

Figure 3A

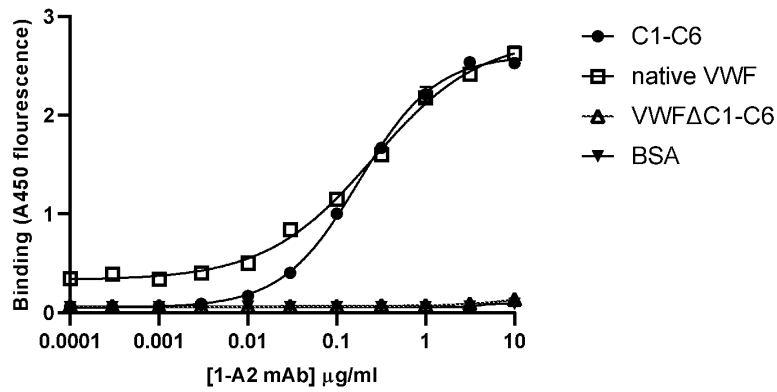


Figure 3B

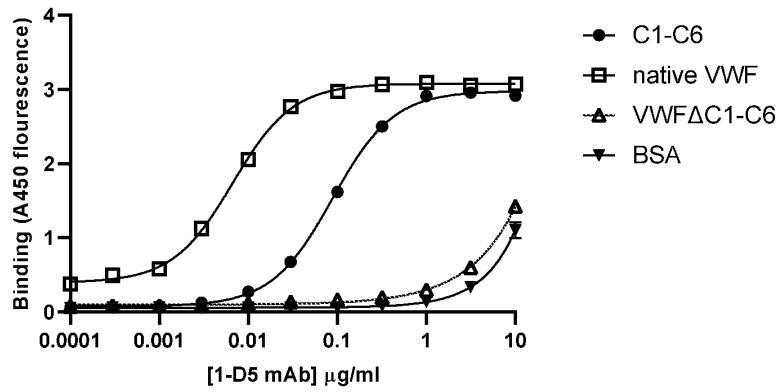


Figure 3C

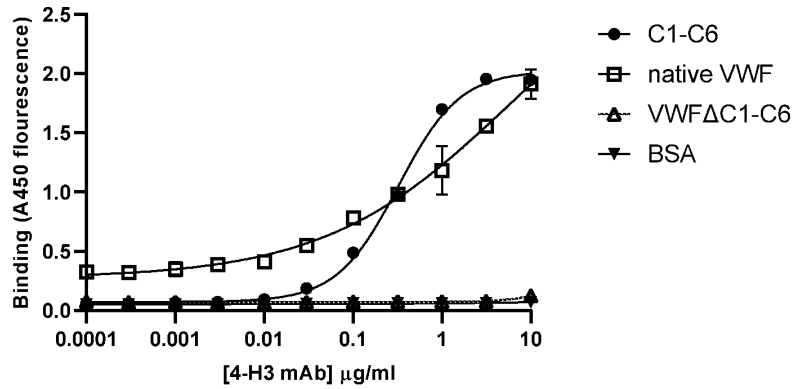


Figure 3D

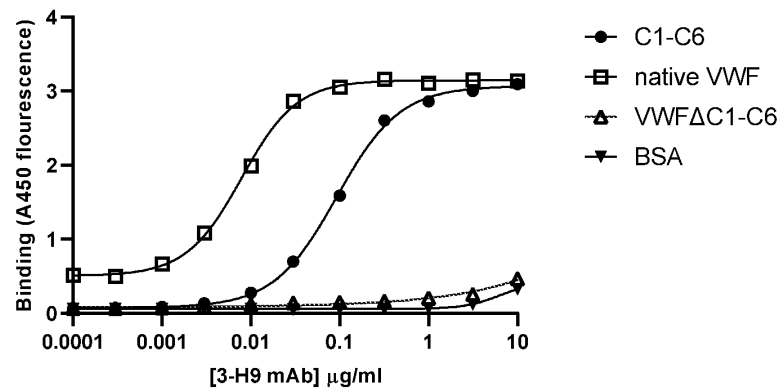


Figure 3E

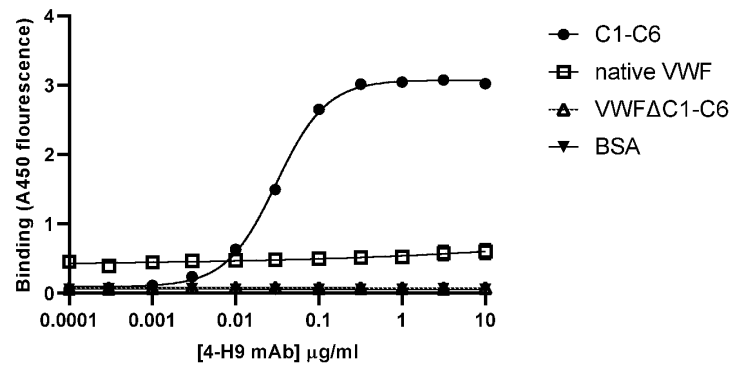


Figure 3F

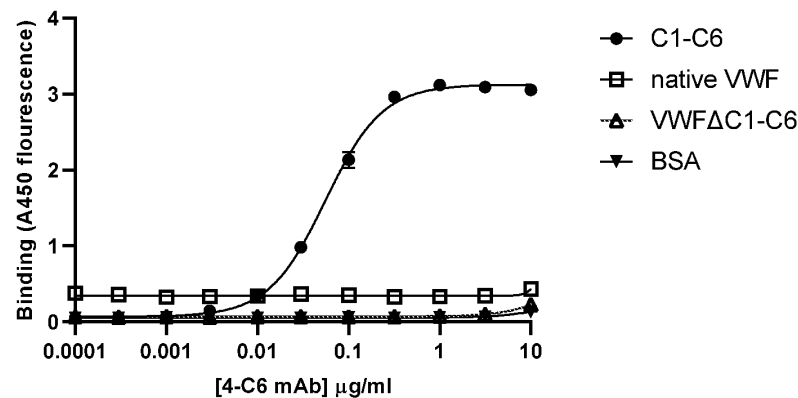


Figure 3G

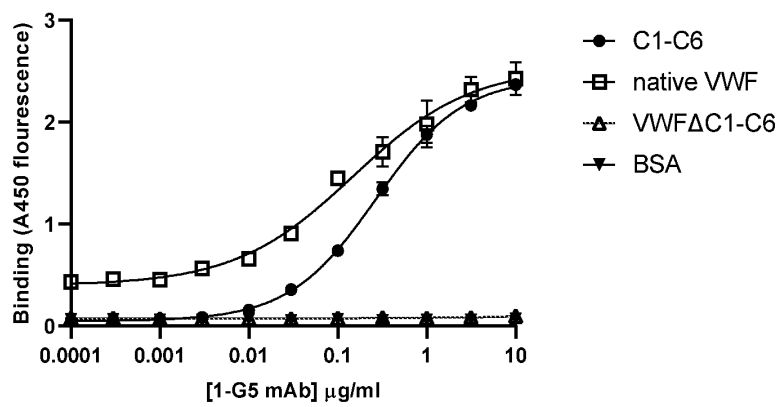


Figure 3H

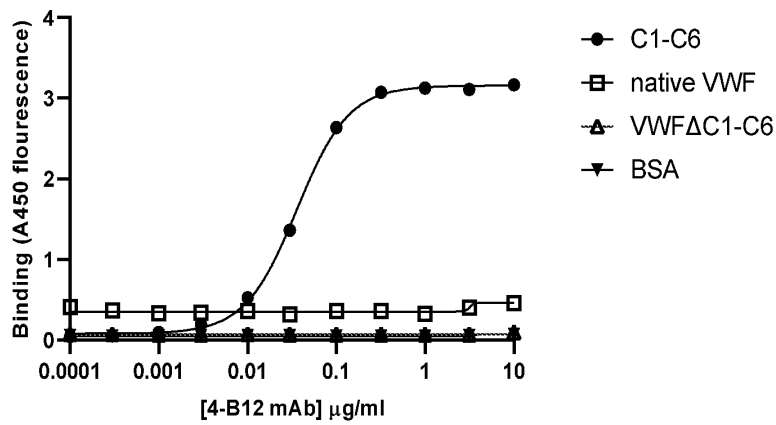


Figure 4

Antibody	Replicate #	ka (1/Ms)	kd (1/s)	KD (M)
1-A2	1	73700.00	0.0000121	1.64E-10
1-A2	2	24500.00	0.0000129	5.27E-10
4-H3	1	113000.00	0.0000139	1.23E-10
4-H3	2	108000.00	0.0000167	1.54E-10
1-D5	1	151000.00	0.00000376	2.50E-11
1-D5	2	125000.00	0.00000477	3.81E-11
1-D5	3	130000.00	0.00000834	6.41E-11
3-H9	1	188000.00	0.00000915	4.87E-11
3-H9	2	127000.00	0.0000107	8.40E-11
3-H9	3	157000.00	0.00000393	2.50E-11
1-G5	1	119000.00	0.00000653	5.49E-11
1-G5	2	70700.00	0.00000562	7.90E-11
1-G5	3	116000.00	0.0000143	1.23E-10

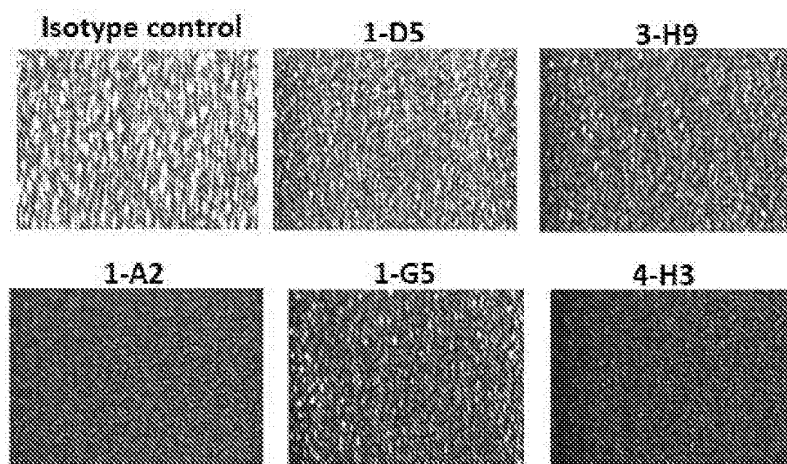
Figure 5

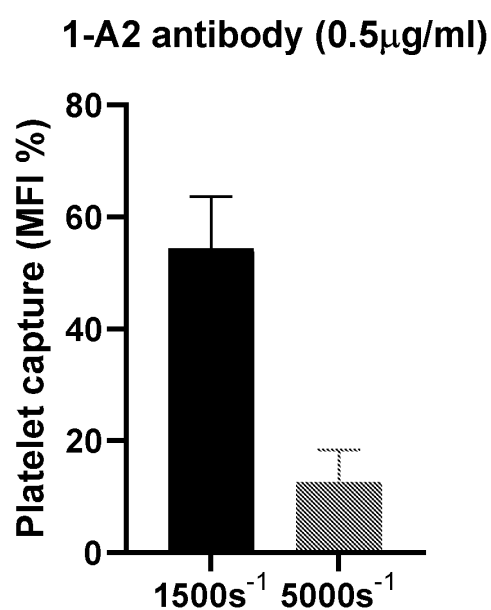
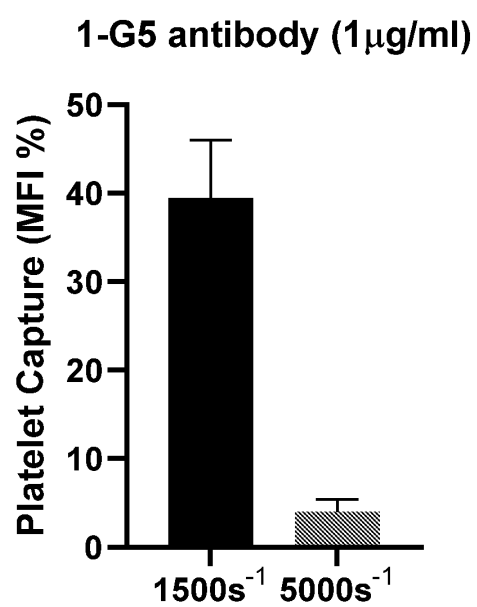
Figure 6A**Figure 6B**

Figure 6C

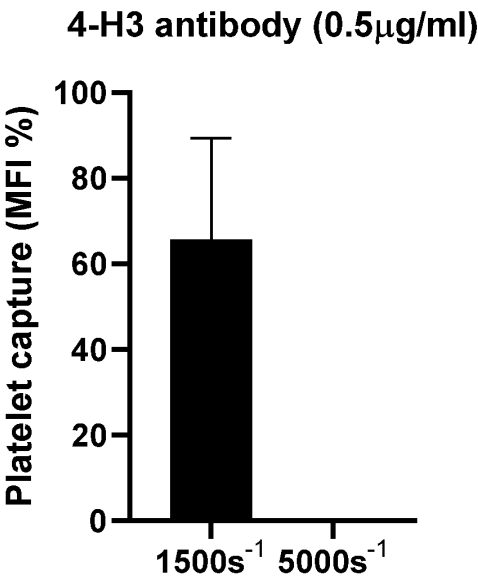


Figure 7A

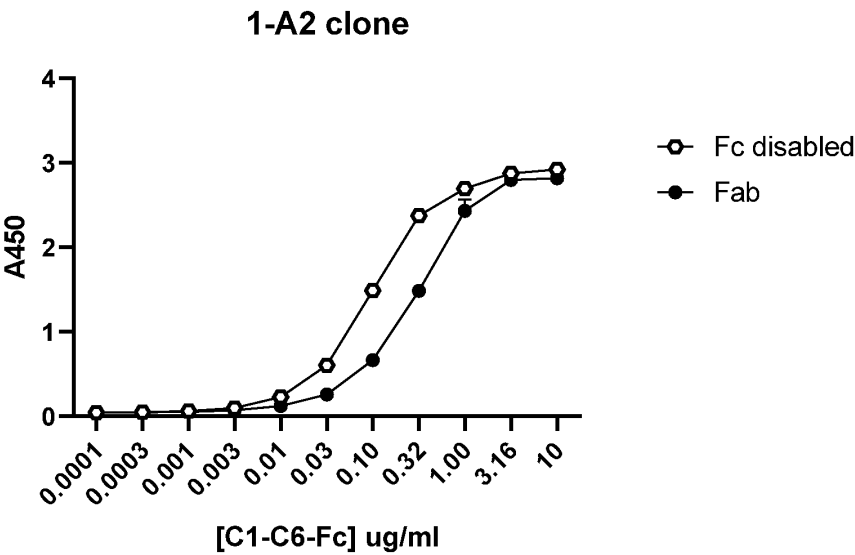


Figure 7B

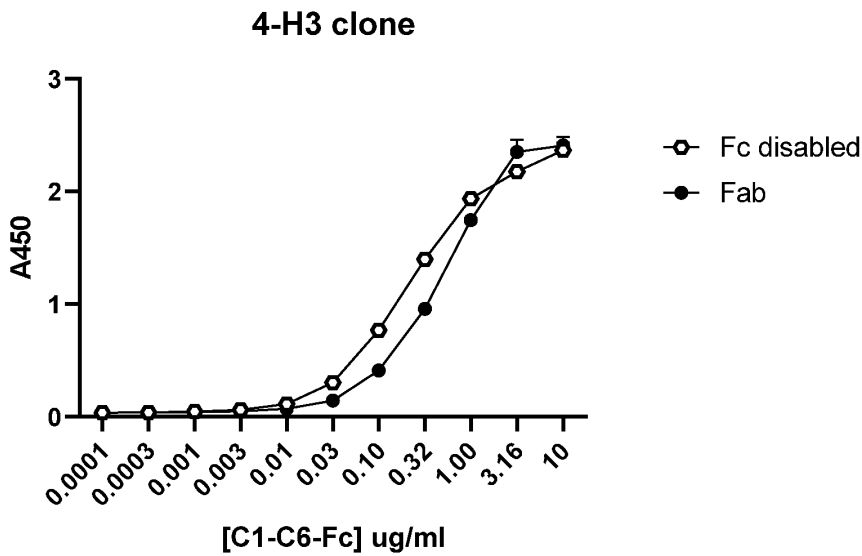


Figure 7C

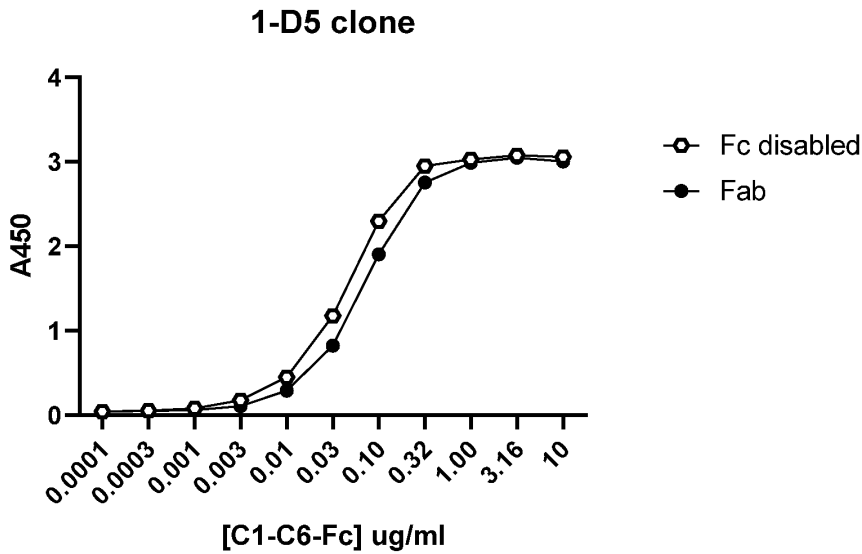


Figure 7D

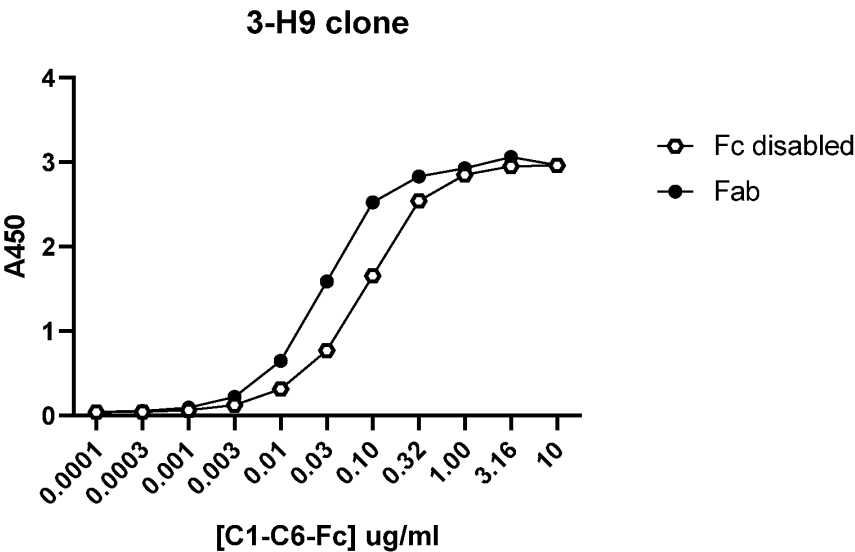
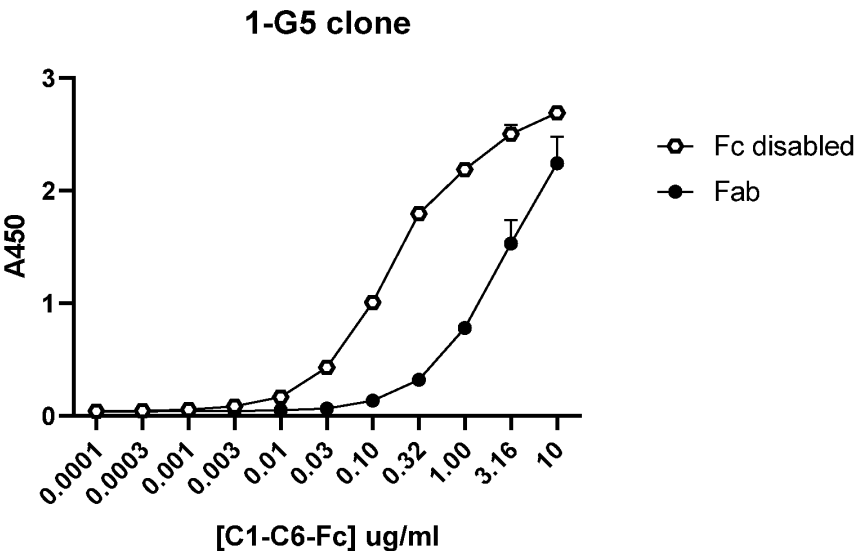


Figure 7E



- 10/34 -

Figure 8

Antibody	CDR -H1	CDR- H2	CDR -H3	FR- H1	FR- H2	FR- H3	FR- H4	CDR -L1	CDR -L2	CDR -L3	FR- L1	FR- L2	FR- L3	FR- L4	VH	VL
1-A2	SEQ ID NO: 9	SEQ ID NO: 10	SEQ ID NO: 11	SEQ ID NO: 12	SEQ ID NO: 13	SEQ ID NO: 14	SEQ ID NO: 15	SEQ ID NO: 18	SEQ ID NO: 19	SEQ ID NO: 20	SEQ ID NO: 21	SEQ ID NO: 22	SEQ ID NO: 23	SEQ ID NO: 24	SEQ ID NO: 16	SEQ ID NO: 25
4-H3	SEQ ID NO: 27	SEQ ID NO: 28	SEQ ID NO: 29	SEQ ID NO: 30	SEQ ID NO: 31	SEQ ID NO: 32	SEQ ID NO: 33	SEQ ID NO: 36	SEQ ID NO: 37	SEQ ID NO: 38	SEQ ID NO: 39	SEQ ID NO: 40	SEQ ID NO: 41	SEQ ID NO: 42	SEQ ID NO: 34	SEQ ID NO: 43
1-D5	SEQ ID NO: 45	SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 48	SEQ ID NO: 49	SEQ ID NO: 50	SEQ ID NO: 51	SEQ ID NO: 54	SEQ ID NO: 55	SEQ ID NO: 56	SEQ ID NO: 57	SEQ ID NO: 58	SEQ ID NO: 59	SEQ ID NO: 60	SEQ ID NO: 52	SEQ ID NO: 61
3-H9	SEQ ID NO: 63	SEQ ID NO: 64	SEQ ID NO: 65	SEQ ID NO: 66	SEQ ID NO: 67	SEQ ID NO: 68	SEQ ID NO: 69	SEQ ID NO: 72	SEQ ID NO: 73	SEQ ID NO: 74	SEQ ID NO: 75	SEQ ID NO: 76	SEQ ID NO: 77	SEQ ID NO: 78	SEQ ID NO: 70	SEQ ID NO: 79

Figure 9

human VWF protein residues	Domain	Antibody	ka (1/Ms)	kd (1/s)	KD (M)
2255-2333	C1	1-A2			
2334-2402	C2	1-A2			
2430-2496	C3	1-A2			
2497-2577	C4	1-A2			
2578-2646	C5	1-A2	1.70E+05	7.93E-05	4.66E-10
2647-2722	C6	1-A2			
2255-2333	C1	1-D5			
2334-2402	C2	1-D5			
2430-2496	C3	1-D5	1.64E+03	2.43E-03	1.49E-06
2497-2577	C4	1-D5			
2578-2646	C5	1-D5	1.55E+05	1.43E-04	9.22E-10
2647-2722	C6	1-D5			
2255-2333	C1	1-G5			
2334-2402	C2	1-G5			
2430-2496	C3	1-G5			
2497-2577	C4	1-G5			
2578-2646	C5	1-G5	2.14E+07	4.78E-03	2.23E-10
2647-2722	C6	1-G5			
2255-2333	C1	3-H9			
2334-2402	C2	3-H9			
2430-2496	C3	3-H9			
2497-2577	C4	3-H9	3.04E+04	1.42E-03	4.66E-08
2578-2646	C5	3-H9	1.60E+05	3.19E-05	1.99E-10
2647-2722	C6	3-H9			
2255-2333	C1	4-H3			
2334-2402	C2	4-H3			
2430-2496	C3	4-H3			
2497-2577	C4	4-H3			
2578-2646	C5	4-H3	4.36E+07	1.22E-02	2.79E-10
2647-2722	C6	4-H3			

Figure 10

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-A2_parental (IgG4)	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSTTD LT (SEQ ID NO: 20)	SQSVESGRLVTFGTPLTL TCTVSGIDLTSMANWVRQA PKGLEWIGSIHAIHTIYYA AWAKGEFTISKTSITVLEKLM TRPTIDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 156)	AIEMTQTFPSLSASVG ETVRLIRGLASDIIYSG ISWYQQKPFQKPEPTLLI YGASNLESQVPPRFSG SGSGTDYTLTIIGSVQA EDAATYCYLGGHSHST TDLTFGAGTKYEIK (SEQ ID NO: 25)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKVEKPKCKDTHICPC PAPELLLGPSVFLPEPKPKDTLMISRTPEVTCVAVDVSHEDEVEKFNMYVDGVVH NAKTREREQYHSTYRVSVSLTVLHQW LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQFNKKYKTIPEV LQSDGSFELYSKLIVDKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYFREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
4-H3_parental (IgG4)	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	SQSLEESGRLVTFGTPLTL TCTVSGIDLTSMANWVRQA PKGLEWIGSIHAIHTIYYA AWAKGEFTISKTSITVLEKLM TRPTIDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 159)	AYDMTQTFPSLSASVG ETVRLIRGLASDIIYSG ISWYQQKPKPEPTLLI YGASNLESQVPPRFSG SGSGTDYTLTIIGSVQA EDAATYCYLGGHSHST TDLTFGAGTKYEIK (SEQ ID NO: 43)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKVEKPKCKDTHICPC PAPELLLGPSVFLPEPKPKDTLMISRTPEVTCVAVDVSHEDEVEKFNMYVDGVVH NAKTREREQYHSTYRVSVSLTVLHQW LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQFNKKYKTIPEV LQSDGSFELYSKLIVDKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYFREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
1-D5_parental (IgG4)	GFLSNYYI (SEQ ID NO: 45)	IETGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSISNG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHIYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVTFGTPLTL TCAVSFGLNNHYIMGWVRQA PKGLEWIGSIHAIHTIYYA SWAKGEFTISKTSITVLEKLM TSLTIEDTATYFCARGGSA GAGNFWGFIILVTISS (SEQ ID NO: 52)	DIWMTQTFPSVSAANG DTVTIQCQASQISNG LAWYQQKPKQPKRRLI YKASTLASGVSPRFRG SGSGTDFTLTISDLCE ADAATYCYQSYHIYISA NGATFGGTEVVE (SEQ ID NO: 61)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKVEKPKCKDTHICPC PAPELLLGPSVFLPEPKPKDTLMISRTPEVTCVAVDVSHEDEVEKFNMYVDGVVH NAKTREREQYHSTYRVSVSLTVLHQW LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQFNKKYKTIPEV LQSDGSFELYSKLIVDKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYFREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
3-H9_parental (IgG4)	GFLSNYYD (SEQ ID NO: 63)	IHAIGT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSGWY NT (SEQ ID NO: 74)	SQSLEESGRLVTFGTPLTL TCSVSFGLNNHYIMGWVRQA PKGLEWIGSIHAIHTIYYA NMAWGEFTISKTSITVLEKLM TSLTIEDTATYFCARGLVDL NMWGFGLVTISS (SEQ ID NO: 160)	AIKMTQTFPSVSAANG DTVTIQCQASQISNG LAWYQQKPKQPKRRLI YKASTLASGVSPRFRG SGSGTDFTLTISDLCE ADAATYCYQSYHIYISA NGATFGGTEVVE (SEQ ID NO: 79)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKVEKPKCKDTHICPC PAPELLLGPSVFLPEPKPKDTLMISRTPEVTCVAVDVSHEDEVEKFNMYVDGVVH NAKTREREQYHSTYRVSVSLTVLHQW LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQFNKKYKTIPEV LQSDGSFELYSKLIVDKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYFREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-G5_parental (hlgG1)	GFSLGSVD (SEQ ID NO: 81)	IHAIGIT (SEQ ID NO: 82)	ARGLVLDLM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGGWD TA (SEQ ID NO: 92)	SQSLBEISGGRLVFTGPTLTL TCSVSEFSLSSDMMWVRQA FGKGLVEYIGSIHAIGITFYA NMAKGRFTISKTSITVOLDK TSLTIEDTATYFCARGLVLD NMMGFGLTVTSS (SEQ ID NO: 161)	DPVMTQTASSVSAVG GTVTINCAQSQSYNN NLYLWQKQCPQPKL LIYDASTLASGTSFV SONSGSTQFTLISGV QCQDAATYYCGSYYTS GGWDATFGGKTVMVK (SEQ ID NO: 97)	ASTKGFSVFFLAFSSKSTSGTAAAGCL VKDYFFPEVTVSMNSGALTSGVHTFFAV LQSSGLYLSGVTVVPSSLSIGTIYICN VNHKFSNTVKRVKRFKSCDKTHCTPCP FAEEAAGGSFVLFPPFRKDTLMISRT EVTCCVVVDVSHDEPVENRWYVDGVEVH NAKTRFREQVNSTYRVSVLVLIHQDWM LNKGKYCKVKNALGAPFTEKTSKAGK QPREQVYTLTFPSRDELTKNQVSLTCLV KGFTFSQDIAVESNGQFENNTKTPFP LSDSGSFFLYSKLTVDKSRMQQGNVFSC SYMHEALHHNYTKQSLSISFGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQLK SGTASVCLLNNFIPREA KQVMKVDNALQSGNSQES VTEQDSKOSTYSLASLT LSEKADYEKHKVYACEVTH QQLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_parental (hlgG1-L234A- L235A-P329G)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTIS (SEQ ID NO: 28)	ARGFLYFDI (SEQ ID NO: 29)	EDIYSG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	SQSLBEISGGRLVFTGPTLTL TCTVYSIDILTSNMMWVRQA FGKGLVEYIGSIHADSYNYA AMAKGRFTISRTISITVOLDK TRPTTDDTATYFCARGFYF DIMTGTTLTVTSS (SEQ ID NO: 159)	AYDMTQTFFPSLSAVG ETVRICLAESDITISG ISWYQKQKGRFPTLLI YGASNLGSEVFPNFSG SSSGIDYTLTIIGQVA EQAATYYCLGGSFSS NGLTFAGTKVEIK (SEQ ID NO: 43)	ASTKGFSVFFLAFSSKSTSGTAAAGCL VKDYFFPEVTVSMNSGALTSGVHTFFAV LQSSGLYLSGVTVVPSSLSIGTIYICN VNHKFSNTVKRVKRFKSCDKTHCTPCP FAEEAAGGSFVLFPPFRKDTLMISRT EVTCCVVVDVSHDEPVENRWYVDGVEVH NAKTRFREQVNSTYRVSVLVLIHQDWM LNKGKYCKVKNALGAPFTEKTSKAGK QPREQVYTLTFPSRDELTKNQVSLTCLV KGFTFSQDIAVESNGQFENNTKTPFP LSDSGSFFLYSKLTVDKSRMQQGNVFSC SYMHEALHHNYTKQSLSISFGK (SEQ ID NO: 162)	TVAAPSVFIFFPSDEQLK SGTASVCLLNNFIPREA KQVMKVDNALQSGNSQES VTEQDSKOSTYSLASLT LSEKADYEKHKVYACEVTH QQLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_parental (hlgG1-L234A- L235A-P329G)	GFSLNNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVLDLM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSGGW NT (SEQ ID NO: 74)	SQSLBEISGGRLVFTGPTLTL TCSVSEFSLSSDMMWVRQA FGKGLVEYIGSIHAIGITFYA NMAKGRFTISKTSITVOLDK TSLTIEDTATYFCARGLVLD NMMGFGLTVTSS (SEQ ID NO: 160)	AIKMTQTFFSSVAVG GTVTINCAQSQSYNN NLLSWYQKQKQPKRLI LIYDASTLSEGVSRF KSSSGSTQFTLISGV QCEAATYYCGSYYTS SGMWNTFFGGGTVEVVE (SEQ ID NO: 70)	ASTKGFSVFFLAFSSKSTSGTAAAGCL VKDYFFPEVTVSMNSGALTSGVHTFFAV LQSSGLYLSGVTVVPSSLSIGTIYICN VNHKFSNTVKRVKRFKSCDKTHCTPCP FAEEAAGGSFVLFPPFRKDTLMISRT EVTCCVVVDVSHDEPVENRWYVDGVEVH NAKTRFREQVNSTYRVSVLVLIHQDWM LNKGKYCKVKNALGAPFTEKTSKAGK QPREQVYTLTFPSRDELTKNQVSLTCLV KGFTFSQDIAVESNGQFENNTKTPFP LSDSGSFFLYSKLTVDKSRMQQGNVFSC SYMHEALHHNYTKQSLSISFGK (SEQ ID NO: 162)	TVAAPSVFIFFPSDEQLK SGTASVCLLNNFIPREA KQVMKVDNALQSGNSQES VTEQDSKOSTYSLASLT LSEKADYEKHKVYACEVTH QQLSSPVTKSFNRGEC (SEQ ID NO: 158)

WO 2022/223966

PCT/GB2022/050989

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-G5_parental (hlgG1-L234A-L235A-P329G)	GFSLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGVLDM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWD TA (SEQ ID NO: 92)	SQSLESGRLVFPGLTL TCVSGFSLSSVDMWRQA PGKLEWIGSIHATGIFYA NMAKGRFTISRTISITVLDLM TSLTIEDTATYFCARGVLNL NMWPGTLTVSS (SEQ ID NO: 161)	DPVMTQASSVSAAGV GTVTINQASQSYVNN NLLSWYQKQKPPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYVS GMDTAFGGGKVK (SEQ ID NO: 97)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK PAPRAAGPSPVLEFPKPKOTLMISRTIP EVTCCVAVDSHEDFEVKNWVGVGVH NAKTEREEQYHSTYVAVSLVTLQKAG LAKGEVKYKSKALGAPIKTLISKAG QPREQVTLTLPSSRDLTKNQVSLTCLV KGFYPSDIAYWESNQENNYKTTPEV LQSSGFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKSLSLSEFK (SEQ ID NO: 162)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
1-A2_parental (hlgG1-Fab)	GIDLTSNA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGHSHSTTD LT (SEQ ID NO: 20)	SQSLESGRLVFPGLTL TCTVSGIOLTSNMMWRQA PGKLEWIGSIHGHDTSYA AMAKGRFTISRTISITVLDLM TRPTIDDATYFCARGEIYF DIWGTGLTVLSS (SEQ ID NO: 156)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQKQKPPKLTLI YGASNLSESGVFPFSG SGSGDTVTLTIGGVQA EDAAATYTCQGSYVS TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
4-H3_parental (hlgG1-Fab)	GIDLTSNA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	SQSLESGRLVFPGLTL TCTVSGIOLTSNMMWRQA PGKLEWIGSIHGHDTSYA AMAKGRFTISRTISITVLDLM TRPTIDDATYFCARGEIYF DIWGTGLTVLSS (SEQ ID NO: 159)	AYDMTQTFPSLSASVG ETVIRCLASEDIASG ISWYQKQKPPKLTLI YGASNLSESGVFPFSG SGSGDTVTLTIGGVQA EDAAATYTCQGSYVS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
1-D5_parental (hlgG1-Fab)	GFSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGSSAGAG FNT (SEQ ID NO: 47)	QSINS (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG NT (SEQ ID NO: 56)	QQQLVESGRLVFPGLTL TCVSGFSLNNYIMGWQRQA PGKLEWIGSIHGHDTSYA SWAKGRFTISRTISITVLDLM TSLTIEDTATYFCARGGSA GAGFNWPGTLTVLTVSS (SEQ ID NO: 52)	DIVMTQTFSSVSAAGV DIVILQCSQSSINS LAWYQKQKPPKLTLI IKASHLASGVFSRFG SGSGDTVTLTISOLBC ADAAATYTCQGSYVS NGLTFGAGTKVEIK (SEQ ID NO: 61)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
3-H9_parental (hlgG1-Fab)	GFSLSYD (SEQ ID NO: 63)	IHAIGT (SEQ ID NO: 64)	ARGVLDM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSGWD NT (SEQ ID NO: 74)	SQSLESGRLVFPGLTL TCVSGFSLSSVDMWRQA PGKLEWIGSIHATGIFYA NMAKGRFTISRTISITVLDLM TSLTIEDTATYFCARGVLNL NMWPGTLTVSS (SEQ ID NO: 160)	DPVMTQASSVSAAGV GTVTINQASQSYVNN NLLSWYQKQKPPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYVS GMDTAFGGGKVK (SEQ ID NO: 79)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
1-G5_parental (hlgG1-Fab)	GFSLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGVLDM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWD TA (SEQ ID NO: 92)	SQSLESGRLVFPGLTL TCVSGFSLSSVDMWRQA PGKLEWIGSIHATGIFYA NMAKGRFTISRTISITVLDLM TSLTIEDTATYFCARGVLNL NMWPGTLTVSS (SEQ ID NO: 161)	DPVMTQASSVSAAGV GTVTINQASQSYVNN NLLSWYQKQKPPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYVS GMDTAFGGGKVK (SEQ ID NO: 97)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSWNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITSLSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
4-H3_Ho (hlgG ₁)	GFTFSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 165)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 194)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
4-H3_H2 (hlgG ₁)	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 166)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 167)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
4-H3_H3 (hlgG ₁)	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 168)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNANMWRA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDIWQQGTLIVTSS (SEQ ID NO: 168)	AYDMTQTFPSLSASVG ETVRIKRLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLTIIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFPELAPSSKSTSGGTAALGCL VKDYFPEEVTVMNSGALTSGVHIFPAV LQSSGLYSLSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSCDKHTCPCC FAPELLGGPSPVLPFPEKDKTLMISRT EVTCVVDVSHDEPVEKFNWVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREFQVTLTPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKITPEV LQSDGSFFLYSKLTVDKGRWQQQNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFFPDSBQLK SGTASVVCILLINFIYREA KYQMKVDNALQSNQS VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)

WO 2022/223966

PCT/GB2022/050989

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-D ₅ _H ₀ (hlgG ₁)	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTFNINIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGGS SAGAGENIWQGGTLVTVSS (SEQ ID NO: 174)	DIVMTQTPSSVSAVNG DVTIIQCAQSOSINSG LAMYQKQKQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLSC ADAAITYCQSVHYISA NGATFGGTEVYVE (SEQ ID NO: 61)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 158)
	GFTSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTSLNINIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGSLV SAGAGENIWQGGTLVTVSS (SEQ ID NO: 175)	DIVMTQTPSSVSAVNG DVTIIQCAQSOSINSG LAMYQKQKQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLSC ADAAITYCQSVHYISA NGATFGGTEVYVE (SEQ ID NO: 61)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	TVAAPSVTIFPFSDEQLK SGTASVVCLLNNFYPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLSLSTLT LSKADTEKHKVYACAEVTH QGLSSPVTKSGFNRGEC (SEQ ID NO: 158)
1-D ₅ _H ₂ (hlgG ₁)	GFTSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QQQLVESGGGVQFGRSLRL SCAASGFTSLNINIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNMTLQM NSLEAEDTAVYTCARGSSA GAGFNITWQGGTLVTVSS (SEQ ID NO: 176)	DIVMTQTPSSVSAVNG DVTIIQCAQSOSINSG LAMYQKQKQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLSC ADAAITYCQSVHYISA NGATFGGTEVYVE (SEQ ID NO: 61)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	TVAAPSVTIFPFSDEQLK SGTASVVCLLNNFYPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLSLSTLT LSKADTEKHKVYACAEVTH QGLSSPVTKSGFNRGEC (SEQ ID NO: 158)
	GFTSLNYD (SEQ ID NO: 177)	IHTAGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSQWY NT (SEQ ID NO: 74)	QVQLVESGGGVQFGRSLRL SCAASGFTFNINIMGWYRQA PKGLEWVAIIISIGSTYYA NWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV DLNHWQQTILVTVSS (SEQ ID NO: 178)	AIKMTQTPSSVSAVNG GTVTINQCAQSOSVYN NLISWYQKQKQPPKRLI LYDASTLASGVPSFRFG KSGSGDTFTLTISGLV QCEDAATYTCQGSYYS SGWNTFGGTEVYVE (SEQ ID NO: 79)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	TVAAPSVTIFPFSDEQLK SGTASVVCLLNNFYPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLSLSTLT LSKADTEKHKVYACAEVTH QGLSSPVTKSGFNRGEC (SEQ ID NO: 158)
3-H ₉ _H ₁ (hlgG ₁)	GFTSLNYD (SEQ ID NO: 63)	IHTAGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSQWY NT (SEQ ID NO: 74)	QVQLVESGGGVQFGRSLRL SCAASGFTSLNINIMGWYRQA PKGLEWVAIIISIGSTYYA NWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV DLNHWQQTILVTVSS (SEQ ID NO: 179)	AIKMTQTPSSVSAVNG GTVTINQCAQSOSVYN NLISWYQKQKQPPKRLI LYDASTLASGVPSFRFG KSGSGDTFTLTISGLV QCEDAATYTCQGSYYS SGWNTFGGTEVYVE (SEQ ID NO: 79)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	TVAAPSVTIFPFSDEQLK SGTASVVCLLNNFYPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLSLSTLT LSKADTEKHKVYACAEVTH QGLSSPVTKSGFNRGEC (SEQ ID NO: 158)
	GFTSLNYD (SEQ ID NO: 63)	IHTAGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSQWY NT (SEQ ID NO: 74)	QVQLVESGGGVQFGRSLRL SCAASGFTSLNINIMGWYRQA PKGLEWVAIIISIGSTYYA NWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV DLNHWQQTILVTVSS (SEQ ID NO: 179)	AIKMTQTPSSVSAVNG GTVTINQCAQSOSVYN NLISWYQKQKQPPKRLI LYDASTLASGVPSFRFG KSGSGDTFTLTISGLV QCEDAATYTCQGSYYS SGWNTFGGTEVYVE (SEQ ID NO: 79)	ASTKGESVFELAFSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSGVHTFPFV LQSSGLYSLSVTVTFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPFRFKDTIMLSRTP EVTCVVDVSHEDPEFVENWYVDGVEVH NAKTREREQNSITRYRVSVTLVHLQDW LNKREYKCKVSKNALPAFIEKTIISKAKG QFREQVYTLFPSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNTKTPFP LSDSGSFFLYSKLTIVDKSRWQQGNVFSC SVMEHALHNHYTKQSLSLSFSGK (SEQ ID NO: 157)	TVAAPSVTIFPFSDEQLK SGTASVVCLLNNFYPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLSLSTLT LSKADTEKHKVYACAEVTH QGLSSPVTKSGFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
3-H9_H2 (hlgG1)	GFLSNYD (SEQ ID NO: 63)	IYHGDT (SEQ ID NO: 64)	ARGFLVDM (SEQ ID NO: 65)	QSVYSHNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSGWY NT (SEQ ID NO: 74)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMWVRQAP GRGLEWIGSYTHAIGTYYAN WAGREFTISRDNKNTVYLQAN SLRAEDTAIFYCARGLVDLN MWGGTLVTYSS (SEQ ID NO: 180)	AIKMTQTFPSLSASVG ETVIRCLASEDIYSG NLISWYQQKPKPTLLI LITDASTLESQVPSRP KGSGSGFTLTITISGV QCEDAATYICQGSYIS SGWNTATFGGTEVVE (SEQ ID NO: 79)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGKREYKVKSKALPAFIEKTIISKAG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWKRVNDALOSNGSQS VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)
1-A2_Ho (hlgG1)	GFTFSNA (SEQ ID NO: 164)	IYHGDT (SEQ ID NO: 10)	ARGFLYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQVQGRSIRL SCAASGIDITSNAMWVRQA PGKLEWVAGIYGHDTSYIA AWAKGRTISRDNKNTLYL QMSLRADTAIFYCARGFI YFDIWQQGTLVTYSS (SEQ ID NO: 165)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYLTITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGKREYKVKSKALPAFIEKTIISKAG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWKRVNDALOSNGSQS VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)
1-A2_H1 (hlgG1)	GIDLTSA (SEQ ID NO: 9)	IYHGDT (SEQ ID NO: 10)	ARGFLYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQVQGRSIRL SCAASGIDITSNAMWVRQA PGKLEWVAGIYGHDTSYIA AWAKGRTISRDNKNTLYL QMSLRADTAIFYCARGFI YFDIWQQGTLVTYSS (SEQ ID NO: 194)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYLTITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGKREYKVKSKALPAFIEKTIISKAG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWKRVNDALOSNGSQS VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)
1-A2_H2 (hlgG1)	GIDLTSA (SEQ ID NO: 9)	IYHGDT (SEQ ID NO: 10)	ARGFLYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMWVRQAP GRGLEWIGIYGHDTSYAA WAKGRTISRDNKNTVYLQAN SLRAEDTAIFYCARGIFYD IWGGTLVTYSS (SEQ ID NO: 172)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYLTITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGKREYKVKSKALPAFIEKTIISKAG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWKRVNDALOSNGSQS VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)

WO 2022/223966

PCT/GB2022/050989

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-G ₅ _H ₀ (hlgG ₁)	GFTFSYD (SEQ ID NO: 181)	IHAIGT (SEQ ID NO: 82)	ARGLVLLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSVYSGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSYDMTWRRQ PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLRADTAVYFCARGIV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKQPKPKLL LYYDASTLASGVSRFP SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGKTVVK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
	GFTLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVLLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSVYSGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSYDMTWRRQ PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLRADTAVYFCARGIV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKQPKPKLL LYYDASTLASGVSRFP SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGKTVVK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
1-G ₅ _H ₂ (hlgG ₁)	GFTLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVLLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSVYSGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSYDMTWRRQ PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLRADTAVYFCARGIV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKQPKPKLL LYYDASTLASGVSRFP SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGKTVVK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
	GFTLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVLLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSVYSGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSYDMTWRRQ PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLRADTAVYFCARGIV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKQPKPKLL LYYDASTLASGVSRFP SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGKTVVK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
4-H ₃ _L ₀ (hlgGK)	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	SQSLEESGRLVFPFGTEPLTL TCTVSGIDLTSMAMWRRQ PCKGLEWIGSYGHDTSYIA AMAKGRFTISRSTIVDLRM TRPTDIDTATYFCARGIYF DIWGTGTIVTSS	DIQMTQSPFSLASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISLQAP EDFATYTLGGYSFAS NGLTPGGTKYELK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	SQSLEESGRLVFPFGTEPLTL TCTVSGIDLTSMAMWRRQ PCKGLEWIGSYGHDTSYIA AMAKGRFTISRSTIVDLRM TRPTDIDTATYFCARGIYF DIWGTGTIVTSS	DIQMTQSPFSLASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISLQAP EDFATYTLGGYSFAS NGLTPGGTKYELK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
4-H ₃ _L ₁ (hlgGK)	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	SQSLEESGRLVFPFGTEPLTL TCTVSGIDLTSMAMWRRQ PCKGLEWIGSYGHDTSYIA AMAKGRFTISRSTIVDLRM TRPTDIDTATYFCARGIYF DIWGTGTIVTSS	DIQMTQSPFSLASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISLQAP EDFATYTLGGYSFAS NGLTPGGTKYELK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	SQSLEESGRLVFPFGTEPLTL TCTVSGIDLTSMAMWRRQ PCKGLEWIGSYGHDTSYIA AMAKGRFTISRSTIVDLRM TRPTDIDTATYFCARGIYF DIWGTGTIVTSS	DIQMTQSPFSLASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISLQAP EDFATYTLGGYSFAS NGLTPGGTKYELK	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGHTFPFPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKRSCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAPSVFIFPPSDQKLK SGTASVVCCLLNINFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTKSFNGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-D5_Lo (hlgGK)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSIING (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVFTGPTLTL TCVAVSGFLSNVYIMGWVQA PCKGLGYIGISTGGSTYYA SWAKGRFTISKSTIMDLKM TSLTTEDTATYFCARGSSA GAGFNIMPGTGLTVSS (SEQ ID NO: 52)	DIQMTQSFSSLSASVG DRAVITTCQASQISNG LVLLYQKQKGRKAPKLLI YKASTLASGVSPRFSG SSGSGTDFLTILISLQF EQAFTIYQSVHYISA NGATFGGGTKVEIK (SEQ ID NO: 187)	RGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQKL SGTASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLASLT LTKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
								ASTKGFQSVFFLAESKSKTSGGTAALGCL LQSSGLYSLSSVTVFPSSLSIGTQYICN VNHKFSNTVKVKRFBKSCDKTHCTPCC PAPELLLGSGSVFLFFPEKDKTLMILSRTP EVTCCVVVDVSHDEPVENRWYVDGVGVH NAKTKPREQNYSTRYRVSVLVLIHQDM LNGKYEYKVKSNALPAFTEKTIISKAG QPREQVYITLFPSSRDELTKNQVSLTCLV KGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)		
1-D5_L1 (hlgGK)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSIING (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVFTGPTLTL TCVAVSGFLSNVYIMGWVQA PCKGLGYIGISTGGSTYYA SWAKGRFTISKSTIMDLKM TSLTTEDTATYFCARGSSA GAGFNIMPGTGLTVSS (SEQ ID NO: 52)	DIQMTQSFSSLSASVG DRAVITTCQASQISNG LVLLYQKQKGRKAPKLLI YKASTLASGVSPRFSG SSGSGTDFLTILISLQF EQAFTIYQSVHYISA NGATFGGGTKVEIK (SEQ ID NO: 188)	RGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQKL SGTASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLASLT LTKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
								ASTKGFQSVFFLAESKSKTSGGTAALGCL LQSSGLYSLSSVTVFPSSLSIGTQYICN VNHKFSNTVKVKRFBKSCDKTHCTPCC PAPELLLGSGSVFLFFPEKDKTLMILSRTP EVTCCVVVDVSHDEPVENRWYVDGVGVH NAKTKPREQNYSTRYRVSVLVLIHQDM LNGKYEYKVKSNALPAFTEKTIISKAG QPREQVYITLFPSSRDELTKNQVSLTCLV KGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)		
3-H9_Lo (hlgGK)	GFSLNNYD (SEQ ID NO: 63)	THAIGIT (SEQ ID NO: 64)	ARGVLDAIM (SEQ ID NO: 65)	QSVYSNNIL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYTSYSGWY NT (SEQ ID NO: 74)	QSQIESGRLVFTGPTLTL TCVSVSGFLSNVYIMGWVQA PCKGLEWFTGISHTGYIA NBAEGRFTISKSTIVDLKM TSLTTEDTATYFCARGLVOL NMGKRGTLTVSS (SEQ ID NO: 160)	DIQMTQSFSSLSASVG DRAVITTCQASQSYIEN NLLSWYQKQKGRKAPRL LIYDASTLQSGVSPRFL SSGSGSGTDFLTILISL QPREQFATYICQGSYIS SGWNTFGGGTKVEIK (SEQ ID NO: 189)	RGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQKL SGTASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLASLT LTKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
								ASTKGFQSVFFLAESKSKTSGGTAALGCL LQSSGLYSLSSVTVFPSSLSIGTQYICN VNHKFSNTVKVKRFBKSCDKTHCTPCC PAPELLLGSGSVFLFFPEKDKTLMILSRTP EVTCCVVVDVSHDEPVENRWYVDGVGVH NAKTKPREQNYSTRYRVSVLVLIHQDM LNGKYEYKVKSNALPAFTEKTIISKAG QPREQVYITLFPSSRDELTKNQVSLTCLV KGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)		
1-A2_Lo (hlgGK)	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFTYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTID LT (SEQ ID NO: 20)	QSQVYESGRLVFTGPTLTL TCTVSVGIDLTSNAMVWVQA PCKGLEWFTGISHTGYIA AMAKGRFTISKSTIVDLKM TRPTTDDTATYFCARGEYIF DIMTGTGLTVSS (SEQ ID NO: 156)	DIQMTQSFSSLSASVG DRAVITTCASDITYSG LSWYQKQKGRKAPKLLI YKASNLGSGVSPRFSG SSGSGTDFLTILISLQF EQAFTIYCLGHHSHST TDLTFGGGTKVEIK (SEQ ID NO: 190)	RGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQKL SGTASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKOSTYSLASLT LTKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
								ASTKGFQSVFFLAESKSKTSGGTAALGCL LQSSGLYSLSSVTVFPSSLSIGTQYICN VNHKFSNTVKVKRFBKSCDKTHCTPCC PAPELLLGSGSVFLFFPEKDKTLMILSRTP EVTCCVVVDVSHDEPVENRWYVDGVGVH NAKTKPREQNYSTRYRVSVLVLIHQDM LNGKYEYKVKSNALPAFTEKTIISKAG QPREQVYITLFPSSRDELTKNQVSLTCLV KGFYFSDIAVWESNGQFENNKTITPPV LSDSGSFFLYSKLTVDKSRWQQGNVFC SYMHEALHHYTKQSLSISFSGK (SEQ ID NO: 157)		

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-A2_L1 (hlgGK)	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHITD LT (SEQ ID NO: 20)	SQSVEESGRLVFGTEPLTL TCTVSGIDLTSMAMWRQAP CGKLEWIGISIHATGTFYA AMAKGRTIISRTISYVLQNM TRPTIDDTATYFCARGFIYFD DIWGTGLTVTSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLESQVSRFSG SGSGTDYTLTISSLP EDFATYICLGGHSHIT TDLTPGGTKVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GFSLSYD (SEQ ID NO: 8)	IHAIGT (SEQ ID NO: 82)	ARGVLQNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWMD TA (SEQ ID NO: 92)	SQSLEESGRLVFGTEPLTL TCTVSGFSLSSVDMWRQAP CGKLEWIGISIHATGTFYA NAKGRFTISRTISYVLQNM TSLTIDEDTATYFCARGVLVDL NMGPGTILVTVSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG NLYSWYQKPKGKAPKLLI LYLDASTLASGVSRF SGSGTDFTLTISLL QPEDFATYICGGSYYS GGMDFATGGGTVKEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
1-G5_L1 (hlgGK)	GFSLSYD (SEQ ID NO: 8)	IHAIGT (SEQ ID NO: 82)	ARGVLQNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWMD TA (SEQ ID NO: 92)	SQSLEESGRLVFGTEPLTL TCTVSGFSLSSVDMWRQAP CGKLEWIGISIHATGTFYA NAKGRFTISRTISYVLQNM TSLTIDEDTATYFCARGVLVDL NMGPGTILVTVSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG NLYSWYQKPKGKAPKLLI LYLDASTLASGVSRF SGSGTDFTLTISLL QPEDFATYICGGSYYS GGMDFATGGGTVKEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
1-A2_H2_L1	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHITD LT (SEQ ID NO: 20)	QQLVESGGGVQFGRSIRLS CAASGIDLTSMAMWRQAP CGKLEWIGISIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLESQVSRFSG SGSGTDYTLTISSLP EDFATYICLGGHSHIT TDLTPGGTKVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHITD LT (SEQ ID NO: 20)	QQLVESGGGVQFGRSIRLS CAASGIDLTSMAMWRQAP CGKLEWIGISIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLESQVSRFSG SGSGTDYTLTISSLP EDFATYICLGGHSHIT TDLTPGGTKVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
1-A2_H2_Lo	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHITD LT (SEQ ID NO: 20)	QQLVESGGGVQFGRSIRLS CAASGIDLTSMAMWRQAP CGKLEWIGISIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLESQVSRFSG SGSGTDYTLTISSLP EDFATYICLGGHSHIT TDLTPGGTKVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHITD LT (SEQ ID NO: 20)	QQLVESGGGVQFGRSIRLS CAASGIDLTSMAMWRQAP CGKLEWIGISIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLESQVSRFSG SGSGTDYTLTISSLP EDFATYICLGGHSHIT TDLTPGGTKVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGK QPREPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEEKHYACIEVTH QGLSSPVTIKSFNAGEC (SEQ ID NO: 158)

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-A2_H1_L1	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGILTSSNAMWVRA PGKLEWVAGIYGHDTSYIA AMAKGRFTISRDNKNTLYL QMSLRADTAVYICARGEI YFDLWGQGITLVVSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 191)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSLTSGVHTFPV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNKREYKCKVSKALPAFIEKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFFLYSLKLTVDKSRWQQGNVFC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKVNDALQSGNSQES VTEQSKDSKSTYSLSLT LQKADYEKHKVYACEVTH QGSSPVTKSNRGC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 9)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGILTSSNAMWVRA PGKLEWVAGIYGHDTSYIA AMAKGRFTISRDNKNTLYL QMSLRADTAVYICARGEI YFDLWGQGITLVVSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 190)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSLTSGVHTFPV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNKREYKCKVSKALPAFIEKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFFLYSLKLTVDKSRWQQGNVFC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKVNDALQSGNSQES VTEQSKDSKSTYSLSLT LQKADYEKHKVYACEVTH QGSSPVTKSNRGC (SEQ ID NO: 158)
1-A2_Ho_L1	GFTSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGFTSSNAMWVRA PGKLEWVAGIYGHDTSYIA AMAKGRFTISRDNKNTLYL QMSLRADTAVYICARGEI YFDLWGQGITLVVSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 191)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSLTSGVHTFPV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNKREYKCKVSKALPAFIEKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFFLYSLKLTVDKSRWQQGNVFC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKVNDALQSGNSQES VTEQSKDSKSTYSLSLT LQKADYEKHKVYACEVTH QGSSPVTKSNRGC (SEQ ID NO: 158)
	GFTSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGFTSSNAMWVRA PGKLEWVAGIYGHDTSYIA AMAKGRFTISRDNKNTLYL QMSLRADTAVYICARGEI YFDLWGQGITLVVSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 190)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSLTSGVHTFPV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNKREYKCKVSKALPAFIEKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFFLYSLKLTVDKSRWQQGNVFC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKVNDALQSGNSQES VTEQSKDSKSTYSLSLT LQKADYEKHKVYACEVTH QGSSPVTKSNRGC (SEQ ID NO: 158)

[illegible]

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
4-H3_H6_Lo			ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 170)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	RGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 169)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSLT LTKADYEKKHYACIEVTH LQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H5_L1			ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 169)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSLT LTKADYEKKHYACIEVTH LQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 168)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSLT LTKADYEKKHYACIEVTH LQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H4_L1			ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 168)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSLT LTKADYEKKHYACIEVTH LQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQVQGRSIRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYICARGFIYFD IWGGGLTVTSS (SEQ ID NO: 168)	DIQMTQSPSSLSASVG DRVTITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTSSSLQ EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTSGVTHFPV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPEPKKOTLMISRT EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYINSTRYVSVLTVLHQW LNKREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSLT LTKADYEKKHYACIEVTH LQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
4-H3_H1_L1	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGIDLTSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 194)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGIDLTSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 194)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)
4-H3_Ho_L1 rep	GFTFSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGFTFSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 165)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)
	GFTFSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGFTFSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 165)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)
4-H3_Ho_Lo	GFTFSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGFTFSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 165)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)
	GFTFSSNA (SEQ ID NO: 164)	IYGHDT (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVQPGSRSLR SCAASGFTFSSANMWVRQ PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMSLRADITAVYCARGEI YFDLWQQGITLVSS (SEQ ID NO: 165)	DYQMTPSFSSLSASVG DRVITITCLASEDTASG ISWYQKPKGAPKLLI YGASNLESGVSRFSG SGSGDTFTLTLSLQIP EDFATYICLGSGFS NGLTFGGGKVEIK (SEQ ID NO: 186)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEPTVMSNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEPKSCDKTHICPC PAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQDW LNGREYKCKVSKALPAFIEKTIISKAG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQDSGSFFLYSKLTVDKSRWQQGNFSC SVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPDSQQLK SGTASVCLLNNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYLSLSSTLT LQKADYEEKHYACAEVTH QGLSSPVTKSNRGEIC (SEQ ID NO: 158)

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-D ₅ _H ₂ _L ₁	GFSLNYYI (SEQ ID NO: 45)	ISTGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QTSNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVSGGGVQVQPSRLRL SCAASGFSLLNIYIMGWQRA PKGLEWAIILISTGSTYYA SWAKGFTIIRSDNKNLTLYL QMSLRABDTAVTYCARGSSA SAGAGFTIWQGGTLVTYSS (SEQ ID NO: 176)	DIQMTQSPSSLSASVG LWYITTCQASQNSNG LWYKQKPKGKAPKRLI YKASTLASGVPSPRFG SGSGDTFTLTSSLOP EDFATYTCQSYHYISA NGATEGGGTKYEIK (SEQ ID NO: 188)	ASTKGSVFPELAPSSKSTSGGTAALGCL VKDYFFPEVTVMSNGALITSGVHTFPFV LQSSGLYSLSSVTVFSSSISGTTQYICN VNHKFSNTKDKVPEKSCDKTHCTCPCC PAFELLGGSESVFLPFPEKQKTLIMLSRTP EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPREQYINSTYAVSVTLVTHQDW LNKGEYKCVSNKALPAEIKETISKARG QRFEPQVTLTPESRDLTKNQVSLTCLV KGFFYSDIADVEMESNQEPENNTKTFPFV LQSGSGFFFLYSKLTVDKSRQQQGNVFSC SVNHEALHNHYTQKSILSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQLK SGTASVVCCLLNINFPREA KYQWKVDNALQSGNSQES VTEQDSKSTYSISLTIL LSKADVEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D ₅ _H ₂ _L ₀	GFSLNYYI (SEQ ID NO: 45)	ISTGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QTSNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVSGGGVQVQPSRLRL SCAASGFSLLNIYIMGWQRA PKGLEWAIILISTGSTYYA SWAKGFTIIRSDNKNLTLYL QMSLRABDTAVTYCARGSSA SAGAGFTIWQGGTLVTYSS (SEQ ID NO: 176)	DIQMTQSPSSLSASVG LWYITTCQASQNSNG LWYKQKPKGKAPKRLI YKASTLASGVPSPRFG SGSGDTFTLTSSLOP EDFATYTCQSYHYISA NGATEGGGTKYEIK (SEQ ID NO: 187)	ASTKGSVFPELAPSSKSTSGGTAALGCL VKDYFFPEVTVMSNGALITSGVHTFPFV LQSSGLYSLSSVTVFSSSISGTTQYICN VNHKFSNTKDKVPEKSCDKTHCTCPCC PAFELLGGSESVFLPFPEKQKTLIMLSRTP EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPREQYINSTYAVSVTLVTHQDW LNKGEYKCVSNKALPAEIKETISKARG QRFEPQVTLTPESRDLTKNQVSLTCLV KGFFYSDIADVEMESNQEPENNTKTFPFV LQSGSGFFFLYSKLTVDKSRQQQGNVFSC SVNHEALHNHYTQKSILSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQLK SGTASVVCCLLNINFPREA KYQWKVDNALQSGNSQES VTEQDSKSTYSISLTIL LSKADVEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D ₅ _H ₁ _L ₀	GFSLNYYI (SEQ ID NO: 45)	ISTGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QTSNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVSGGGVQVQPSRLRL SCAASGFSLLNIYIMGWQRA PKGLEWAIILISTGSTYYA SWAKGFTIIRSDNKNLTLYL QMSLRABDTAVTYCARGGS SAGAGFTIWQGGTLVTYSS (SEQ ID NO: 175)	DIQMTQSPSSLSASVG LWYITTCQASQNSNG LWYKQKPKGKAPKRLI YKASTLASGVPSPRFG SGSGDTFTLTSSLOP EDFATYTCQSYHYISA NGATEGGGTKYEIK (SEQ ID NO: 188)	ASTKGSVFPELAPSSKSTSGGTAALGCL VKDYFFPEVTVMSNGALITSGVHTFPFV LQSSGLYSLSSVTVFSSSISGTTQYICN VNHKFSNTKDKVPEKSCDKTHCTCPCC PAFELLGGSESVFLPFPEKQKTLIMLSRTP EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPREQYINSTYAVSVTLVTHQDW LNKGEYKCVSNKALPAEIKETISKARG QRFEPQVTLTPESRDLTKNQVSLTCLV KGFFYSDIADVEMESNQEPENNTKTFPFV LQSGSGFFFLYSKLTVDKSRQQQGNVFSC SVNHEALHNHYTQKSILSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQLK SGTASVVCCLLNINFPREA KYQWKVDNALQSGNSQES VTEQDSKSTYSISLTIL LSKADVEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D ₅ _H ₀ _L ₁	GFTEFSNYYI (SEQ ID NO: 173)	ISTGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QTSNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVSGGGVQVQPSRLRL SCAASGFTFSNIIYIMGWQRA PKGLEWAIILISTGSTYYA SWAKGFTIIRSDNKNLTLYL QMSLRABDTAVTYCARGGS SAGAGFTIWQGGTLVTYSS (SEQ ID NO: 174)	DIQMTQSPSSLSASVG LWYITTCQASQNSNG LWYKQKPKGKAPKRLI YKASTLASGVPSPRFG SGSGDTFTLTSSLOP EDFATYTCQSYHYISA NGATEGGGTKYEIK (SEQ ID NO: 188)	ASTKGSVFPELAPSSKSTSGGTAALGCL VKDYFFPEVTVMSNGALITSGVHTFPFV LQSSGLYSLSSVTVFSSSISGTTQYICN VNHKFSNTKDKVPEKSCDKTHCTCPCC PAFELLGGSESVFLPFPEKQKTLIMLSRTP EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPREQYINSTYAVSVTLVTHQDW LNKGEYKCVSNKALPAEIKETISKARG QRFEPQVTLTPESRDLTKNQVSLTCLV KGFFYSDIADVEMESNQEPENNTKTFPFV LQSGSGFFFLYSKLTVDKSRQQQGNVFSC SVNHEALHNHYTQKSILSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIFFPSDEQLK SGTASVVCCLLNINFPREA KYQWKVDNALQSGNSQES VTEQDSKSTYSISLTIL LSKADVEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

[illegible]

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-G ₅ _H ₂ _L ₁	GFSLSSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 184)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 193)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GFSLSSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 184)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 192)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)
1-G ₅ _H ₁ _L ₁	GFSLSSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 183)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 193)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GFSLSSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 182)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 193)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)
1-G ₅ _H ₀ _L ₁	GTFSSYD (SEQ ID NO: 181)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 182)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 193)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GTFSSYD (SEQ ID NO: 181)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QQLVESGGGVVQFGRSLRL CAASGFSLSYSDMTWVRQAP PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQGSLIVTVSS (SEQ ID NO: 182)	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK (SEQ ID NO: 193)	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFVAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKHTCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKALFAPIEKTIISKAGG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSITYSLSSTLT LQKADYEKHKVYACEVTH LQGLSSPVTKSFNGRGC (SEQ ID NO: 158)

WO 2022/223966

PCT/GB2022/050989

Antibody	CDR-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
									RGFYFSDIAVEWESNGQFENNYKTTPEV LSDSGSFFLYSKLTVDKSRWQQGNFSC SYMHEALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	
1-G5_Ho_Lo	GFTFSSYD (SEQ ID NO: 181)	IHAIGIT (SEQ ID NO: 82)	ARGLDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWD TA (SEQ ID NO: 92)	QVQLVESGGGVYQPGRLRL SCAASGFTFSSYDMTWQRA PGKGLWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLRADTAVYICARGLV DLNHWGGTILTVGS (SEQ ID NO: 182)	DIQMTQSPFSSLSASVG DRVLTITCQASQSYNN NYLSWYQQKPKGAPKL LIYDASTCLASGVFSRP SGSGSGDFTLTISLL QPEDFATYYCQGSYYS GGMDTAFGGGKVEIK (SEQ ID NO: 192)	ASTKGISVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTISGVHTFPV LQSSGLYSLSVVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKSCDKTHICPC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEYH NAKTREDEQYNSTYRVSVLTVVLHQDW LNKREYKEKYNKALFAPIEKTIISKAG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYFSDIAVEWESNGQFENNYKTTPEV LSDSGSFFLYSKLTVDKSRWQQGNFSC SYMHEALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDRLK SGTASVVCLLNNFYREA KVQWKVDNALQSGNSQES VTEQDSKDSSTYSLSSTLT LGRADYEKKYVACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Figure 11

Antibody	ka (1/Ms)	kd (1/s)	KD (M)
1-A2 parent	5.93E+04	4.76E-07	8.02E-12
1-A2_VH-par_VL-par	6.64E+04	8.30E-09	1.25E-13
1-A2_VH-par_L1	2.56E+04	1.81E-07	7.07E-12
1-A2_VH-par_L0	5.96E+04	7.44E-07	1.25E-11
1-A2_H2_VL-par	2.45E+04	7.80E-06	3.18E-10
1-A2_H2_L1	1.90E+04	3.84E-08	2.03E-12
1-A2_H2_L0	3.61E+04	3.50E-06	9.69E-11
1-A2_H1_VL-par	3.98E+04	9.49E-07	2.38E-11
1-A2_H1_L1	2.38E+04	1.40E-07	5.89E-12
1-A2_H1_L0	3.49E+04	6.54E-07	1.87E-11
1-A2_H0_VL-par	3.51E+04	6.18E-07	1.76E-11
1-A2_H0_L1	6.32E+04	2.73E-06	4.32E-11
1-A2_H0_L0	1.19E+05	2.74E-08	2.31E-13

Antibody	ka (1/Ms)	kd (1/s)	KD (M)
4-H3 parent	1.86E+05	2.84E-06	1.53E-11
4-H3_VH-par_VL-par	1.37E+05	9.81E-06	7.17E-11
4-H3_VH-par_L1	1.23E+04	1.75E-08	1.43E-12
4-H3_VH-par_L0	4.88E+04	8.46E-08	1.73E-12
4-H3_H8_VL-par	5.49E+04	5.99E-07	1.09E-11
4-H3_H8_L1	5.28E+04	9.15E-07	1.73E-11
4-H3_H8_L0	4.52E+04	5.66E-07	1.25E-11
4-H3_H7_VL-par	2.93E+04	3.05E-07	1.04E-11
4-H3_H7_L1	6.54E+04	3.82E-07	5.84E-12
4-H3_H7_L0 rep	1.08E+05	1.73E-07	1.61E-12
4-H3_H6_VL-par rep	5.53E+04	3.63E-07	6.55E-12
4-H3_H6_L1	6.57E+04	1.14E-07	1.73E-12
4-H3_H6_L0	4.12E+04	2.67E-08	6.49E-13
4-H3_H5_VL-par	2.69E+04	4.34E-07	1.61E-11
4-H3_H5_L1	1.03E+05	5.95E-08	5.75E-13
4-H3_H5_L0	1.35E+05	4.93E-08	3.66E-13

4-H3_H4_VL-par	Binding confirmed		
4-H3_H4_L1	4.45E+04	6.25E-09	1.4E-13
4-H3_H4_L0	2.71E+04	5.24E-07	1.93E-11
4-H3_H3_VL-par	5.42E+04	1.59E-06	2.94E-11
4-H3_H3_L1	1.15E+05	1.72E-07	1.49E-12
4-H3_H3_L0	7.56E+04	1.45E-07	1.92E-12
4-H3_H2_VL-par	9.00E+04	1.75E-06	1.94E-11
4-H3_H2_L1	2.99E+04	1.36E-07	4.53E-12
4-H3_H2_L0	3.35E+04	9.13E-07	2.73E-11
4-H3_H1_VL-par	2.82E+04	1.87E-07	6.64E-12
4-H3_H1_L1	3.10E+04	4.27E-07	1.38E-11
4-H3_H1_L0	1.34E+05	2.49E-06	1.87E-11
4-H3_H0_VL-par	2.21E+04	2.89E-07	1.31E-11
4-H3_H0_L1 rep	3.69E+04	1.52E-07	4.12E-12
4-H3_H0_L0	No binding		

Antibody	ka (1/Ms)	kd (1/s)	KD (M)
1-D5 parent	1.72E+05	4.20E-06	2.43E-11
1-D5_VH-par_VL-par	1.50E+05	3.34E-06	2.23E-11
1-D5_VH-par_L1	9.60E+04	7.91E-06	8.24E-11
1-D5_VH-par_L0	1.32E+05	6.59E-06	5E-11
1-D5_H2_VL-par	1.35E+05	4.20E-06	3.12E-11
1-D5_H2_L1	2.98E+05	1.13E-05	3.8E-11
1-D5_H2_L0	1.38E+05	1.06E-06	7.66E-12
1-D5_H1_VL-par	7.80E+04	2.37E-08	3.04E-13
1-D5_H1_L1	7.10E+04	6.72E-09	9.46E-14
1-D5_H1_L0	7.79E+04	1.25E-07	1.6E-12
1-D5_H0_VL-par	7.70E+04	2.38E-09	3.1E-14
1-D5_H0_L1	1.69E+05	2.99E-07	1.77E-12
1-D5_H0_L0	7.52E+04	1.13E-08	1.5E-13

Antibody	ka (1/Ms)	kd (1/s)	KD (M)
3-H9 parent	1.50E+05	9.05E-06	6.03E-11
3-H9_VH-par_VL-par	2.06E+05	8.94E-06	4.34E-11

3-H9_VH-par_L0	1.92E+05	2.12E-05	1.11E-10
3-H9_H2_VL-par	9.20E+04	1.14E-06	1.24E-11
3-H9_H2_L0	7.81E+04	8.74E-07	1.12E-11
3-H9_H1_VL-par	2.29E+04	7.18E-08	3.13E-12
3-H9_H1_L0	1.82E+04	2.84E-07	1.56E-11
3-H9_H0_VL-par	8.77E+04	3.59E-07	4.09E-12
3-H9_H0_L0	8.09E+04	8.46E-08	1.05E-12

Antibody	ka (1/Ms)	kd (1/s)	KD (M)
1-G5 parent	8.16E+04	2.07E-06	2.53E-11
1-G5_VH-par_VL-par	1.78E+05	8.45E-08	4.75E-13
1-G5_VH-par_L1	1.07E+05	1.28E-06	1.2E-11
1-G5_VH-par_L0	1.06E+05	3.80E-07	3.58E-12
1-G5_H2_VL-par	2.62E+04	3.78E-07	1.44E-11
1-G5_H2_L1	1.29E+05	2.25E-08	1.74E-13
1-G5_H2_L0	2.99E+04	3.90E-07	1.3E-11
1-G5_H1_VL-par	2.46E+04	1.66E-07	6.77E-12
1-G5_H1_L1	4.07E+04	6.03E-07	1.48E-11
1-G5_H1_L0	No binding		
1-G5_H0_VL-par rep	8.45E+04	7.20E-07	8.52E-12
1-G5_H0_L1	7.90E+04	1.02E-06	1.29E-11
1-G5_H0_L0	8.24E+04	9.05E-08	1.1E-12

Figure 12