

TABLA 11: SÍNTESIS DEL LISTADO DE SECUENCIAS

SEQ ID	Descripción	Secuencia
1	Isoforma 1 de GTR humano	MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGT GTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCC TTCRHHPCCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCK PWTDCQFGFLTVPFGNKTHNAVCPGSPPAEPLGWLTVVLLA VAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDA RSCQFP EEERGERSAEEKGRLGDLWV
2	Isoforma 2 de GTR humano	MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGT GTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCC TTCRHHPCCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCK PWTDCWRCRRRPKTPEAASSPRKSGASDRQRRRGWETCGCE PGRPPGPPTAASPSPGAPQAAGALRSALGRALLPWQQKWVQEG GSDQRPGPCSSAAAAGPCRRERETQSWPPSSLAGPDGVGS
3	Isoforma 3 de GTR humano	MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGT GTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCC TTCRHHPCCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCK PWTDCQFGFLTVPFGNKTHNAVCPGSPPAEPLGWLTVVLLA VAACVLLLTSAQLGLHIWQLRKTQLLLEVPPSTEDARSCQFPE EERGERSAEEKGRLGDLWV
4	GTR humano (maduro)	QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCS EWDCMCVQPEFHCGDPCCCTTCRHHPCCPPGQGVQSQGKFSFGFQ CIDCASGTFSGGHEGHCKPWTDCQFGFLTVPFGNKTHNAVCP PGSPPAEP
5	GTR de <i>Macaca fascicularis</i>	MCASGTLCCALLCAASLGQRPTGGPGCGPGRLLLGTGKDARC CRVHPTTRCCRDYQGECCSEWDCVCVQPEFHCGNPCCTTCQHH PCPSGQGVQPQKGKFSFGFRCDALGTFSRGHDGHCKPWTDCQ QFGFLTVPFGNKTHNAVCPGSPPAEPPGWLTIIILLAVAACVL LLTSAQLGLHIWQLRSQPTGPRETQLLLEVPPSTEDASSCQFP EEERGERLAEEKGRLGDLWV
6	GTR-L humano	MTLHPSPIITCEFLFSTALISPKMCLSHLENMPLSHSRTQGAQR SSWKLWLFCSIVMLLFLCSFSWLIFIFLQLETAKEPCMAKFGP LPSKWQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANY NDVAPFEVRLYKNKDMIQTLTNKSQI QNVGGTYELHVGDTIDL IFNSEHQVLKNNTYWGIIILLANPQFIS
7	Dominio constante de IgG1 humana	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSR ~~E~~ EMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
8	Dominio constante de IgG1 humana (variante alotípica)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSR ~~E~~ DELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
9	Dominio constante de IgG1 humana con mutaciones L234A, L235E y G237A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKRVKPKSCDKTHTCPPCPAEP AEGAPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE

		VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
10	Dominio constante de IgG1 humana con mutaciones A330S y P331S	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPSSIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
11	Dominio constante de IgG1.1 humana (mutaciones L234A, L235E, G237A, A330S y P331S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKRVKPKSCDKTHTCPPCPAEEGAPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPG
12	Región constante de la cadena liviana kappa de IgG1 humana (CL)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC
13	28F3 (VH)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAWIWYEGSNKYYADSVKGRFTISRDNKNTLYLQMNSL RAEDTAVYYCARGGSMVRGDYYYGMDVWGQGTITVTVSS
14	28F3 (VL)	AIQLTQSPSSLSASVGDRTITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPYTFGQGTKLEIK
15	28F3 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAWIWYEGSNKYYADSVKGRFTISRDNKNTLYLQMNSL RAEDTAVYYCARGGSMVRGDYYYGMDVWGQGTITVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSN TKVDKTVKRCCKVECPCCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNHYTQKSLSLSPGK
16	28F3 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	AIQLTQSPSSLSASVGDRTITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY YSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
17	28F3.IgG1 (VH + IgG1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAWIWYEGSNKYYADSVKGRFTISRDNKNTLYLQMNSL RAEDTAVYYCARGGSMVRGDYYYGMDVWGQGTITVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSN TKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE

		WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPG
18	28F3.IgG1.1 (VH + IgG1.1)	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVIWIYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGDY YYGMDVWGQGT TTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVPEPKSCDKTHTCPPCPAPEAEAGAPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVHLQDNLNGKEYKCKVSNKALPSSIEKTI S KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPG
19	28F3.IgG1 (VL + CL)	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
20	28F3 VH CDR1	SYGMH
21	28F3 VH CDR2	VIWYEGSNKYYADSVKG
22	28F3 VH CDR3	GGSMVRGDY YYGMDV
23	28F3 VL CDR1	RASQGISSALA
24	28F3 VL CDR2	DASSLES
25	28F3 VL CDR3	QQFNSYPYT
26	19D3 (VH)	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYGFHWVRQAPGK GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSS
27	19D3 (VL)	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQQYNSYPYTFGQGT KLEIK
28	19D3 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYGFHWVRQAPGK GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNT KVDKTKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQFNST FRVSVSLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MEALHNHYTQKSLSLSPGK
29	19D3 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
30	19D3.IgG1 (VH + IgG1)	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYGFHWVRQAPGK GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKRVPEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ

		PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
44	18E10.IgG1.1 (VH + IgG1.1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVIWYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGRIAVAFYYSM DVWGQGT TTVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSG VHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNT KVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
45	18E10.IgG1 (VL + CL)	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATY YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
46	18E10 VH CDR1	SYGMH
47	18E10 VH CDR2	VIWYAGSNKYYADSVKG
48	18E10 VH CDR3	GGRIAVAFYYSM DV
49	18E10 VL CDR1	RASQGISSWLA
50	18E10 VL CDR2	AASSLQS
51	18E10 VL CDR3	QQYNSYPYT
52	3C3 (VH)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDI WGQGTMTVTVSS
53	3C3 (VL1)	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATY YCQQYNSYPYTFGQGTKLEIK
54	3C3 (VL2)	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGPGTDFTLTIS SLEPEDFAVY YCQQRSNWHTFGQGTKLEIK
55	3C3 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDI WGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTKVDKR VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGK
56	3C3 L1 (cadena liviana 1 de tipo silvestre de longitud completa) La región constante está subrayada	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATY YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
57	3C3 L2 (cadena liviana 2 de tipo silvestre de longitud	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGPGTDFTLTIS SLEPEDFAVY

	completa) La región constante está subrayada	<u>YCQQRSNWHTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTA</u> <u>SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY</u> <u>SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC</u>
58	3C3.IgG1 (VH + IgG1)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
59	3C3.IgG1.1 (VH + IgG1.1)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPG
60	3C3.IgG1 (VL1 + CL)	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
61	3C3IgG1.2 (VL2 + CL)	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGPGTDFTLTISLQPEDFAVY YCQQRSNWHTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
62	3C3 VH CDR1	GYWT
63	3C3 VH CDR2	KINHSGNTNYPNPSLKS
64	3C3 VH CDR3	LGAFDAFDI
65	3C3 VL1 CDR1	RASQGISSWLA
66	3C3 VL1 CDR2	AASSLQS
67	3C3 VL1 CDR3	QQYNSYPYT
68	3C3 VL2 CDR1	RASQGVSSYLA
69	3C3 VL2 CDR2	DASNRAT
70	3C3 VL2 CDR3	QQRSNWHT
71	2G6 (VH)	QVQLVESGGGVVQPGGSLRLSCAASGFI ¹ LSDYGMHWVRQAPGK GLEWTVI ² WYDGSNKFYVDSVKGRFTISRDN ³ SKNTLYLQMN ⁴ SL RVEDTAVYYCARGRLATGHFY ⁵ YVMDVWGQGT ⁶ TVTVSS
72	2G6 (VL)	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPYTFGQGTKLEIK
73	2G6 (cadena pesada de tipo silvestre de longitud completa)	QVQLVESGGGVVQPGGSLRLSCAASGFI ¹ LSDYGMHWVRQAPGK GLEWTVI ² WYDGSNKFYVDSVKGRFTISRDN ³ SKNTLYLQMN ⁴ SL RVEDTAVYYCARGRLATGHFY ⁵ YVMDVWGQGT ⁶ TVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS

	La región constante está subrayada	<u>GVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSN</u> <u>TKVDKTVERKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVVSVLTIVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFS</u> <u>MHEALHNHYTQKSLSLSPGK</u>
74	2G6 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	<u>DIQMTQSPSSLSASVGDRVTITCRASQGIISSWLAWYQQKPEKA</u> <u>PKSLIYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATY</u> <u>YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT</u> <u>ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST</u> <u>YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC</u>
75	2G6.IgG1 (VH + IgG1)	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI</u> LSDYGMHWVRQAPGK GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL RVEDTAVYYCARGRLATGHFYVMDVWGQGTTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
76	2G6.IgG1.1 (VH + IgG1.1)	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI</u> LSDYGMHWVRQAPGK GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL RVEDTAVYYCARGRLATGHFYVMDVWGQGTTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTL MISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
77	2G6.IgG1 (VL + CL)	<u>DIQMTQSPSSLSASVGDRVTITCRASQGIISSWLAWYQQKPEKA</u> <u>PKSLIYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATY</u> <u>YCQQYNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT</u> <u>ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST</u> <u>YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC</u>
78	2G6 VH CDR1	DYGMH
79	2G6 VH CDR2	VIWYDGSNKFYVDSVKG
80	2G6 VH CDR3	GGRLATGHFYVMDV
81	2G6 VL CDR1	RASQGIISSWLA
82	2G6 VL CDR2	AASSLQS
83	2G6 VL CDR3	QQYNSYPYT
84	8A6 (VH)	<u>QVQLVESGGGVVQGRSLRLSCTASGFTFSSYGMQWVRQAPGK</u> GLEWVAVIWYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGTTVTVSS
85	8A6 (VL)	<u>AIQLTQSPSSLSASVGDRVTITCRASQGIISSALAWYQQKPGKA</u> <u>PKFLIYDASSLESGVPSRFRSGSGSGTDFTLTISLQPEDFATY</u> <u>YCQQFNSYPYTFGQGTKLEIK</u>
86	8A6 (cadena pesada de tipo silvestre de longitud	<u>QVQLVESGGGVVQGRSLRLSCTASGFTFSSYGMQWVRQAPGK</u> GLEWVAVIWYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGTTVTVSSASTKG

	completa) La región constante está subrayada	<u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTV ERKCCVECP PCPAPPVAGPSVFLFPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TRFVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV</u> <u>MHEALHNHYTQKSLSLSPGK</u>
87	8A6 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	<u>AIQLTQSPSSLSASVGDRVTITCRASQG ISSALAWYQQKPGKA</u> <u>PKFLIYDASSLESGVPSRFSGSGSGTDFTLT ISSLQPEDFATY</u> <u>YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT</u> <u>ASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST</u> <u>YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC</u>
88	8A6.IgG1 (VH + IgG1)	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGMQWVRQAPGK GLEWVAVIWIYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPG
89	8A6.IgG1.1 (VH + IgG1.1)	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGMQWVRQAPGK GLEWVAVIWIYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPG
90	8A6.IgG1 (VL + CL)	AIQLTQSPSSLSASVGDRVTITCRASQG ISSALAWYQQKPGKA PKFLIYDASSLESGVPSRFSGSGSGTDFTLT ISSLQPEDFATY YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
91	8A6 VH CDR1	SYGMQ
92	8A6 VH CDR2	VIWIYEGSNKYYADSVKG
93	8A6 VH CDR3	GGLMVRGLFYYGMDV
94	8A6 VL CDR1	RASQGISSALA
95	8A6 VL CDR2	DASSLES
96	8A6 VL CDR3	QQFNSYPYT
97	9G7 (VH)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSTVTVSS
98	9G7 (VL1)	EIVLTQSPGTL SLPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPWTFGQGTKVEIK
99	9G7 (VL2)	EIVLTQSPGTL SLPGERATLSCRASQSVTSSSYLAWYQQKPGQ APRLLIYGASSRATGIPERFSGSGSGTDFTLTISRLEPEDFAV

		YYCQQYGSSPITFGQGTRLEIK
100	9G7 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	EVQLVESGGGLV ^K PGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTE ^D TAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLG ^T KTYTCNV ^D HKPS NTKVDKR ^V ESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK ^T ISK ^A KGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC SVMHEALHNHYTQKSLSLSLGK
101	9G7 L2 (cadena liviana 2 de tipo silvestre de longitud completa) La región constante está subrayada	EIVLTQSPGTLSLSPGERATLSCRASQSVTSSYLAWYQQKPGQ APRLLIYGASSRATGIPERFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
102	9G7.IgG1 (VH + IgG1)	EVQLVESGGGLV ^K PGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTE ^D TAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLG ^T QTYICNVN ^H KPS NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMI ^S RTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK ^T I SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
103	9G7.IgG1.1 (VH + IgG1.1)	EVQLVESGGGLV ^K PGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTE ^D TAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLG ^T QTYICNVN ^H KPS NTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDT LMI ^S RTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEK ^T I SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
104	9G7.IgG1 (VL1 + CL)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
105	9G7.IgG1.2 (VL2 + CL)	EIVLTQSPGTLSLSPGERATLSCRASQSVTSSYLAWYQQKPGQ APRLLIYGASSRATGIPERFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
106	9G7 VH CDR1	TVWMS
107	9G7 VH CDR2	RIKSKTDGGTTDYAAPVKG
108	9G7 VH CDR3	GQLIPYSYYYGMDV
109	9G7 VL1 CDR1	RASQSVSSSYLA
110	9G7 VL1 CDR2	GASSRAT

111	9G7 VL1 CDR3	QQYGSSPWT
112	9G7 VL2 CDR1	RASQSVTSSYLA
113	9G7 VL2 CDR2	GASSRAT
114	9G7 VL2 CDR3	QQYGSSPIT
115	14E3 (VH)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSS
116	14E3 (VL)	DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPPTFGQGTKVEIK
117	14E3 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGK
118	14E3 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
119	14E3.IgG1 (VH + IgG1)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
120	14E3.IgG1.1 (VH + IgG1.1)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPG
121	14E3.IgG1 (VL + CL)	DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYNSYPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
122	14E3 VH CDR1	GYYS

123	14E3 VH CDR2	EINHSGNTYYNP ~~SLKS~~
124	14E3 VH CDR3	FGSND ~~AFDI~~
125	14E3 VL CDR1	RASQGISS ~~WLA~~
126	14E3 VL CDR2	AASSL ~~QS~~
127	14E3 VL CDR3	QQYNSYP ~~PT~~
128	19H8 (VH)	QVQLVESGGGVVQPG ~~RS~~ LRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDN ~~SKNSLSLQMN~~ SL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGT ~~TVTVSS~~
129	19H8 (VL1)	AIQLTQSPSSLSASV ~~GDRVTITCRASQGISSALAWYQQKPGKA~~ PKFLIYDASSLESGVPSR ~~FSGSGSGTDFTLT~~ ISSLQPEDFATY YCQQFNSYPQT ~~FGQGTKVEIK~~
130	19H8 (VL2)	EIVLTQSPATLSLSPGERATLSC ~~RASQSVSSYLAWYQQKPGQA~~ PRLLIYDASNRATGIPAR ~~FSGSGSGTDFTLT~~ ISSLEPEDFAVY YCQQRSNWPLT ~~FGGGTKVEIK~~
131	19H8 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLVESGGGVVQPG ~~RS~~ LRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDN ~~SKNSLSLQMN~~ SL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGT ~~TVTVSSASTKG~~ PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT ~~SVNSGALTS~~ GVHTFPAVLQSSGLYSLSSVTV ~~PSSNFGTQTYTCNV~~ DHKPSN TKVDKTV ~~ERKCCVECP~~ PCPAPPVAGPSVFLFP ~~PKPKD~~ TL ~~MISR~~ TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA ~~TKPREEQFNS~~ TFRVVS ~~VLTVVHQDLN~~ GKEYKCKVSNKGLPAPIE ~~KTISK~~ TKG QPREPQVYTLPPSREEMTKN ~~QVSLTCLVKGFYPSDIAVEWESN~~ GQPENNYK ~~TTTPMLDS~~ DGSFFLYSKLTVDKSRW ~~QQGNVF~~ FSCSV MHEALHNHYTQKSLSLSPGK
132	19H8 L1 (cadena liviana 1 de tipo silvestre de longitud completa) La región constante está subrayada	AIQLTQSPSSLSASV ~~GDRVTITCRASQGISSALAWYQQKPGKA~~ PKFLIYDASSLESGVPSR ~~FSGSGSGTDFTLT~~ ISSLQPEDFATY YCQQFNSYPQT ~~FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT~~ ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK ~~DST~~ YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
133	19H8 L2 (cadena liviana 2 de tipo silvestre de longitud completa)	EIVLTQSPATLSLSPGERATLSC ~~RASQSVSSYLAWYQQKPGQA~~ PRLLIYDASNRATGIPAR ~~FSGSGSGTDFTLT~~ ISSLEPEDFAVY YCQQRSNWPLT ~~FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT~~ ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK ~~DST~~ YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
134	19H8.IgG1 (VH + IgG1)	QVQLVESGGGVVQPG ~~RS~~ LRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDN ~~SKNSLSLQMN~~ SL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGT ~~TVTVSSASTKG~~ PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT ~~SVNSGALTS~~ GVHTFPAVLQSSGLYSLSSVTV ~~PSSSLGTQTYICNV~~ NHKPSN TKVDKRVEPKSCDKTHTCP ~~PCPAPELLGGPSVFLF~~ PPKPKD ~~TL~~ MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNA ~~TKPREEQYN~~ STYRVVSVLTVLHQDLN ~~GKEYKCKV~~ SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN ~~QVSLT~~ CLVKGFYPSDIAVEWESNGQPENNYK ~~TTTPVLDSDGSFFLYSK~~ LTVDKSRWQ ~~QGNVF~~ FSCVMHEALHNHYTQKSLSLSPG
135	19H8.IgG1.1 (VH + IgG1.1)	QVQLVESGGGVVQPG ~~RS~~ LRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDN ~~SKNSLSLQMN~~ SL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGT ~~TVTVSSASTKG~~ PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT ~~SVNSGALTS~~ GVHTFPAVLQSSGLYSLSSVTV ~~PSSSLGTQTYICNV~~ NHKPSN TKVDKRVEPKSCDKTHTCP ~~PCPAEAGAPSVFLFP~~ PKPKD ~~TL~~ MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA ~~TKPREE~~ QYNSTYRVVSVLTVLHQDLN ~~GKEYKCKVSNKALPSSIEKTIS~~

		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV SCSVMHEALHNHYTQKSLSLSPG
136	19H8.IgG1 (VL1 + CL)	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKA PKFLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPQTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
137	19H8.IgG1.2 (VL2 + CL)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGSGTDFTLTISLQPEDFAVY YCQQRSNWPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
138	19H8 VH CDR1	NYGMH
139	19H8 VH CDR2	VIWYGGSNKFYADSVKG
140	19H8 VH CDR3	GGAMVRGVYYYGMDV
141	19H8 VL1 CDR1	RASQGISSALA
142	19H8 VL1 CDR2	DASSLES
143	19H8 VL1 CDR3	QQFNSYPQT
144	19H8 VL2 CDR1	RASQSVSSYLA
145	19H8 VL2 CDR2	DASNRAT
146	19H8 VL2 CDR3	QQRSNWPLT
147	Secuencia de nucleótidos de 28F3 (VH)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGAAGGAAGTAATA AATATTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGGA GTATGGTTCGGGGGGACTACTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA
148	Secuencia de nucleótidos de 28F3 (VL)	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGCTCCTGATCTATGATGCCTCCAGTTTGAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACTTAT TACTGTCAACAGTTTAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAA
149	Secuencia de nucleótidos de 28F3 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGAAGGAAGTAATA AATATTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGGA GTATGGTTCGGGGGGACTACTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGC <u>CCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG</u> <u>AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC</u> <u>CGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCTCTGACCAGC</u> <u>GGCGTGCACACCTTCCCAGCTGTCTTACAGTCTCAGGACTCT</u> <u>ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGG</u> <u>CACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC</u> <u>ACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGTCAGT</u>

		<u>GCCCACCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTT</u> <u>CCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGG</u> <u>ACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAG</u> <u>ACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGT</u> <u>GCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC</u> <u>ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT</u> <u>GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGG</u> <u>CCTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG</u> <u>CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG</u> <u>AGGAGATGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAA</u> <u>AGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT</u> <u>GGGCAGCCGGAGAACAATAACAAGACCACACCTCCCATGCTGG</u> <u>ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGA</u> <u>CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG</u> <u>ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT</u> <u>CCCTGTCTCCGGGTAAA</u>
150	Secuencia de nucleótidos de 28F3 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	<u>GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG</u> <u>TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT</u> <u>TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT</u> <u>CCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGG</u> <u>TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC</u> <u>TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT</u> <u>TACTGTCAACAGTTTAAATAGTTACCCGTACACTTTTGGCCAGG</u> <u>GGACCAAGCTGGAGATCAAACGAAGTGTGGCTGCACCATCTGT</u> <u>CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT</u> <u>GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG</u> <u>CCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA</u> <u>CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC</u> <u>TACAGCCTCAGCAGCACCCGTGACGCTGAGCAAAGCAGACTACG</u> <u>AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT</u> <u>GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</u>
151	Secuencia de nucleótidos de 28F3.IgG1 (VH + IgG1)	caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct ccaggcaagg ggtctggagt ggtggcagtt atatggtatg aaggaagtaa taaatattat gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggg agtatggttc ggggggacta ctactacggt atggacgtct ggggccaagg gaccacggtc accgtctcct cagctagcac caagggccca tcggtcttcc ccctggcacc ctocctocaag agcacctctg ggggcacagc ggccctgggc tgccctggta aggactactt ccccgaaccg gtgacggtgt cgtggaaactc aggcgcacctg accagcggcg tgcacacctt cccggtctgc ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag agagttgagc ccaaactctg tgacaaaact cacacatgcc caccgtgcc agcactgaa ctcctggggg gaccgtcagt ctctctctc ccccaaaac ccaaggacac cctcatgata tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggctc tccaacaaag ccctcccagc ccccatcgag aaaacctct ccaagccaa

		agggcagccc cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtttctat ccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tccccgggtt ga
152	Secuencia de nucleótidos de 28F3.IgG1.1 (VH + IgG1.1)	caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggagggtc cctgagactc tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct ccaggcaagg ggtggagtg ggtggcagtt atatggtag aaggaagtaa taaatattat gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggg agtatggttc ggggggacta ctactacggt atggacgtct gggggccaagg gaccacggtc accgtctcct cagctagcac caagggccca tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc tgctgggtca aggactactt ccccgaaccg gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag agagttgagc ccaaactctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa gccgaagggg ccccgctcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga cctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccaag cagcatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtttctat ccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tccccgggtt ga
153	Secuencia de nucleótidos de 28F3.IgG1 (VL + CL)	gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc atcacttgcc gggcaagtca gggcattagc agtgcttttag cctgggtatca gcagaaacca gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaagtggt ggtcccatca aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct gaagattttg caacttatta ctgtcaacag tttaatatgtt acccgtacac ttttggccag gggaccaagc tggagatcaa acgtacgggtg gctgcaccat ctgtcttcat cttcccgcc tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac agcacctaca

		gcctcagcag caccctgacg ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtag
154	Secuencia de nucleótidos de 19D3 (VH)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAACCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTT CAGTAGCTATGGCTTCCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGCTGGAAGTAATA AATTCTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTA AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGAC AGTTGGACTACTACTATTACGTTATGGACGTCTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
155	Secuencia de nucleótidos de 19D3 (VL)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAA
156	Secuencia de nucleótidos de 19D3 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAACCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTT CAGTAGCTATGGCTTCCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGCTGGAAGTAATA AATTCTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTA AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGAC AGTTGGACTACTACTATTACGTTATGGACGTCTGGGGCCA AGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCCA TCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCAGCTCCGAGA GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGA ACCGGTGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGC GTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACT CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGGCAC CCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCC CACCGTGCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCT CTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACC CCTGAGGTACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACG TTCCGTGTGGTCAGCGTCCTCACC GTTGTGCACCAGGACTGGC TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCT CCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAGGGCAG CCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGG AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG CTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAATAACAAGACCACACCTCCCATTGCTGGACT CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC TGTCTCCGGGTAAA
157	Secuencia de nucleótidos de 19D3 (cadena liviana de tipo silvestre de longitud	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG

	completa) La secuencia que codifica la región constante está subrayada	<u>TCCCATCAAGGTT</u> <u>CAGCGGCAGTGGATCTGGGACAGATTT</u> <u>CAC</u> <u>TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT</u> <u>TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGGCCAGG</u> <u>GGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGT</u> <u>CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA</u> <u>ACT</u> <u>GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG</u> <u>CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAA</u> <u>CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC</u> <u>TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACG</u> <u>AGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCT</u> <u>GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</u>
158	Secuencia de nucleótidos de 18E10 (VH)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGCTGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGGC GTATAGCAGTGGCCTTCTACTACAGTATGGACGTCTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
159	Secuencia de nucleótidos de 18E10 (VL)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTGCGGGCAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGG TCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGATTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGGCCAGG GGACCAAGCTGGAGATCAAA
160	Secuencia de nucleótidos de 18E10 (cadena pesada de tipo silvestre de longitud completa)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGCTGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGGC GTATAGCAGTGGCCTTCTACTACAGTATGGACGTCTGGGGCCA AGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGA GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGA ACCGGTGACGGTGTCTGGAAGTCAAGGCGCTCTGACCAGCGGC GTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACT CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGGCAC CCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC AAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGTGCC CACCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCT CTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC CCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGAGGTGCA TAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAGC TTCCGTGTGGTCAAGCTCCTCACC GTTGTGCACCAAGGACTGGC TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCT CCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGGCAG CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGG AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG CTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACCTACAAGACCACACCTCCCATGCTGGACT CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA

		<u>GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG</u> <u>CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC</u> <u>TGTCTCCGGGTAAA</u>
161	Secuencia de nucleótidos de 18E10 (cadena liviana de tipo silvestre de longitud completa)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
162	Secuencia de nucleótidos de 3C3 (VH)	CAGGTGCAACTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCTT CAGTGGTTACTACTGGACCTGGATCCGCCAGCCCCCAGGGAAG GGGCTGGAGTGGATTGGGAAAATCAATCATAGTGGAACACCA ACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCCGCGGACACGGCTGTGTATTACTGTGCGAGACTGGGGGCCT TTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCA
163	Secuencia de nucleótidos de 3C3 (VL1)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAA
164	Secuencia de nucleótidos de 3C3 (VL2)	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGT TAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT CCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCA TCCCAGCCAGGTTTCAGTGGCAGTGGGCCTGGGACAGACTTCAC TCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGAGTTTAT TACTGTCAGCAGCGTAGCAACTGGCACACTTTTGCCAGGGGA CCAAGCTGGAGATCAAA
165	Secuencia de nucleótidos de 3C3 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAACTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCTT CAGTGGTTACTACTGGACCTGGATCCGCCAGCCCCCAGGGAAG GGGCTGGAGTGGATTGGGAAAATCAATCATAGTGGAACACCA ACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCCGCGGACACGGCTGTGTATTACTGTGCGAGACTGGGGGCCT TTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA

		<u>CGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT</u> <u>GAGCCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCC</u> <u>CAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCC</u> <u>CCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG</u> <u>GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG</u> <u>TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC</u> <u>CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT</u> <u>GTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATG</u> <u>GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGC</u> <u>CCCCATCGAGAAAACCATCTCCAAGCCAAAGGCCAGCCCCGA</u> <u>GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGTGA</u> <u>CCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA</u> <u>TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG</u> <u>GAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG</u> <u>GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAG</u> <u>GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG</u> <u>GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTC</u> <u>CGGGTAAA</u>
166	Secuencia de nucleótidos de 3C3 L1 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	<u>GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG</u> <u>TAGGAGACAGAGTCACCATCACTTGTGCGGGCAGTCAGGGTAT</u> <u>TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC</u> <u>CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGG</u> <u>TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC</u> <u>TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT</u> <u>TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGGCCAGG</u> <u>GGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGT</u> <u>CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC</u> <u>GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG</u> <u>CCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA</u> <u>CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC</u> <u>TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACG</u> <u>AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT</u> <u>GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</u>
167	Secuencia de nucleótidos de 3C3 L2 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	<u>GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTC</u> <u>CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGT</u> <u>TAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT</u> <u>CCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCA</u> <u>TCCCAGCCAGGTTTCAGTGGCAGTGGGCCTGGGACAGACTTCAC</u> <u>TCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTAT</u> <u>TACTGTCAGCAGCGTAGCAACTGGCACACTTTTGGCCAGGGGA</u> <u>CCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTT</u> <u>CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACGCC</u> <u>TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCA</u> <u>AAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTC</u> <u>CCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTAC</u> <u>AGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGA</u> <u>AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG</u> <u>CTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</u>
168	Secuencia de nucleótidos de 2G6 (VH)	<u>CAGGTTACAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG</u> <u>GGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTTCATCTT</u> <u>GAGTGACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG</u> <u>GGACTGGAGTGGGTGACAGTTATCTGGTATGATGGAAGTAATA</u> <u>AATTCTATGTAGACTCCGTGAAGGGCCGATTACCATCTCCAG</u> <u>AGACAATTCCAAGAACACGTTGTATCTGCAAATGAACAGCCTG</u> <u>AGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGAC</u> <u>GTCTAGCAACAGGTCACCTTCTACTACGTTATGGACGTCTGGGG</u> <u>CCAAGGGACCACGGTCACCGTCTCCTCA</u>

169	Secuencia de nucleótidos de 2G6 (VL)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGGCCAGG GGACCAAGCTGGAGATCAAA
170	Secuencia de nucleótidos de 2G6 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTTTCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTTCATCTT GAGTGACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGACTGGAGTGGGTGACAGTTATCTGGTATGATGGAAGTAATA AATTCTATGTAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGTTGTATCTGCAAATGAACAGCCTG AGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGAC GTCTAGCAACAGGTCACCTTCTACTACGTTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCAGGTGACGGTGTCTGTGGAAGTCAAGGCGCTCTGACCAGC GGCGTGCACACCTTCCCAGCTGTCTTACAGTCTCAGGACTCT ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGG CACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC ACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGT GCCCACCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTT CCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCCG ACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAG ACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCACGGGAGGAGAGCTTCAACAGC ACGTTCCGTGTGGTCAGCGTCCTCACCCTTGTGCACCAAGGACT GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGG CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCCGGG AGGAGATGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAA AGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACCTACAAGACCACACCTCCCATGCTGG ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT CCCTGTCTCCGGGTAAA
171	Secuencia de nucleótidos de 2G6 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCGTACACTTTTGGCCAGG GGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
172	Secuencia de nucleótidos de	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTT

	8A6 (VH)	CAGTAGCTATGGCATGCAGTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGAAGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGAAAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCGGTC TTATGGTTCCGGGTCTCTTCTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCAC CGTCTCCTCA
173	Secuencia de nucleótidos de 8A6 (VL)	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGTTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGG TCCCATCAAGGTTTACGCGGCAGTGGATCTGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGTCAACAGTTTAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAA
174	Secuencia de nucleótidos de 8A6 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTT CAGTAGCTATGGCATGCAGTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGAAGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGAAAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCGGTC TTATGGTTCCGGGTCTCTTCTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGC GGCGTGCACACCTTCCCAGCTGTCTTACAGTCTCAGGACTCT ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGG CAGCCAGACCTACACCTGCAACGTAGATCACAAGCCCAAGAAC ACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGT GCCCACCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTT CCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTACAGTGCCTGGTGGTGGACGTGAGCCACGAAG ACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGG CCTCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAA AGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAATAAGACCACACCTCCCATGCTGG ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT CCCTGTCTCCGGGTAAA
175	Secuencia de nucleótidos de 8A6 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGTTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGG TCCCATCAAGGTTTACGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGTCAACAGTTTAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAACGAAGTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGG

		<u>CCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA</u> <u>CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC</u> <u>TACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACG</u> <u>AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT</u> <u>GAGCTCGCCCCGTACAAAAGAGCTTCAACAGGGGAGAGTGT</u>
176	Secuencia de nucleótidos de 9G7 (VH)	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTAAAGCCTG GGGGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTT CAGTACCGTCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTGGCCGTATTAAAAGCAAACTGATGGTG GGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACCAT CTCAAGAGATGATTCAAAAAACACGCTGTATCTGCAAATGAAC AGCCTGCACACCGAGGACACAGCCGTGTATTACTGTACCACAG GGCAGCTGATCCCTTACTCCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCTCGGT CACCGTCTCCTCA
177	Secuencia de nucleótidos de 9G7 (VL1)	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCC AAGGGACCAAGGTGGAATCAAA
178	Secuencia de nucleótidos de 9G7 (VL2)	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TACCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGAGAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCACCGATCACCTTCGGCC AAGGGACACGACTGGAGATTAAA
179	Secuencia de nucleótidos de 9G7 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTAAAGCCTG GGGGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTT CAGTACCGTCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTGGCCGTATTAAAAGCAAACTGATGGTG GGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACCAT CTCAAGAGATGATTCAAAAAACACGCTGTATCTGCAAATGAAC AGCCTGCACACCGAGGACACAGCCGTGTATTACTGTACCACAG GGCAGCTGATCCCTTACTCCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCTCGGTACCGTCTCCTCAGCTTCCACCAAG <u>GGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCT</u> <u>CCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTT</u> <u>CCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACC</u> <u>AGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGAC</u> <u>TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT</u> GGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGC AACACCAAGGTGGACAAGAGAGTTGAGTCCAAATATGGTCCCC CATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATC AGTCTTCCTGTTCCCCCAAAACCAAGGACACTCTCATGATC TCCCGGACCCCTGAGGTACGTGCGTGGTGGTGAGCGTGAGCC AGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGT GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTT AACAGCACGTACCGTGTGGTCAGCGTCCTACCGTCTCTGCACC AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAA CAAAGGCCTCCCGTCTCTCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCAT CCCAGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCT GGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAG

		<u>AGCAATGGGCAGCCGGAGAACAAC</u> <u>TACAAGACCACGCCTCCCG</u> <u>TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAAC</u> <u>CGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGC</u> <u>TCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGA</u> <u>GCCTCTCCCTGTCTCTGGGTAAA</u>
180	Secuencia de nucleótidos de 9G7 L2 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TACCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGAGAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCACCGATCACCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATC TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACT ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCCGTACAAAGAGCTTCAACAGGGGAGAGTGT
181	Secuencia de nucleótidos de 9G7 L1 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCC AAGGGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATC TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACT ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCCGTACAAAGAGCTTCAACAGGGGAGAGTGT
182	Secuencia de nucleótidos de 14E3 (VH)	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCTT CAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAG GGGCTGGAGTGGATTGGAGAAATCAATCATAGTGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGCGTCACCATATCAGTAGA CACGTCCAAGAACCAGTTATCCCTGAAGCTGAGCTCTGTGACC GCCGCGGACACGGCTGTGTATTACTGTGCGAGATTTGGGAGTA ATGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCA
183	Secuencia de nucleótidos de 14E3 (VL)	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTGGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCCTCCGACGTTTCGGCCAAG GGACCAAGGTGGAATCAAA
184	Secuencia de nucleótidos de 14E3 (cadena pesada de tipo silvestre de longitud completa)	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCTT CAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAG GGGCTGGAGTGGATTGGAGAAATCAATCATAGTGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGCGTCACCATATCAGTAGA

	La secuencia que codifica la región constante está subrayada	CACGTCCAAGAACCAGTTATCCCTGAAGCTGAGCTCTGTGACC GCCGCGGACACGGCTGTGTATTACTGTGCGAGATTTGGGAGTA ATGATGCTTTTGTATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA CGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT GAGCCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCC CAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCCCTCTTCCC CCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGC CCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGA GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCCTCTACAGCAAGCTCACCGTGGACAAGAGCAG GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTC CGGGTAAA
185	Secuencia de nucleótidos de 14E3 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTGCGGCGAGTCAGGGTAT TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACAGTATAATAGTTACCCTCCGACGTTTCGGCCAAG GGACCAAGGTGGAATCAAACGAAGTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
186	Secuencia de nucleótidos de 19H8 (VH)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGATGGCAGTTATATGGTATGGTGGAAAGTAATA AATTCTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACTCGCTGTCTCTGCAAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGG CTATGGTTTCGGGGAGTCTACTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCAC CGTCTCCTCA
187	Secuencia de nucleótidos de 19H8 (VL1)	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGTTCCCTGATCTATGATGCCTCCAGTTTGAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT

		TACTGTCAACAGTTTAAATAGTTACCCTCAGACGTTTCGGCCAAG GGACCAAGGTGGAAATCAAA
188	Secuencia de nucleótidos de 19H8 (VL2)	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCT CCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCA TCCCAGCCAGGTTTCAAGTGGCAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTAT TACTGTCAGCAGCGTAGCAACTGGCCGCTCACTTTTCGGCGGAG GGACCAAGGTGGAGATCAAA
189	Secuencia de nucleótidos de 19H8 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTT CAGTAACATATGGCATGCAGTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGATGGCAGTTATATGGTATGGTGGAAGTAATA AATTCTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACTCGCTGTCTCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGG CTATGGTTTCGGGAGTCTACTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGC CCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG <u>AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC</u> <u>CGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCTCTGACCAGC</u> <u>GGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCAGGACTCT</u> <u>ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGG</u> <u>CACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC</u> <u>ACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGT</u> <u>GCCCACCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTT</u> <u>CCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGG</u> <u>ACCCCTGAGGTACAGTGCCTGGTGGTGGACGTGAGCCAGGAAG</u> <u>ACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGT</u> <u>GCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC</u> <u>ACGTTCCGTGTGGTCAAGCGTCTCACCCTGTCACAGGACT</u> <u>GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGG</u> <u>CCTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAGGG</u> <u>CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG</u> <u>AGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAA</u> <u>AGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT</u> <u>GGGCAGCCGGAGAACAACATAAGACCACACCTCCCATGCTGG</u> <u>ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGA</u> <u>CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG</u> <u>ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT</u> <u>CCCTGTCTCCGGGTAAA</u>
190	Secuencia de nucleótidos de 19H8 L1 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGTTCCTGATCTATGATGCCTCCAGTTTGAAAGTGGGG TCCCATCAAGGTTTCAAGCGCAGTGGATCTGGGACAGATTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGAACCTTAT TACTGTCAACAGTTTAAATAGTTACCCTCAGACGTTTCGGCAAG GGACCAAGGTGGAATCAAACGAAGTGTGGCTGCATCCAGTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

191	Secuencia de nucleótidos de 19H8 L2 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCT CCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCA TCCCAGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTAT TACTGTCAGCAGCGTAGCAACTGGCCGCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGGAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
192	VH 3-33 (28F3, 18E10, 19D3, 2G6, 8A6, 19H8)	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVIWDGNSKYYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCAR
193	VH 3-10 (28F3, 8A6)	MVRG
194	VH 3-10 (9G7)	YYYG
195	VH 3-10 (19H8)	YYY
196	VH JH6 (28F3, 19H8)	YYYGMDVWGQGT TTVTVSS
197	VH JH6 (18E10, 2G6, 8A6)	YYGMDVWGQGT TTVTVSS
198	VH JH6 (19D3, 9G7)	YYYYYGMVWGQGT TTVTVSS
199	VH 6-19 (18E10)	IAVA
200	VH 3-16 (19D3)	DY
201	VH 4-34 (3C3, 14E3)	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGSTNYNPSLKSRTVISVDTSKNQFSKLSSVT AADTAVYYCAR
202	VH JH3 (3C3, 14E3)	DAFDIWGQGTMTTVSS
203	VH 3-15 (9G7)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLKTEDTAVYYCTT
204	VL L18 (28F3, 8A6, 19H8VK1)	AIQLTQSPSSLSASVGDRVITITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNYY
205	VL JK2 (28F3, 18E10, 19D3, 3C3VK1, 8A6, 2G6)	YTFGQGTKLEIK
206	VL JK2 (3C3VK2)	TFGQGTKLEIK
207	VL L15 (18E10, 19D3, 3C3VK1, 2G6, 14E3)	DIQMTQSPSSLSASVGDRVITITCRASQGISSWLAWYQQKPEKA PKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYNSY
208	VL L20 (3C3VK2)	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGPGTDFTLTISLLEPEDFAVY YCQQRSNW
209	VL A27 (9G7VK1, 9G7VK2)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YICQQYGSS
210	VL JK1 (9G7VK1)	WTFGQGTKVEIK
211	VL JK1 (14E3, 19H8VK1)	TFGQGTKVEIK
212	VL JK5 (9G7VK2)	ITFGQGTRLEIK
213	VL L6 (19H8VK2)	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA PRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVY YCQQRSNW

214	VL JK4 (19H8VK2)	LTFGGGTKVEIK
215	Epítopo de G1TR	QRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGE
216	Epítopo de G1TR	QRPTGGPGCGPGRLLLTGTGT
217	Epítopo de G1TR (región 1)	PTGGPGCGPGRLLLTGTGT
218	Epítopo de G1TR (región 2)	CRDYPGEE
219	Ligador peptídico	PVGVV
220	Terminales C de la cadena pesada	LSPGK
221	Región constante de G2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKCCVECPPEPPVAGPSVFLFPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT SKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPG
222	Región constante de G2(C219S)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKSCVECPPEPPVAGPSVFLFPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE EQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT SKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPG
223	Región constante modificada de G2.g1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKCCVECPPEPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPG
224	Región constante modificada de G2.g1.1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKCCVECPPEPPVAGPSVFLFPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPG
225	Región constante modificada de G2(C219S).g1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKSCVECPPEPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPG
226	Región constante modificada de G2(C219S).g1.1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNS GALTSGVHTFPAVLQSSGLYSLSSVTPSSNFGTQTYTCNV HKPSNTKVDKTKVERKSCVECPPEPPVAGPSVFLFPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV

		FSCSVMEALHNHYTQKSLSLSPG
15	28F3 (VH + G2) o 28F3-IgG2	SEQ ID NO: 15
227	28F3 (VH + G2(C219S)) o 28F3-IgG2-C219S	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAVIWYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGSMVRGDIYYGMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
228	28F3 (VH + G2.g1) o 28F3-IgG2-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAVIWYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGSMVRGDIYYGMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISR</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN</u> <u>STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
229	28F3 (VH + G2.g1.1) o 28F3-IgG2-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAVIWYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGSMVRGDIYYGMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
230	28F3 (VH + G2(C219S).g1) o 28F3-IgG2-C219S-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAVIWYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGSMVRGDIYYGMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMISR</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN</u> <u>STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
231	28F3 (VH + G2(C219S).g1.1) o 28F3-IgG2-C219S-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAVIWYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGSMVRGDIYYGMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u>

		<u>GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
28	19D3 (VH + G2) o 19D3-IgG2	SEQ ID NO: 28
232	19D3 (VH + G2(C219S)) o 19D3-IgG2-C219S	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGFWVRQAPGK</u> <u>GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTV PSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPPVAGPSVFLFPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST</u> <u>FRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQ</u> <u>PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG</u> <u>QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>HEALHNHYTQKSLSLSPG</u>
233	19D3 (VH + G2.g1) o 19D3-IgG2-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGFWVRQAPGK</u> <u>GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTV PSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKCCVECP PCPAPELLGGPSVFLFPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
234	19D3 (VH + G2.g1.1) o 19D3-IgG2-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGFWVRQAPGK</u> <u>GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTV PSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKCCVECP PCPAPPVAGPSVFLFPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST</u> <u>YRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQ</u> <u>PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>HEALHNHYTQKSLSLSPG</u>
235	19D3 (VH + G2(C219S).g1) o 19D3-IgG2-C219S-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGFWVRQAPGK</u> <u>GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTV PSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPELLGGPSVFLFPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
236	19D3 (VH + G2(C219S).g1.1) o 19D3-IgG2-C219S-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGFWVRQAPGK</u> <u>GLEWVAVIWIYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGQLDY YYYVMDVWGQGT TTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTV PSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPPVAGPSVFLFPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST</u> <u>YRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQ</u>

		<u>PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG</u> <u>QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>HEALHNHYTQKSLSLSPG</u>
41	18E10 (VH + G2) o 18E10-IgG2	SEQ ID NO: 41
237	18E10 (VH + G2(C219S)) o 18E10-IgG2-C219S	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAWIYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGRIAVAFYYSM DVWGQGTTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPPVAGPSVFLFPPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST</u> <u>FRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQ</u> <u>PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG</u> <u>QPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>HEALHNHYTQKSLSLSPG</u>
238	18E10 (VH + G2.g1) o 18E10-IgG2-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAWIYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGRIAVAFYYSM DVWGQGTTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKCCVECP PCPAPELLGGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
239	18E10 (VH + G2.g1.1) o 18E10-IgG2-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAWIYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGRIAVAFYYSM DVWGQGTTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKCCVECP PCPAPPVAGPSVFLFPPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST</u> <u>YRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQ</u> <u>PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG</u> <u>QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>HEALHNHYTQKSLSLSPG</u>
240	18E10 (VH + G2(C219S).g1) o 18E10-IgG2-C219S-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAWIYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGRIAVAFYYSM DVWGQGTTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPELLGGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
241	18E10 (VH + G2(C219S).g1.1) o 18E10-IgG2-C219S-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK</u> <u>GLEWVAWIYAGSNKYYADSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGRIAVAFYYSM DVWGQGTTVTVSSASTKGP</u> <u>SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG</u> <u>VHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSNT</u> <u>KVDKTVERKSCVECP PCPAPPVAGPSVFLFPPKPKDTLMISRT</u> <u>PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST</u>

		YRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIISKAKGQ PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
242	3C3 (VH + G2) o 3C3-IgG2	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSV LTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV YITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG
243	3C3 (VH + G2(C219S)) o 3C3-IgG2-C219S	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSV LTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV YITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG
244	3C3 (VH + G2.g1) o 3C3-IgG2-IgG1	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG
245	3C3 (VH + G2.g1.1) o 3C3-IgG2-IgG1.1	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPSSIEKTIISKAKGQPREPQV YITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG
246	3C3 (VH + G2(C219S).g1) o 3C3-IgG2-C219S-IgG1	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARLGAFDAFDIWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN

		<u>YKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG</u>
247	3C3 (VH + G2(C219S).g1.1) o 3C3-IgG2-C219S-IgG1.1	<u>QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGK</u> <u>GLEWIGKINHSGNTNYPNPSLKSRVTISVDTSKNQFSLKLSSVT</u> <u>AADTAVYYCARLGAFDAFDIWQGGMVTVSSASTKGPSVFPLA</u> <u>PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA</u> <u>VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV</u> <u>ERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV</u> <u>VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV</u> <u>LTVLHQDWLNGKEYKCKVSNKALPSSIEKTIKAKGQPREPQV</u> <u>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY</u> <u>KTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG</u>
248	2G6 (VH + G2) o 2G6-IgG2	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI LSDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
249	2G6 (VH + G2(C219S)) o 2G6-IgG2-C219S	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI LSDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
250	2G6 (VH + G2.g1) o 2G6-IgG2-IgG1	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI LSDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN</u> <u>STYRVVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>VMHEALHNHYTQKSLSLSPG</u>
251	2G6 (VH + G2.g1.1) o 2G6-IgG2-IgG1.1	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI LSDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTISRDN SKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQGT TTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN</u> <u>TKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVSLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>

252	2G6 (VH + G2(C219S).g1) o 2G6-IgG2-C219S-IgG1	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI</u> <u>LS</u> <u>SDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTI</u> <u>SR</u> <u>DNSKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQ</u> <u>GT</u> <u>TVT</u> <u>VSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYF</u> <u>PE</u> <u>PVT</u> <u>TVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFG</u> <u>TQ</u> <u>TYTC</u> <u>NVDHKPSN</u> <u>TKVDKTVERKSCVECP</u> <u>PC</u> <u>PAPELLGGPSV</u> <u>FLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDG</u> <u>VE</u> <u>VHNAKTKPREEQYN</u> <u>STYRVVSVLTVLHQDWLNGKEYKCKVSN</u> <u>KAL</u> <u>PAPIEKTISKAK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCL</u> <u>VK</u> <u>GFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDSDGSFFLYSKLT</u> <u>VD</u> <u>KSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
253	2G6 (VH + G2(C219S).g1.1) o 2G6-IgG2-C219S-IgG1.1	<u>QVQLVESGGGVVQPGGSLRLSCAASGFI</u> <u>LS</u> <u>SDYGMHWVRQAPGK</u> <u>GLEWVTVIWYDGSNKFYVDSVKGRFTI</u> <u>SR</u> <u>DNSKNTLYLQMNSL</u> <u>RVEDTAVYYCARGRLATGHFYVMDVWGQ</u> <u>GT</u> <u>TVT</u> <u>VSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYF</u> <u>PE</u> <u>PVT</u> <u>TVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFG</u> <u>TQ</u> <u>TYTC</u> <u>NVDHKPSN</u> <u>TKVDKTVERKSCVECP</u> <u>PC</u> <u>PAPPVAGPSV</u> <u>FLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDG</u> <u>VE</u> <u>VHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSN</u> <u>KAL</u> <u>PSSIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCL</u> <u>VK</u> <u>GFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLT</u> <u>VD</u> <u>KSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
86	8A6 (VH + G2) o 8A6-IgG2	SEQ ID NO: 86
254	8A6 (VH + G2(C219S)) o 8A6-IgG2-C219S	<u>QVQLVESGGGVVQPGRSLRLSCTASGFT</u> <u>FS</u> <u>SYGMQWVRQAPGK</u> <u>GLEWVAVIWIYEGSNKYYADSVKGRFTI</u> <u>S</u> <u>RENSKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGLMVRGLFYYGMDV</u> <u>WGQ</u> <u>GT</u> <u>TVT</u> <u>VSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYF</u> <u>PE</u> <u>PVT</u> <u>TVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFG</u> <u>TQ</u> <u>TYTC</u> <u>NVDHKPSN</u> <u>TKVDKTVERKSCVECP</u> <u>PC</u> <u>PAPPVAGPSV</u> <u>FLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDG</u> <u>VE</u> <u>VHNAKTKPREEQFNS</u> <u>TFRVVS</u> <u>SVLTVVHQDWLNGKEYKCKVSN</u> <u>KGL</u> <u>PAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCL</u> <u>VK</u> <u>GFYPSDIAVEWESN</u> <u>GQPENNYKTTPPMLDSDGSFFLYSKLT</u> <u>VD</u> <u>KSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
255	8A6 (VH + G2.g1) o 8A6 -IgG2-IgG1	<u>QVQLVESGGGVVQPGRSLRLSCTASGFT</u> <u>FS</u> <u>SYGMQWVRQAPGK</u> <u>GLEWVAVIWIYEGSNKYYADSVKGRFTI</u> <u>S</u> <u>RENSKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGLMVRGLFYYGMDV</u> <u>WGQ</u> <u>GT</u> <u>TVT</u> <u>VSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYF</u> <u>PE</u> <u>PVT</u> <u>TVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFG</u> <u>TQ</u> <u>TYTC</u> <u>NVDHKPSN</u> <u>TKVDKTVERKCCVECP</u> <u>PC</u> <u>PAPELLGGPSV</u> <u>FLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDG</u> <u>VE</u> <u>VHNAKTKPREEQYN</u> <u>STYRVVSVLTVLHQDWLNGKEYKCKVSN</u> <u>KAL</u> <u>PAPIEKTISKAK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCL</u> <u>VK</u> <u>GFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDSDGSFFLYSKLT</u> <u>VD</u> <u>KSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
256	8A6 (VH + G2.g1.1) o 8A6 -IgG2-IgG1.1	<u>QVQLVESGGGVVQPGRSLRLSCTASGFT</u> <u>FS</u> <u>SYGMQWVRQAPGK</u> <u>GLEWVAVIWIYEGSNKYYADSVKGRFTI</u> <u>S</u> <u>RENSKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGLMVRGLFYYGMDV</u> <u>WGQ</u> <u>GT</u> <u>TVT</u> <u>VSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYF</u> <u>PE</u> <u>PVT</u> <u>TVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFG</u> <u>TQ</u> <u>TYTC</u> <u>NVDHKPSN</u> <u>TKVDKTVERKCCVECP</u> <u>PC</u> <u>PAPPVAGPSV</u> <u>FLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDG</u> <u>VE</u> <u>VHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSN</u> <u>KAL</u> <u>PSSIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCL</u> <u>VK</u> <u>GFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSDGSFFLYSKLT</u> <u>VD</u> <u>KSRWQQGNVFSCSV</u>

		<u>MHEALHNHYTQKSLSLSPG</u>
257	8A6 (VH + G2(C219S).g1) o 8A6-IgG2-C219S-IgG1	<u>QVQLVESGGGVVQPGRLRLSCTASGFTFSSYGMQWVRQAPGK</u> <u>GLEWVAVIWIYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGTTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN</u> <u>STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
258	8A6 (VH + G2(C219S).g1.1) o 8A6-IgG2-C219S-IgG1.1	<u>QVQLVESGGGVVQPGRLRLSCTASGFTFSSYGMQWVRQAPGK</u> <u>GLEWVAVIWIYEGSNKYYADSVKGRFTISRENSKNTLYLQMNSL</u> <u>RAEDTAVYYCARGGLMVRGLFYYGMDVWGQGTTVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN</u> <u>TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS</u> <u>TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
259	9G7 (VH + G2) o 9G7-IgG2	<u>EVQLVESGGGLVKPGGSLRLSCAASGFTFSTVWMSWVRQAPGK</u> <u>GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN</u> <u>SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSTVTVSSASTK</u> <u>GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT</u> <u>SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS</u> <u>NTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN</u> <u>STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
260	9G7 (VH + G2(C219S)) o 9G7-IgG2-C219S	<u>EVQLVESGGGLVKPGGSLRLSCAASGFTFSTVWMSWVRQAPGK</u> <u>GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN</u> <u>SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSTVTVSSASTK</u> <u>GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT</u> <u>SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS</u> <u>NTKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS</u> <u>RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN</u> <u>STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK</u> <u>GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES</u> <u>NGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSCS</u> <u>VMHEALHNHYTQKSLSLSPG</u>
261	9G7 (VH + G2.g1) o 9G7-IgG2-IgG1	<u>EVQLVESGGGLVKPGGSLRLSCAASGFTFSTVWMSWVRQAPGK</u> <u>GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN</u> <u>SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSTVTVSSASTK</u> <u>GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT</u> <u>SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS</u> <u>NTKVDKTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMI</u> <u>SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY</u> <u>NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA</u> <u>KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE</u> <u>SNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSC</u> <u>SVMHEALHNHYTQKSLSLSPG</u>

262	9G7 (VH + G2.g1.1) o 9G7-IgG2-IgG1.1	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS NTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
263	9G7 (VH + G2(C219S).g1) o 9G7-IgG2-C219S-IgG1	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS NTKVDKTVERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG
264	9G7 (VH + G2(C219S).g1.1) o 9G7-IgG2-C219S-IgG1.1	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSTVWMSWVRQAPGK GLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMN SLHTEDTAVYYCTTGQLIPYSYYYGMDVWGQGTSVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPS NTKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
265	14E3 (VH + G2) o 14E3-IgG2	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSV LTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG
266	14E3 (VH + G2(C219S)) o 14E3-IgG2-C219S	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT AADTAVYYCARFGSNDADFIDWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSV LTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG
267	14E3 (VH + G2.g1) o	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT

	14E3-IgG2-IgG1	<u>AADTAVYYCARFGSNDAFDIWGQGTMTVTSSASTKGPSVFPLA</u> <u>PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA</u> <u>VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV</u> <u>ERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC</u> <u>VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS</u> <u>VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ</u> <u>VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN</u> <u>YKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH</u> <u>NHYTQKSLSLSPG</u>
268	14E3 (VH + G2.g1.1) o 14E3-IgG2-IgG1.1	<u>QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK</u> <u>GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT</u> <u>AADTAVYYCARFGSNDAFDIWGQGTMTVTSSASTKGPSVFPLA</u> <u>PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA</u> <u>VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV</u> <u>ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV</u> <u>VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV</u> <u>LTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQV</u> <u>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY</u> <u>KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN</u> <u>HYTQKSLSLSPG</u>
269	14E3 (VH + G2(C219S).g1) o 14E3-IgG2-C219S-IgG1	<u>QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK</u> <u>GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT</u> <u>AADTAVYYCARFGSNDAFDIWGQGTMTVTSSASTKGPSVFPLA</u> <u>PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA</u> <u>VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV</u> <u>ERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC</u> <u>VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS</u> <u>VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ</u> <u>VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN</u> <u>YKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH</u> <u>NHYTQKSLSLSPG</u>
270	14E3 (VH + G2(C219S).g1.1) o 14E3-IgG2-C219S-IgG1.1	<u>QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK</u> <u>GLEWIGEINHSGNTYYNPSLKSRTISVDTSKNQLSLKLSSVT</u> <u>AADTAVYYCARFGSNDAFDIWGQGTMTVTSSASTKGPSVFPLA</u> <u>PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA</u> <u>VLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV</u> <u>ERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV</u> <u>VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV</u> <u>LTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQV</u> <u>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY</u> <u>KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN</u> <u>HYTQKSLSLSPG</u>
131	19H8 (VH + G2) o 19H8-IgG2	SEQ ID NO: 131
271	19H8 (VH + G2(C219S)) o 19H8-IgG2-C219S	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK</u> <u>GLEWMAVIWYGGSNKFYADSVKGRFTISRDNKNSLSLQMNSL</u> <u>RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGTITVTVSSASTKG</u> <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN</u> <u>TKVDKTVVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSV</u> <u>MHEALHNHYTQKSLSLSPG</u>
272	19H8 (VH + G2.g1) o	<u>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK</u>

	19H8-IgG2-IgG1	GLEWMAVIWYGGSNKFYADSVKGRFTISRDNKNSLSLQMNSL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGTTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN TKVDKTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
273	19H8 (VH + G2.g1.1) o 19H8-IgG2-IgG1.1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDNKNSLSLQMNSL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGTTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN TKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
274	19H8 (VH + G2(C219S).g1) o 19H8-IgG2-C219S-IgG1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDNKNSLSLQMNSL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGTTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
275	19H8 (VH + G2(C219S).g1.1) o 19H8-IgG2-C219S-IgG1.1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWMAVIWYGGSNKFYADSVKGRFTISRDNKNSLSLQMNSL RAEDTAVYYCARGGAMVRGVYYYGMDVWGQGTTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVDHKPSN TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
276	Terminales C de la cadena pesada	LSPG
277	-	
278	CH1 de IgG1 humana de tipo silvestre	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKV
279	CH1 de IgG2 humana de tipo silvestre	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVD HKPSNTKVDKTV
280	CH2 de IgG1 humana de tipo silvestre	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAK
281	CH2 de IgG1 humana con	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD

	A330S/P331S	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPSSIEKTI SKAK
282	CH3 de IgG1 humana de tipo silvestre	GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPG
283	IgG1-IgG2-IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKCCVECPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPG
284	IgG1-IgG2CS-IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKSCVECPPCAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
285	IgG1-IgG2-IgG1.1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKCCVECPPCAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTI ISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
286	IgG1-IgG2CS-IgG1.1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKSCVECPPCAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTI ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
287	IgG1-IgG2-1gG1f2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKCCVECPPCAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
288	IgG1-IgG2(C219S)-IgG1f2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVERKSCVECPPCAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPG
289	IgG2-IgG1f2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKPKDT

		LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPG
290	IgG2(C219S)-IgG1f2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWSNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTKVERKSCVECPPCPAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPG
291	Bisagra de IgG2 humana WT	ERKCCVECPPCPAPPVAG
292	Bisagra de IgG2 humana con C219S	ERKSCVECPPCPAPPVAG
293	Bisagra de IgG2/IgG1	ERKCCVECPPCPAPELLGG
294	Bisagra de IgG2 (C219S)/IgG1	ERKSCVECPPCPAPELLGG
295	Bisagra de IgG1 humana de tipo silvestre	EPKSCDKTHTCPPCPAPELLGG
296	Bisagra de IgG1.1 (L234A/L235E/G237A)	EPKSCDKTHTCPPCPAPEAEGA
297	CH2 de IgG2 humana de tipo silvestre	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKV SNKGLPAPIEKTISKTK
298	CH3 de IgG2 humana de tipo silvestre	GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
299	Terminal C C _H 1 de IgG1 (igual para IgG3 (17-15-15-15), IgG3 (17-15-15), IgG3 (17-15), IgG3 (15-15-15), IgG3 (15) e IgG4	VDKRV
300	Terminal C C _H 1 de IgG2	VDKTV
301	Bisagra superior de IgG1	EPKSCDKTHT
302	Bisagra superior de IgG3 (17-15-15-15) (igual para IgG3 (17-15-15) e IgG3 (17-15))	ELKTPLGDTTHT
303	Bisagra superior de IgG3 (15-15-15) (igual para IgG3(15))	EPKS
304	Bisagra superior de IgG4	ESKYGPP
305	Bisagra intermedia de IgG1	CPPCP
306	Bisagra intermedia de IgG2	CCVECPPCP
307	Bisagra intermedia de IgG3 (17-15-15-15)	CPRCP (EPKSCDTPPPCPRCP) ₃
308	Bisagra intermedia de IgG3 (17-15-15)	CPRCP (EPKSCDTPPPCPRCP) ₂

309	Bisagra intermedia de IgG3 (17-15)	CPRCPEPKSCDTPPPCPRCP
310	Bisagra intermedia de IgG3 (15-15-15)	CDTPPPCPRCP (EPKSCDTPPPCPRCP) ₂
311	Bisagra intermedia de IgG3 (15)	CDTPPPCPRCP
312	Bisagra intermedia de IgG4	CPSCP
313	Bisagra inferior de IgG1 (igual para IgG3 (17-15-15-15), IgG3 (17-15-15), IgG3 (17-15), IgG3 (15-15-15), IgG3 (15) e IgG4)	APELLGG
314	Bisagra inferior de IgG2	APPVAG
315	Secuencia de señal VH de 28F3 (igual para 18E10, 19D3, 19H8, 6G10)	MEFGLSWVFLVALLRGVQC
316	Secuencia de señal VH de 28F3 (secuencia de nucleótidos)	ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAA GAGGTGTCCAGTGT
317	Secuencia de señal VL de 28F3 (igual para 18E10, 8A6, 19H8VL1, 6G10)	MDMRVPAQLLGLLLLWLPGARC
318	Secuencia de señal VL de 28F3 (secuencia de nucleótidos)	ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTTCTGCTGC TCTGGCTCCCAGGTGCCAGAT
319	Secuencia de señal VL de 19D3	MRVLAQLLGLLLLCPFGARC
320	Secuencia de señal VL de 19D3 (secuencia de nucleótidos)	ATGAGGGTCCTCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGTT TCCCAGGTGCCAGATGT
321	Secuencia de señal VH de 3C3 (igual para 14E3)	MKHLWFFLLLVAAPRWLS
322	Secuencia de señal VH de 3C3 (secuencia de nucleótidos)	ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCA GATGGGTCCTGTCC
323	Secuencia de señal VL de 3C3 (igual para 14E3)	MDMRVLAQLLGLLLLCPFGARC
324	Secuencia de señal VL de 3C3 (secuencia de nucleótidos)	ATGGACATGAGGGTCCTCGCTCAGCTCCTGGGGCTCCTGCTGC TCTGTTTCCCAGGTGCCAGATGT
325	Secuencia de señal VL2 de 3C3 (igual para 19H8 VL2)	MEAPAQLLFLLLLWLPDTTG
326	Secuencia de señal VL2 de 3C3 (secuencia de nucleótidos)	ATGGAAGCCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGC TCCCAGATACCACCGGA
327	Secuencia de señal VH de 8A6	MEFGLNWVFLVALLRGVQC
328	Secuencia de señal VH de 8A6 (secuencia de nucleótidos)	ATGGAGTTTGGGCTGAACTGGGTTTTCTCGTTGCTCTTTTAA GAGGTGTCCAGTGT

329	Secuencia de señal VH de 9G7	MEFGLSWIFLAAILKGVQC
330	Secuencia de señal VH de 9G7 (secuencia de nucleótidos)	ATGGAGTTTGGGCTGAGCTGGATTTTCCTTGCTGCTATTTTAA AAGGTGTCCAGTGT
331	Secuencia de señal VL1 y VL2 de 9G7	METPAQLLFLLLLWLPDTTG
332	Secuencia de señal VL1 y VL2 de 9G7 (secuencia de nucleótidos)	ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGC TCCCAGATACCACCGGA
333	Secuencia de señal VH de 14E3	MKHLWFFLLLVAAPRWLS
334	Secuencia de señal VH de 14E3 (secuencia de nucleótidos)	ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCA GATGGGTCTGTCC
335	6G10 (VH)	QVQLVESGGDVVQPGRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGTITVTVSS
336	6G10 (VL)	AIQLTQSPSSLSASVGDRVITITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPYTFGQGTKLEIK
337	6G10 (cadena pesada de tipo silvestre de longitud completa) La región constante está subrayada	QVQLVESGGDVVQPGRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGTITVTVSSASTKG <u>PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS</u> <u>GVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDHKPSN</u> <u>TKVDKTVERKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISR</u> <u>TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS</u> <u>TFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG</u> <u>QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN</u> <u>GQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV</u> <u>MHEALHNHYTQKSLSLSPGK</u>
338	6G10 (cadena liviana de tipo silvestre de longitud completa) La región constante está subrayada	AIQLTQSPSSLSASVGDRVITITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT <u>ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST</u> <u>YLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC</u>
339	6G10.IgG1 (VH + IgG1)	QVQLVESGGDVVQPGRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGTITVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYICNVNHKPSN TKVDKRVEPKCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPG
340	6G10.IgG1.1 (VH + IgG1.1)	QVQLVESGGDVVQPGRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGTITVTVSSASTKG

		PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVPEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPG
341	6G10.IgG1 (VL + CL)	AIQLTQSPSSLSASVGDRVITITCRASQGISSALAWYQQKPGKA PKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLPEDFATY YCQQFNSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
342	6G10 VH CDR1	TYGMH
343	6G10 VH CDR2	VTWYAGSNKFYADSVKG
344	6G10 VH CDR3	GGSMVRGLYYYYGMDV
345	6G10 VL CDR1	RASQGISSALA
346	6G10 VL CDR2	DASSLES
347	6G10 VL CDR3	QQFNSYPYT
337	6G10 (VH + G2) o 6G10-IgG2	SEQ ID NO: 337
348	6G10 (VH + G2(C219S)) o 6G10-IgG2-C219S	QVQLVESGGDVVQPGRSRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
349	6G10 (VH + G2.g1) o 6G10-IgG2-IgG1	QVQLVESGGDVVQPGRSRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN TKVDKTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISR RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV VMHEALHNHYTQKSLSLSPG
350	6G10 (VH + G2.g1.1) o 6G10-IgG2-IgG1.1	QVQLVESGGDVVQPGRSRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYTCNV DHKPSN TKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG

351	6G10 (VH + G2(C219S).g1) o 6G10-IgG2-C219S-IgG1	QVQLVESGGDVVQPGRSRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKIFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNV DHKPSN TKVDKTVERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCS VMHEALHNHYTQKSLSLSPG
352	6G10 (VH + G2(C219S).g1.1) o 6G10- IgG2-C219S-IgG1.1	QVQLVESGGDVVQPGRSRLRLSCAASGFTTFSTYGMHWVRQAPGK GLEWVAVTWYAGSNKIFYADSVKGRFTISRDN SKNTLYLQMNSL RAEDTAVYYCARGGSMVRGLYYYGMDVWGQGT TTVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNV DHKPSN TKVDKTVERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPG
353	Secuencia de nucleótidos de 6G10 (VH)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGACGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTT CAGTACCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTACATGGTATGCTGGAAGTAATA AATTTTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTA GTATGGTTCGGGGACTTTATTATTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA
354	Secuencia de nucleótidos de 6G10 (VL)	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTCAACATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGCTCCTGATCTATGATGCCTCCAGTTTGAAAGTGGGG TCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGATTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGTCAACAGTTTAATAGTTACCCGTACACTTTTGCCAGG GGACCAAGCTGGAGATCAAA
355	Secuencia de nucleótidos de 6G10 (cadena pesada de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	CAGGTGCAGCTGGTGGAGTCTGGGGGAGACGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTT CAGTACCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTACATGGTATGCTGGAAGTAATA AATTTTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTA GTATGGTTCGGGGACTTTATTATTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGC <u>CCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG</u> <u>AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC</u> <u>CGAACCGGTGACGGTGTCGTGGAACCTCAGGCCTCTGACCAGC</u> <u>GGCGTGACACCTTCCCAGCTGTCTACAGTCCTCAGGACTCT</u> <u>ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGG</u> <u>CACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC</u> <u>ACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGT</u> <u>GCCCACCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTT</u> <u>CCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGG</u>

		<u>ACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAG</u> <u>ACCCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGT</u> <u>GCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC</u> <u>ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT</u> <u>GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGG</u> <u>CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG</u> <u>CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG</u> <u>AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA</u> <u>AGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT</u> <u>GGGCAGCCGGAGAACAACATAAGACCACACTCCCATGTCTGG</u> <u>ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGA</u> <u>CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG</u> <u>ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT</u> <u>CCCTGTCTCCGGGTAAA</u>
356	Secuencia de nucleótidos de 6G10 (cadena liviana de tipo silvestre de longitud completa) La secuencia que codifica la región constante está subrayada	GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTG TAGGAGACAGAGTACCATCACTTGCCGGGCAAGTCAGGGCAT TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCT CCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGG TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTTAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGAACCTTAT TACTGTCAACAGTTTAAATAGTTACCCGTACACTTTTGGCCAGG GGACCAAGCTGGAGATCAAACGAAGTGTGGCTGCACCATCTGT CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC TACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
357	28F3 (VH) (SEQ ID NO: 13) con péptido de señal El péptido de señal está subrayado	<u>MRAWIFFLLCLAGRALAQVQLVESGGGVVQPGRSRLRLSCAASG</u> <u>FTFSSYGMHWVRQAPGKGLEWVAVIWEYSNKYYADSVKGRFT</u> <u>ISRDNSTLYLQMNSLRAEDTAVYYCARGGSMVRGDYVYGM</u> <u>VDWGQGTFTVTVSS</u>
358	28F3 (VL) (SEQ ID NO: 14) con péptido de señal El péptido de señal está subrayado	MRAWIFFLLCLAGRALAAIQLTQSPSSLSASVGDRTITCRAS QGISSALAWYQKPGKAPKLLIYDASSLESVPSRFSGSGSGT DFTLTISLQPEDFATYYCQQFNSYPYTFGQGTKLEIK
359	Secuencia de nucleótidos de 28F3 (VH) con péptido de señal SEQ ID NO: 147 con secuencia que codifica el péptido de señal La secuencia que codifica el péptido de señal está subrayada	<u>atgagggccttgatcttctttctgctctgcctggccgggagag</u> <u>cgctcgca</u> CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGA TTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGAAGG AAGTAATAAATATTATGCAGACTCCGTGAAGGGCCGATTACC ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAG AGGGGGGAGTATGGTTCGGGGGGACTACTACTACGGTATGGAC GTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
360	Secuencia de nucleótidos de 28F3 (VL) con péptido de señal SEQ ID NO: 148 con secuencia que codifica el	<u>atgagggccttgatcttctttctgctctgcctggccggggcgcg</u> <u>ccttgccc</u> GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTC TGCATCTGTAGGAGACAGAGTACCATCACTGCCGGGCAAGT CAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACAG GGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGA AAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACA

	péptido de señal La secuencia que codifica el péptido de señal está subrayada	GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTATTACTGTCAACAGTTTAAATAGTTACCCGTACACTTT TGGCCAGGGGACCAAGCTGGAGATCAAA
361	28F3.IgG1 (VH + IgG1) (SEQ ID NO: 17) con péptido de señal El péptido de señal y la región constante están subrayados	<u>MRAWIFFLLCLAGRALAQVQLVESGGGVVQPGRSRLRLSCAASG</u> <u>FTFSSYGMHWVRQAPGKGLEWVAVIWEYSNKKYADSVKGRFT</u> <u>ISRDNSTNTLYLQMNLSRAEDTAVYYCARGGSMVRGDYYYGMD</u> <u>VWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD</u> <u>YFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS</u> <u>SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEL</u> <u>LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW</u> <u>YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK</u> <u>CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV</u> <u>SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL</u> <u>YSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPG</u>
362	28F3.IgG1.1 (VH + IgG1.1) (SEQ ID NO: 18) con péptido de señal El péptido de señal y la región constante están subrayados	<u>MRAWIFFLLCLAGRALAQVQLVESGGGVVQPGRSRLRLSCAASG</u> <u>FTFSSYGMHWVRQAPGKGLEWVAVIWEYSNKKYADSVKGRFT</u> <u>ISRDNSTNTLYLQMNLSRAEDTAVYYCARGGSMVRGDYYYGMD</u> <u>VWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD</u> <u>YFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS</u> <u>SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA</u> <u>EGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW</u> <u>YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK</u> <u>CKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSREEMTKNQV</u> <u>SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL</u> <u>YSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPG</u>
363	28F3.IgG1 (VH + IgG1) con secuencia de nucleótidos del péptido de señal SEQ ID NO: 151 con secuencia que codifica el péptido de señal La secuencia que codifica el péptido de señal está subrayada	atgagggccttgatcttctctctctgctctgcttgccgggagagag cgctcgacacaggtgcagctgggtggagtctgggggagggcgtggg ccagcctgggaggtccctgagactctctctgtgcagcgtctgga ttcaccttcagtagctatggcatgcactgggtccgccaggctc caggcaaggggctggagtgggtggcagttatatggtatgaagg aagtaataaatattatgcagactccgtgaagggccgattcacc atctccagagacaattccaagaacacgctgtatctgcaaatga acagcctgagagccgaggacacggctgtgtattactgtgcgag aggggggagtatggttcggggggactactactacggtatggac gtctggggccaagggaccacgggtcacctgtctcctcagctagca ccaagggcccatcggtcttccccctggcaccctcctccaagag cacctctgggggacacagcgccctgggtgctgctgggtcaaggac tacttccccgaaccgggtgacgggtgtcgtggaactcaggcgccc tgaccagcggcgtgcacaccttcccggctgtcctacagtcctc aggactctactccctcagcagcgtgggtgaccgtgcccctccagc agcttgggcacccagacctacatctgcaacgtgaatcacaagc ccagcaacaccaaggtggacaagagagttgagcccaaatcttg tgacaaaactcacacatgccaccgtgcccagcacctgaactc ctggggggacagctcagtccttctcttccccccaaaacccaagg acaccctcatgatctcccggaaccttgaggtcacatgcgtgggt gggtggacgtgagccacgaagacctgaggtcaagttcaactgg tacgtggacggcgtggaggtgcataatgccaagacaaagccgc gggaggagcagtacaacagcacgtaccgtgtgggtcagcgtcct caccgtcctgcaccaggactgggtgaatggcaaggagtacaag tgcaaggtctccaacaaagccctcccagcccccatcgagaaaa ccatctccaaagccaaagggcagccccgagaaccacaggtgta caccctgcccccatcccgggaggagatgaccaagaaccagggtc agcctgacctgctgggtcaaaggcttctatcccagcgacatcg ccgtggagtgggagagcaatgggcagccggagaacaactacaa

		gaccacgcctcccgtgctggactccgacgggtccttcttctc tatagcaagctcaccgtggacaagagcaggtggcagcagggga acgtcttctcatgctccgtgatgcatgaggctctgcacaacca ctacacgcagaagagcctctccctgtccccgggttga
364	28F3.IgG1.1 (VH + IgG1.1) con secuencia de nucleótidos del péptido de señal SEQ ID NO: 152 con secuencia que codifica el péptido de señal La secuencia que codifica el péptido de señal está subrayada	atgagggccttgatcttcttctgctctgcctggccgggagag <u>cgctcgcacaggtgcagc</u> tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct ccaggcaagg ggctggagtg ggtggcagtt atatggtatg aaggaagtaa taaatattat gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgtgtat ctgcaaatga acagcctgag agccgaggac accgtgtgt attactgtgc gagagggggg agtatggttc ggggggacta ctactacggt atggacgtct ggggccaagg gaccacggtc accgtctcct cagctagcac caagggccca tcggtcttcc ccctggcacc ctccctccaag agcacctctg ggggcacagc ggccctgggc tgcttggtca aggactactt ccccgaaaccg gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc agcgtgggtga ccgtgccctc cagcagcttg ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag agagttgagc ccaaactctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa gccgaagggg ccccgtcagt ctccctcttc ccccaaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtggtg gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaaag ccctcccaag cagcatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc agcctgacct gccttggtcaa aggttctat cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tccccgggtt ga
365	28F3.IgG1 (VL+CL) (SEQ ID NO: 19) con péptido de señal El péptido de señal y la región constante están subrayados	<u>MRWIFFLLCLAGRALAAIQLTQSPSSLSASVGDVRTITCRAS</u> <u>QGISSALAWYQKPGKAPKLLIYDASSLESVPSRFSGSGSGT</u> <u>DFTLTISLQPEDFATYYCQQFNSYPYTFGQGTKLEIKRTVAA</u> <u>PSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ</u> <u>SGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTH</u> <u>QGLSPVTKSFNRGEC</u>
366	28F3.IgG1 (VL+CL) con secuencia de nucleótidos del péptido de señal SEQ ID NO: 153 con secuencia de señal	atgagggccttgatcttcttctgctctgcctggccgggagcgcg <u>ccttggccgccatccagttgaccagtcctccatcctccctgtc</u> tgcatctgtaggagacagagtcaccatcacttgccgggcaagt cagggcattagcagtgctttagcctggtatcagcagaaaccag ggaaagctcctaagctcctgatctatgatgcctccagtttggga aagtgggggtcccatcaagggttcagcggcagtggtctgggaca gatttcactctcaccatcagcagcctgcagcctgaagattttg caacttattactgtcaacagtttaatatgattaccgtagacttt

	La secuencia que codifica el péptido de señal está subrayada	tggccaggggaccaagctggagatcaaacgtacggtggctgca ccatctgtcttcatcttcccgcctctgatgagcagttgaaat ctggaactgcctctgttgtgtgcctgctgaataacttctatcc cagagaggccaaagtacagtggaaggtggataacgccctccaa tcgggtaactcccaggagagtgtcacagagcaggacagcaagg acagcacctacagcctcagcagcaccctgacgctgagcaaagc agactacgagaaacacaaagtctacgcctgcgaagtcacccat cagggcctgagctcgcccgtcacaaagagcttcaacaggggag agtgttag
367	Péptido de señal	MRAWIFFLLCLAGRALA
368	Secuencia de nucleótidos del péptido de señal	atgagggccttgatcttctttctgctctgcctggccgggagag cgctcgca
369	Secuencia de nucleótidos del péptido de señal	atgagggccttgatcttctttctgctctgcctggccgggagcg ccttgcc
370	Fragmento de GTR humano	QRPTGGPGCGPGRLLLTGTGDARCCRVHTTR
371	9G7 L1 (cadena liviana 1 de tipo silvestre de longitud completa) La región constante está subrayada	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPWFQGTKVEIKRTVAAPSVFIFPPSDEQLKSG <u>TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS</u> <u>TYSLSSLTTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC</u>
372	CDR1 de VH degenerada	SYGXH, en donde X es cualquier aminoácido
373	CDR2 de VH degenerada	VIWYX ₁ GSNKX ₂ YADSVKG, en donde X ₁ y X ₂ son cualquier aminoácido
374	CDR2 de VH degenerada	VIWYX ₁ GSNKX ₂ YX ₃ DSVKG, en donde X ₁ , X ₂ y X ₃ son cualquier aminoácido
375	CDR3 de VH degenerada	GGSX ₁ VRGDYYYGMDV, en donde X ₁ es cualquier aminoácido
376	CDR3 de VH degenerada	GGSX ₁ VRGX ₂ YYYGMDV, en donde X ₁ y X ₂ son cualquier aminoácido
377	CDR3 de VH degenerada	GG (6-7aa) MDVWYYX ₁ MDVW, en donde X ₁ es cualquier aminoácido, y los aminoácidos 6-7 son cualquier aminoácido
378	CDR1 de VL degenerada	RASQGISSXLA, en donde X es cualquier aminoácido
379	CDR1 de VL degenerada	RASQG (2-3 aa) SX ₁ LA, en donde X ₁ es cualquier aminoácido, y los aminoácidos 2-3 son cualquier aminoácido
380	CDR2 de VL degenerada	DASSLXS, en donde X es cualquier aminoácido
381	CDR3 de VL degenerada	QQXNSYPYT, en donde X es cualquier aminoácido
382	CDR3 de VL degenerada	QQX ₁ X ₂ SX ₃ PX ₄ T, en donde X ₁ , X ₂ , X ₃ y X ₄ son cualquier aminoácido