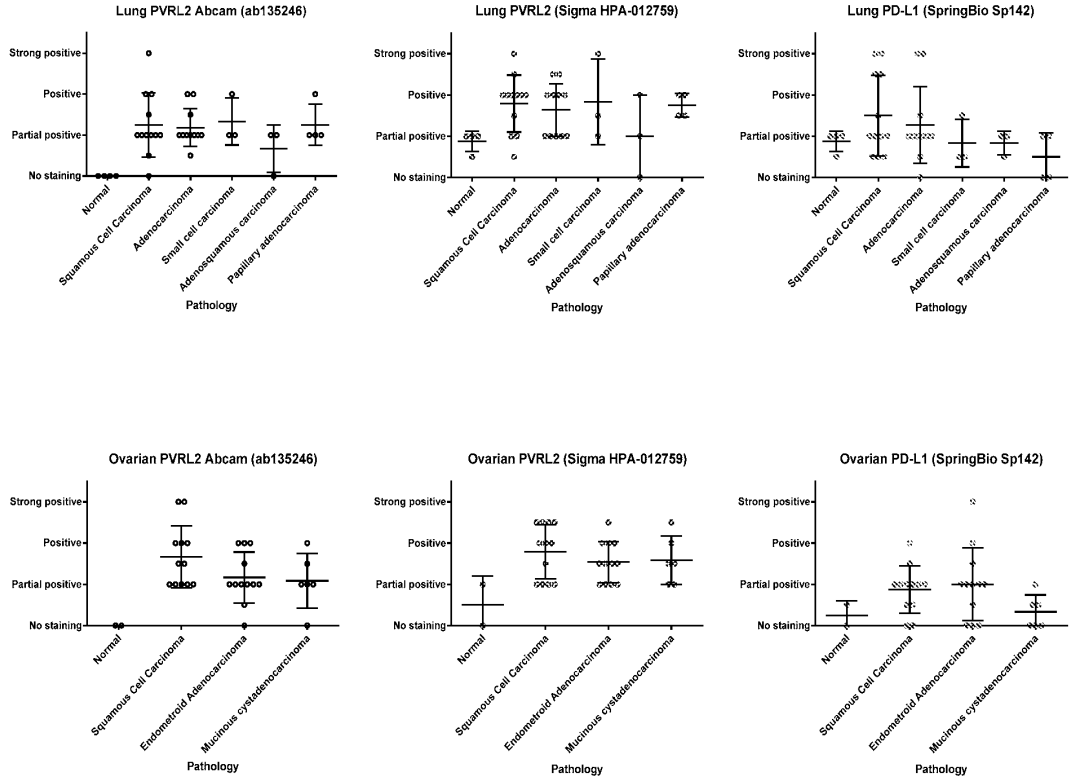

Lung PVRL2 Abcam (ab135246)
Lung PVRL2 (Sigma HPA-012759)
Lung PD-L1 (SpringBio Sp142)
Strong positive
Positive
Partial positive
No staining
Normal
Squamous Cell Carcinoma
Adenocarcinoma
Small cell carcinoma
Adenosquamous carcinoma
Papillary adenocarcinoma
Pathology
Ovarian PVRL2 Abcam (ab135246)
Ovarian PVRL2 (Sigma HPA-012759)
Ovarian PD-L1 (SpringBio Sp142)
Strong positive
Positive
Partial positive
No staining
Normal
Squamous Cell Carcinoma
Endometroid Adenocarcinoma
Mucinous cystadenocarcinoma
Pathology

Figure 21B

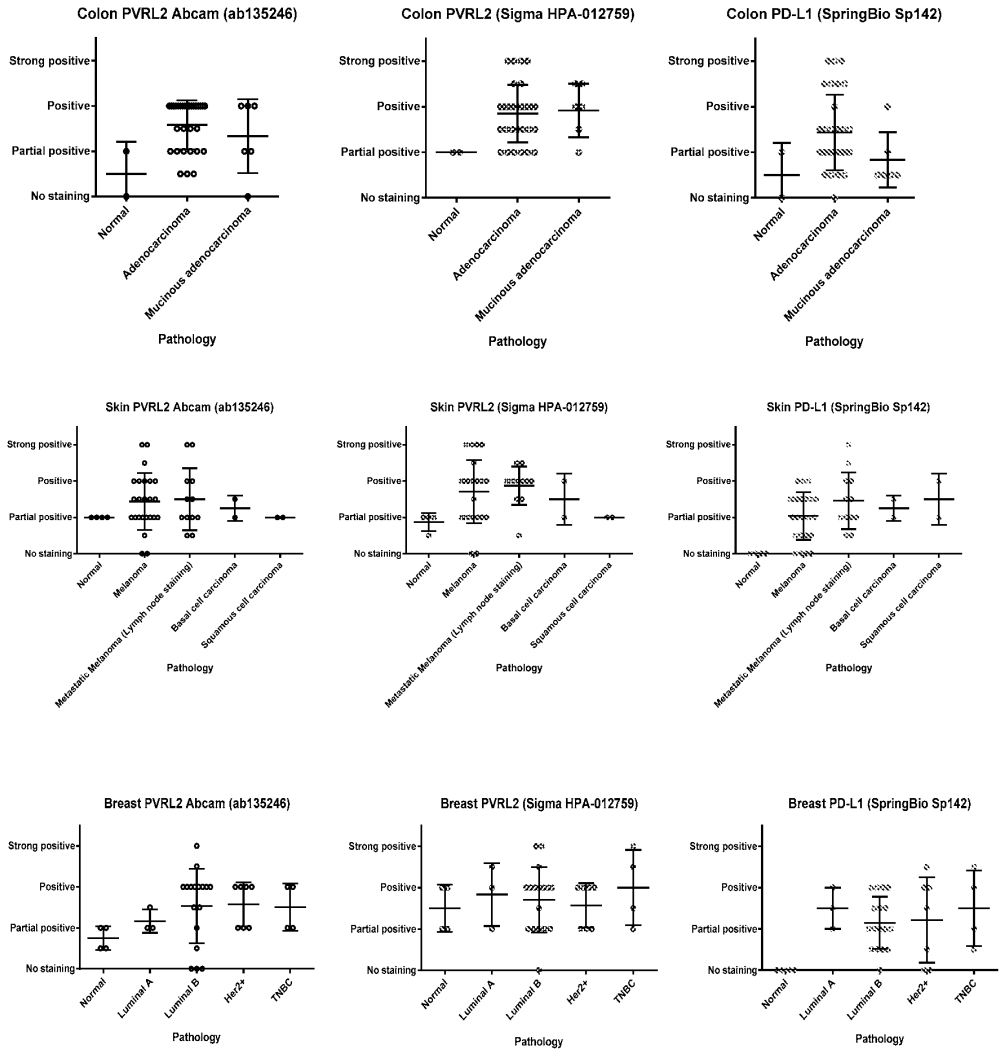
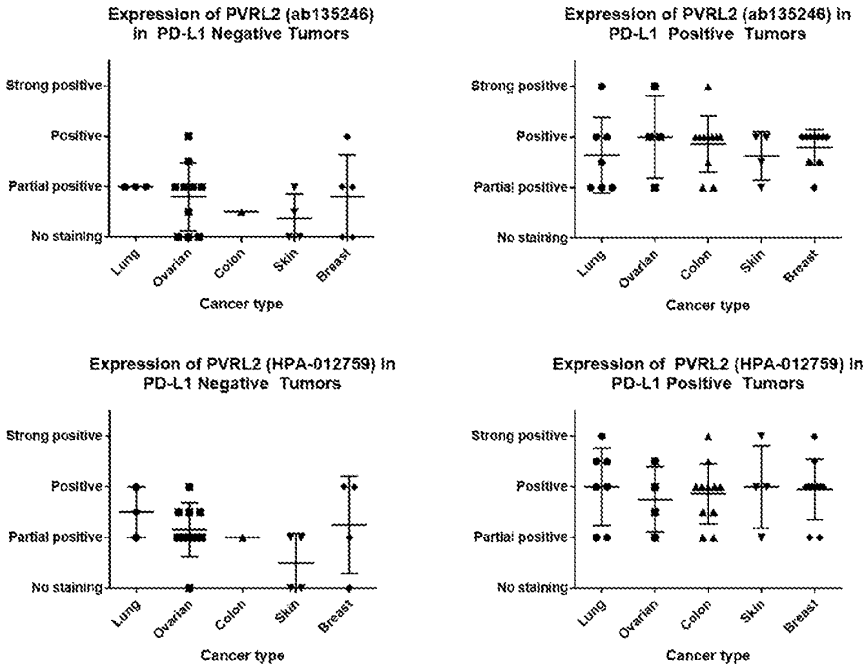

Colon PVRL2 Abcam (ab135246)
Colon PVRL2 (Sigma HPA-012759)
Colon PD-L1 (SpringBio Sp142)
Strong positive
Positive
Partial positive
No staining
Normal
Adenocarcinoma
Mucinous adenocarcinoma
Pathology
Skin PVRL2 Abcam (ab135246)
Skin PVRL2 (Sigma HPA-012759)
Skin PD-L1 (SpringBio Sp142)
Normal
Melanoma
Metastatic Melanoma (Lymph node staining)
Basal cell carcinoma
Squamous cell carcinoma
Pathology
Breast PVRL2 Abcam (ab135246)
Breast PVRL2 (Sigma HPA-012759)
Breast PD-L1 (SpringBio Sp142)
Normal
Luminal A
Luminal B
Her2+
TNBC
Pathology

Figure 22

A



B

Expression of PVRL2 in PD-L1 negative tumors

	Lung	Ovarian	Colon	Skin	Breast
PVRL2 (ab135246)	3/3	6/10	0/1	1/4	3/5
PVRL2 (HPA-012759)	3/3	9/10	1/1	2/4	3/4

Figure 23

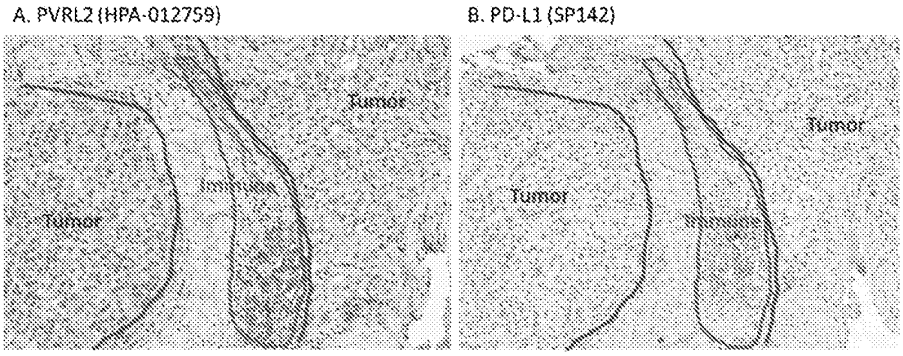
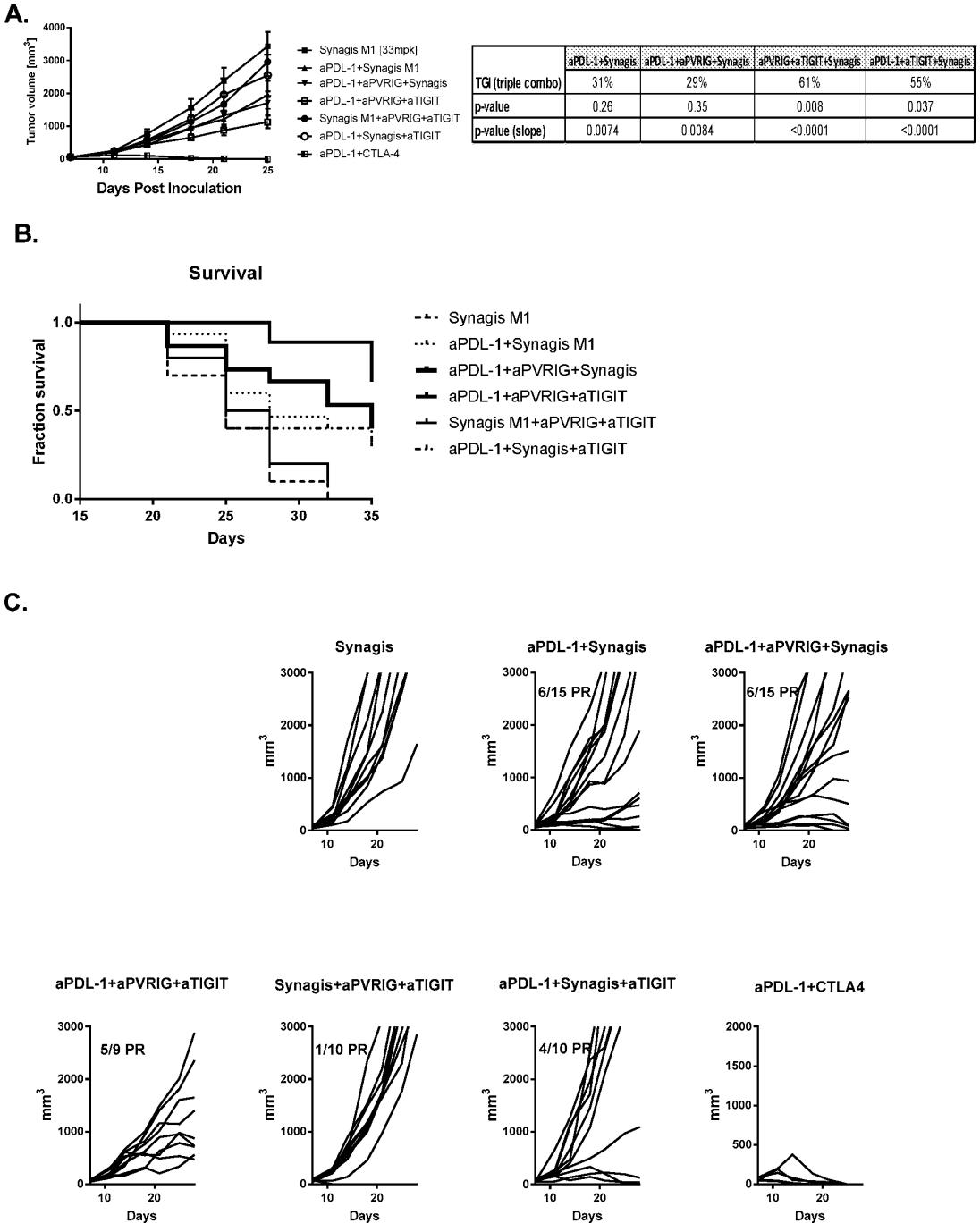
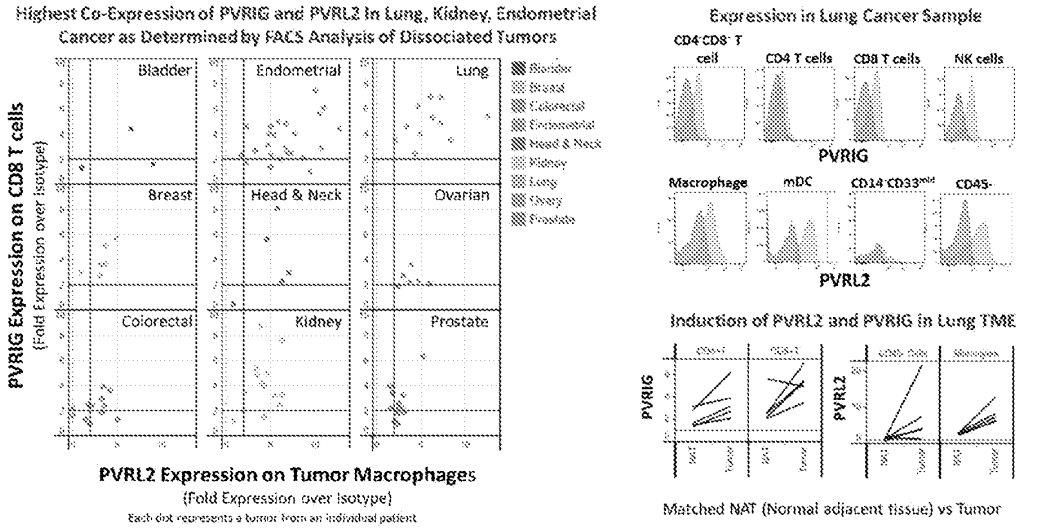


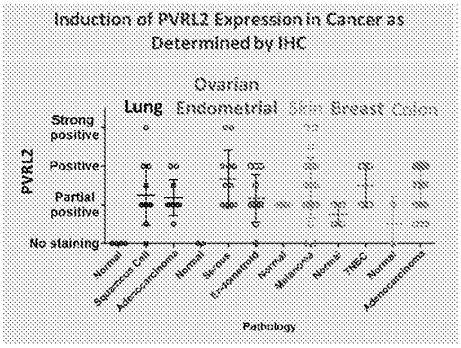
Figure 24



	aPDL-1+Synagis	aPDL-1+aPVRIG+Synagis	aPVRIG+aTIGIT+Synagis	aPDL-1+aTIGIT+Synagis
TGI (triple combo)	31%	29%	61%	55%
p-value	0.26	0.35	0.008	0.037
p-value (slope)	0.0074	0.0084	<0.0001	<0.0001

Figure 25


Highest Co-Expression of PVRIG and PVRL2 in Lung, Kidney, Endometrial Cancer as Determined by FACS Analysis of Dissociated Tumors
PVRIG Expression on CD8 T cells
(Fold Expression over Isotype)
Bladder
Endometrial
Lung
Breast
Head & Neck
Ovarian
Colorectal
Kidney
Prostate
PVRL2 Expression on Tumor Macrophages
(Fold Expression over Isotype)
Each dot represents a tumor from an individual patient
Expression in Lung Cancer Sample
CD4 T cells
CD8 T cells
NK cells
PVRIG
Macrophage
mDC
PVRL2
Induction of PVRL2 and PVRIG in Lung TME
PVRIG
PVRL2
Matched NAT (Normal adjacent tissue) vs Tumor


Induction of PVRL2 Expression in Cancer as Determined by IHC
Ovarian
Lung
Endometrial
Breast
Colon
PVRL2
Strong positive
Positive
Partial positive
No staining
Normal
Squamous Cell
Adenocarcinoma
Nevus
Melanoma
TNBC
Pathology

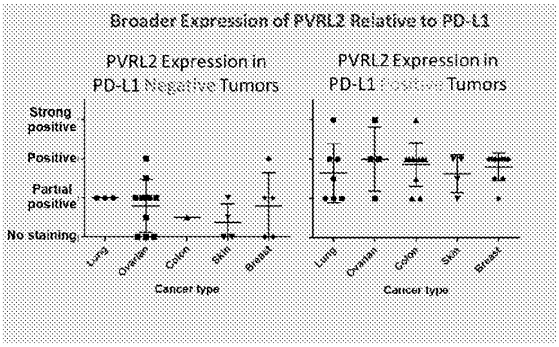
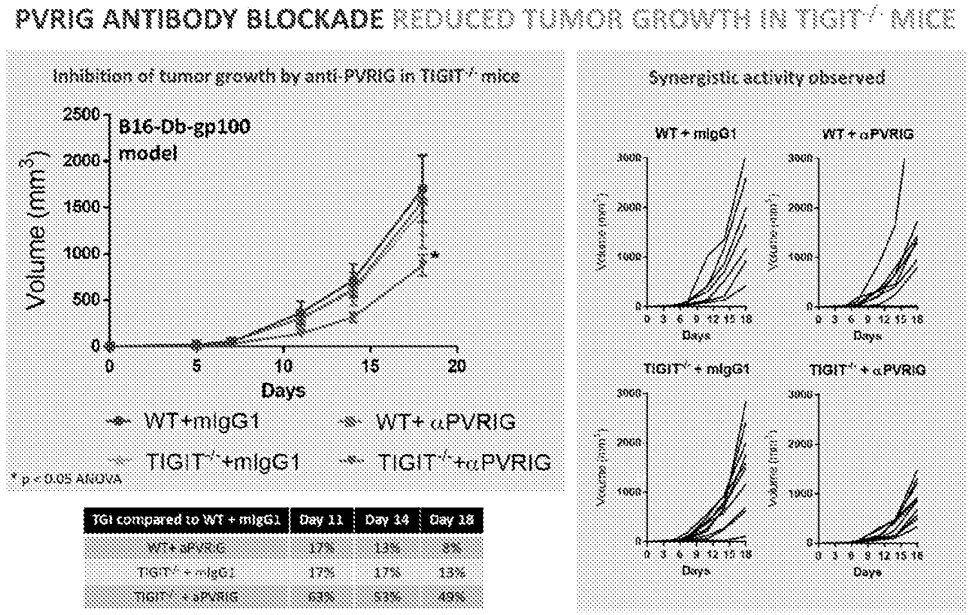

Broader Expression of PVRL2 Relative to PD-L1
PVRL2 Expression in PD-L1 Negative Tumors
PVRL2 Expression in PD-L1 Positive Tumors
Strong positive
Positive
Partial positive
No staining
Lung
Ovarian
Colon
Skin
Breast
Cancer type

Figure 26



TGI compared to WT + mIgG1	Day 11	Day 14	Day 18
WT+ aPVRIG	17%	13%	8%
TIGIT-/- + mIgG1	17%	17%	13%
TIGIT-/- + aPVRIG	63%	53%	49%

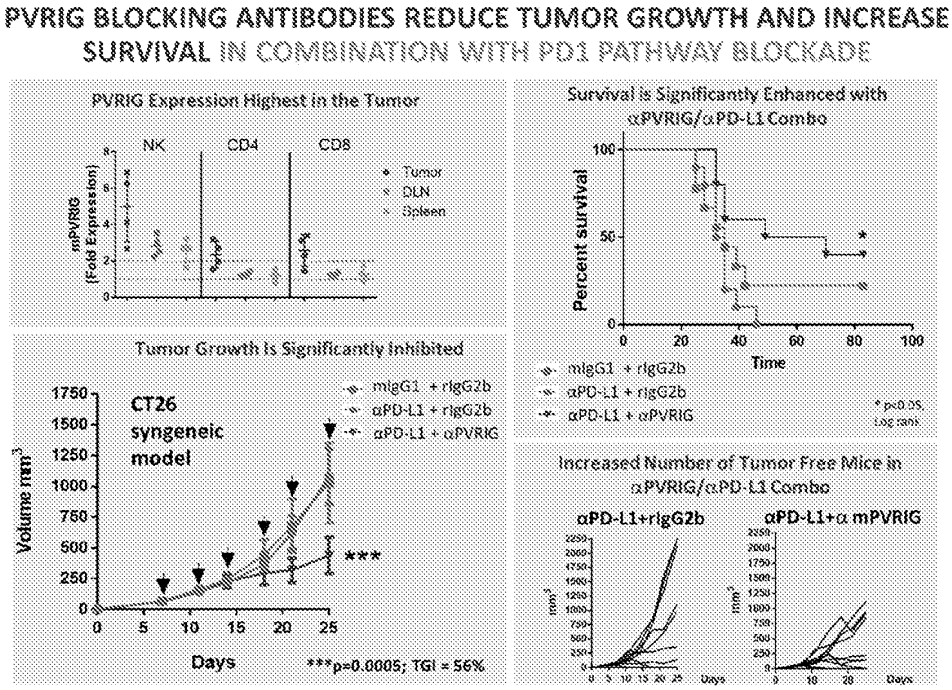
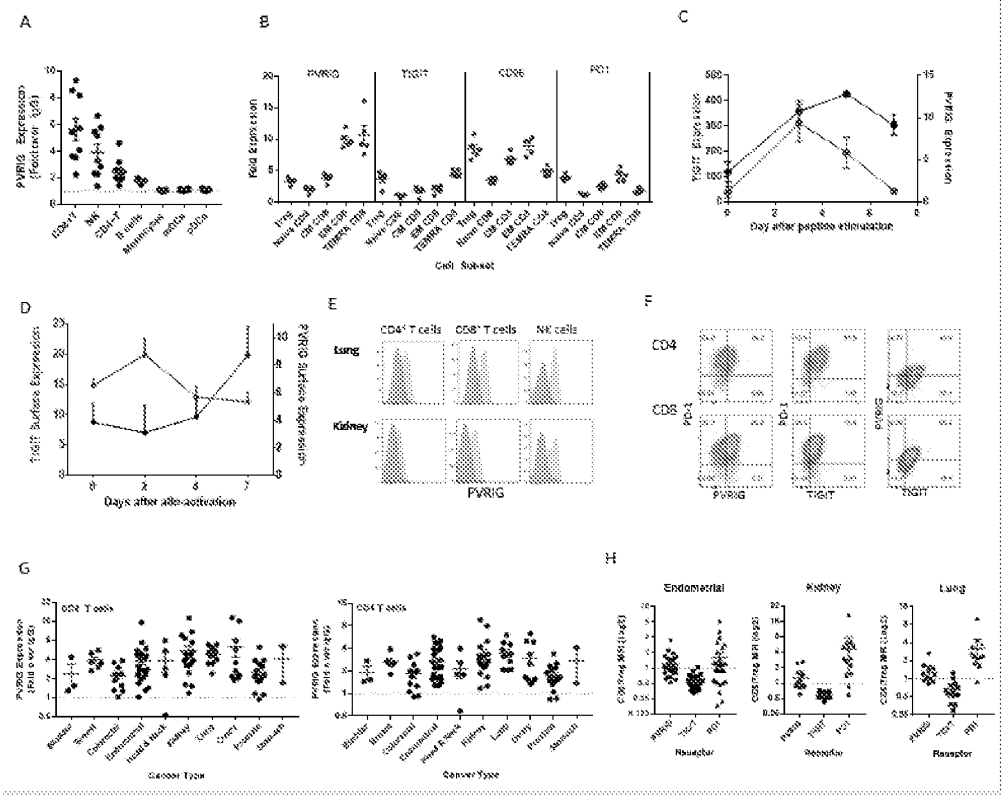


Figure 27


A
B
C
D
E
F
G
H
PVRIG
TIGIT
CD96
PD1
Cell Subset
Day after peptide elimination
Days after allo-activation
Lung
Kidney
CD4+ T cells
CD8+ T cells
NK cells
CD4
CD8
PD-1
Cancer Type
Endometrial
Kidney
Lung
Receptor

Fgiure 28A

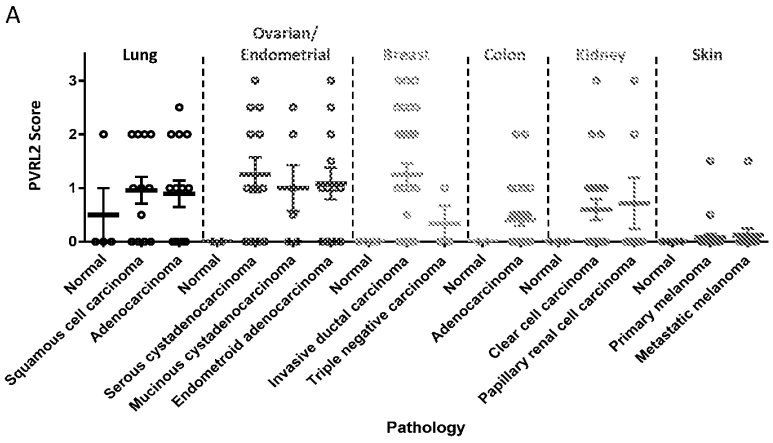


Figure 28B

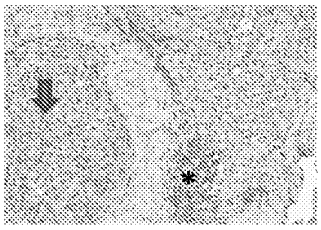


Figure 28C

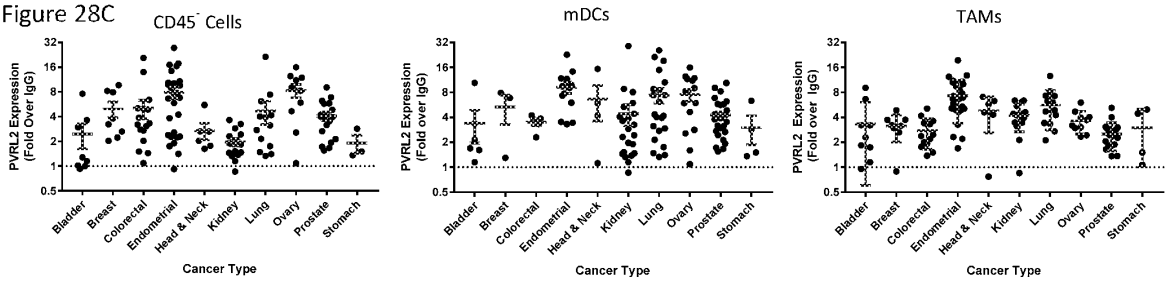


Figure 28D

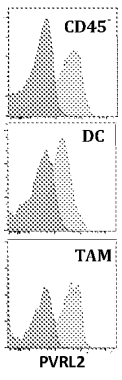


Figure 28 E

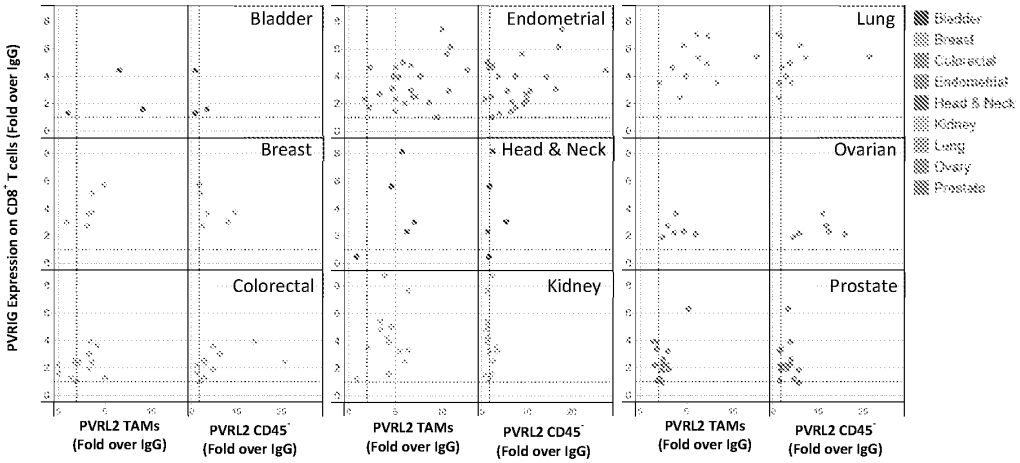


Figure 28F

	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

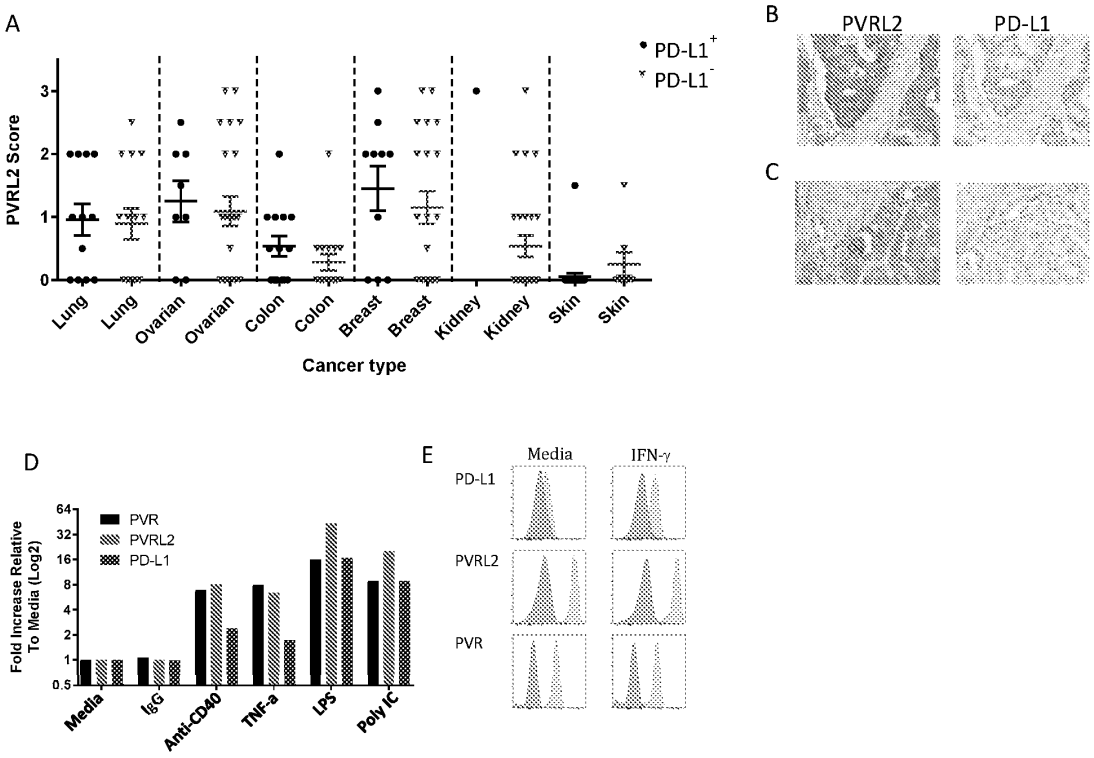

A
PD-L1+
PD-L1-
PVRL2 Score
Lung
Lung
Ovarian
Ovarian
Colon
Colon
Breast
Breast
Kidney
Kidney
Skin
Skin
Cancer type
B
PVRL2
PD-L1
C
D
PVR
PVRL2
PD-L1
Fold Increase Relative To Media (Log2)
Media
IgG
Anti-CD40
TNF-a
LPS
Poly IC
E
Media
IFN-γ
PD-L1
PVRL2
PVR

Figure 30

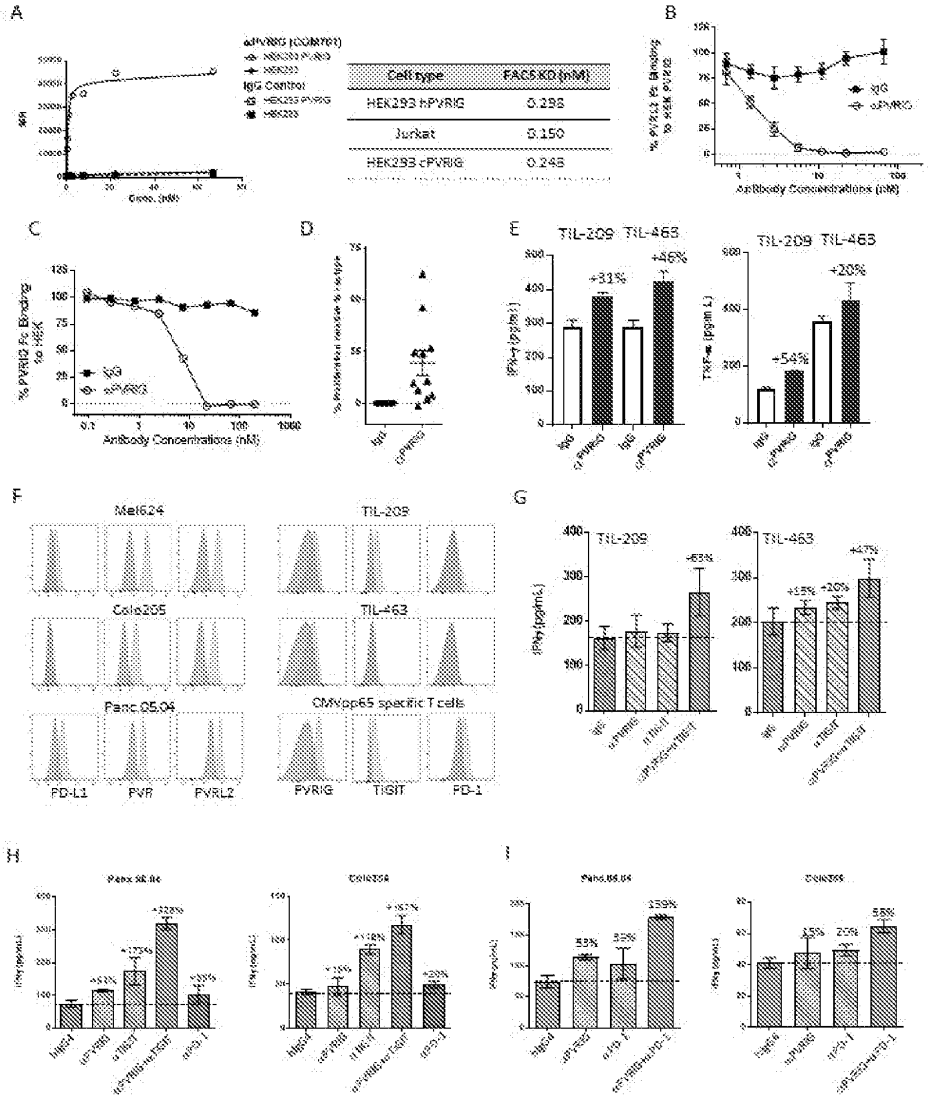

A
B
C
D
E
F
G
H
I
Cell type
FACS KD (nM)
HEK293 hPVRIG
0.298
Jurkat
0.150
HEK293 cPVRIG
0.245
IgG
Antibody Concentrations (nM)
TIL-209
TIL-463
+31%
+46%
+54%
+20%
Melt624
Colo205
Panc 05.04
PD-L1
PVR
PVRL2
OMVpp65 specific T cells
PVRIG
TIGIT
PD-1

Figure 31

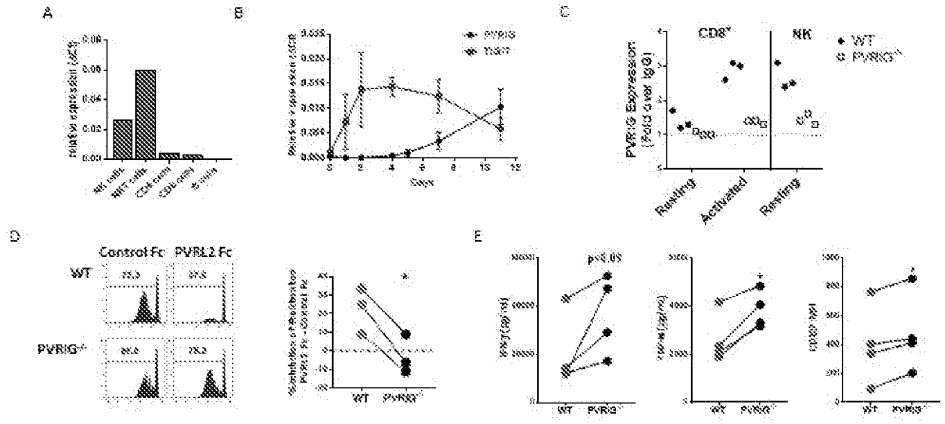

A
B
C
CD8+
NK
WT
PVRIG-/-
Resting
Activated
Resting
D
Control Fc
PVRL2 Fc
WT
PVRIG-/-
E
p<0.05

Figure 32

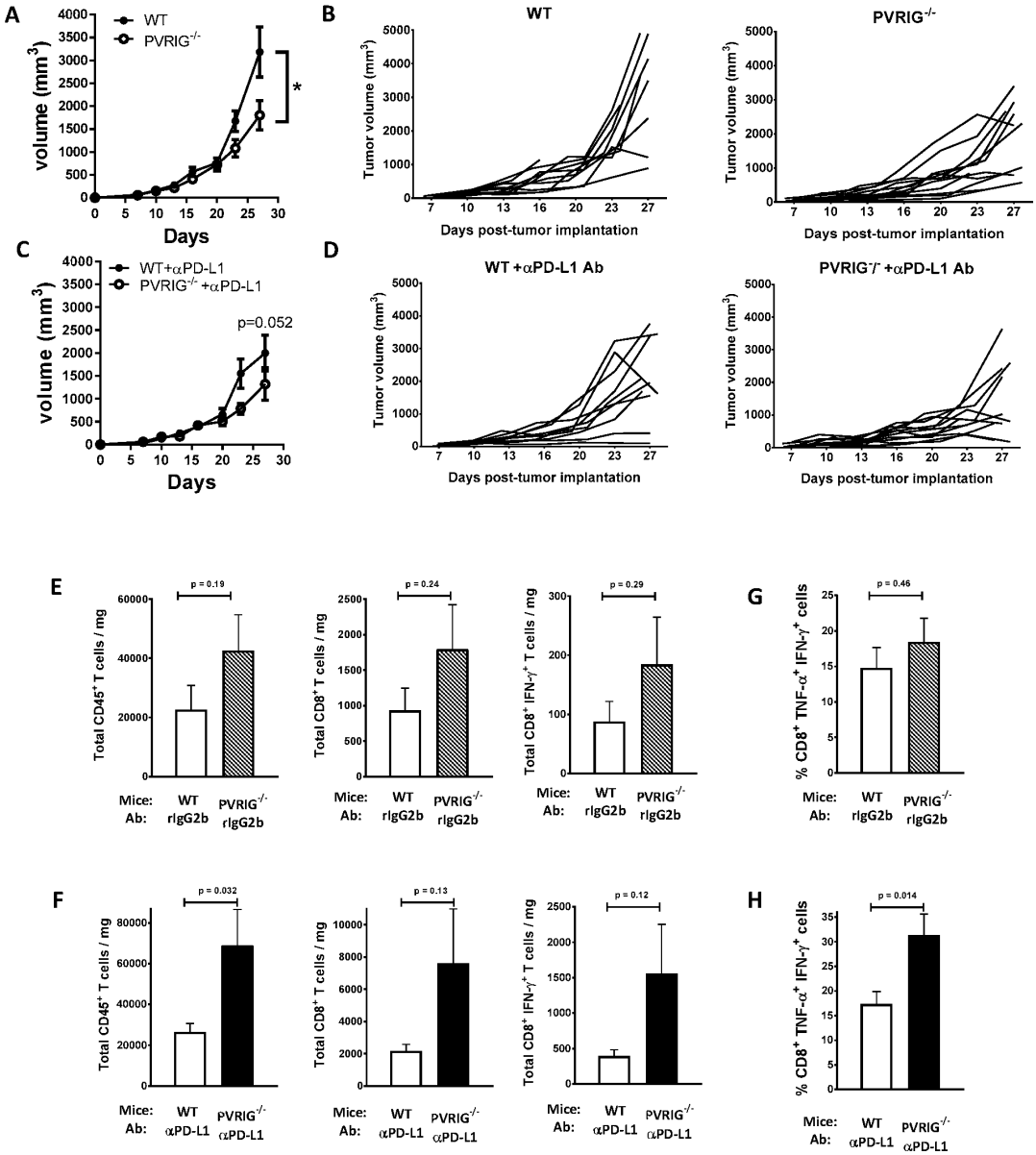

A
WT
PVRIG-/-
volume (mm3)
Days
*
B
WT
PVRIG-/-
Tumor volume (mm3)
Days post-tumor implantation
C
WT+αPD-L1
PVRIG-/- +αPD-L1
p=0.052
volume (mm3)
Days
D
WT +αPD-L1 Ab
PVRIG-/- +αPD-L1 Ab
Tumor volume (mm3)
Days post-tumor implantation
E
Total CD45+ T cells / mg
Total CD8+ T cells / mg
Total CD8+ IFN-γ+ T cells / mg
p = 0.19
p = 0.24
p = 0.29
Mice: WT PVRIG-/-
Ab: rIgG2b rIgG2b
G
% CD8+ TNF-α+ IFN-γ+ cells
p = 0.46
F
Total CD45+ T cells / mg
Total CD8+ T cells / mg
Total CD8+ IFN-γ+ T cells / mg
p = 0.032
p = 0.13
p = 0.12
Mice: WT PVRIG-/-
Ab: αPD-L1 αPD-L1
H
% CD8+ TNF-α+ IFN-γ+ cells
p = 0.014

Figure 33

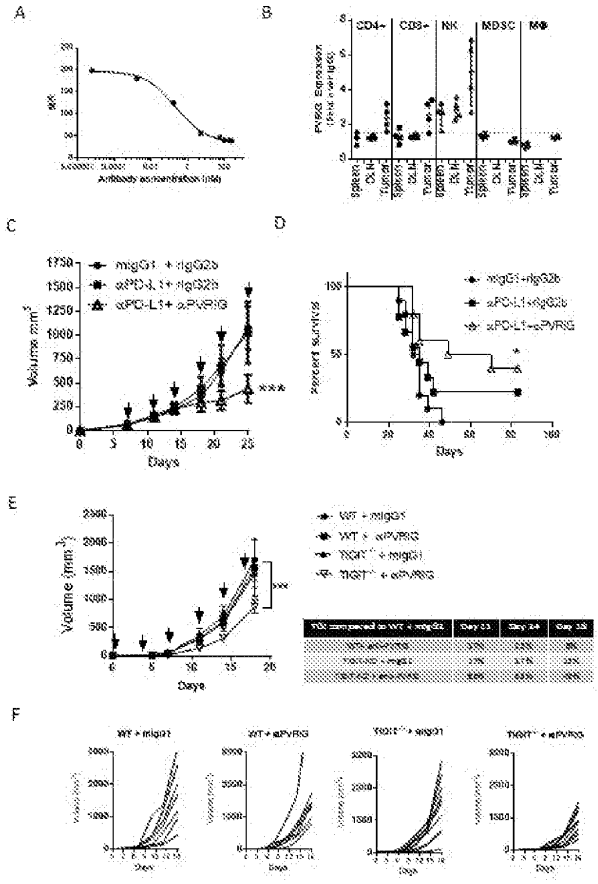


Figure 34

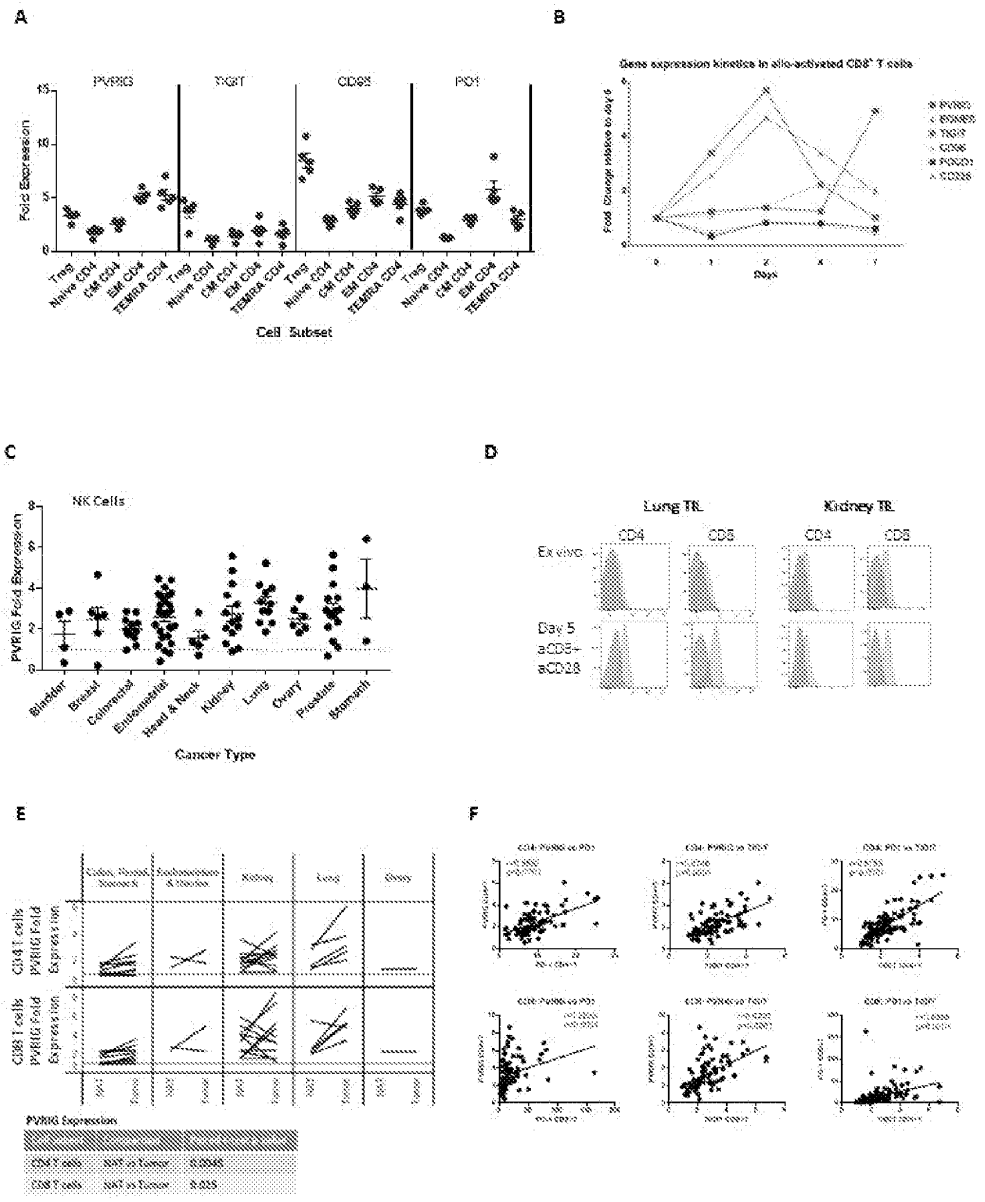
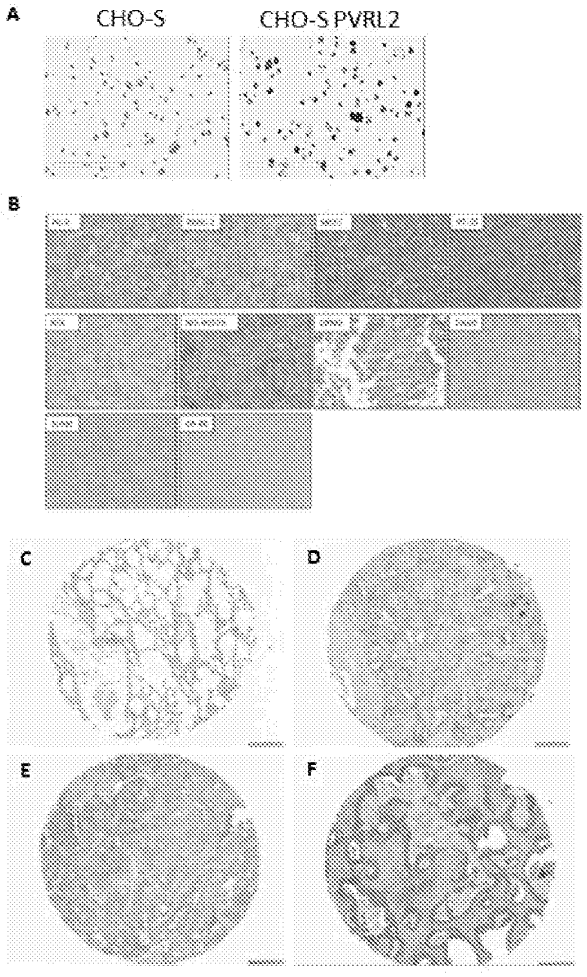

A
PVRIG
TIGIT
CD96
PD1
Fold Expression
Treg
Naive CD4
CM CD4
EM CD4
TEMRA CD4
Cell Subset
B
Gene expression kinetics in allo-activated CD8+ T cells
Fold Change relative to day 0
Days
C
NK Cells
PVRIG Fold Expression
Bladder
Breast
Colorectal
Endometrial
Head & Neck
Kidney
Lung
Ovary
Prostate
Stomach
Cancer Type
D
Lung TIL
Kidney TIL
CD4
CD8
Ex vivo
Day 5
aCD3+
aCD28
E
CD4 T cells PVRIG Fold Expression
CD8 T cells PVRIG Fold Expression
PVRIG Expression
F

Figure 35



Cell Line	PVRL2 Expression by FACS
PC-3	+
PANC-1	+
MCF7	+
HT-29	+
RT-4	+
NCI-H1573	+
OPM2	-
Daudi	-
Jurkat	-
CA-46	-

Figure 36

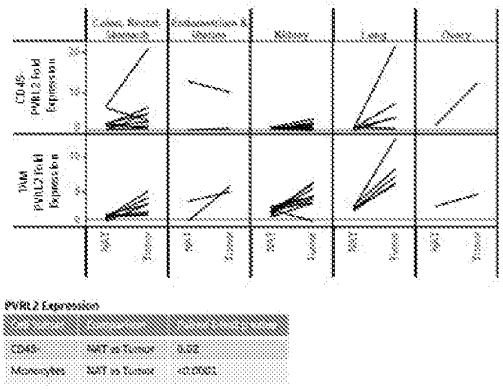

CD45+ PVRL2 fold Expression
TAM PVRL2 fold Expression
NAT
Tumor
PVRL2 Expression
CD45 NAT vs Tumor 0.02
Monocytes NAT vs Tumor <0.0001

Figure 37

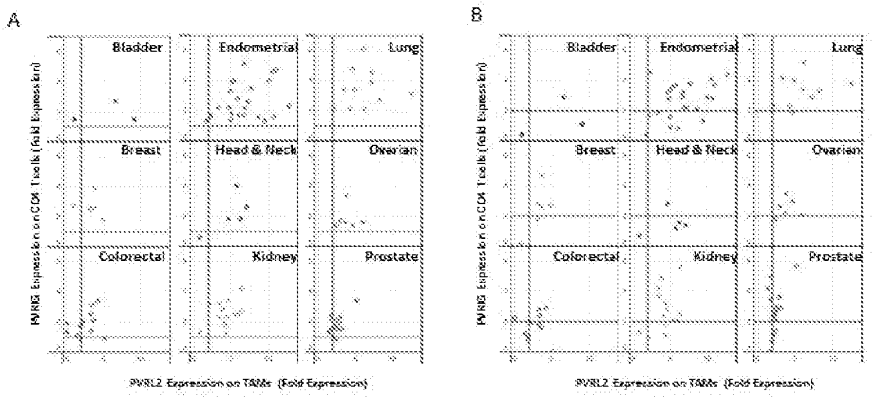

A
Bladder
Endometrial
Lung
Breast
Head & Neck
Ovarian
Colorectal
Kidney
Prostate
B
Bladder
Endometrial
Lung
Breast
Head & Neck
Ovarian
Colorectal
Kidney
Prostate

Figure 38

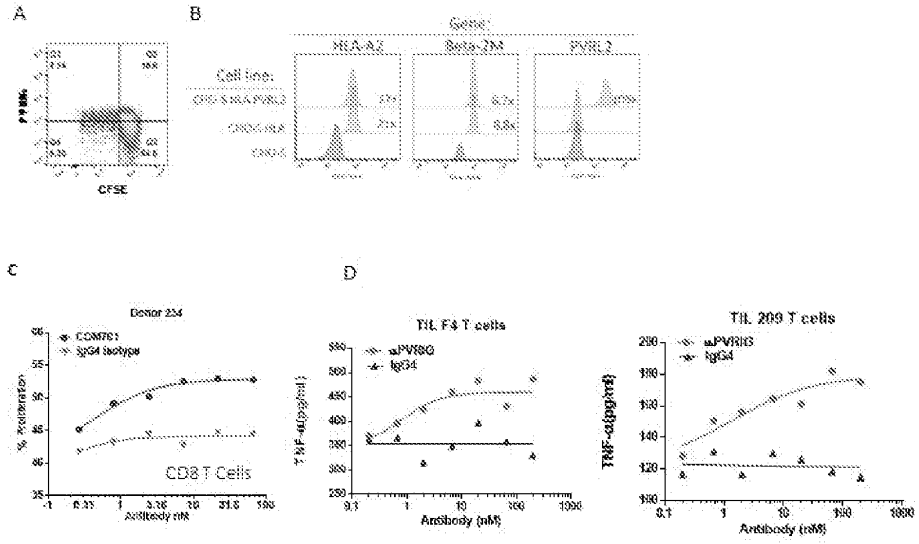

A
B
Gene
HLA-A2
Beta-2M
PVRL2
Cell line
CFSE
C
Donor 254
CD8 T Cells
Antibody nM
D
TIL F4 T cells
TIL 209 T cells
Antibody (nM)

Figure 39

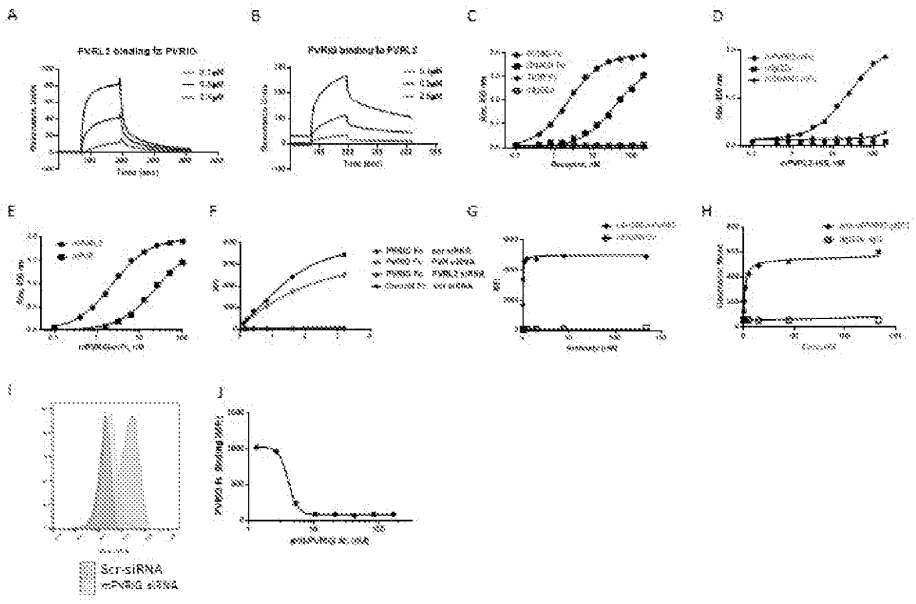


Figure 40

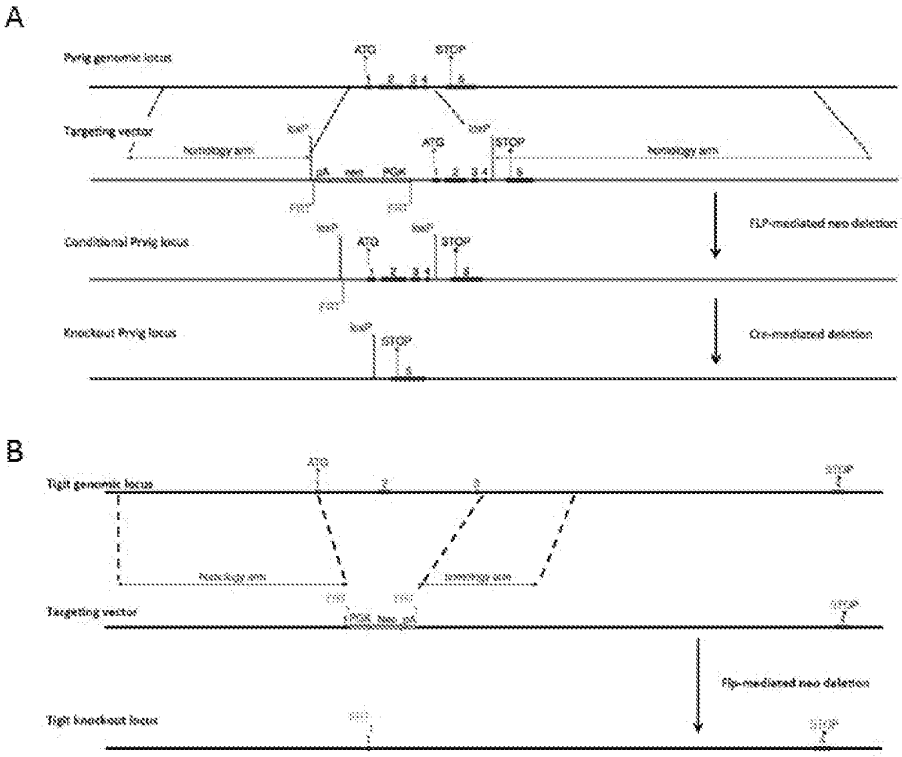

A
Rxrg genomic locus
ATG
STOP
Targeting vector
Neo
Homology arm
Conditional Rxrg locus
FLP-mediated neo deletion
Knockout Rxrg locus
Cre-mediated deletion
B
Tgfr genomic locus
Targeting vector
Flp-mediated neo deletion
Tgfr knockout locus

Figure 41

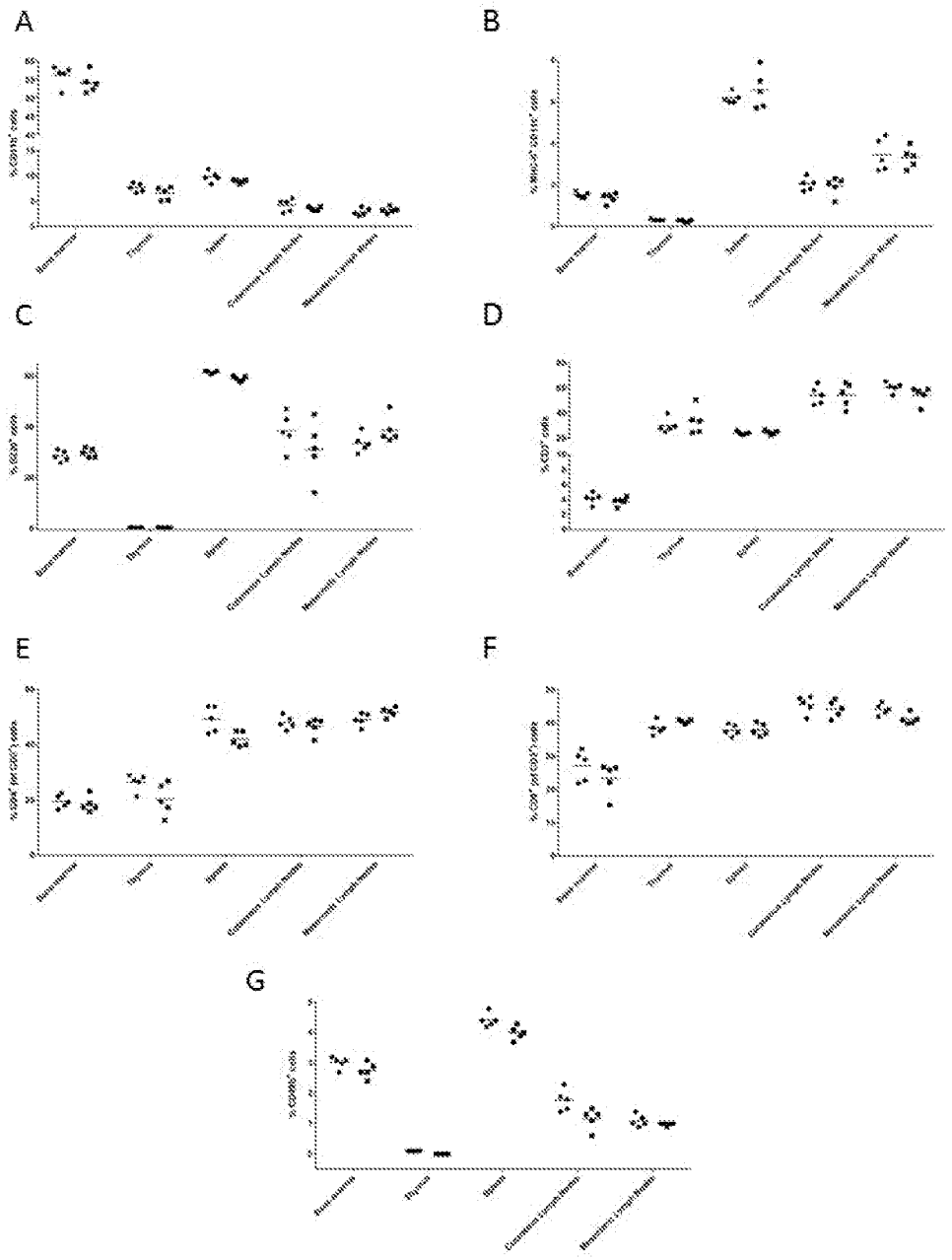


Figure 41 (cont.)

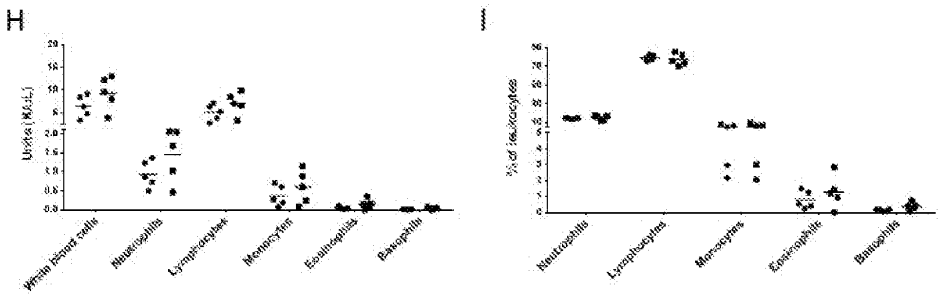


Figure 42

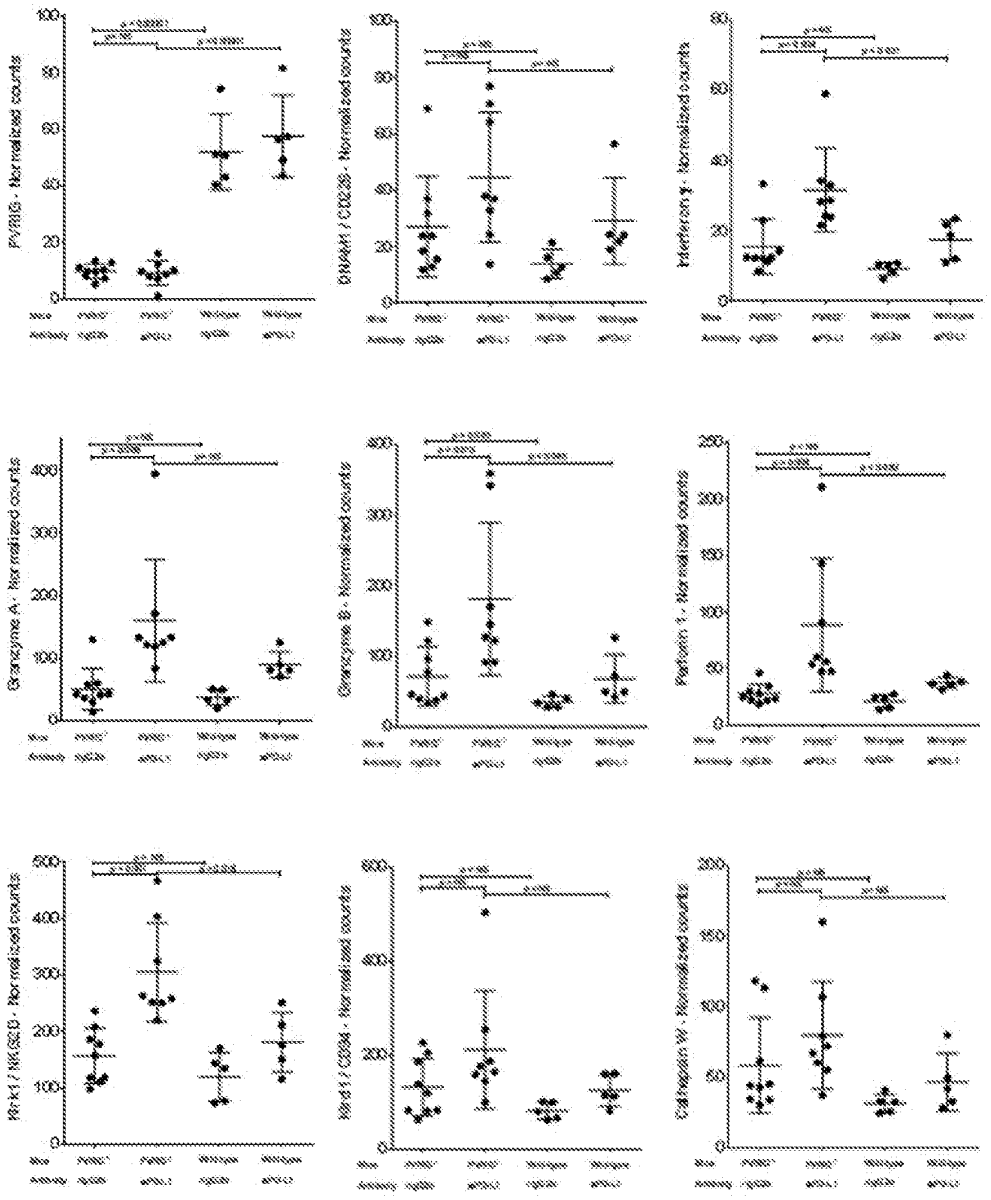

PYRIN - Normalized counts
CD40/41 / CD226 - Normalized counts
Interferon γ - Normalized counts
Granzyme A - Normalized counts
Granzyme B - Normalized counts
Perforin 1 - Normalized counts
Fcrk1 / NKG2D - Normalized counts
Fcrk1 / CD56 - Normalized counts
Cathepsin W - Normalized counts

Figure 43

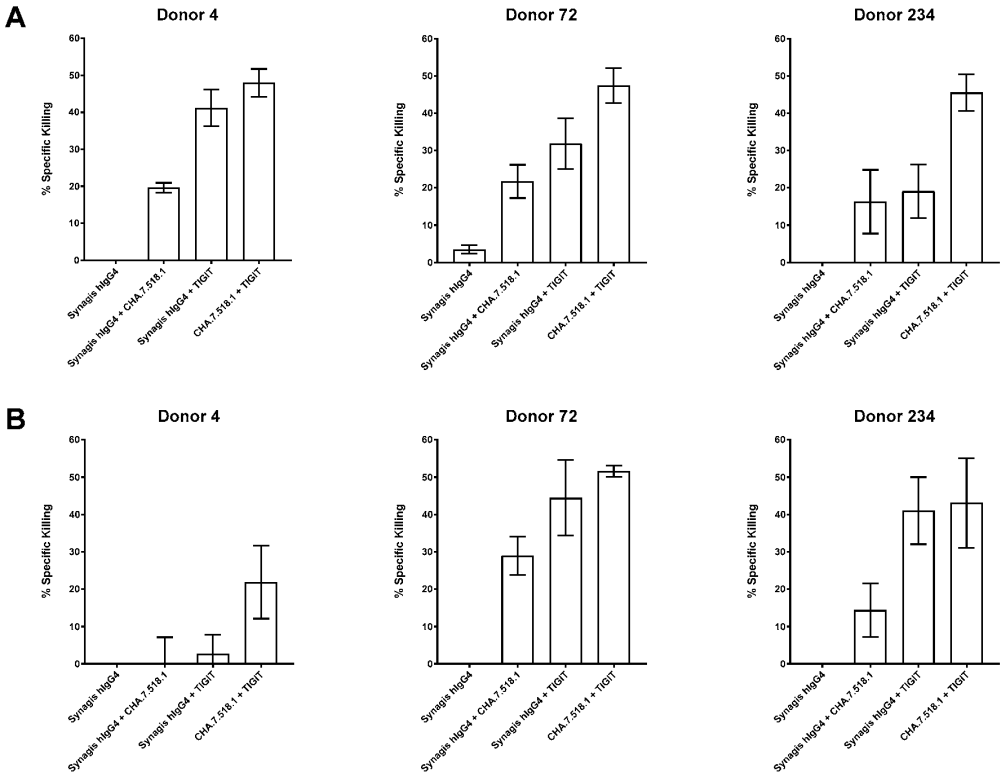

A
Donor 4
Donor 72
Donor 234
% Specific Killing
Synagis hIgG4
Synagis hIgG4 + CHA.7.518.1
Synagis hIgG4 + TIGIT
CHA.7.518.1 + TIGIT
B
Donor 4
Donor 72
Donor 234
% Specific Killing
Synagis hIgG4
Synagis hIgG4 + CHA.7.518.1
Synagis hIgG4 + TIGIT
CHA.7.518.1 + TIGIT

Figure 44

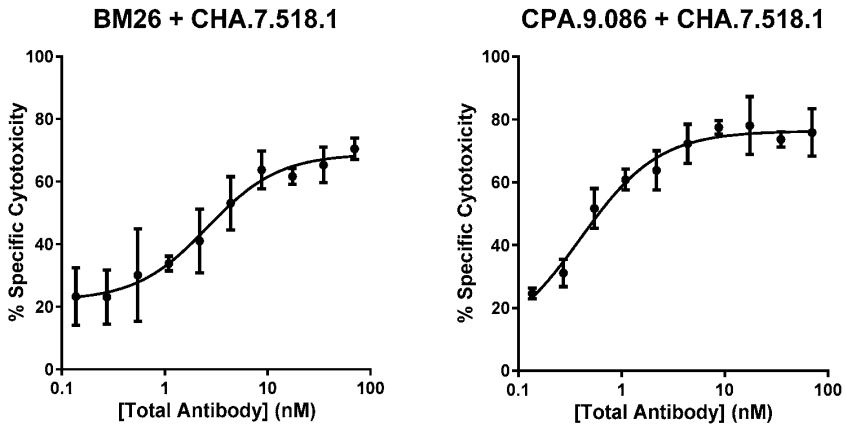
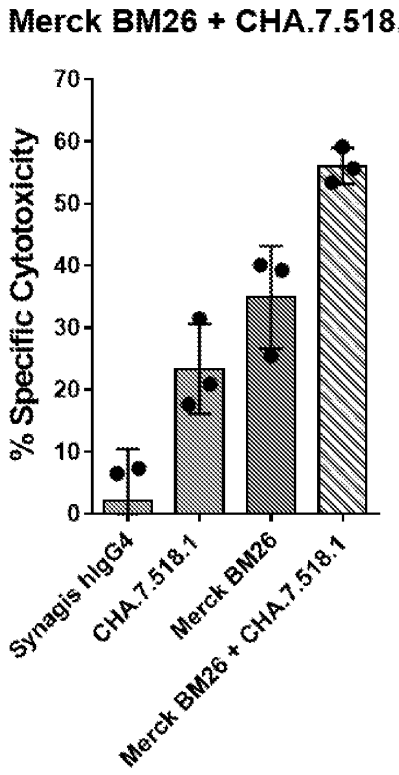

BM26 + CHA.7.518.1
% Specific Cytotoxicity
100
80
60
40
20
0
0.1
1
10
100
[Total Antibody] (nM)
CPA.9.086 + CHA.7.518.1
% Specific Cytotoxicity
100
80
60
40
20
0
0.1
1
10
100
[Total Antibody] (nM)

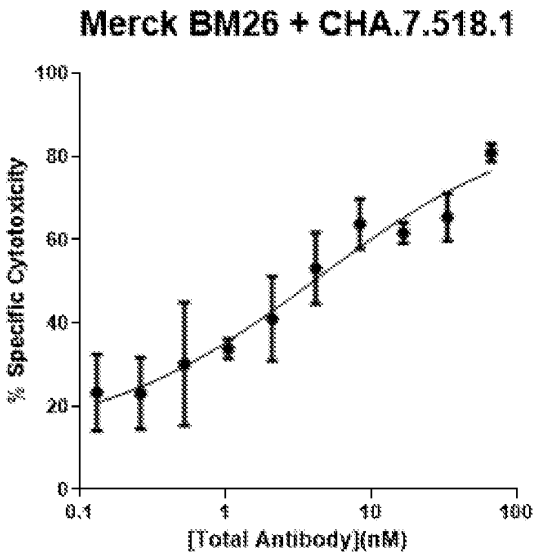
Figure 45

CPA9.086 CDR sequences

Definition	H-CDR1	H-CDR2	H-CDR3	L-CDR1	L-CDR2	L-CDR3
IMGT	GFTFSSYA (SEQ ID NO:1105)	ISYAGEVK (SEQ ID NO:1107)	ARDPLPLHYYGMDV (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)	DPLPLHYYGMDV (SEQ ID NO:1110)	SGSSSNMGRRPVN (SEQ ID NO:1112)	SQNQRPS (SEQ ID NO:1114)	AVWDDIGRVLQ (SEQ ID NO:1116)

Figure 46


Merck BM26 + CHA.7.518.1
% Specific Cytotoxicity
70
60
50
40
30
20
10
0
Synagis hIgG4
CHA.7.518.1
Merck BM26
Merck BM26 + CHA.7.518.1


Merck BM26 + CHA.7.518.1
% Specific Cytotoxicity
100
80
60
40
20
0
0.1
1
10
100
[Total Antibody](nM)

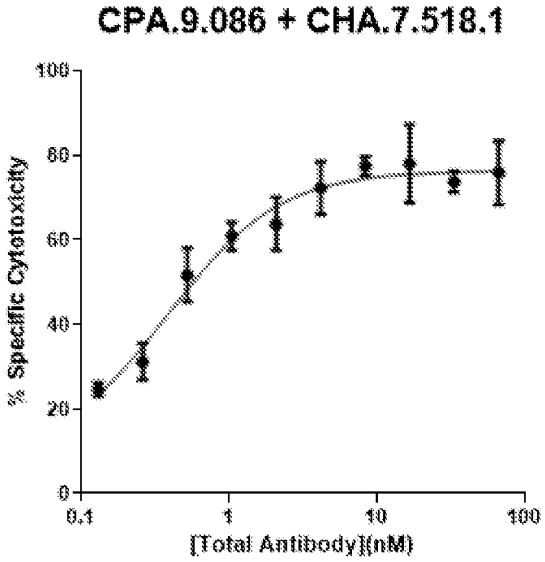

CPA.9.086 + CHA.7.518.1
% Specific Cytotoxicity
100
80
60
40
20
0
0.1
1
10
100
[Total Antibody](nM)

Figure 47

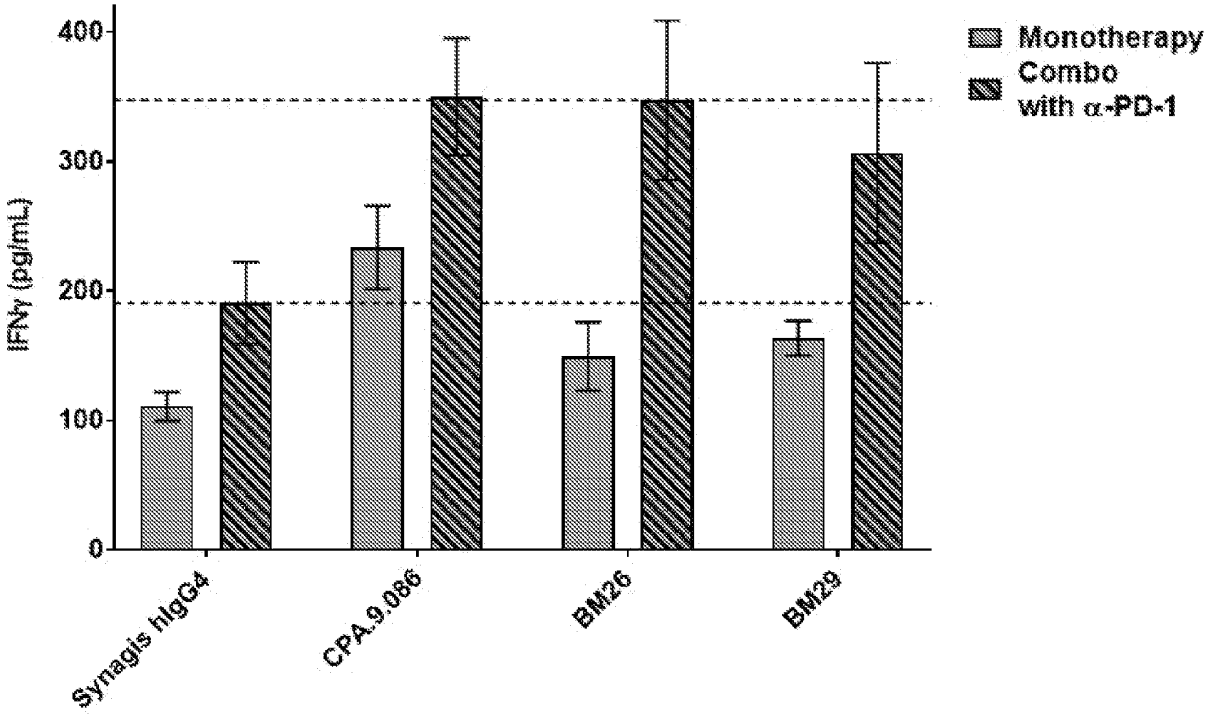

400
300
200
100
0
IFNγ (pg/mL)
Monotherapy
Combo with α-PD-1
Synagis hIgG4
CPA.9.086
BM26
BM29

Figure 48

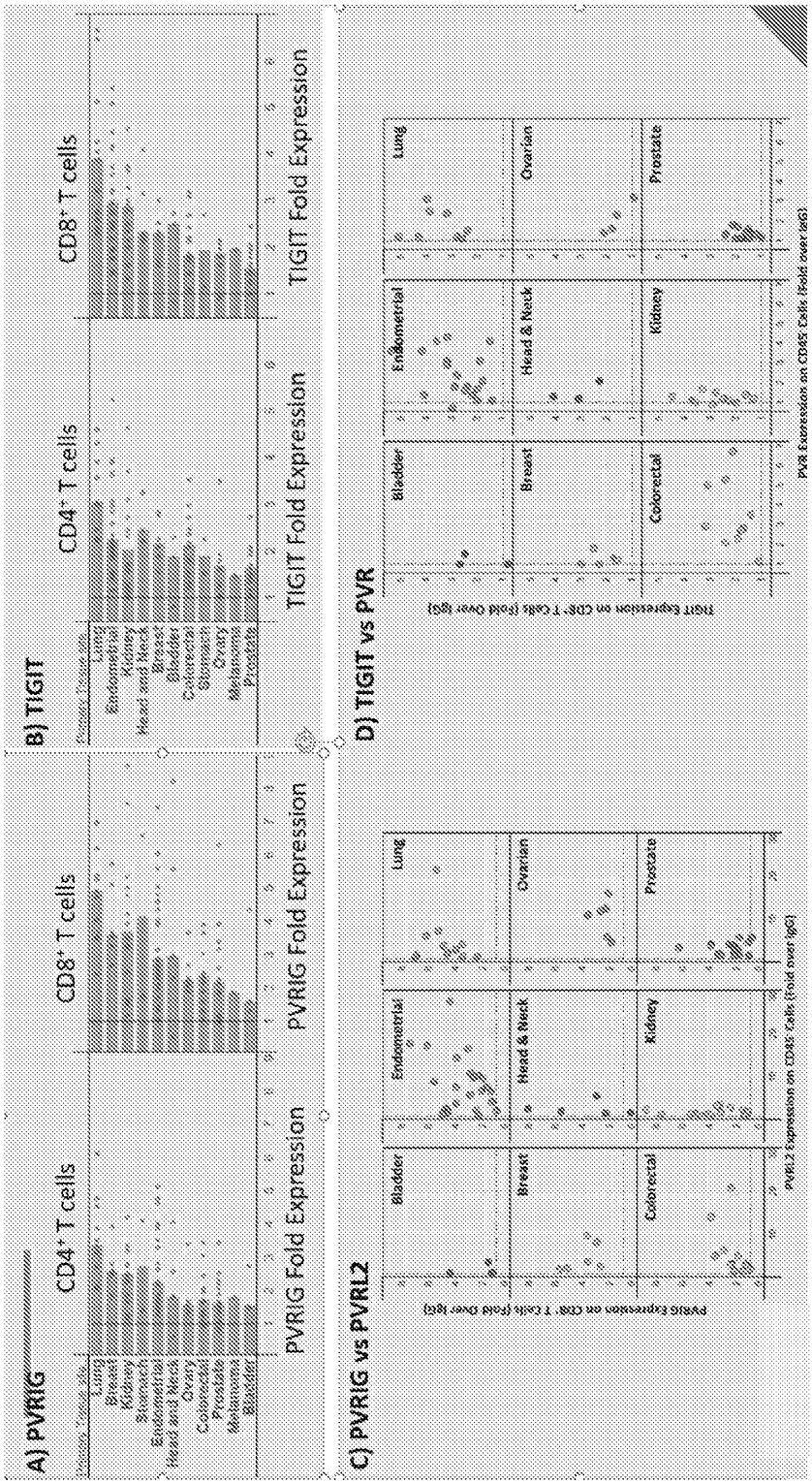

A) PVRIG
CD4+ T cells
CD8+ T cells
Primary Tissue site
Lung
Breast
Kidney
Stomach
Endometrial
Head and Neck
Ovary
Colorectal
Prostate
Melanoma
Bladder
PVRIG Fold Expression
B) TIGIT
TIGIT Fold Expression
C) PVRIG vs PVRL2
PVRIG Expression on CD8+ T Cells (Fold over IgG)
PVRL2 Expression on CD45+ Cells (Fold over IgG)
D) TIGIT vs PVR
TIGIT Expression on CD8+ T Cells (Fold over IgG)
PVR Expression on CD45+ Cells (Fold over IgG)

Figure 49

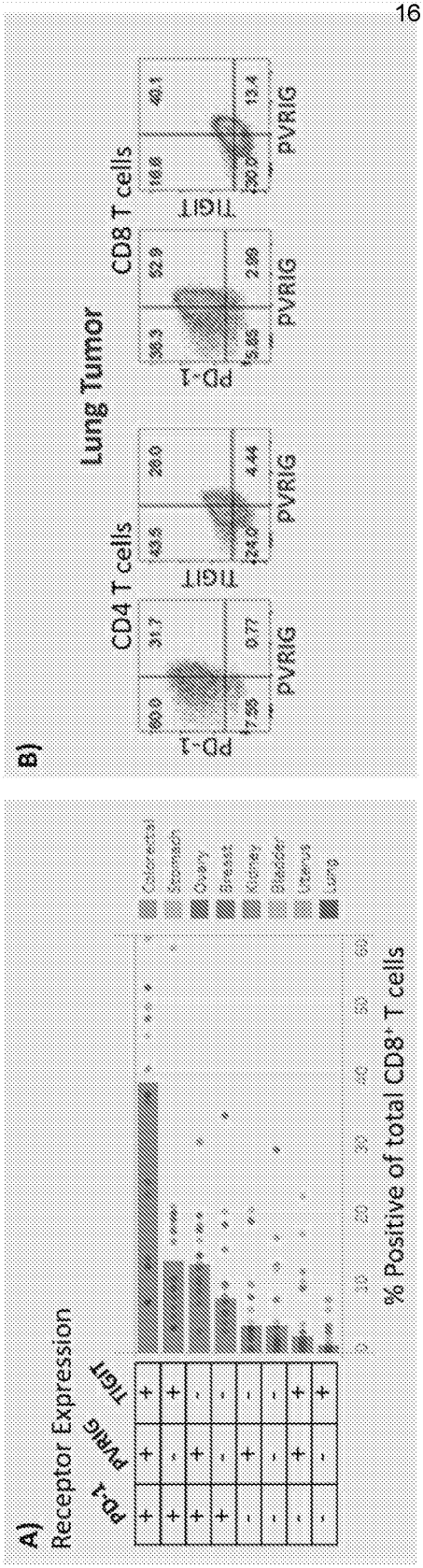
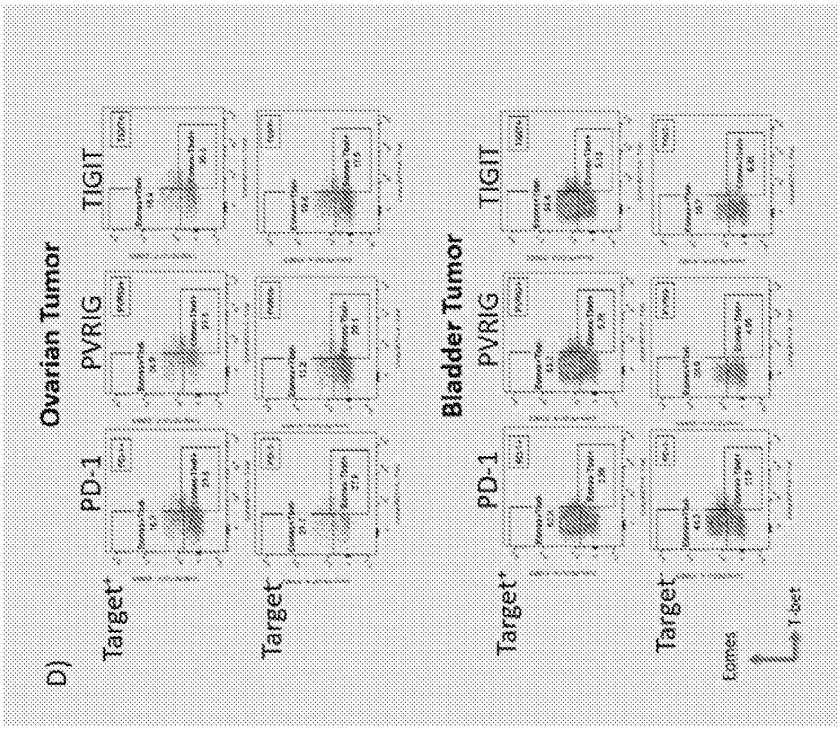

A)
Receptor Expression
PD-1
PVRIG
TIGIT
% Positive of total CD8+ T cells
B)
Lung Tumor
CD4 T cells
CD8 T cells
PD-1
TIGIT
PVRIG

Figure 49 (cont.)



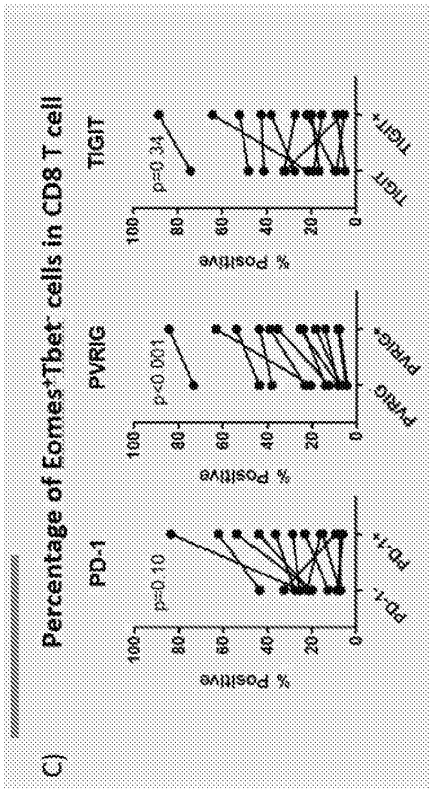


Figure 50

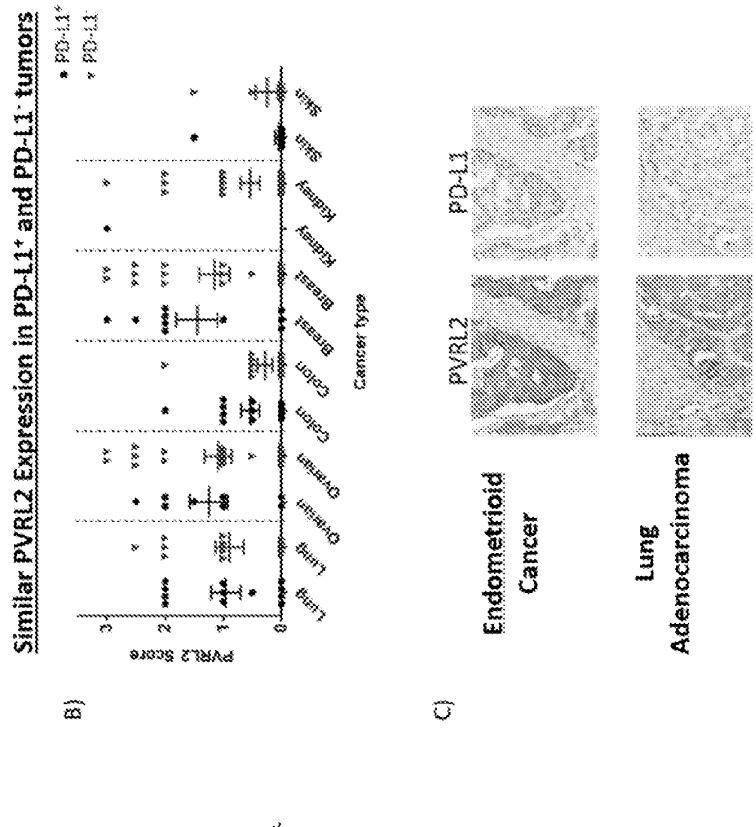

A)
PVRL2 Is Induced in the Tumor
PVRL2 score
Lung
Ovarian/ Endometrial
Breast
Colon
Kidney
Skin
Pathology
B)
Similar PVRL2 Expression in PD-L1+ and PD-L1- tumors
PD-L1+
PD-L1-
PVRL2 score
Cancer type
C)
PVRL2
PD-L1
Endometrioid Cancer
Lung Adenocarcinoma

Figure 51

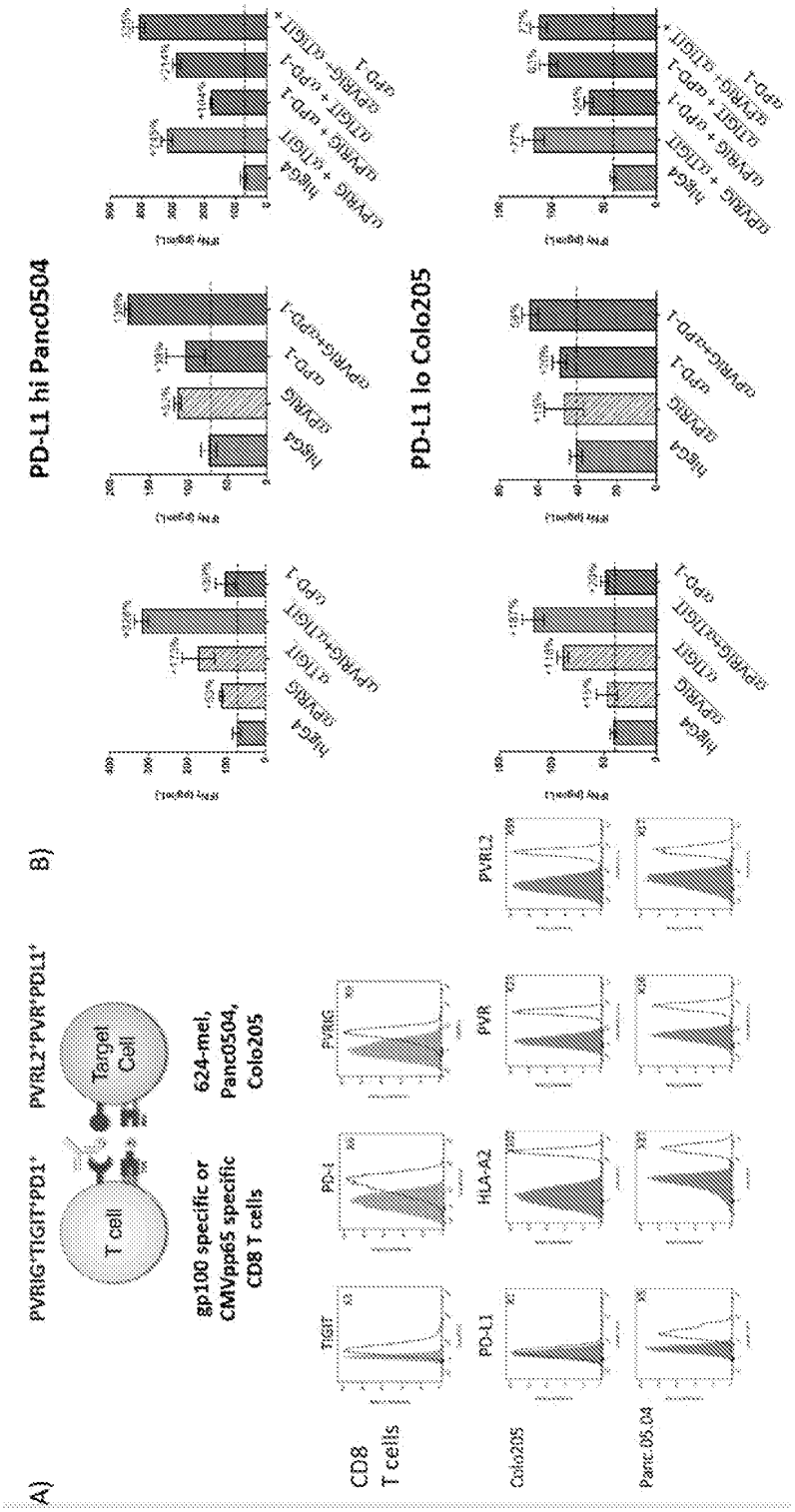
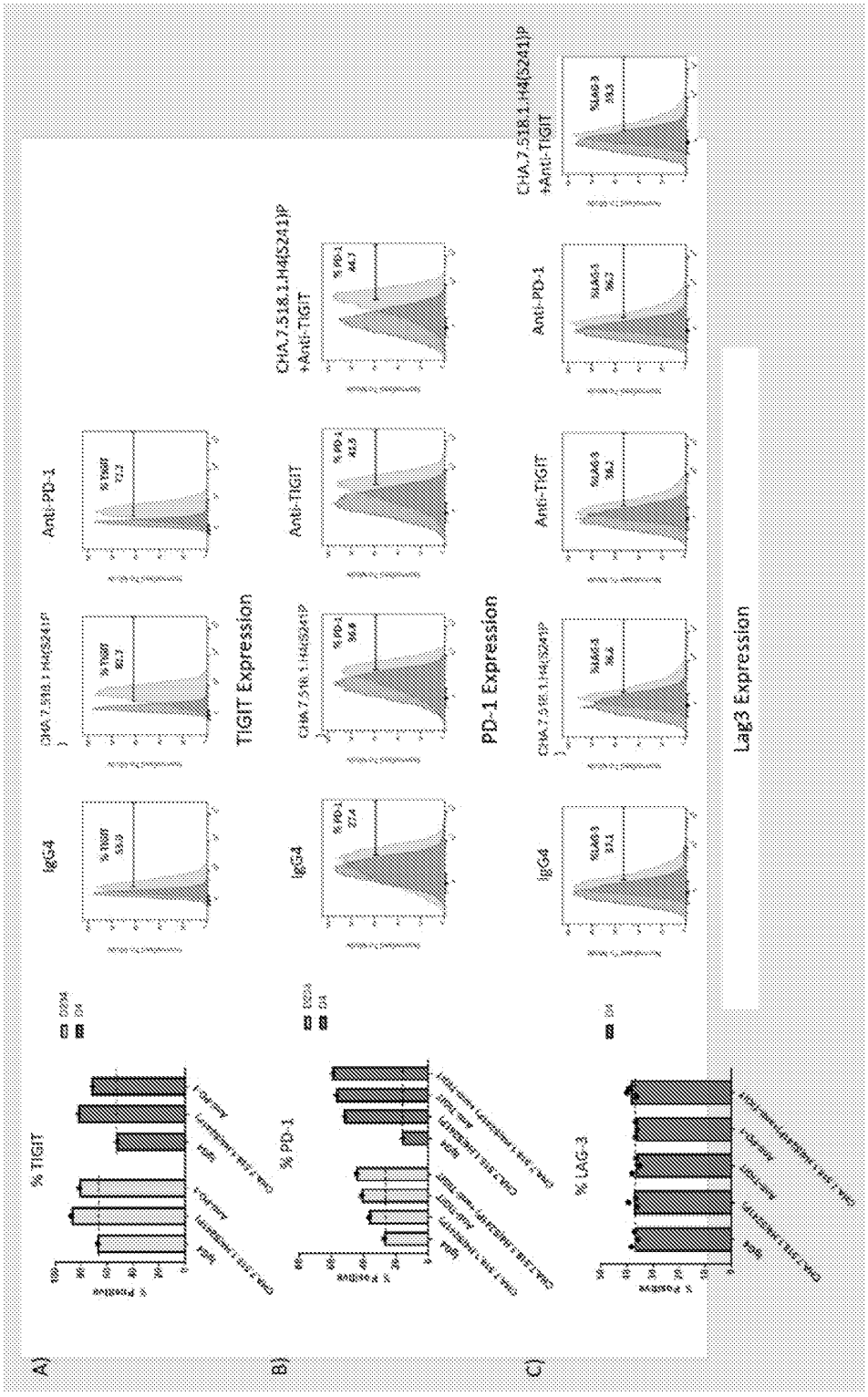

A)
PVRIG+TIGIT+PD1+
PVRL2+PVR+PDL1+
T cell
Target Cell
gp100 specific or CMVpp65 specific CD8 T cells
624-mel, Panc0504, Colo205
CD8 T cells
Colo205
Panc 05.04
TIGIT
PD-1
PVRIG
PD-L1
HLA-A2
PVR
PVRL2
B)
PD-L1 hi Panc0504
PD-L1 lo Colo205
HLA-A2
aPVRIG
aTIGIT
aPD-1
aPVRIG+aTIGIT
aPVRIG + aTIGIT
aTIGIT + aPD-1
aPVRIG + aPD-1
aPVRIG+aTIGIT + aPD-1

Figure 52


A)
% TIGIT
% Positive
IgG4
Anti-PD-1
TIGIT Expression
B)
% PD-1
% Positive
IgG4
Anti-TIGIT
CHA.7.538.1.H4S241P +Anti-TIGIT
PD-1 Expression
C)
% LAG-3
% Positive
IgG4
Anti-PD-1
Anti-TIGIT
CHA.7.538.1.H4S241P +Anti-TIGIT
Lag3 Expression

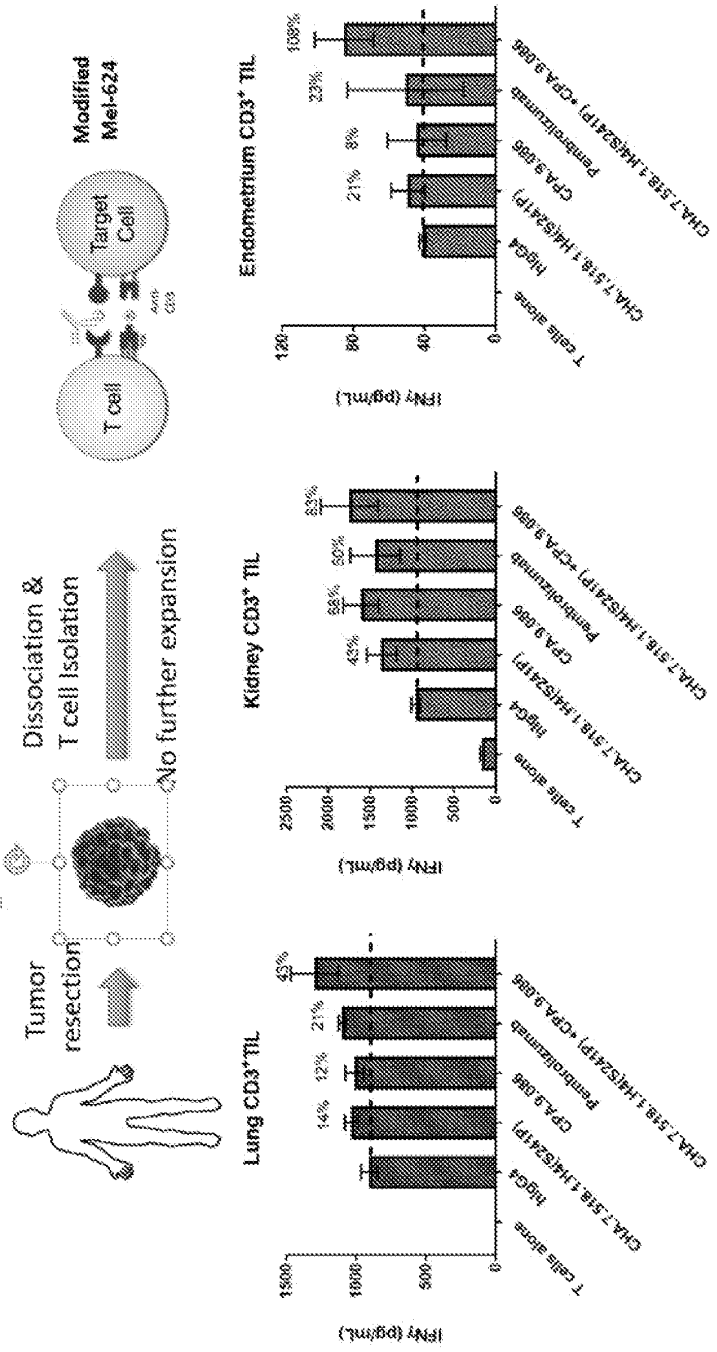

Tumor resection
Dissociation & T cell Isolation
No further expansion
T cell
Target Cell
Modified Mel-624
Lung CD3+ TIL
Kidney CD3+ TIL
Endometrium CD3+ TIL
IFNγ (pg/mL)
T cells alone
hIgG4
CHA.7.518.1.h4/S241P) +CPA.9.086
Pembrolizumab
CPA.9.086
CHA.7.518.1.h4/S241P)
CHA.7.518.1.h4/S241P) +CPA.9.086
14%
12%
21%
43%
45%
68%
60%
82%
8%
21%
23%
108%

Figure 53

Figure 54

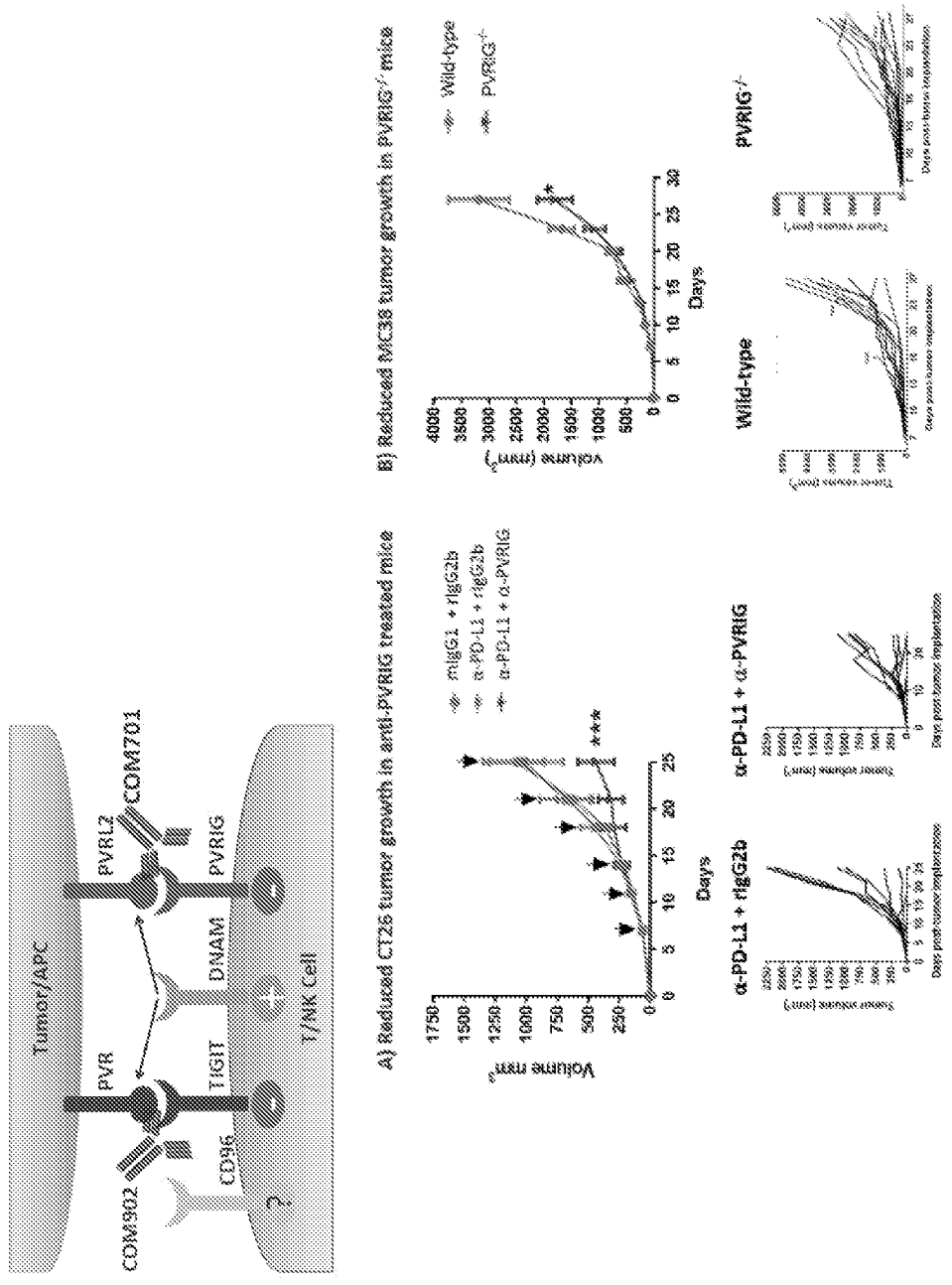

Tumor/APC
PVR
PVRL2
COM701
PVRIG
DNAM
TIGIT
CD96
COM902
?
T/NK cell
A) Reduced CT26 tumor growth in anti-PVRIG treated mice
mIgG1 + rIgG2b
α-PD-L1 + rIgG2b
α-PD-L1 + α-PVRIG
Volume mm³
Days
***
B) Reduced MC38 tumor growth in PVRIG-/- mice
Wild-type
PVRIG-/-
Volume (mm³)
Days
α-PD-L1 + rIgG2b
α-PD-L1 + α-PVRIG
Wild-type
PVRIG-/-

Figure 55

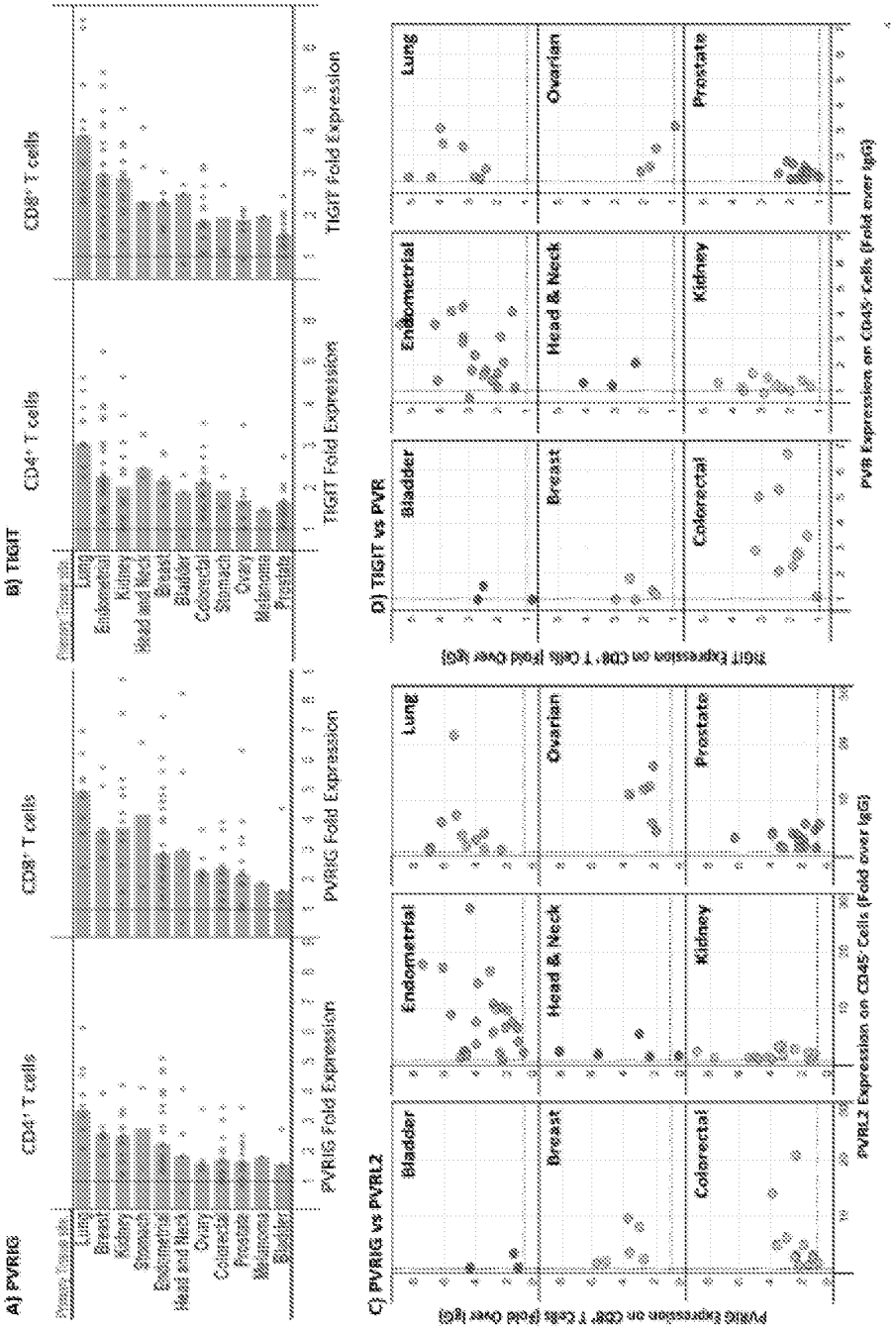

A) PVRIG
CD4+ T cells
CD8+ T cells
Tissue Origin
Lung
Breast
Kidney
Stomach
Endometrial
Head and Neck
Ovary
Colorectal
Prostate
Melanoma
Bladder
PVRIG Fold Expression
B) TIGIT
CD4+ T cells
CD8+ T cells
TIGIT Fold Expression
C) PVRIG vs PVRL2
PVRIG Expression on CD8+ T Cells (Fold over Iso)
PVRL2 Expression on CD45- Cells (Fold over Iso)
Bladder
Endometrial
Lung
Breast
Head & Neck
Ovarian
Colorectal
Kidney
Prostate
D) TIGIT vs PVR
TIGIT Expression on CD8+ T Cells (Fold Over Iso)
PVR Expression on CD45- Cells (Fold over Iso)

Figure 56

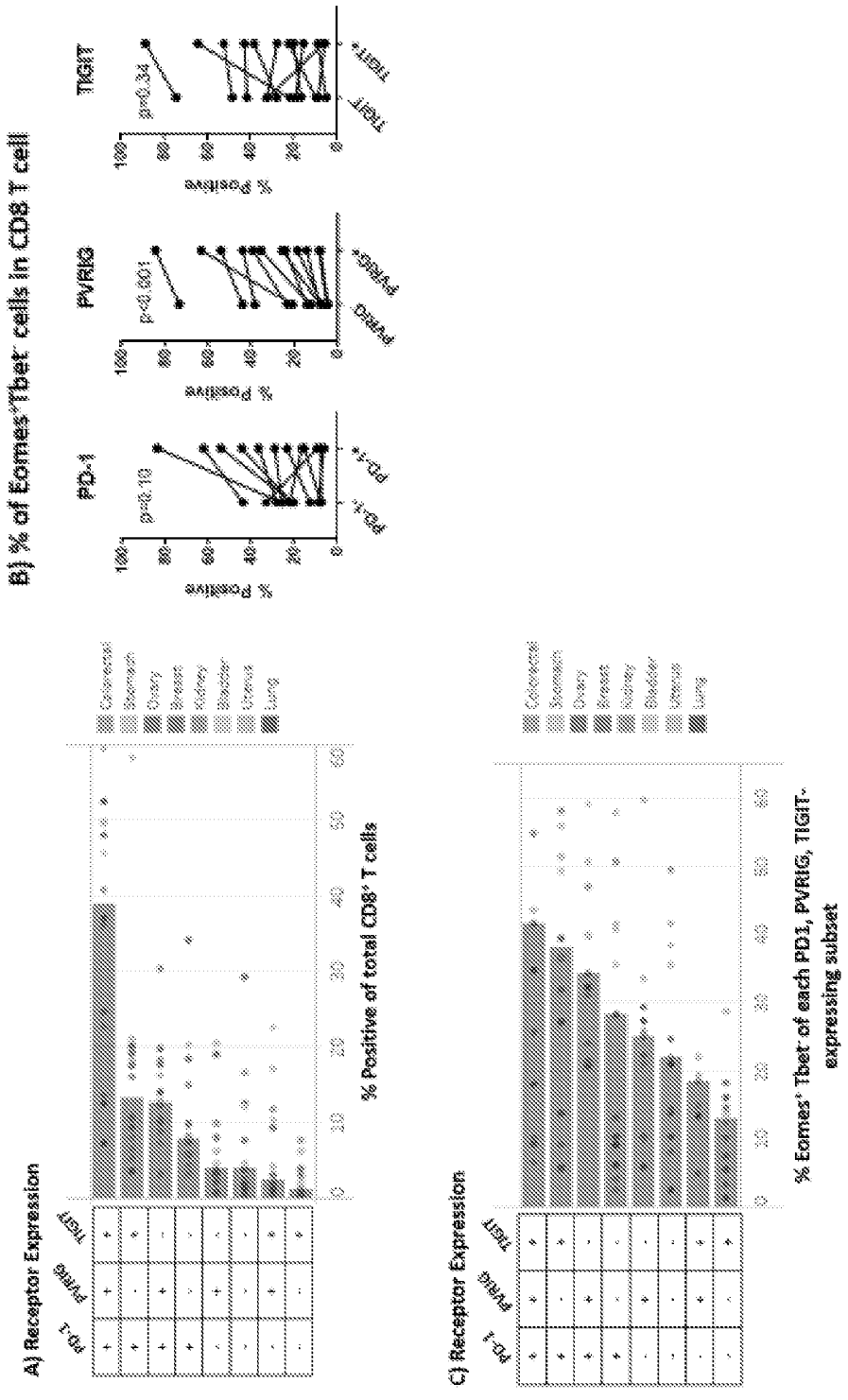

A) Receptor Expression
PD-1
PVRIG
TIGIT
% Positive of total CD8+ T cells
Colorectal
Stomach
Ovary
Breast
Kidney
Bladder
Uterus
Lung
B) % of Eomes+Tbet+ cells in CD8 T cell
PD-1
PVRIG
TIGIT
% Positive
p=0.10
p<0.001
p=0.34
PD-1+
PD-1-
PVRIG+
PVRIG-
TIGIT+
TIGIT-
C) Receptor Expression
% Eomes+ Tbet+ of each PD1, PVRIG, TIGIT-expressing subset

Figure 57

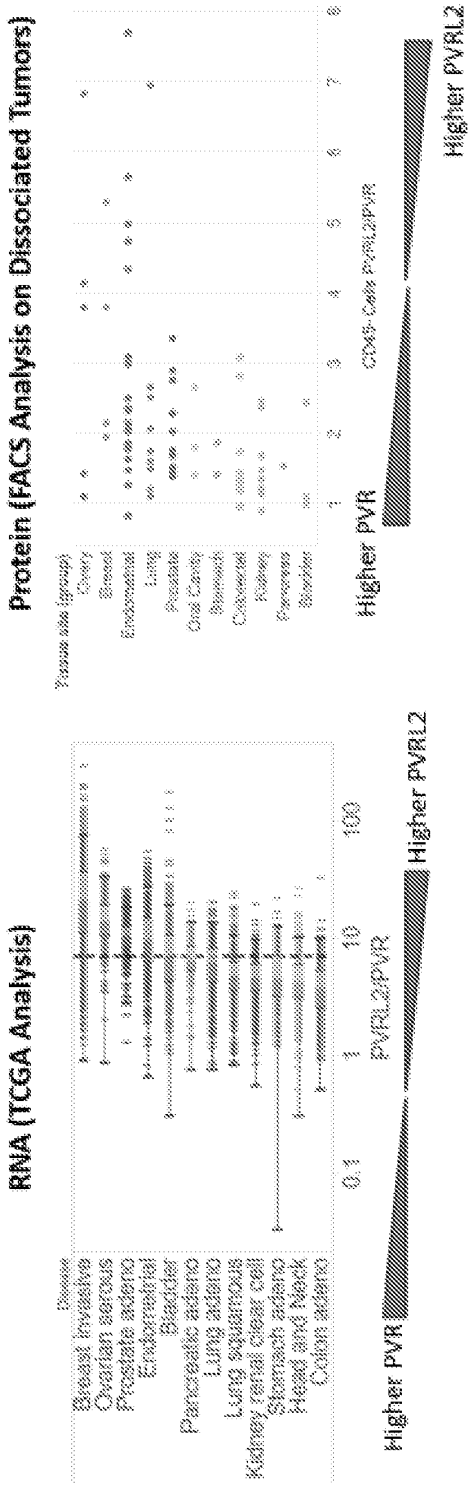
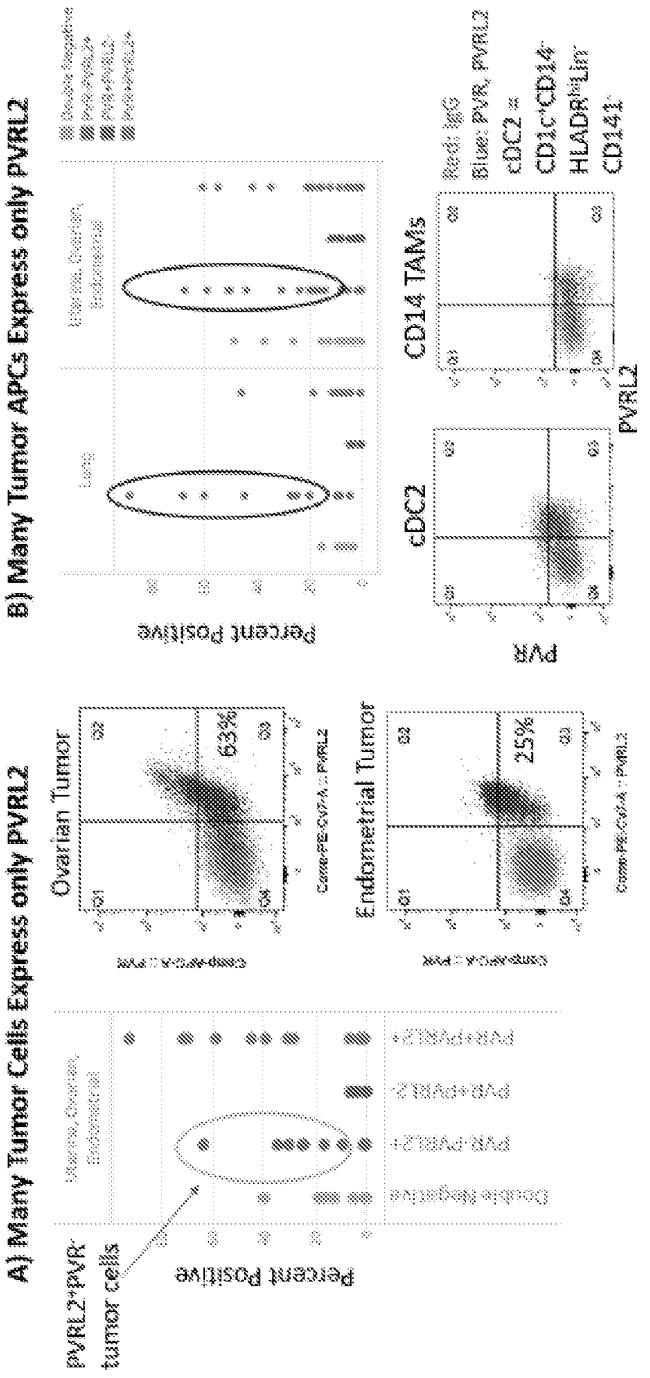

RNA (TCGA Analysis)
Breast invasive
Ovarian serous
Prostate adeno
Endometrial
Bladder
Pancreatic adeno
Lung adeno
Lung squamous
Kidney renal clear cell
Stomach adeno
Head and Neck
Colon adeno
0.1
1
10
100
PVRL2/PVR
Higher PVR
Higher PVRL2
Protein (FACS Analysis on Dissociated Tumors)
Tissue site (group)
Ovary
Breast
Endometrial
Lung
Prostate
Oral Cavity
Stomach
Colorectal
Kidney
Pancreas
Bladder
1
2
3
4
5
6
7
8
CD96-Cells PVRL2/PVR
Higher PVR
Higher PVRL2

Figure 58


A) Many Tumor Cells Express only PVRL2
PVRL2+PVR- tumor cells
Percent Positive
Double Negative
PVR-PVRL2+
PVR+PVRL2-
PVR+PVRL2+
Ovarian Tumor
63%
Endometrial Tumor
25%
B) Many Tumor APCs Express only PVRL2
Lung
Percent Positive
cDC2
CD14 TAMs
Red: IgG
Blue: PVR, PVRL2
cDC2 = CD1c+CD14- HLADRhiLin- CD141-
PVR
PVRL2

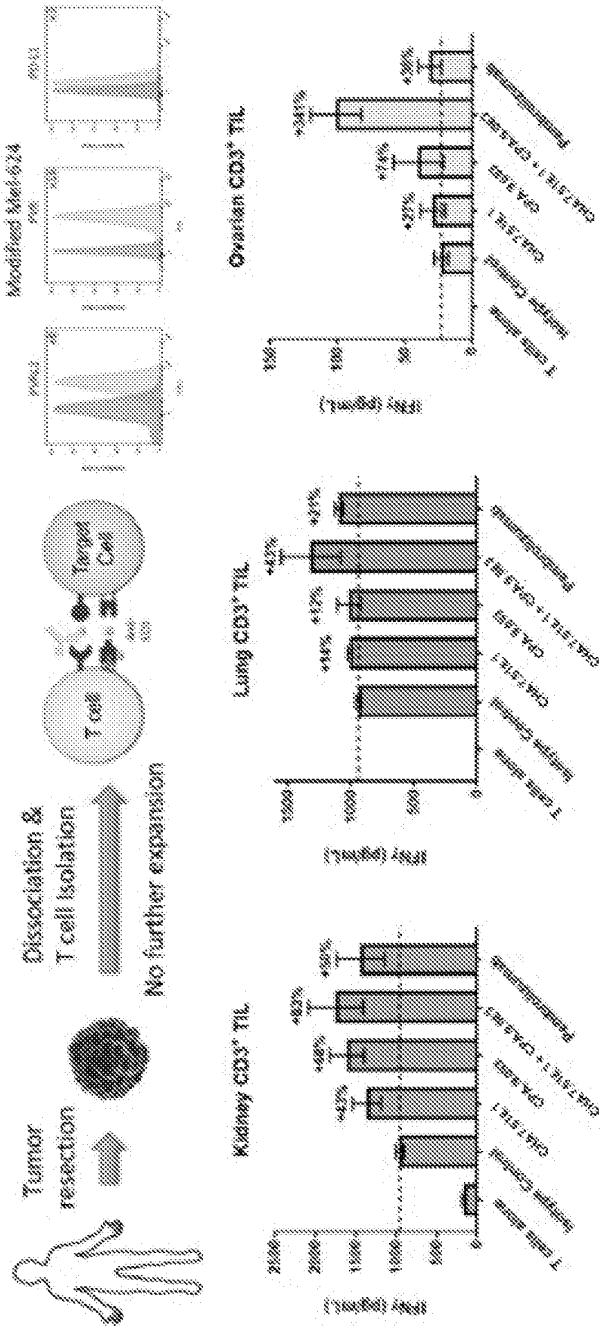

Tumor resection
Dissociation & T cell isolation
No further expansion
T cell
Target Cell
Modified Mel-624
Kidney CD3+ TIL
Lung CD3+ TIL
Ovarian CD3+ TIL
IFNγ (pg/mL)
T cells alone
Tumor Control
OKT3 3ng/
OKT3 3ng/ + CD28.3 3ug/
Autologous

Figure 59

Figure 60

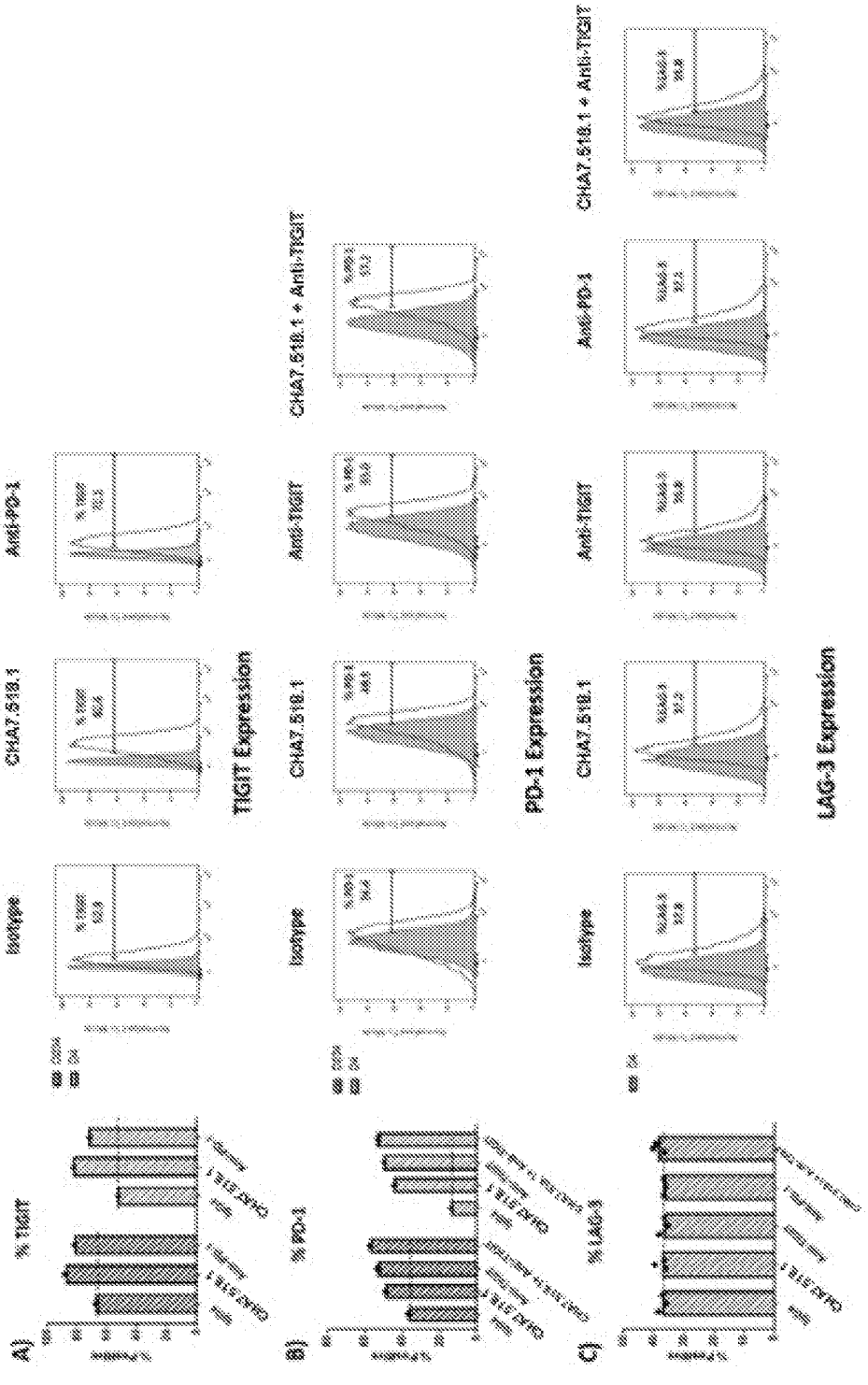
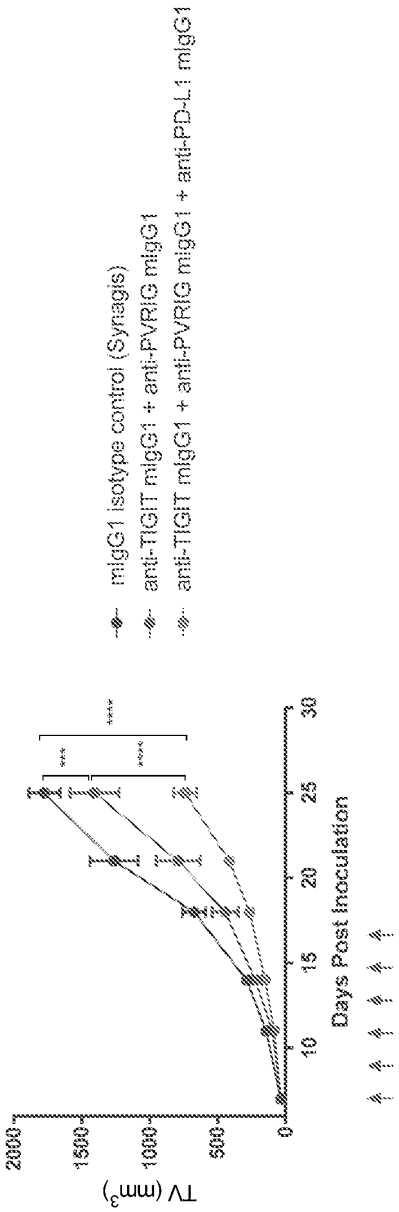

A)
% TIGIT
Isotype
CHA7.518.1
Anti-PD-1
TIGIT Expression
B)
% PD-1
Isotype
CHA7.518.1
Anti-TIGIT
CHA7.518.1 + Anti-TIGIT
PD-1 Expression
C)
% LAG-3
Isotype
CHA7.518.1
Anti-TIGIT
Anti-PD-1
CHA7.518.1 + Anti-TIGIT
LAG-3 Expression

Figure 61A



TGI compared to isotype control mIgG1	Day 18	Day 21	Day 25
anti-TIGIT mIgG1 + anti-PVRIG mIgG1	34	37.3	20.7
anti-TIGIT mIgG1 + anti-PVRIG mIgG1 + anti-PD-L1 mIgG1	60.6	67.2	58.3

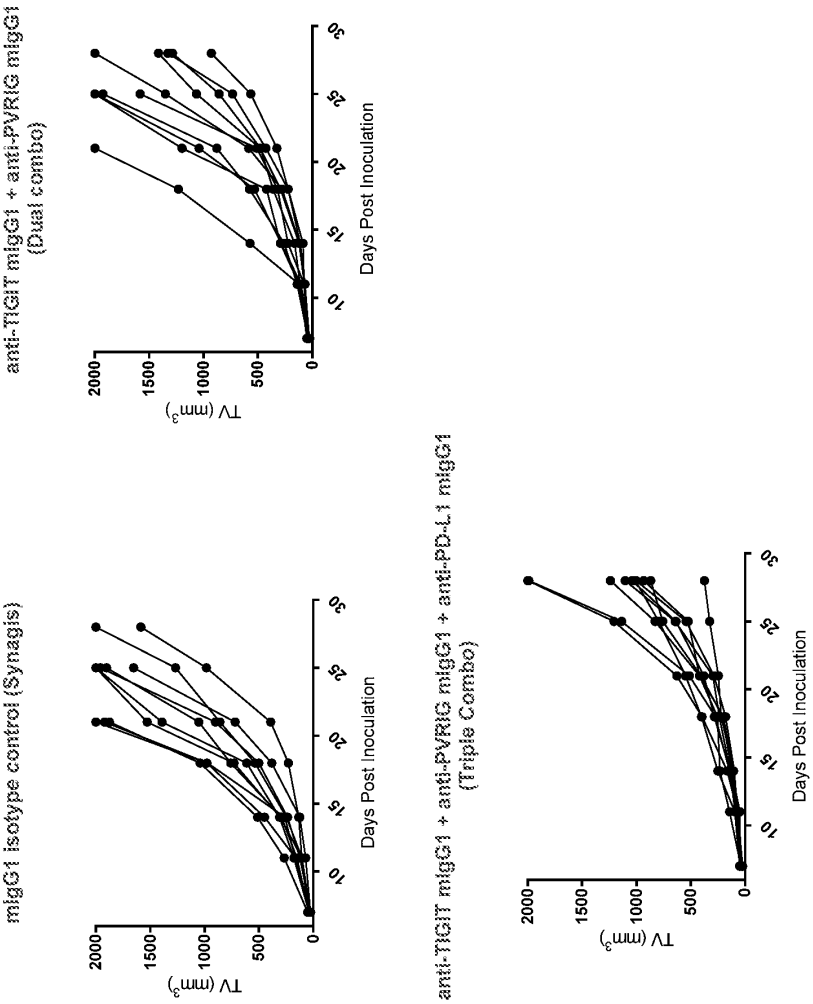

anti-TIGIT mIgG1 + anti-PVRIG mIgG1
(Dual combo)
TV (mm³)
Days Post Inoculation
mIgG1 isotype control (Synagis)
anti-TIGIT mIgG1 + anti-PVRIG mIgG1 + anti-PD-L1 mIgG1
(Triple Combo)

Figure 61B

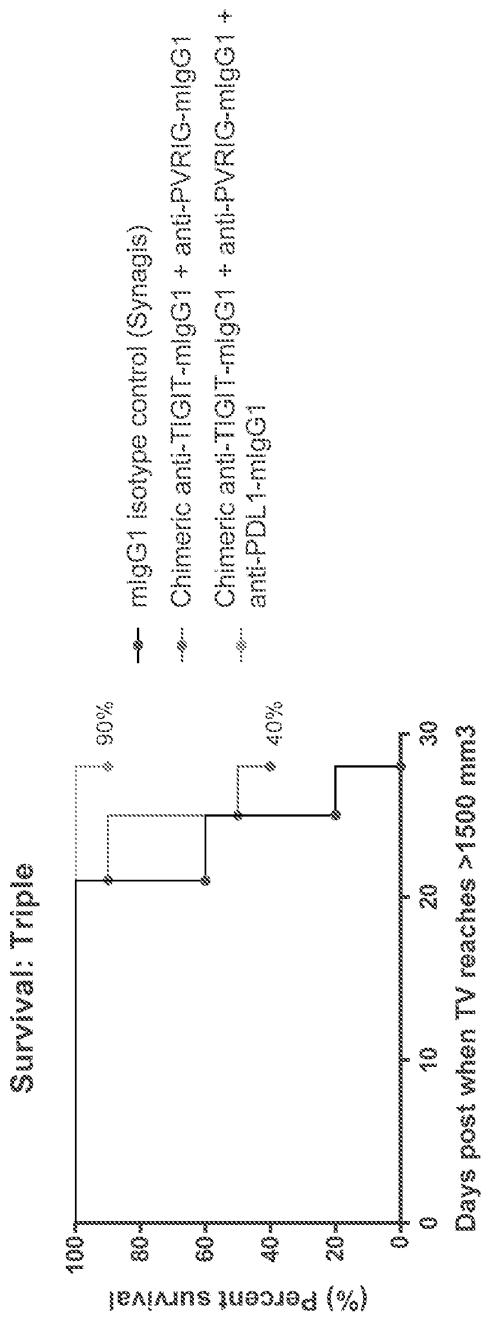

Survival: Triple
mIgG1 isotype control (Synagis)
Chimeric anti-TIGIT-mIgG1 + anti-PVRIG-mIgG1
Chimeric anti-TIGIT-mIgG1 + anti-PVRIG-mIgG1 + anti-PDL1-mIgG1
90%
40%
Percent survival (%)
100
80
60
40
20
0
0
10
20
30
Days post when TV reaches >1500 mm3

Figure 61C

Figure 62A

From W02017100541 (Medimmune, LLC; also US20170306025; Durvalumab)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:2 from W02017100541)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYV DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLVTVSS	1117
vhCDR1 (SEQ ID NO:3 from W02017100541)	RYWMS	1118
vhCDR2 (SEQ ID NO:4 from W02017100541)	NIKQDGSEKYYVDSVKG	1119
vhCDR3 (SEQ ID NO:5 from W02017100541)	EGGWFGELAFD	1120
Light chain (SEQ ID NO:1 from W02017100541)	EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLPWTFGQGTKVEIK	1121
vlCDR1 (SEQ ID NO:6 from W02017100541)	RASQRVSSSYLA	1122
vlCDR2 (SEQ ID NO:7 from W02017100541)	DASSRAT	1123
vlCDR3 (SEQ ID NO:8 from W02017100541)	QQYGSLPWT	1124

Figure 62B

Figure 62B

From US20170281764 (JN Biosciences)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:34 from US20170281764)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADS VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRIWPGGFDYWGQGTLVTVSAASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	1125
Light chain (SEQ ID NO:36 from US20170281764)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYLFTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	1126

Figure 62C

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:23 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT 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)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIKR	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)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWV A WISPYGG STYY ADSVKGRFTISADTSKNTA YLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSSASTK (SEQ ID N0:40), or	1135
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTA VA WYQQKPGKAPKLLIYSASFL YSG VPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQYL YHPATFGQGTKVEIKR (SEQ ID N0:24).	1136

From WO2015009856 (GENENTECH, INC. and F. HOFFMANN-LA ROCHE AG)

What	sequence	SEQ ID NO
Heavy chain (SEQ ID NO: 41 from WO2015009856)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGG STYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTA VYYCARRHWPGGFDYWGQG TLVTVSS	1137
Light chain (SEQ ID NO: from WO2015009856)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIKR	1138

Figure 62E

From US20160222117 (GENENTECH, INC.)

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:20 from US20160222117)	EVQLVESCGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA	1139
Heavy chain (SEQ ID NO:23 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGST YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA	1140
Heavy chain (SEQ ID NO:24 from US20160222117)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSGSWIHWVRQAPGKGLEWVAWILPYGGSS YYADSVKGRFTISRDTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVT VSA	1141

From US20160222117 (GENENTECH, INC.)

What	sequence	SEQ ID NO
Light chain (SEQ ID NO:21 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIKR	1142
Light chain (SEQ ID NO:26 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNVPWTFGQGTKVEIKR	1143
Light chain (SEQ ID NO:27 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYAPPWTFGQGTKVEIKR	1144

Figure 62F

From US20160222117 (GENENTECH, INC.)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:28 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTVPWTFGQGTKVEIKR	1145
Light chain (SEQ ID NO:29 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQNVNTFLAWYQQKPGKAPKLLIYSASTLASGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTVPRTFGQGTKVEIKR	1146
Light chain (SEQ ID NO:30 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGVPRTFGQGTKVEIKR	1147
Light chain (SEQ ID NO:31 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYLFTPPTFGQGTKVEIKR	1148
Light chain (SEQ ID NO:32 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYFITPTTFGQGTKVEIKR	1149
Light chain (SEQ ID NO:33 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYTPPTFGQGTKVEIKR	1150
Light chain (SEQ ID NO:34 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQFFYTPPTFGQGTKVEIKR	1151

Figure 62G

From US20160222117 (GENENTECH, INC.)

What	sequence	SEQ ID NO:
Light chain (SEQ ID NO:35 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSLFTPPTFGQGTKVEIKR	1152
Light chain (SEQ ID NO:36 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSLYTPPTFGQGTKVEIKR	1153
Light chain (SEQ ID NO:37 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSWYHPPTFGQGTKVEIKR	1154
Light chain (SEQ ID NO:38 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYFYIPPTFGQGTKVEIKR	1155
Light chain (SEQ ID NO:39 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYWYTPYTFGQGTKVEIKR	1156
Light chain (SEQ ID NO:40 from US20160222117)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYFIPPTFGQGTKVEIKR	1157

Figure 62H

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

What	sequence	SEQ ID NO:
Heavy chain (SEQ ID NO:32 from WO2013079174)	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADT VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	1158
Light chain (SEQ ID NO: from WO2013079174)	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNR FSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTRVFGTGTKVTVLGQPKANPTVTLFPPSSEE LQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQW KSHRSYSCQVTHEGSTVEKTVAPTECS	1159

Figure 621

From US8217149 (Hoffman La Roche; Atezolizumab)

What	sequence	SEQ ID NO:
Heavy chain (VH) (SEQ ID NO:20 from US8217149)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSA	1160
Light chain (VL) (SEQ ID NO:21 from US8217149)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKWYSASFLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYC QQYLYH PATFGQGTKVEIKR	1161

Atezolizumab (alternate sequence))

What	sequence	SEQ ID NO:
Heavy chain (from IMGT database or DrugBank database)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	
Light chain (from IMGT database or DrugBank database)	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC	1163

Figure 63A

CPA.7.001

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSS	1164
vhCDR1	GGTFSSYA	1165
vhCDR2	IIPIFGTA	1166
vhCDR3	AREEVSSPYGMDV	1167
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1168
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGTSTGAVTSGHYPYWFQQKPGQAPKTLIYDTGNKHSWTPARFSGSLLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLG	1169
vlCDR1	TGAVTSGHY	1170
vlCDR2	DTG	1171
vlCDR3	LLSYSGASWV	1172
Full length light chain	QAVVTQEPSLTVSPGGTVTLTCGTSTGAVTSGHYPYWFQQKPGQAPKTLIYDTGNKHSWTPARFSGSLLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1173

Figure 63B
CPA.7.003

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGFSLSHFSMHWVRQVPGKGLEWLGGFDPEEGGTIPAQKFQGRLTMTEDTST ETAYMELSSLRSEDTAVYYCATGIWYSSGWPVDYWGPGTLVTVSS	1174
vhCDR1	GFSLSHFS	1175
vhCDR2	FDPEEGGT	1176
vhCDR3	ATGIWYSSGWPVDY	1177
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1178
Variable light (vl) domain	DVVMTQSPLSLPVTPGGPASISCRSSQSLLDSSGYNYVDWYLQKPGQSPQLLISLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKR	1179
vlCDR1	QSLLDSSGYNY	1180
vlCDR2	LGS	1181
vlCDR3	MQALQTPIT	1182
Full length light chain	DVVMTQSPLSLPVTPGGPASISCRSSQSLLDSSGYNYVDWYLQKPGQSPQLLISLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1183

Figure 63C
CPA.7.004

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATVSRVRGVINYYYYMDV WGKGTTVTVSS	1184
vhCDR1	GYTLTELS	1185
vhCDR2	FDPEDGET	1186
vhCDR3	ATVSRVRGVINYYYYMDV	1187
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATVSRVRGVINYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1188
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	1189
vlCDR1	QSLLYRNGNNY	1190
vlCDR2	LGS	1191
vlCDR3	MQALQTPPT	1192
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1193

Figure 63D
CPA.7.006

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFGTYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDTAVYYCARGFEYSDGLLDDWGQGTLVTVSS	1194
vhCDR1	GGTFGTYA	1195
vhCDR2	ITPISATI	1196
vhCDR3	ARGFEYSDGLLDD	1197
Full length HC	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFGTYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDTAVYYCARGFEYSDGLLDDWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1198
Variable light (vl) domain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMEEPLTFGGGTKVEIKR	1199
vlCDR1	QSLFYSDDGNTY	1200
vlCDR2	RLS	1201
vlCDR3	MQHMEEPLT	1202
Full length light chain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMEEPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1203

Figure 63E
CPA.7.008

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSGTLSLTCVVSGSISSTNWWTWVRQPPGKGLEWIGEIYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVYYCARVGPAAIYYWGQGTLVTVSS	1204
vhCDR1	SGSISSTNW	1205
vhCDR2	IYHSGST	1206
vhCDR3	ARVGPAAIYY	1207
Full length HC	QVQLQESGPGLVKPSGTLSLTCVVSGSISSTNWWTWVRQPPGKGLEWIGEIYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVYYCARVGPAAIYYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1208
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLG	1209
vlCDR1	SNNVGYEG	1210
vlCDR2	RNN	1211
vlCDR3	SAWDSSLNAVV	1212
Full length light chain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1213

Figure 63F
CPA.7.009

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYYYMDVWGKGTTVTVSS	1214
vhCDR1	GYTLTELS	1215
vhCDR2	FDPEDGET	1216
vhCDR3	ATAKPGIAVAGQNYYYYYMDV	1217
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1218
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	1219
vlCDR1	QSLLYRNGNNY	1220
vlCDR2	LGS	1221
vlCDR3	MQALQTPPT	1222
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1223

Figure 63G
CPA.7.010

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGQGTTVTVSS	1224
vhCDR1	GFTFSSYA	1225
vhCDR2	ISYDGSNK	1226
vhCDR3	ASSPIGYSYGYWGGMDV	1227
Full length HC	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1228
Variable light (vl) domain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEDEADYYCLIWHTSGWVFGGGTQLTVLG	1229
vlCDR1	SGIDVRTNK	1230
vlCDR2	FQSDSDK	1231
vlCDR3	LIWHTSGWV	1232
Full length light chain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEDEADYYCLIWHTSGWVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK ADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1233

Figure 63H
CPA.7.011

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYYMDV WGKGTTVTVSS	1234
vhCDR1	GYTLTELS	1235
vhCDR2	FDPEDGET	1236
vhCDR3	ATGPAAAGVGYYYYMDV	1237
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1238
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKR	1239
vlCDR1	QSLLYRNGYNY	1240
vlCDR2	LGS	1241
vlCDR3	MQALQTPPT	1242
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1243

Figure 63I
CPA7.012

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSS	1244
vhCDR1	GFTFSSYA	1245
vhCDR2	ISYDGSNK	1246
vhCDR3	ARDVMVYCSSTSCYFYGMDV	1247
Full length HC	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1248
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKPGKAPKLLIYDASNLEAGVPSRFSGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTRLEIKR	1249
vlCDR1	QDIRDY	1250
vlCDR2	DAS	1251
vlCDR3	QQFENLPIT	1252
Full length light chain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKPGKAPKLLIYDASNLEAGVPSRFSGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1253

Figure 63J
CPA.7.013

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYYMDV WGKGTTVTVSS	1254
vhCDR1	GYTLTELS	1255
vhCDR2	FDPEDGET	1256
vhCDR3	ATGGYSSGFNYYYYYMDV	1257
Full length HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1258
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	1259
vlCDR1	QSLLYRNGNNY	1260
vlCDR2	LGS	1261
vlCDR3	MQALQTPPT	1262
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1263

Figure 63K
CPA.7.014

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVTTYYYYGMDVWGQGTTVTVSS	1264
vhCDR1	GYTLTELS	1265
vhCDR2	FDPEDGET	1266
vhCDR3	ATGVTTYYYYGMDV	1267
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVTTYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1268
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGQGTKVEIKR	1269
vlCDR1	QSLLYSNGNNF	1270
vlCDR2	LGS	1271
vlCDR3	MQALQTPPT	1272
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1273

Figure 63L
CPA.7.015

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QITLKESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLFDFWWDGMDVWGQGTTVTVSS	1274
vhCDR1	GFTFSSYG	1275
vhCDR2	IRYDGSNK	1276
vhCDR3	ARDLFDFWWDGMDV	1277
Full length HC	QITLKESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLFDFWWDGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1278
Variable light (vl) domain	EIVLTQSPGTLSLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLLIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTKLEIKR	1279
vlCDR1	QSVSSMY	1280
vlCDR2	GAS	1281
vlCDR3	QQYVSSPMYT	1282
Full length light chain	EIVLTQSPGTLSLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLLIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1283

Figure 63M
CPA.7.017

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMAVFDYWGQGTLVTVSS	1284
vhCDR1	GGTFNNYG	1285
vhCDR2	IIPLFGTT	1286
vhCDR3	ARDRMAADGMAVFDY	1287
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMAVFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1288
Variable light (vl) domain	QSVLTQPPSVSGTPGQKVIISCSGSSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLG	1289
vlCDR1	SSNIGRHF	1290
vlCDR2	KND	1291
vlCDR3	SSWDAALNGVV	1292
Full length light chain	QSVLTQPPSVSGTPGQKVIISCSGSSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1293

Figure 63N
CPA.7.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYYYMDVWGKGTTVTVSS	1294
vhCDR1	GYTLTELS	1295
vhCDR2	FDPEDGET	1296
vhCDR3	ATEVPMVRGARRYYYYMDV	1297
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1298
Variable light (vl) domain	DVVMTQSPLFLAVTPGEPASISCRSSQTLLYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVPDRFSGGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKR	1299
vlCDR1	QTLLYINENNY	1300
vlCDR2	LGS	1301
vlCDR3	MQGLQTPPT	1302
Full length light chain	DVVMTQSPLFLAVTPGEPASISCRSSQTLLYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVPDRFSGGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1303

Figure 630
CPA.7.019

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKSSETLSLTCSVSGGSISNSNYYWGWIRQPPGKGLEWIGGIYYSGSTYYNPSLESRVTISEDTSKNQIS LKLSSVTAADTAVYYCARGAWELSLGDWFDPWGPGTLVTVSS	1304
vhCDR1	GGSISNSNYY	1305
vhCDR2	IYYSGST	1306
vhCDR3	ARGAWELSLGDWFDP	1307
Full length HC	QVQLQESGPGLVKSSETLSLTCSVSGGSISNSNYYWGWIRQPPGKGLEWIGGIYYSGSTYYNPSLESRVTISEDTSKNQIS LKLSSVTAADTAVYYCARGAWELSLGDWFDPWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1308
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLG	1309
vlCDR1	SSNIGAGYD	1310
vlCDR2	GNN	1311
vlCDR3	QSYDSSLSVYVV	1312
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1313

Figure 63P
CPA.7.021

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHYADSVKGRFTISRDNSKST VFLQMNSLRPDDTALYYCAKGSGNIYFYSGMDVWGQGTTVTVSS	1314
vhCDR1	GFTFGTSS	1315
vhCDR2	ISFDGTEI	1316
vhCDR3	AKGSGNIYFYSGMDV	1317
Full length HC	EVQLVESGGGVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHYADSVKGRFTISRDNSKST VFLQMNSLRPDDTALYYCAKGSGNIYFYSGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1318
Variable light (vl) domain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESGVPSRFSGSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKVEIKR	1319
vlCDR1	QSISGW	1320
vlCDR2	ETS	1321
vlCDR3	QQYYSYPLT	1322
Full length light chain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESGVPSRFSGSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1323

Figure 63Q
CAP.7.022

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSS	1324
vhCDR1	GYTLTELS	1325
vhCDR2	FDPEDGET	1326
vhCDR3	ATGVPAAIGVYYYYYYMDV	1327
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1328
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGTKVEIKR	1329
vlCDR1	QSLLYSNGYNY	1330
vlCDR2	LGS	1331
vlCDR3	MQALQSPVT	1332
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1333

Figure 63R
CPA.7.023

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYYYYMDVWGQGTTVTVSS	1334
vhCDR1	GYTLTELS	1335
vhCDR2	FDPEDGET	1336
vhCDR3	ATDSRDGPAARGGYYYYMDV	1337
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYYYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1338
Variable light (vl) domain	DVVMTQSPLSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKR	1339
vlCDR1	QSLLYINGYNY	1340
vlCDR2	LGS	1341
vlCDR3	MQALQTPPT	1342
Full length light chain	DVVMTQSPLSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1343

Figure 635
CPA.7.024

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSEDTAVYYCARDAYYYDSSGYYNPDAFDIWGQGTMVTVSS	1344
vhCDR1	GGTFSSYA	1345
vhCDR2	IIPIFGTA	1346
vhCDR3	ARDAYYYDSSGYYNPDAFDI	1347
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSEDTAVYYCARDAYYYDSSGYYNPDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1348
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSSRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKR	1349
vlCDR1	QSLLHSNGYNY	1350
vlCDR2	LGS	1351
vlCDR3	MQGLQTPRT	1352
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSSRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1353

Figure 63T

CPA.7.033

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1354
vhCDR1	GGTFSSSA	1355
vhCDR2	IIPIYGIT	1356
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1357
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1358
Variable light (vl) domain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAAYYFCLQHDNLPLTFGGGTKVDIKR	1359
vlCDR1	QDIDDD	1360
vlCDR2	EAS	1361
vlCDR3	LQHDNLPLT	1362
Full length light chain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAAYYFCLQHDNLPLTFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1363

Figure 63U

CPA.7.034

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYYGMDVWGQGTTVTVSS	1364
vhCDR1	GYTLTELS	1365
vhCDR2	FDPEDGET	1366
vhCDR3	ATEDPGPVAGPYYYYGMDV	1367
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1368
Variable light (vl) domain	DVVMTQSPLVLPVTPGEPASISCRSSQSLLYINGYHYLDWYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKR	1369
vlCDR1	QSLLYINGYHY	1370
vlCDR2	LGS	1371
vlCDR3	MQALQTPPT	1372
Full length light chain	DVVMTQSPLVLPVTPGEPASISCRSSQSLLYINGYHYLDWYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1373

Figure 63V

CPA.7.036

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1374
vhCDR1	GGTFSSSA	1375
vhCDR2	IIPIYGIT	1376
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1377
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1378
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASISCRPSQSLLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQRLQFPLTFGGGTKVEIKR	1379
vlCDR1	QSLLDSDDGNTY	1380
vlCDR2	TLS	1381
vlCDR3	MQRLQFPLT	1382
Full length light chain	DIVMTQTPLSLPVTPGEPASISCRPSQSLLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQRLQFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1383

Figure 63W

CPA.7.040

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSS	1384
vhCDR1	GYTLTELS	1385
vhCDR2	FDPEDGET	1386
vhCDR3	ATGVPAAIGVYYYYYYMDV	1387
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1388
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVDIKR	1389
vlCDR1	QSLLYRNGYNY	1390
vlCDR2	WGS	1391
vlCDR3	MQAVQNPPT	1392
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1393

Figure 63X

CPA.7.046

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1394
vhCDR1	GGTFSSSA	1395
vhCDR2	IIPIYGIT	1396
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1397
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1398
Variable light (vl) domain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISSV QSEDFALYYCQQYGDWLPITFGQGTRLEIKR	1399
vlCDR1	QTMNNY	1400
vlCDR2	DAS	1401
vlCDR3	QQYGDWLPIT	1402
Full length light chain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISSV QSEDFALYYCQQYGDWLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1403

Figure 63Y

CPA.7.047

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAFPEATISYYYYMDVWGKGTTVTVSS	1404
vhCDR1	GYTLTELS	1405
vhCDR2	FDPEDGET	1406
vhCDR3	ATAFPEATISYYYYMDV	1407
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAFPEATISYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1408
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVEIKR	1409
vlCDR1	QSLLYRNGYNY	1410
vlCDR2	WGS	1411
vlCDR3	MQAVQNPPT	1412
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1413

Figure 63Z

CPA.7.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1414
vhCDR1	GGTFSSSA	1415
vhCDR2	IIPIYGIT	1416
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1417
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1418
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDRFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLTFGGGTKVEIKR	1419
vlCDR1	RSLLDSDDGNTH	1420
vlCDR2	SLS	1421
vlCDR3	MQRKEFPLT	1422
Full length light chain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDRFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1423

Figure 63AA

CPA.7.050

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSS	1424
vhCDR1	GGTFSSYA	1425
vhCDR2	IIPIFGTA	1426
vhCDR3	ARGPWYYDSSGYSSYAYYMDV	1427
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1428
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKR	1429
vlCDR1	QSLLHSDGYNY	1430
vlCDR2	LGS	1431
vlCDR3	MQALHTPGVT	1432
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1433

Figure 63BB
CPA.7.028

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QLQLQESGPGLVKPSETLSLTCTVTGGSISSSSYYWAWIRQPPGKGLEWIGGIYYSGSTYYNVSLESRVTISQDTSKNQFS LKLTSVTAADTAVYYCARGAWELRLGDWFDPWGQGTLVTVSS	1434
vhCDR1	GGSISSSSYY	1435
vhCDR2	IYYSGST	1436
vhCDR3	ARGAWELRLGDWFDP	1437
Full length HC	QLQLQESGPGLVKPSETLSLTCTVTGGSISSSSYYWAWIRQPPGKGLEWIGGIYYSGSTYYNVSLESRVTISQDTSKNQFS LKLTSVTAADTAVYYCARGAWELRLGDWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1438
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAA	1439
vlCDR1	SSNIGAGYD	1440
vlCDR2	GYS	1441
vlCDR3	QSYDSSLSVYVV	1442
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1443

Figure 63CC
CPA.7.030

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLEWVSGISWKSGGINYADSVKGRFTISRDNAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNIWGQGTMVTVSS	1444
vhCDR1	RFTFEDYA	1445
vhCDR2	ISWKSGGI	1446
vhCDR3	VKDPTLVATDRAFNI	1447
Full length HC	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLEWVSGISWKSGGINYADSVKGRFTISRDNAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1448
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQYLQTPDTFGQGTKLEIKRAAPS	1449
vlCDR1	QSLLHSNGYNY	1450
vlCDR2	LGS	1451
vlCDR3	MQYLQTPDT	1452
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQYLQTPDTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1453

Figure 63DD
CPA.7.041

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1454
vhCDR1	GGTFSSSA	1455
vhCDR2	IIPIYGIT	1456
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1457
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1458
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQNIDSSLHWYQQKPGQSPKLLINYASQSFSGVPSRFSGSGSGTDFTLTIDSLEPE DAATYFCHQSSSLPLTFGGGTKVEIRRTVAAPS	1459
vlCDR1	QNIDSS	1460
vlCDR2	YAS	1461
vlCDR3	HQSSSLPLT	1462
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	1463

Figure 63EE
CPA.7.016

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKTSGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTSTA YMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1464
vhCDR1	GGTFSSSA	1465
vhCDR2	IIPIYGIT	1466
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1467
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKTSGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTSTA YMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1468
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLQSE DFAVYYCQQYDDWPQTFGQGTRLEIKRTVAAPS	1469
vlCDR1	QSVSSY	1470
vlCDR2	DAS	1471
vlCDR3	QQYDDWPQT	1472
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLQSE DFAVYYCQQYDDWPQTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1473

Figure 63FF
CPA.7.020

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDES TSTAYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1474
vhCDR1	GGTFSSSA	1475
vhCDR2	IIPIYGIT	1476
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1477
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDES TSTAYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1478
Variable light (vl) domain	EIVMTQSPATLSLSTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYYCQQRRDWPITFGQGTRLEIKRTVAAPS	1479
vlCDR1	QNVYGE	1480
vlCDR2	DTF	1481
vlCDR3	QQRRDWPIT	1482
Full length light chain	EIVMTQSPATLSLSTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYYCQQRRDWPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1483

Figure 63GG
CPA.7.038

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1484
vhCDR1	GGTFSSSA	1485
vhCDR2	IIPIYGIT	1486
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1487
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1488
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCQASRDISDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGSGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKVEIKRTVAAPS	1489
vlCDR1	RDISDS	1490
vlCDR2	DAS	1491
vlCDR3	HQYDNLPLT	1492
Full length light chain	DIQMTQSPSSLSASVGDRVTITCQASRDISDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGSGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1493

Figure 63HH
CPA.7.044

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	1494
vhCDR1	GGTFSSSA	1495
vhCDR2	IIPIYGIT	1496
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	1497
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1498
Variable light (vl) domain	EIVMTQSPATLSLSPGERATLSCRASESVTTFLAWYQQKPGQAPRLLITDASNRATGIPGRFSGSGSGTDFTLTISSLEPE DFAVYYCHQHTNWPLTFGGGTKLEIKRTVAAPS	1499
vlCDR1	ESVTTF	1500
vlCDR2	DAS	1501
vlCDR3	HQHTNWPLT	1502
Full length light chain	EIVMTQSPATLSLSPGERATLSCRASESVTTFLAWYQQKPGQAPRLLITDASNRATGIPGRFSGSGSGTDFTLTISSLEPE DFAVYYCHQHTNWPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1503

Figure 63II
CPA.7.045

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYYGMDVWGQGTTVTVSS	1504
vhCDR1	GYTLTELS	1505
vhCDR2	FDPEDGET	1506
vhCDR3	ATEVGYCSGGSCYISYYYGMDV	1507
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1508
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKLEIKRTVAAPS	1509
vlCDR1	QSLLYRNGHNF	1510
vlCDR2	LGS	1511
vlCDR3	MQALQTPPT	1512
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1513

Figure 63JJ

CHA.7.502

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLVESGGDLVQPGGSRKLSCTASGFTFSNFGMHWVRQAPEKGLEWVAYISSGS STIYYADTVKGRFTISRDNPENTLFLQMTSLRSEDTAMYYCTRLDYYTNSYSMDHWG QGTSVTVSS	1514
vhCDR1	GFTFSNFG	1515
vhCDR2	ISSGSSTI	1516
vhCDR3	TRLDYYTNSYSMDH	1517
Variable light (vl) domain	QIVLTQSPALMSASPGEKVTLTCSASSSLPYIYWYQQKPGSSPKPWIYLTSNLASGVP ARFSGSRSGTSYSLTISSVEAEDAATYYCQQWSSNPFTFGSGTKLEIK	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 SNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTSADSAVYYCALMISAWLPYWG QGTLVTVSA	1522
vhCDR1	GYTFTSNW	1523
vhCDR2	INPSNGYT	1524
vhCDR3	ALMISAWLPY	1525
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRASQSVSASSYSYVHWYQQKPGQPPKLLIKYASSLE SGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCLHTWEIPYTFGGGTKLEIK	1526
vlCDR1	QSVSASSYSY	1527
vlCDR2	YAS	1528
vlCDR3	LHTWEIPYT	1529

Figure 63LL

CHA.7.506

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELTRPGASVNLSCKASGYTFTSYWMQWVKQRPGQGLEWIGAIYPG DGDTRFNQKFKGKATLTADESSSTAYMQLSSLASEDSAVYYCATYYRYDDYWGQGT TLTVSS	1530
vhCDR1	GYTFTSYW	1531
vhCDR2	IYPGDGDT	1532
vhCDR3	ATYYRYDDY	1533
Variable light (vl) domain	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASG VPTRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK	1534
vlCDR1	SSVSY	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	DIQMTQSPASLSVSVGETVTITCRASENIFSNLAWYQQKQGKSPQLLVYGEANLAD GVPSRFSGSGSGTQYSLKINSLQSEDFGNYYCQHFWGTPYTFGGGTTLEIK	1542
vlCDR1	ENIFSN	1543
vlCDR2	GEA	1544
vlCDR3	QHFWGTPYT	1545

Figure 63NN

CHA.7.510

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

Figure 63OO

CHA.7.512

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKKPRETVKISCKASGYTFTDYSMHWVKQAPGKGLKWMGWINTETGEPTYADDFKGRFAFSLEASASSAYLQINILKDEDTATYFCARSRGGYYEDYYALDYWGQGTSVTVSS	1554
vhCDR1	GYTFTDYS	1555
vhCDR2	INTETGEP	1556
vhCDR3	ARSRGGYYEDYYALDY	1557
Variable light (vl) domain	DIQMTQSPASLSASVGESVTITCRASGNIHYYLAWYQQKQGKSPQLLVYNAKNLADGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHFWISPPTFGGGTKLEIK	1558
vlCDR1	GNIHYY	1559
vlCDR2	NAK	1560
vlCDR3	QHFWISPPT	1561

Figure 63PP

CHA.7.514

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

Figure 63QQ

CHA.7.516

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVRPGVSVKISCKVSGYTFTDYVMHWVKQSHAKSLEWIGIISPYSGNTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDSAIYYCAREGDLPMFAYWGQGTLVTVSA	1570
vhCDR1	GYTFTDYV	1571
vhCDR2	ISPYSGNT	1572
vhCDR3	AREGDLPMFAY	1573
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVSYIYWYQQNPGSSPRLLIYDTSILASGVPFRFSGSGSGTSYSLTISRMEAEDAATYYCQQWTSYPLTFGSGTKLELK	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	DIQMTQSPASLSVSVGETVTIICRVSENIYSNLAWYQQKQGKSPQLLVYEATNLAEG VPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTKLEIK	1582
vlCDR1	ENIYSN	1583
vlCDR2	EAT	1584
vlCDR3	QHFWGTPYT	1585

Figure 635S

CHA.7.520_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSG STSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARHYRYPPYAMDYWGQG TSVTVSS	1586
vhCDR1	GYSITSDYA	1587
vhCDR2	ISYSGST	1588
vhCDR3	ARHYRYPPYAMDY	1589
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKPGQSPKLLVY FASTRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	1590
vlCDR1	QSLLNSSNQKNY	1591
vlCDR2	FAS	1592
vlCDR3	QQHYSTPFT	1593

Figure 63TT

CHA.7.520_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSFGVHWVRQSPGKGLEWLGVIWSGGTTVYDAAFISRLSISKDNSKSQVFFKMNSLQTNDTAIYYCARKRGNFYVMDYWGQGTSVTVSS	1594
vhCDR1	GFSLTSFG	1595
vhCDR2	IWSGGTT	1596
vhCDR3	ARKRGNFYVMDY	1597
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	1598
vlCDR1	QSLLNSSNQKNY	1599
vlCDR2	FAS	1600
vlCDR3	QQHYSTPFT	1601

Figure 63UU

CHA.7.522

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGSELVRPGTSVKLSCKASGYTFTSYWVHWVRQRHGQGLEWIGNVYPG SGSTNYDEKFKSKGTLTVDTSSSTAYMHLSSLTSEDSAVYYCTRGVLRFPLDYWGQG TTLTVSS	1602
vhCDR1	GYTFTSYW	1603
vhCDR2	VYPGSGST	1604
vhCDR3	TRGVLRFPLDY	1605
Variable light (vl) domain	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQSPHLLIYRMS NLASGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK	1606
vlCDR1	KSLLHSNGNTY	1607
vlCDR2	RMS	1608
vlCDR3	MQHLEYPLT	1609

Figure 63VV

CHA.7.524

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPEVVRPGVSVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGIISIYSG NTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAREGDLPMFAYWGQG TLVTVSA	1610
vhCDR1	GYKFPDYV	1611
vhCDR2	ISIYSGNT	1612
vhCDR3	AREGDLPMFAY	1613
Variable light (vl) domain	QIVLTQSPAIMSASPGEKVTMTCNASSSVSYMYWYQQKPISSPRLLIYDTSNLASGV PVRFSGSGSGTSYSLTIGRMEAEDAATYYCQQWSSYPLTFGAGTKVEVK	1614
vlCDR1	SSVSY	1615
vlCDR2	DTS	1616
vlCDR3	QQWSSYPLT	1617

Figure 63WW

CHA.7.526

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLTAYNINWVRQPPGKGLEWLGMIWGDG NTDYNSPLKSRLTISKDNSKSQVFLKMDSLQTDDTARYYCARDLKVRRDSPYTMDY WGQGTSVTVSS	1618
vhCDR1	GFSLTAYN	1619
vhCDR2	IWGDGNT	1620
vhCDR3	ARDLKVRRDSPYTMDY	1621
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIY WASNRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK	1622
vlCDR1	QSVLYSSNQKNY	1623
vlCDR2	WAS	1624
vlCDR3	HQYLSSYT	1625

Figure 63XX

CHA.7.527

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLSLTCTVTGYSLTSDYAWNWIRQFPGNKLEWMGYITYSGGTTYNPSLKSRISITRDTSKNQFFLQLTSVTTEDTATYYCARRGSGTTVVGDWYFDVWGAGTTVTVSS	1626
vhCDR1	GYSLTSDYA	1627
vhCDR2	ITYSGGT	1628
vhCDR3	ARRGSGTTVVGDWYFDV	1629
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKYYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTPTISSVTAEDLAVYYCQQFYTYPYTFGGGTKLEMK	1630
vlCDR1	QSLLYSFNQKYY	1631
vlCDR2	WAS	1632
vlCDR3	QQFYTYPYT	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	DIQMTQSPASLSVSVGETVTITCRASDNIFSNLAWYHQKQGKSPHLLVYGATNLAD GVPSRFSGSGSGTQYSLKINSLQSEDFGDYYCQHFWGTPYTFGGGTKLEIK	1638
vlCDR1	DNIFSN	1639
vlCDR2	GAT	1640
vlCDR3	QHFWGTPYT	1641

Figure 63ZZ

CHA.7.530

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

Figure 63AAA

CHA.7.534

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGAELVKPGASVRLSCTASGFSIRDTYIHWVKQRPEQGLDWIGKIDPANG KSEYDPKFQGRATMTTDTSSNTAYLQLSSLTSEDTAVYYCTRYGYYPYFDVWGAGTT VTVFS	1650
vhCDR1	GFSIRDTY	1651
vhCDR2	IDPANGKS	1652
vhCDR3	TRYGYYPYFDV	1653
Variable light (vl) domain	SIVMTQTPKFLLVSAGDRVAITCKASQSVRHDVVWYQQKPGQSPKLLIYYASSRYTG VPDRFTGSGYGTDFTFTISTVQAEDLALYFCLQDFSSPWTFGGGTKLEIK	1654
vlCDR1	QSVRHD	1655
vlCDR2	YAS	1656
vlCDR3	LQDFSSPWT	1657

Figure 63BBB

CHA.7.535

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

Figure 63CCC

CHA.7.537

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLIGHGVNWIRQPPGKGLEWLGVIWGDGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDTARYFCAVNSAMDYWGQGTAVTVSS	1666
vhCDR1	GFSLIGHG	1667
vhCDR2	IWGDGNT	1668
vhCDR3	AVNSAMDY	1669
Variable light (vl) domain	NIVMTQSPKSMSMSVGERVTLNCTASENVASFVSWYQQKPEQSPKLLIYGTSNRYTGVPDRFTGSGSATDFTLTISSVQAEDLGDYHCGQSYNYPFTFGSGTKLEIE	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	QVQLQQSGAELVRPGASVKVSCKTSGYAFTNYLIEWVKQRPGQGLEWIGVINPGSG GIYYNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCARSETHDTWFAYWGQG TLVTVSA	1674
vhCDR1	GYAFTNYL	1675
vhCDR2	INPGSGGI	1676
vhCDR3	ARSETHDTWFAY	1677
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTG VPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNYPYTFGGGTKLEIKR	1678
vlCDR1	QSVRIA	1679
vlCDR2	LAS	1680
vlCDR3	LQHWNYPYT	1681

Figure 63EEE

CHA.7.538_2

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

Figure 63FFF

CHA.7.543

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

Figure 63GGG

CHA.7.544

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYAITWVRQPPGKGLEWLGVIWPGGGT NYNSALKSRLSISKDNSKSHLFLKMNSLQTDDTARYYCVRSYDGYLDWYFDVWGTG TTVTVSS	1698
vhCDR1	GFSLTSYA	1699
vhCDR2	IWPGGGT	1700
vhCDR3	VRSYDGYLDWYFDV	1701
Variable light (vl) domain	NIVMTQSPKSMSMSVGERVTLSCKASENVGTYVSWYQQKPDQSPKLLIYGASNRYT GVPDRFTGSGSATDFTLIISSVQAEDLSDYHCGQSYSYPYTFGGGTKLEII	1702
vlCDR1	ENVGTY	1703
vlCDR2	GAS	1704
vlCDR3	GQSYSYPYT	1705

Figure 63HHH

CHA.7.545

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

Figure 63III

CHA.7.546

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

Figure 63JJJ

CHA.7.547

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

Figure 63KKK

CHA.7.548

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYSMNWVKQSHGKSLEWIGDITPNNGSPNYNQKFKDKATLTVDKSSSTVYMELRSLTSEDSAVYYCASLFFDYWGHGTTLTVSS	1730
vhCDR1	GYTFTDYS	1731
vhCDR2	ITPNNGSP	1732
vhCDR3	ASLFFDY	1733
Variable light (vl) domain	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTRDSGVPDRFTGSGSGTDFTLTITSVQAEDLAVYYCQNDHTYPYTFGGGTKLEIK	1734
vlCDR1	QSLLNSGNQKNY	1735
vlCDR2	GAS	1736
vlCDR3	QNDHTYPYT	1737

Figure 63LLL

CHA.7.549

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

Figure 63MMM

CHA.7.550

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWIHWVKQRPGQGLEWIGNINPSNGGTNYNEKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVYYCARRGLPYFFDYWGQGTTLTVSS	1746
vhCDR1	GYTFTSYW	1747
vhCDR2	INPSNGGT	1748
vhCDR3	ARRGLPYFFDY	1749
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKGSQNVGYNVAWYQQKPGQSPKALVYSASDRHSGVPDRFAGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGAGTKLELK	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 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1754)

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

```
seq                10        20        30        40        50        60        70        80        90
AbM                10        20        30        40        50  a     60        70        80  abc   90
                 b b b     p   p b b b   b b   b  bi i     i ibb  b     i  b   b b b x   b b b  b     bibibb
518              EVQLQQSGPELVKPGASVKISCKAS GYTFTDYNIN WVKQSHGKSLEWIG YIYPYIGGSG YNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVYYCAR
                 *   *   * **   *         *         *  * ** **  *              *   ****  *** ***  *   *   *   *
1-46*01          QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h518H1           QVQLVQSGAEVKKPGASVKVSCKAS GYTFTDYNIN WVRQAPGQGLEWMG YIYPYIGGSG YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h518H2           QVQLVQSGAEVKKPGASVKVSCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h518H3           QVQLVQSGAEVKKPGASVKISCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAR
h518H4           QVQLVQSGAEVKKPGASVKISCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRATLTADNSTSTAYMELSSLRSEDTAVYYCAR
                                     V                   #                   N
```

```
seq              100       110       120
AbM                      110
                       i  b b b
518              EDKTARNAMDY WGQGTPVTVSS (SEQ ID NO: 1756)
                             *
h518H1           EDKTARNAMDY WGQGTLVTVSS (SEQ ID NO: 1758)
h518H2           EDKTARNAMDY WGQGTLVTVSS (SEQ ID NO: 1759)
h518H3           EDKTARNAMDY WGQGTLVTVSS (SEQ ID NO: 1760)
h518H4           EDKTARNAMDY WGQGTLVTVSS (SEQ ID NO: 1761)
                           #
```

"1-46*01" sequence is disclosed as SEQ ID NO: 1757)

deamidation substitutions: Q/S/A

Figure 63000
Humanized sequences of CHA.7.518 antibody VL

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework

IGKV1-39*01
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP (SEQ ID NO: 1762)

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (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   bi bi i    ii ibbi     i   b   b     b b b b   b     ib bib
518              DIQMTQSPASLSVSVGETVTIIC RVSENIYSNLA WYQQKQGKSPQLIVY EATNLAE GVPSRFSGSGSGTQYSLKINSLQSEDFGSYYC
                     *   *  **  *                  * * * *                  *** * * *   *   **
IGKV1-39         DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h518L1           DIQMTQSPSSLSASVGDRVTITC RVSENIYSNLA WYQQKPGKAPKLLIY EATNLAE GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h518L2           DIQMTQSPSSLSASVGDRVTITC RVSENIYSNLA WYQQKPGKAPKLLIY EATNLAE GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC
h518L3           DIQMTQSPSSLSASVGDRVTITC RVSENIYSNLA WYQQKPGKAPKLLVY EATNLAE GVPSRFSGSGSGTDYTLTISSLQPEDFGTYYC
                                          V                 # #       S         #

seq              90        100
AbM              90        100
                 ibi  iib  i   b b b
518              QHFWGTPYT EGGGTKLEIK (SEQ ID NO: 1764)
                           *

IGKV1-39         QQSYSTPP (SEQ ID NO: 1765)
h518L1           QHFWGTPYT FGQGTKLEIK (SEQ ID NO: 1766)
h518L2           QHFWGTPYT FGQGTKLEIK (SEQ ID NO: 1767)
h518L3           QHFWGTPYT FGQGTKLEIK (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
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO:
1769)
Joining region   IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1770)

seq                10        20        30        40        50        60        70        80        90
AbM                10        20        30        40        50  a     60        70        80  abc   90
                b b b     p   p b b b   b b   b  bi i    i ibb  b     i  b   b b b x   b b b  b     bibibb
538_1    QVQLQQSGAELVRPGASVKVSCKTS GYAFTNYLIE WVKQRPGQGLEWIG VINPGSGGIY YNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCAR
                   *    ***       *           * *       *              **  **** * * * *  *  ^    * * *   *
1-46*01  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5381H1  QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNYLIE WVRQAPGQGLEWMG VINPGSGGIY YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5381H2  QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h5381H3  QVQLVQSGAEVKKPGASVKVSCKTS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTLTADTSTSTAYMELSSLRSEDTAVYYCAR
h5381H4  QVQLVQSGAEVKKPGASVKVSCKTS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTLTADKSTSTAYMELSSLRSEDTAVYYCAR
                          V                   #           #  N     T                                   F
                          @

seq  100       110
AbM            110
               i  b b b
538_1    SETHDTWFAY WGQGTLVTVSA (SEQ ID NO: 1771)
                          * ("1-46*01" sequence is disclosed as SEQ ID NO: 1772)
h5381H1  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1773)
h5381H2  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1774)
h5381H3  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1775)
h5381H4  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1776)
                   @

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

Figure 63QQQ
humanized sequences of CHA.7.538_1 antibody VL

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

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

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

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   b   bi bi i   ii ibbi     i   b   b     b b b   b     ib bib
538              DIVMTQSQKFISTSVGDRVSITC KASQSVRIAVA WFQQKPGQSPKALIY LASTRHT GVPDRFTGSGSGTDFTLTISNVQSEDLADYFC
                   *    ****  *     *               *     **  *               *   *                 **  *  * * *
IGKV1-39         DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h538L1           DIQMTQSPSSLSASVGDRVTITC KASQSVRIAVA WYQQKPGKAPKLLIY LASTRHT GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h538L2           DIQMTQSPSSLSASVGDRVTITC KASQSVRIAVA WFQQKPGKAPKALIY LASTRHT GVPSRFSGSGSGTDFTLTISSVQPEDFATYYC
                                  I T                                                                   S                                                                   L   F

seq              90        100
AbM              90        100
                 ibi  iib  i   b b b
538              LQHWNYPYT FGGGTKLEIK (SEQ ID NO: 1780)
                           *
IGKV1-39         QQSYSTPP (SEQ ID NO: 1781)
h538L1           LQHWNYPYT FGQGTKLEIK (SEQ ID NO: 1782)
h538L2           LQHWNYPYT FGQGTKLEIK (SEQ ID NO: 1783)
                    @#

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

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

```
Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework
IGHV1-46*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO:
1784)
Joining region
IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1785)

seq              10        20        30        40        50        60        70        80        90
AbM              10        20        30        40        50  a     60        70        80  abc   90
                 b b b     p   p b b b   b b   b  bi i    i ibb  b     i  b   b b b x   b b b  b    bibibb
538_2    QVQLQQSGAELVRPGTSVKMSCKAA GYTFTNYWIG WVKQRPGHGLEWIG DIYPGGGYTN YNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCAS
           *     ***  *   *   *                 * *  *    *                **  * ** * *   *  *  *    *  * *   *
1-46*01  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5382H1  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTNYWIG WVRQAPGQGLEWMG DIYPGGGYTN YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5382H2  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTNYWIG WVRQAPGQGLEWIG DIYPGGGYTN YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAS
h5382H3  QVQLVQSGAEVKKPGASVKMSCKAS GYTFTNYWIG WVRQAPGQGLEWIG DIYPGGGYTN YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAS
                       V                  # @                                  # N                                 I

seq      100       110
AbM                110
                 i   b b b
538_2    PYYGSSYGFAF WGQGTLVTVSA (SEQ ID NO: 1786)
                     *           ("1-46*01" sequence is disclosed as SEQ ID NO: 1787)
h5382H1  PYYGSSYGFAF WGQGTLVTVSS (SEQ ID NO: 1788)
h5382H2  PYYGSSYGFAF WGQGTLVTVSS (SEQ ID NO: 1789)
h5382H3  PYYGSSYGFAF WGQGTLVTVSS (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 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1791)

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

```
seq              10        20        30        40        50        60        70        80        90
AbM              10        20        30        40        50  a     60        70        80  abc   90
          b b b     p     p b b b   b b    b  bi i     i ibb  b          i  b   b b b x    b b b  b     bibibb
524       QVQLQQSGPEVVRPGVSVKISCKGS GYKFPDYVMH WVKQSHAKSLEWIG IISIYSGNTN YNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAR
              *   *  **  *   *   *              * *****   *              *   * **   * * *  *    ** *   * *
1-46*01   QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h524H1    QVQLVQSGAEVKKPGASVKVSCKAS GYKFPDYVMH WVRQAPGQGLEWMG IISIYSGNTN YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h524H2    QVQLVQSGAEVKKPGASVKVSCKAS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRVTMTVDTSTSTVYMELSSLRSEDTAVYYCAR
h524H3    QVQLVQSGAEVKKPGASVKISCKGS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRATMTVDTSTSTAYMELSSLRSEDTAVYYCAR
h524H4    QVQLVQSGAEVKKPGASVKISCKGS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRATMTVDKSTSTAYMELSSLRSEDTAVYYCAR
                  V                                                       # #  N                                I
```

```
seq     100       110
AbM                   110
                  i   b b b
524       EGDLPMFAY WGQGTLVTVSA (SEQ ID NO: 1793)
                              * ("1-46*01" sequence disclosed as SEQ ID NO: 1794)
h524H1    EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1795)
h524H2    EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1796)
h524H3    EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1797)
h524H4    EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1798)
             @
```

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

RECTIFIED SHEET (RULE 91) ISA/EP

Figure 63TTT

Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework (AbM CDR definition)
IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP
(SEQ ID NO: 1799)

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (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   bi bi i    ii ibbi      i   b   b        b b b  b    ib bib
524       QIVLTQSPAIMSASPGEKVTMTC NASSSVS-YMY WYQQKPISSPRLLIY DTSNLAS GVPVRFSGSGSGTSYSLTIGRMEAEDAATYYC
          *        ** *    ** **                    ***                * *         ***   *** *  * *
IGKV3-11  EIVLTQSPATLSLSPGERATLSC RASQSVSSYLA WYQQKPGQAPRLLIY DASNRAT GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC
h524L1    EIVLTQSPATLSLSPGERATLSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC
h524L2    EIVLTQSPATLSLSPGERATLSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GIPARFSGSGSGTDYTLTISSLEPEDFAVYYC
h524L3    EIVLTQSPATLSLSPGERVTMSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GVPARFSGSGSGTDYTLTISSMEPEDFAVYYC
                    M A           #                   S         #                                  A
```

```
seq        90        100
AbM        90        100
           ibi  iib  i   b b b
524        QQWSSYPLT FGAGTKVEVK (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)
             @               V
```

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

RECTIFIED SHEET (RULE 91) ISA/EP

Figure 63UUU

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

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

seq             10        20        30        40        50        60        70        80        90
AbM             10        20        30        40        50  a     60        70        80  abc       90
         b b b     p     p b b b   b b    b  bi i     i ibb  b          i  b   b b b x    b b b  b     bibibb
530      QVQLQQSGAELMRPGTSVKVSCKAS GYAFTNHLIE WIKQRPGQGLEWIG VINPGSDSTD YNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR
             *     ***  *                      ** *       *              **  **** * * * *  *  *    * * *   *
1-46*01  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h530H1   QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WVRQAPGQGLEWMG VINPGSDSTD YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h530H2   QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WVRQAPGQGLEWIG VINPGSDSTD YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h530H3   QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WIRQAPGQGLEWIG VINPGSDSTD YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAR
h530H4   QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WIRQAPGQGLEWIG VINPGSDSTD YAQKFQGRATLTADKSTSTAYMELSSLRSEDTAVYYCAR
                 M                   #                     #         N                                   F

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

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

RECTIFIED SHEET (RULE 91) ISA/EP

Figure 63VV

```
Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework (AbM CDR definition)
IGKV1-39*01 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP (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   bi bi i   ii ibbi    i   b   b     b b b b   ib bib
530  DIQMTQSPASLSASVGETVTITC RASENIYSYLA WYQQKRGKSPQLLVY NAKTLVE GVPSRFSGSGSGTQFSLKINSLQPEDFGSYYC
               *      **                  * * * *                 * * * *     **
IGKV1-39 DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h530L1   DIQMTQSPSSLSASVGDRVTITC RASENIYSYLA WYQQKPGKAPKLLIY NAKTLVE GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h530L2   DIQMTQSPSSLSASVGDRVTITC RASENIYSYLA WYQQKPGKAPKLLVY NAKTLVE GVPSRFSGSGSGTDFTLTISSLQPEDFGTYYC
                                      #                   S         #


seq          90        100
AbM          90        100
             ibi  iib  i   b b b
530  QHHYGTPYT FGGGTKLEIK (SEQ ID NO: 1816)
                  *
IGKV1-39 QQSYSTPP          (SEQ ID NO: 1817)
h530L1   QHHYGTPYT FGQGTKLEIK (SEQ ID NO: 1818)
h530L2   QHHYGTPYT FGQGTKLEIK (SEQ ID NO: 1819)


# deamidation substitutions: Q/S/A/D
```

Figure 63WWW

What	Sequences
humanized CHA.7.518 VH h518HH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS **(SEQ ID NO: 1820)**
humanized CHA.7.518 VH h518HH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQG RVTMTADTSTSTVYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS **(SEQ ID NO: 1821)**
humanized CHA.7.518 VH h518HH3	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQG RATLTADTSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS **(SEQ ID NO: 1822)**
humanized CHA.7.518 VH h518HH4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGR ATLTADNSTSTAYMELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS **(SEQ ID NO: 1823)**
humanized CHA.7.518 VL h518HL1	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQHFWGTPYTFGQGTKLEIK **(SEQ ID NO: 1824)**
humanized CHA.7.518 VL h518HL2	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGT DYTLTISSLQPEDFATYYCQHFWGTPYTFGQGTKLEIK **(SEQ ID NO: 1825)**
humanized CHA.7.518 VL h518HL3	DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLVYEATNLAEGVPSRFSGSGSG TDYTLTISSLQPEDFGTYYCQHFWGTPYTFGQGTKLEIK **(SEQ ID NO: 1826)**

Figure 63XX

What	Sequences
humanized CHA.7.538_1 VH h5381HH1	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWMGVINPGSGGIYYAQKFQ GRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS **(SEQ ID NO: 1827)**
humanized CHA.7.538_1 VH h5381HH2	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQG RVTMTADTSTSTVYMELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS **(SEQ ID NO: 1828)**
humanized CHA.7.538_1 VH h5381HH3	QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQG RVTLTADTSTSTAYMELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS **(SEQ ID NO: 1829)**
humanized CHA.7.538_1 VH h5381HH4	QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQG RVTLTADKSTSTAYMELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS **(SEQ ID NO: 1830)**
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWYQQKPGKAPKLLIYLASTRHTGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCLQHWNYPYTFGQGTKLEIK **(SEQ ID NO: 1831)**
humanized CHA.7.538_1/538_2 VL h538HL2	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAW**F**QQKPGKAPK**AL**IYLASTRHTGVPSRFSGSGSGT DFTLTISSVQPEDFATYYCLQHWNYPYTFGQGTKLEIK **(SEQ ID NO: 1832)**

Figure 63YYY

What	Sequences
humanized CHA.7.538_2 VH h5382HH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWMGDIYPGGGYTNYAQKF QGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1833)
humanized CHA.7.538_2 VH h5382HH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQ GRVTMTADTSTSTVYMELSSLRSEDTAVYYCASPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1834)
humanized CHA.7.538_2 VH h5382HH3	QVQLVQSGAEVKKPGASVKMSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQ GRATLTADTSTSTAYMELSSLRSEDTAVYYCASPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1835)
humanized CHA.7.538_1/538_2 VL h538HL1	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWYQQKPGKAPKLLIYLASTRHTGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCLQHWNYPYTFGQGTKLEIK (SEQ ID NO: 1836)
humanized CHA.7.538_1/538_2 VL h538HL2	DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIYLASTRHTGVPSRFSGSGSGT DFTLTISSVQPEDFATYYCLQHWNYPYTFGQGTKLEIK (SEQ ID NO: 1837)

Figure 63ZZ

What	Sequences
humanized CHA.7.524 VH h524H1	QVQLVQSGAEVKKPGASVKVSCKASGYKFPDYVMHWVRQAPGQGLEWMGIISIYSGNTNYAQKFQGRV TMTRDTSTSTVYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1838)
humanized CHA.7.524 VH h524H2	QVQLVQSGAEVKKPGASVKVSCKASGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRVT MTVDTSTSTVYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1839)
humanized CHA.7.524 VH h524H3	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRAT MTVDTSTSTAYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1840)
humanized CHA.7.524 VH h524H4	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRAT MTVDKSTSTAYMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1841)
humanized CHA.7.524 VL h524L1	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPARFSGSGSGTDFTLT ISSLEPEDFAVYYCQQWSSYPLTFGQGTKLEIK (SEQ ID NO: 1842)
humanized CHA.7.524 VL h524L2	EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPARFSGSGSGTDYTL TISSLEPEDFAVYYCQQWSSYPLTFGQGTKLEIK (SEQ ID NO: 1843)
humanized CHA.7.524 VL h524L3	EIVLTQSPATLSLSPGERVTMSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGVPARFSGSGSGTDYT LTISSMEPEDFAVYYCQQWSSYPLTFGQGTKVEIK (SEQ ID NO: 1844)

Figure 63AAAA

What	Sequences
humanized CHA.7.530 VH h530H1	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWMGVINPGSDSTDYAQKFQGRV TMTRDTSTSTVYMELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1845)
humanized CHA.7.530 VH h530H2	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEW**I**GVINPGSDSTDYAQKFQGRVT MT**A**DTSTSTVYMELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1846)
humanized CHA.7.530 VH 530H3	hQVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEW**I**RQAPGQGLEW**I**GVINPGSDSTDYAQKFQGR**A**T **L**T**A**DTSTST**A**YMELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1847)
humanized CHA.7.530 VH h530H4	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSTDYAQKFQGRATL TAD**K**STSTAYMELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1848)
humanized CHA.7.530 VL h530L1	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYNAKTLVEGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQHHYGTPYTFGQGTKLEIK (SEQ ID NO: 1849)
humanized CHA.7.530 VL h530L2	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLL**V**YNAKTLVEGVPSRFSGSGSGTDF TLTISSLQPEDF**G**TYYCQHHYGTPYTFGQGTKLEIK (SEQ ID NO: 1850)