

Figure 1

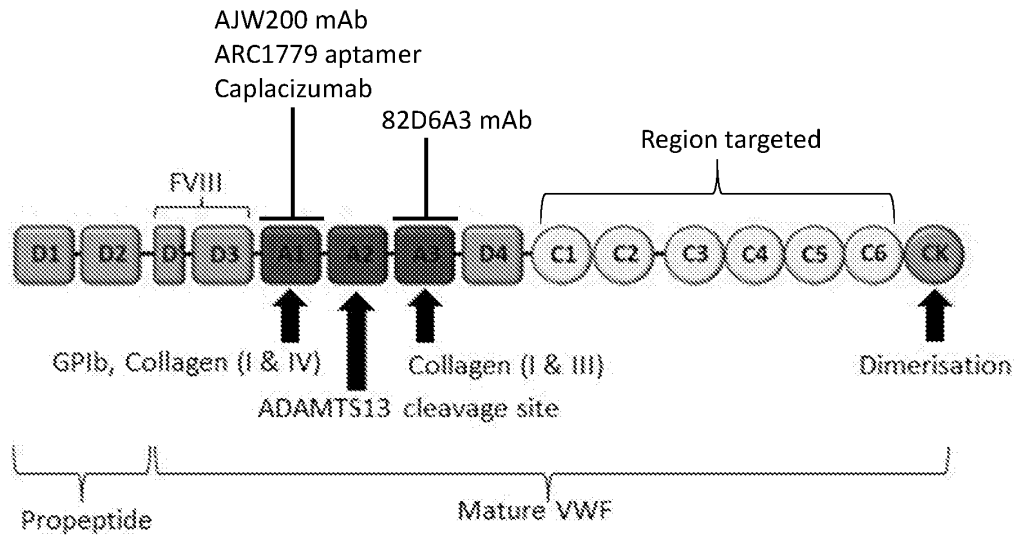


Figure 2

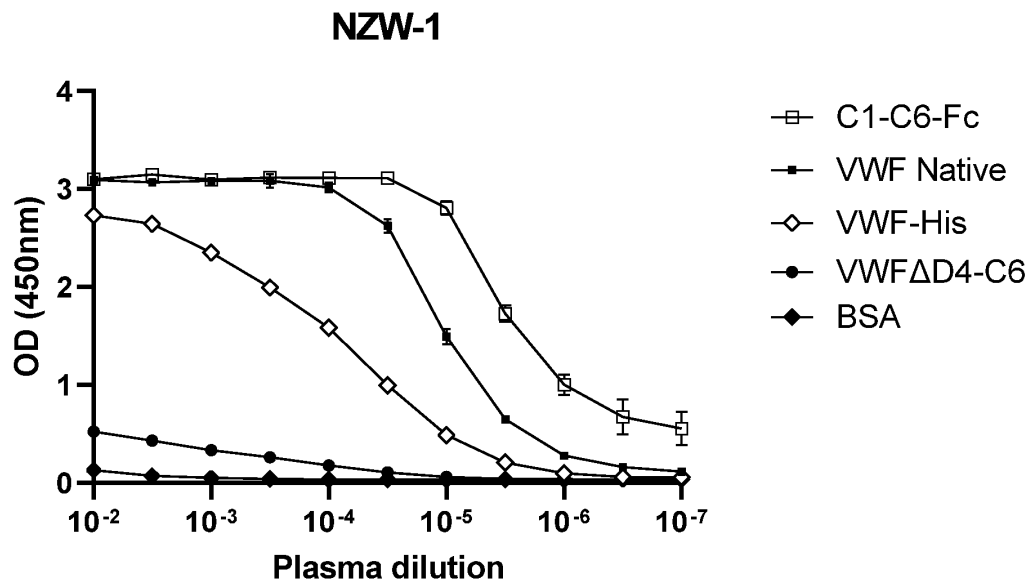


Figure 3A

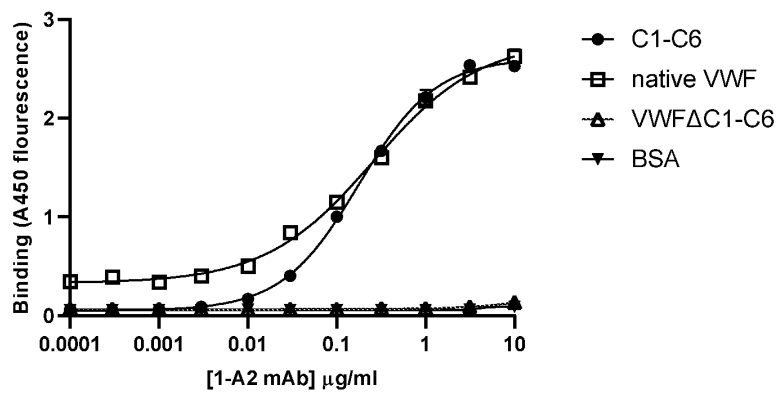


Figure 3B

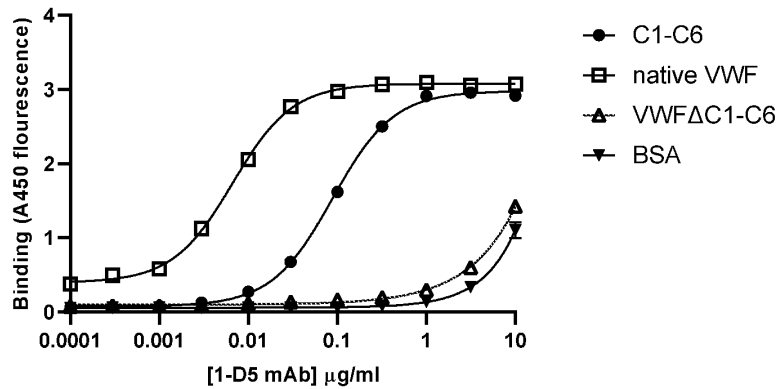


Figure 3C

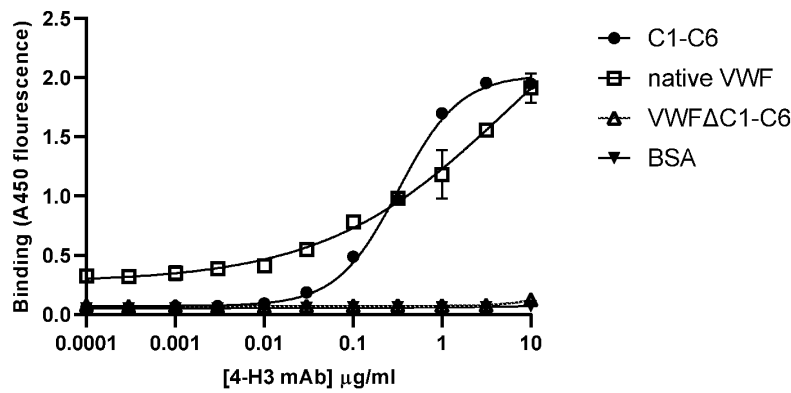


Figure 3D

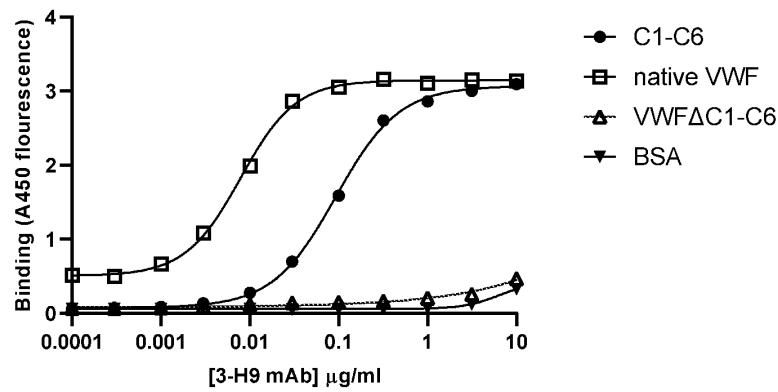


Figure 3E

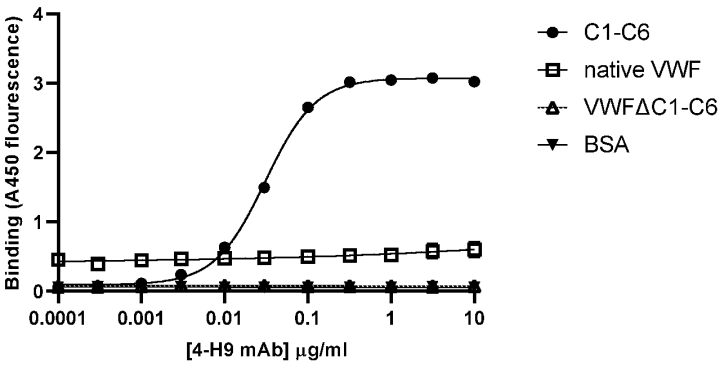


Figure 3F

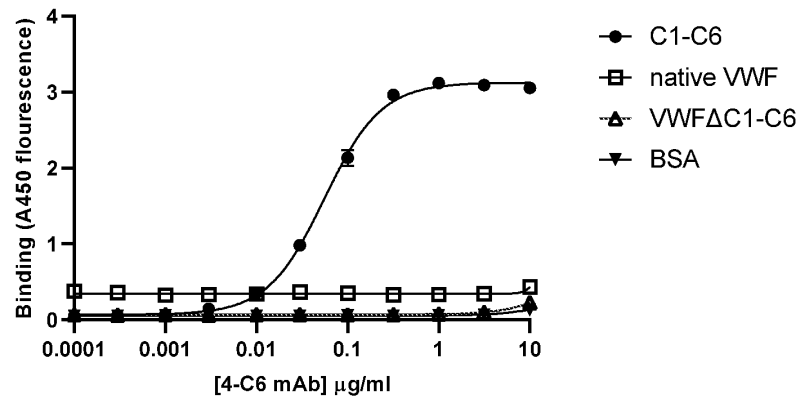


Figure 3G

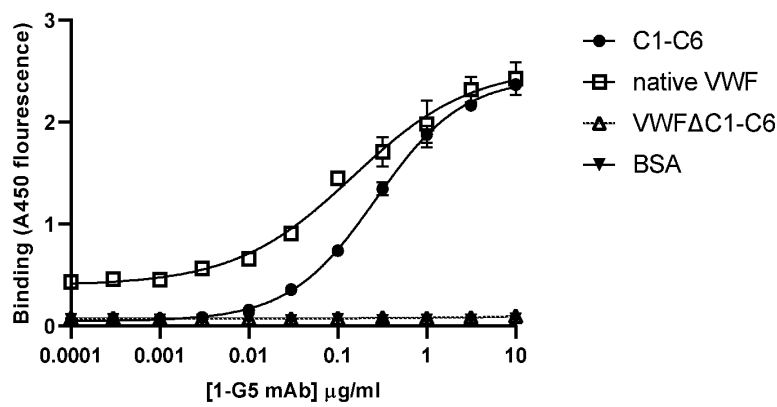


Figure 3H

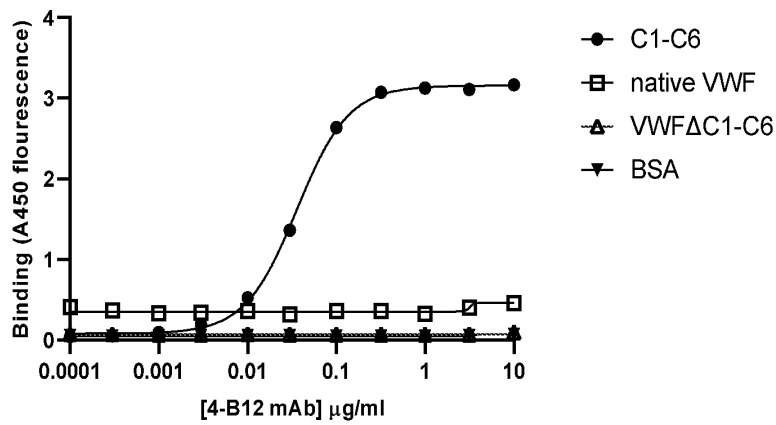


Figure 4

Antibody	Replicate #	k_a (1/Ms)	k_d (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

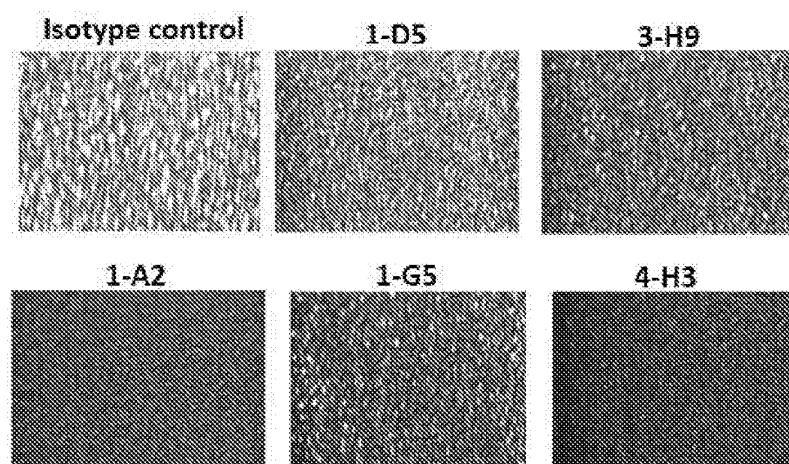
Figure 5

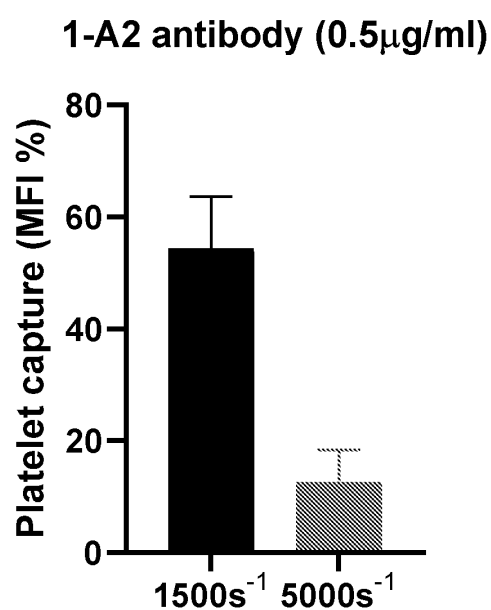
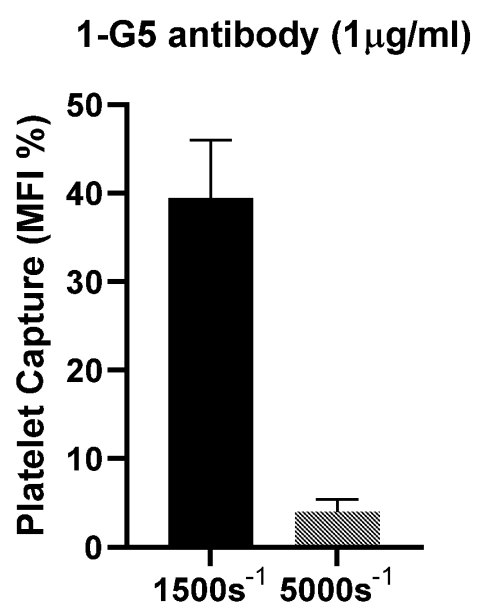
Figure 6A**Figure 6B**

Figure 6C

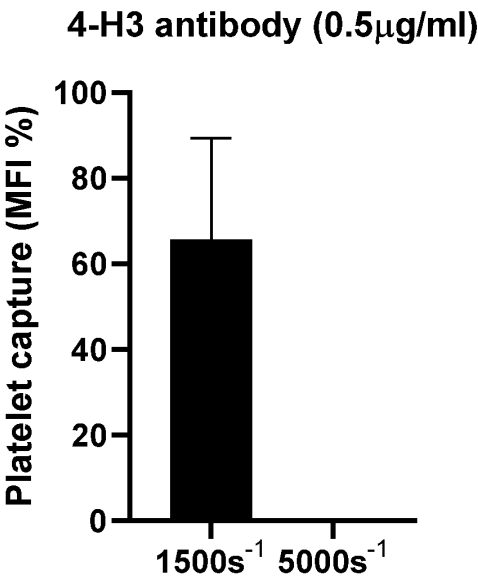


Figure 7A

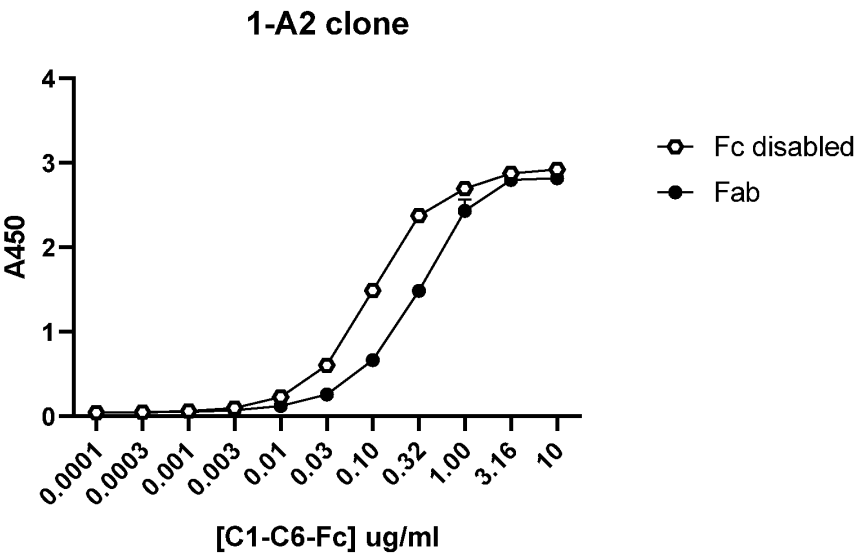


Figure 7B

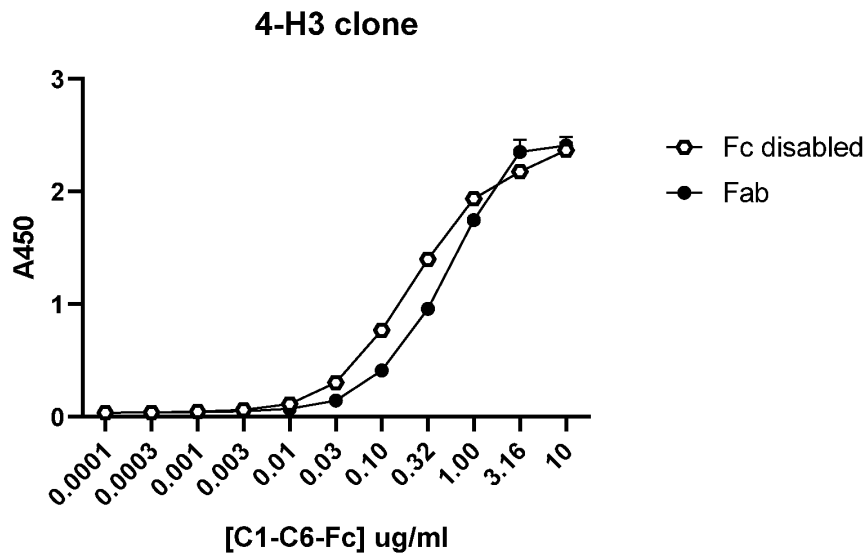


Figure 7C

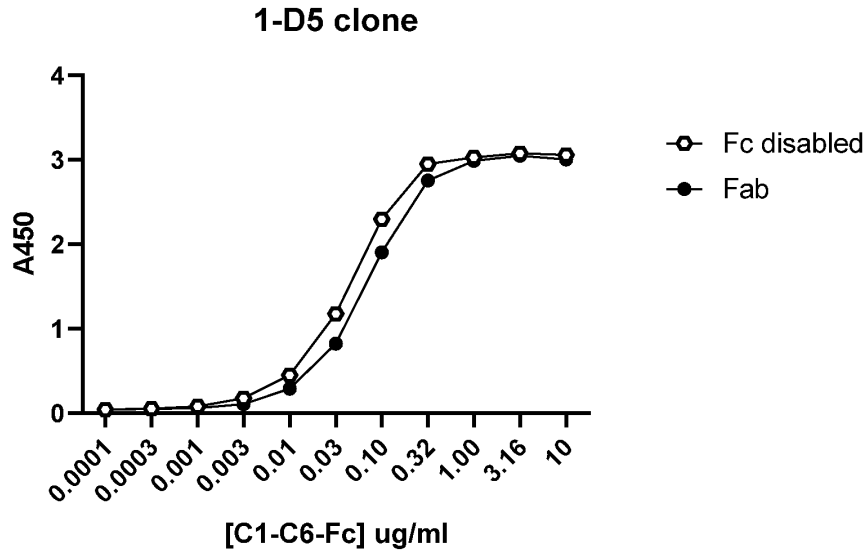


Figure 7D

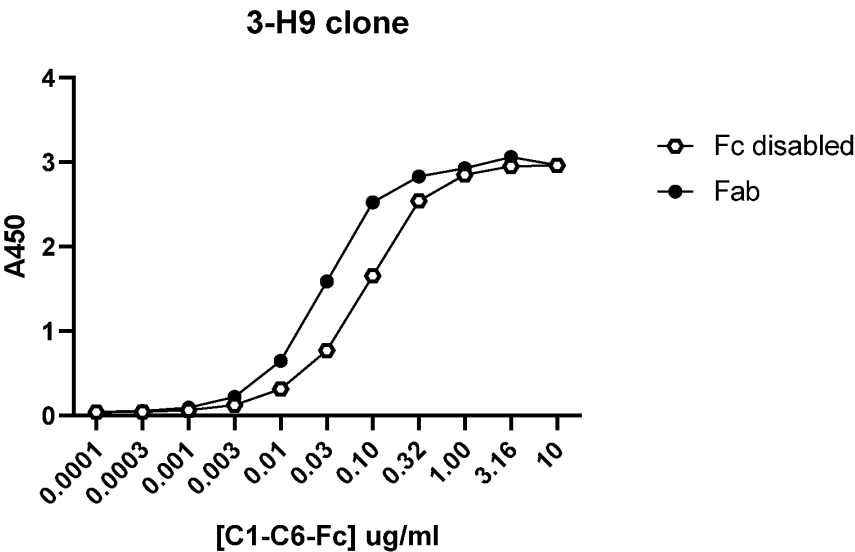
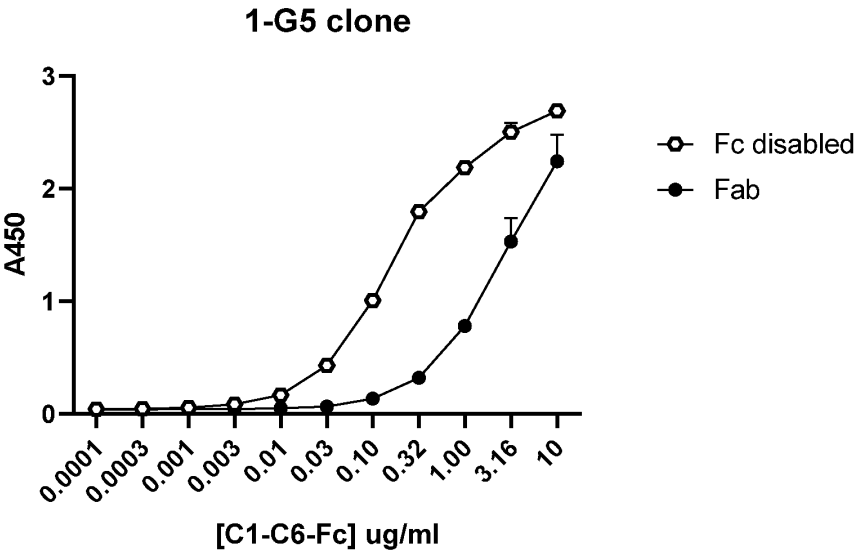


Figure 7E



- 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-H ₁	CDR-H ₂	CDR-H ₃	CDR-L ₁	CDR-L ₂	CDR-L ₃	VH	VL	HC	LC
1-A ₂ _parental (IgG ₄)	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 TCTVSGIDLTSMAMWVRQA PKGLEWIGSIHAIHTIYYA AWAKGEFTISKTSITVLEKLM TRPTIDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 156)	AIEMTQTFPSLSASVG ETVRLIRGLASDIIYSG ISWYQQKPFQKPEPTLLI YGASNLESQVPPFRFS SGSGTDYTLTIIGSVQA EDAATYCYLGGHSHST TDLTFGAGTKYEIK (SEQ ID NO: 25)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTSVGHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKKVEKSKCKTHICPFC PAPELLLGPSVFLPEPKPKDTLMISRTP EVTCVVAVDSHEDPEVKENMYVDGVEVH NAKTEREQQYNTSTYRVSVLTIVLHQWM LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQENNYKTIPEV LQSDGSFELYSLKLVOKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYPREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
4-H ₃ _parental (IgG ₄)	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 TCTVSGIDLTSMAMWVRQA PKGLEWIGSIHAIHTIYYA AWAKGEFTISKTSITVLEKLM TRPTIDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 159)	AYDMTQTFPSLSASVG ETVRLIRGLASDIIYSG ISWYQQKPEKPEPTLLI YGASNLESQVPPFRFS SGSGTDYTLTIIGSVQA EDAATYCYLGGHSHST NKTQSGTKYEIK (SEQ ID NO: 43)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTSVGHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKKVEKSKCKTHICPFC PAPELLLGPSVFLPEPKPKDTLMISRTP EVTCVVAVDSHEDPEVKENMYVDGVEVH NAKTEREQQYNTSTYRVSVLTIVLHQWM LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQENNYKTIPEV LQSDGSFELYSLKLVOKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYPREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
1-D ₅ _parental (IgG ₄)	GFSLNNYI (SEQ ID NO: 45)	ISTGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVTFGTPLTL TCAVSFGLNNHYIMGWVRQA PKGLEWIGSIHAIHTIYYA SWAKGEFTISKTSITVLEKLM TSLTIEDTATYFCARGGSA GAGNFWGFIQTLVTISS (SEQ ID NO: 52)	DIWMTQTFPSVSAANG DVTITQQASQSIKNSG LWYKQKPFQKPKRLI YKASTLASGVSPFRFG SGSGTDFTLTISDLCE ADAATYCYQSIVHISA NGATFGGTEVVE (SEQ ID NO: 61)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTSVGHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKKVEKSKCKTHICPFC PAPELLLGPSVFLPEPKPKDTLMISRTP EVTCVVAVDSHEDPEVKENMYVDGVEVH NAKTEREQQYNTSTYRVSVLTIVLHQWM LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQENNYKTIPEV LQSDGSFELYSLKLVOKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYPREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
3-H ₉ _parental (IgG ₄)	GFSLSNYD (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 NMWGFQTLVTISS (SEQ ID NO: 160)	AIKMTQTFPSVSAANG GTUTLILQQSSQSVYAN NLLSWYKQREQKPKRL LIYDASDLQSSVFSF KSGSGGQYTLIIISG CEDDAATYCYQSIIIS SWATHTFGGTEVVE (SEQ ID NO: 79)	ASTKGSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTSVGHFFPAV LQSSGLVSLSSVTVFSSSLGTQIYICN VNHKFSNTKYDKKVEKSKCKTHICPFC PAPELLLGPSVFLPEPKPKDTLMISRTP EVTCVVAVDSHEDPEVKENMYVDGVEVH NAKTEREQQYNTSTYRVSVLTIVLHQWM LNKREYKVKYSHKALPAFIKTIISKAKG QRFEPQVTLTPPSRDELTKNQVSLTCLV KGIFYSDIAYWESNGQENNYKTIPEV LQSDGSFELYSLKLVOKSRWQQGNFSC SVNHEALHNHYTQKSLSLSPFGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDQQLK SGTASVVCILLNNFYPREA KYQMKVDNALQSGNQES VTEQDSKDSYTSLSLTIT LGRADYEKHKYIACAEVTH QGLSSPVTIKSNRGECC (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 _parental (hlgG1)	GFLSSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSSGWD TA (SEQ ID NO: 92)	SQSLEESGRLVTFGTEPLTL TCVSYGFLSLNDVMWRQA PGKLEWIGSIHAIGTIYFA NMAKGFTISRTISITVLDLM TSLTIEDTATYFCARGLVDL NMWPGTILTVSS (SEQ ID NO: 161)	DPVMTQTASSVSAVG GVTLINQASQSYAN NLLSYQKQKQPKL LTYDASTLESQVSRF SGSGGTFTLTISGV QCDDAIYCGGSYS GQMDATGCGTGVVK (SEQ ID NO: 97)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 158)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 158)
1-A ₂ _parental (hlgG1-L234A-L235A-P329G)	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)	SQSVESGRLVFPCTPLTL TCTVSGIDLTSMANWWRQA AWAKGRFTISRTISITVLDLM TRPTIDDATYFCARGIYF DIWGTGTLTVSS (SEQ ID NO: 156)	AIEMTQTFFSLASVG ISWYKQKQKPEPTLLI YGASNLSSGVPRFSG SGSGDTYLTITGGVQA EDAATYCLGGYSS TDLTGAGTKVEIK (SEQ ID NO: 25)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 162)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 158)
4-H ₃ _parental (hlgG1-L234A-L235A-P329G)	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)	SQSLEESGRLVTFGTEPLTL TCVSYGIDLTSMANWWRQA PGKLEWIGSIHAIGTIYFA NMAKGFTISRTISITVLDLM TRPTIDDATYFCARGIYF DIWGTGTLTVSS (SEQ ID NO: 159)	AYDMTQTFFSLASVG GVTLIRCLASDITASG ISWYKQKQKPEPTLLI YGASNLSSGVPRFSG SGSGDTYLTITGGVQA EDAATYCLGGYSS NGLTGAGTKVEIK (SEQ ID NO: 43)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 162)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 158)
1-D ₅ _parental (hlgG1-L234A-L235A-P329G)	GFLSNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSHYISANG AI (SEQ ID NO: 56)	QQQLVESGRLVTFGTEPLTL TCVSYGFLSLNDVMWRQA PGKLEWIGSIHAIGTIYFA NMAKGFTISRTISITVLDLM TSLTIEDTATYFCARGGSSA GAGFNWPGTILTVSS (SEQ ID NO: 52)	DIVMTQTFFSVSAVG GVTLINQASQSYAN NLLSYQKQKQPKL LTYDASTLESQVSRF SGSGDTFTLTISOLEC ADAAITCOSHHISA NGATPGGTEVVVE (SEQ ID NO: 61)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 162)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 158)
3-H ₉ _parental (hlgG1-L234A-L235A-P329G)	GFLSNYD (SEQ ID NO: 63)	IHAIGT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYSSGWI NT (SEQ ID NO: 74)	SQSLEESGRLVTFGTEPLTL TCVSYGFLSLNDVMWRQA PGKLEWIGSIHAIGTIYFA NMAKGFTISRTISITVLDLM TSLTIEDTATYFCARGLVDL NMWPGTILTVSS (SEQ ID NO: 160)	AIEMTQTFFSVSAVG GVTLINQASQSYAN NLLSYQKQKQPKL LTYDASTLESQVSRF SGSGDTFTLTISOLEC ADAAITCOSHHISA NGATPGGTEVVVE (SEQ ID NO: 79)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (SEQ ID NO: 162)	ASTKGSVFFLAPSSKTSGGTAALGCL VKDYFEEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKYDKVEKSKCKTHCTPCP FAPELLNGPQSVLPFPEKCKOTLMISRT EVTCCVVDVSHDEPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQWM LNKREYKCKVSKALGAPIEKTIISKAKG QFREPQVTVLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKQSLSLSPCK (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 PGKLEWIGSIHATGITYA NMAKGRFTISRTSTIVDLRM TSLTDEDATYFCARGVLDM NMWPGTLTVSS (SEQ ID NO: 161)	DPVMTQASSVSAAG GTVTINQASQSYNN NLLSWYQKPGQPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYS GMDTAFGGGKVK (SEQ ID NO: 97)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK PAPRAAGSPSVLEFPKPKOTLMISRTIP EVTGVVDVSHEDFEVKNWVGVGVH NAKTEREEQYHSTYAVSVLTVLQGM LAKGEVKYKSKALGAPIKTLISKAG QPREQVTVLPFSDRLTKNQVSLTCLV KGFYPSDIAYWESNQENNYKTTPEV LQSSGFLYSKLTVDKSRWQQNVFSC SYMHEALHNHYTKSLSLSEFK (SEQ ID NO: 162)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (SEQ ID NO: 158)
1-A2_parental (hlgG1-Fab)	GIDLTSNA (SEQ ID NO: 9)	IYGHDS (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 PGKLEWIGSIHGHDSITYA AMAKGRFTISRTSTIVDLRM TRPTIDDTATYFCARGEIYF DIWGTIGLTVSS (SEQ ID NO: 156)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQKPGKPTLLI YGASNLESQVFPFSG SGSGDTVTLTIGGVQA EDAAITYCUGGHSHST LDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (SEQ ID NO: 158)
4-H3_parental (hlgG1-Fab)	GIDLTSNA (SEQ ID NO: 27)	IYGHDS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGYVSFSSNG LT (SEQ ID NO: 38)	SQSLESGRLVFPGLTL TCTVSGIOLTSNMMWRQA PGKLEWIGSIHGHDSITYA AMAKGRFTISRTSTIVDLRM TRPTIDDTATYFCARGEIYF DIWGTIGLTVSS (SEQ ID NO: 159)	AYDMTQTFPSLSASVG ETVIRCLASEDIASG ISWYQKPGKPTLLI YGASNLESQVFPFSG SGSGDTVTLTIGGVQA EDAAITYCUGGYFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (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)	QSINSQ (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG NT (SEQ ID NO: 56)	QQQLVESGRLVFPGLTL TCVSGFSLNNYIMGWQRQA PGKLEWIGSIHGTGITYA SWAKGRFTISRTSTIVDLRM TSLTDEDATYFCARGGSA GAGFNWPGTLTVSS (SEQ ID NO: 52)	DIVMTQTFSSVSAAG DIVILQCSQSIKSG LAWYQKPGQPKL IKASHLASGVFSRFG SGSGDTVTLTISOLBC ADAAITYCOSIHLISA NGATPFGGTEVWVE (SEQ ID NO: 61)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (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 PGKLEWIGSIHATGITYA NMAKGRFTISRTSTIVDLRM TSLTDEDATYFCARGVLDM NMWPGTLTVSS (SEQ ID NO: 160)	DPVMTQASSVSAAG GTVTINQASQSYNN NLLSWYQKPGQPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYS SGWNTFEGGTEVWVE (SEQ ID NO: 79)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (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 PGKLEWIGSIHATGITYA NMAKGRFTISRTSTIVDLRM TSLTDEDATYFCARGVLDM NMWPGTLTVSS (SEQ ID NO: 161)	DPVMTQASSVSAAG GTVTINQASQSYNN NLLSWYQKPGQPKL LIYDASTLASGVFSR SGSGGTQTLTISGV QCDAAATYTCQGSYS GMDTAFGGGKVK (SEQ ID NO: 97)	ASTKGEVFFLAPSSKSTSGGTAALGCL VKDYFEVTVSMNSGALISGVHFFPAV LQSSGLVSLSSVTVFSSSLGTQTYICN VNHKPSNTKVDKVKVEFSCGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPDSDEQLK SGTASVVCCLNNFYREA KQWKVDNALQSGNSQES VTEQSKDSTYSLSLTIL LQKADYKEKHYACAEVTH QGLSSPVTKFSNGEC (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 165)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 158)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (SEQ ID NO: 158)
	GIDLTISNA (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 194)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (SEQ ID NO: 158)
4-H3_H2 (hlgG ₁)	GIDLTISNA (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 166)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (SEQ ID NO: 158)
	GIDLTISNA (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 167)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (SEQ ID NO: 158)
4-H3_H4 (hlgG ₁)	GIDLTISNA (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 168)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (SEQ ID NO: 158)
	GIDLTISNA (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 SCAASGFTTSSNMMWRQA PCKGLEWVAGIYGHDTSYIA AWAKGRFTISRDNKNTLYL QMNSLRADTAVYICARGEI YFDLWQQGTLIVTSS (SEQ ID NO: 168)	AYDMTQTFPSLSASVG ETVRLIRCLASDITAGS ISWYQKPKGKPTLLI YGASNLESQVPRFSG SGSGTDYTLITIGGVQA EDAATYICLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFPEVTVSNWNGALTISGVIHFPFVAV LQSSGLYSLSVTVFSSSLGQTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKYSHKALFAPIEKTIISKAG QFREPOVTLTLPFSRDELTKNQVSLTCLV KGFYFSDIAYEWESNGQFNENYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LRSKADYEKHKVYACEVTH QGLSSPVTIKSNRGEC (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 ₀ (hlgG ₁)	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	AHGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV SAGAGENIWQGGLVTIVSS (SEQ ID NO: 174)	DIVMTQTPSSVSAVNG DVTIIQQCASQSI NSG LAMYQQKRPQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLCC ADAATYYCCQSVHYISA NGATFGGGEVYVE (SEQ ID NO: 61)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GFSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	AHGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV SAGAGENIWQGGLVTIVSS (SEQ ID NO: 175)	DIVMTQTPSSVSAVNG DVTIIQQCASQSI NSG LAMYQQKRPQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLCC ADAATYYCCQSVHYISA NGATFGGGEVYVE (SEQ ID NO: 61)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (SEQ ID NO: 158)
1-D ₅ _H ₂ (hlgG ₁)	GFTSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	AHGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV SAGAGENIWQGGLVTIVSS (SEQ ID NO: 176)	DIVMTQTPSSVSAVNG DVTIIQQCASQSI NSG LAMYQQKRPQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLCC ADAATYYCCQSVHYISA NGATFGGGEVYVE (SEQ ID NO: 61)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GFTSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	AHGSSAGAG FNI (SEQ ID NO: 47)	QSI NSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSVHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA SWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV SAGAGENIWQGGLVTIVSS (SEQ ID NO: 177)	DIVMTQTPSSVSAVNG DVTIIQQCASQSI NSG LAMYQQKRPQPPKRLI YKASTLASGVPSFRFG SGSGDTFTLTISDLCC ADAATYYCCQSVHYISA NGATFGGGEVYVE (SEQ ID NO: 61)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (SEQ ID NO: 158)
3-H ₉ _H ₀ (hlgG ₁)	GFTFSNYD (SEQ ID NO: 177)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYVSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA NWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV DLNHWQQTILVTIVSS (SEQ ID NO: 178)	AIKMTQTPSSVSAVNG GTVTINQQCSQSVSYIN NLLSWYQQKRPQPPKRLI LYLDASTLSSGVPSFRFG KSGSGTQFTLTISG QCEDAATYYCCGSIYS SGWYVTFGGGEVYVE (SEQ ID NO: 79)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (SEQ ID NO: 158)
	GFTSLNYYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYVSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVQFGRSLRL SCAASGFTFSNYIMGWYRQA PKGLEWVAIIISIGSTYYA NWAKGRTTISRDNKNTLLY QMSLSRAEDTAVYTCARGLV DLNHWQQTILVTIVSS (SEQ ID NO: 179)	AIKMTQTPSSVSAVNG GTVTINQQCSQSVSYIN NLLSWYQQKRPQPPKRLI LYLDASTLSSGVPSFRFG KSGSGTQFTLTISG QCEDAATYYCCGSIYS SGWYVTFGGGEVYVE (SEQ ID NO: 79)	ASTKGESVFELAPSSKSTSGGTAALGCL VKDYFPEPTVSWNSGALTSVGHITPAV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKVDKKVEPKSCDKTHICPEP FAPELLGGPSVFLPPEPKKOTIMLSRTP EVTCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKAGG QFREPVVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTIVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCLLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACIEVTH QGLSSPVTKSFNGRGC (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)	QQLVESGGGVQFGRSRL CAASGIDISNMMWVQAP GRGLEWISGTHAIGTYYAN WAGREFTISRDNTVYLQAN SLRAEDTAIVFCARGLVDLN MWGGTLVTYSS (SEQ ID NO: 180)	AIKMTQTFPSLSASVG ETVIRCLASEDIYSG NLISWYQQKPKPTLLI LITDASTLESQVPSRP KGSGSGFTLTITISGV QCEDAATYICQGSYIS SGMTATFGGTEVVE (SEQ ID NO: 79)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGREYKCKVSKALFAPEIKTISKAKG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYPSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVVCCLLNINFYREA KQWKRVNALQSGNSQES 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)	QVQLVESGGGVQFGRSRL SCAASGIDISNMMWVQAP PGLGLEWVAGIYGHDTSYIAA AWAKGRFTISRDNSKNTLYL QMSLRADTAIVFCARGFI YFDIWQQGTLVTYSS (SEQ ID NO: 165)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYTLITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGREYKCKVSKALFAPEIKTISKAKG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYPSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVVCCLLNINFYREA KQWKRVNALQSGNSQES VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)
1-A2_H1 (hlgG1)	GIDLTSNA (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)	QVQLVESGGGVQFGRSRL SCAASGIDISNMMWVQAP PGLGLEWVAGIYGHDTSYIAA AWAKGRFTISRDNSKNTLYL QMSLRADTAIVFCARGFI YFDIWQQGTLVTYSS (SEQ ID NO: 194)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYTLITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGREYKCKVSKALFAPEIKTISKAKG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYPSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVVCCLLNINFYREA KQWKRVNALQSGNSQES VTEQSKDSKSTYSLSSTLT VTEQSKDSKSTYSLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNAGEC (SEQ ID NO: 158)
1-A2_H2 (hlgG1)	GIDLTSNA (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)	QQLVESGGGVQFGRSRL CAASGIDISNMMWVQAP GRGLEWISGTHAIGTYYAA WAKGRFTISRDNTVYLQAN SLRAEDTAIVFCARGIYFD IWGGTLVTYSS (SEQ ID NO: 172)	AIEMTQTFPSLSASVG ETVIRCLASEDIYSG ISWYQQKPKPTLLI YGASNLDSGVPFRFSG SGSGDTYTLITGGVQA EDAATYICLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGSEVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSNMNGSLTSGVHTFPV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLFPPKPKDTLMISRT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTREREQYHSTYRVSVLTVHLQW LNGREYKCKVSKALFAPEIKTISKAKG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYPSDIAVEMESNGQFENNYKITPEV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQQLK SGTASVVCCLLNINFYREA KQWKRVNALQSGNSQES 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)	GFTFSSYD (SEQ ID NO: 181)	IHAIGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYISGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSIDMTWVRQA PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYFCARGLV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKPKPPEKL LIYDASTLASGVSRF SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGTVVVK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
	GFTLSSYD (SEQ ID NO: 81)	IHAIGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYISGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSIDMTWVRQA PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYFCARGLV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKPKPPEKL LIYDASTLASGVSRF SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGTVVVK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
1-G ₅ _H ₁ (hlgG ₁)	GFTLSSYD (SEQ ID NO: 81)	IHAIGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYISGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSIDMTWVRQA PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYFCARGLV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKPKPPEKL LIYDASTLASGVSRF SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGTVVVK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
1-G ₅ _H ₂ (hlgG ₁)	GFTLSSYD (SEQ ID NO: 81)	IHAIGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYISGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVQFGRSLRL SCAASGFTFSIDMTWVRQA PCKGLEWVASIHATGIIFYA NMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYFCARGLV DLNHWGQGITLVSS	DPVMTQTASSVSAVG GTVTINQASQSYNN NYLSWYQQKPKPPEKL LIYDASTLASGVSRF SNGSGTQFTLTISGV QCDDAATYCCGGSYS GMDTAFGGGTVVVK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
4-H ₃ _L ₀ (hlgGK)	GIDLTSA (SEQ ID NO: 27)	IYGHDTIS (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)	SQSLEESGGRVLPFGTEPLTL TCTVSYGIOLTSNMMWVRQA PCKGLEWIGSYGHDTISYYA AMAKGRFTISRSTIYVLDLKM TRPTTDDTATYFCARGFIYF DIWGTGTIATVSS	DIQMTQSPFSSLSASVG DRVTITCLASDITASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISGV EDFATYTLGGYSFAS NGITPGGKTVKIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDTIS (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)	SQSLEESGGRVLPFGTEPLTL TCTVSYGIOLTSNMMWVRQA PCKGLEWIGSYGHDTISYYA AMAKGRFTISRSTIYVLDLKM TRPTTDDTATYFCARGFIYF DIWGTGTIATVSS	DIQMTQSPFSSLSASVG DRVTITCLASDITASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISGV EDFATYTLGGYSFAS NGITPGGKTVKIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
4-H ₃ _L ₁ (hlgGK)	GIDLTSA (SEQ ID NO: 27)	IYGHDTIS (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)	SQSLEESGGRVLPFGTEPLTL TCTVSYGIOLTSNMMWVRQA PCKGLEWIGSYGHDTISYYA AMAKGRFTISRSTIYVLDLKM TRPTTDDTATYFCARGFIYF DIWGTGTIATVSS	DIQMTQSPFSSLSASVG DRVTITCLASDITASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISGV EDFATYTLGGYSFAS NGITPGGKTVKIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (SEQ ID NO: 158)
	GIDLTSA (SEQ ID NO: 27)	IYGHDTIS (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)	SQSLEESGGRVLPFGTEPLTL TCTVSYGIOLTSNMMWVRQA PCKGLEWIGSYGHDTISYYA AMAKGRFTISRSTIYVLDLKM TRPTTDDTATYFCARGFIYF DIWGTGTIATVSS	DIQMTQSPFSSLSASVG DRVTITCLASDITASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SNGSGTQFTLTISGV EDFATYTLGGYSFAS NGITPGGKTVKIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSNWNGALTSVGHITPAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNGKEYKCKVSKKALPAPIEKTIISKAG QFREPVTVTLFPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNQGFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVNHEALHNHYTQKSLSLSPECK	TVAAESVFIFFPDSBQLK SGTASVVCILLNINFYREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGECC (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)	GFSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGSSAGAG FNI (SEQ ID NO: 47)	QSTNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVPTGPTLTL TCVSVSGSLNNVIMGWRRQA PGKLGLEIGGIISGTYTAA SWAKGFTIISRTSITMLKRM TSLTIEDTATYFCARGSSA GAGFNWGFGLIVTVSS (SEQ ID NO: 52)	DIQMTQSPFSLASVSG DVTITTCQASQSVIN LAWYQKPKGAPKRLI YKASTLASGFSRFG SSGGIDFTLITLSLQF EDPALTTCGSHIISA NGATFFGGGKVEIK (SEQ ID NO: 187)	ASTKGSVFPEFLAPSSKSTSGGTAALGCL VKDTFFPEVTVSMNSGALITSGVHITFFAV LQSSGLSLSSVTVFSSSGIGTIYICN VNHKFSNTKVKDKVEPKSCDKTHICPPC FAPELLLGGSVFLEFPPEKPKTILMLSRPT EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPEQYNSTYAVSVLVTLHQDW LNKREYKCKVSNKALPAFIEKTIISKAG QFREFQVYTLPEPSROBLTKNQVSLTCLV KGFFYSDIAVEMESNQEPENNYKTIPTFV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTKQSLSLSFEGK (SEQ ID NO: 158)	KGFYPSDIAVEMESNQEPENNYKTIPTFV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTKQSLSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIPTFSDEQLK SGTASVVCCLNNFIPREA KYQWKVDNALQSGNSQES VTEQDSKSTYISLSITL LQKADTEKHKVYACEVTH QGLSGSPVTKFSFNRGEC (SEQ ID NO: 158)
	1-D5_L1 (hlgGK)	GFSLNYYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGSSAGAG FNI (SEQ ID NO: 47)	QSTNSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGRLVPTGPTLTL TCVSVSGSLNNVIMGWRRQA PGKLGLEIGGIISGTYTAA SWAKGFTIISRTSITMLKRM TSLTIEDTATYFCARGSSA GAGFNWGFGLIVTVSS (SEQ ID NO: 52)	DIQMTQSPFSLASVSG DVTITTCQASQSVIN LAWYQKPKGAPKRLI YKASTLASGFSRFG SSGGIDFTLITLSLQF EDPALTTCGSHIISA NGATFFGGGKVEIK (SEQ ID NO: 188)	ASTKGSVFPEFLAPSSKSTSGGTAALGCL VKDTFFPEVTVSMNSGALITSGVHITFFAV LQSSGLSLSSVTVFSSSGIGTIYICN VNHKFSNTKVKDKVEPKSCDKTHICPPC FAPELLLGGSVFLEFPPEKPKTILMLSRPT EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPEQYNSTYAVSVLVTLHQDW LNKREYKCKVSNKALPAFIEKTIISKAG QFREFQVYTLPEPSROBLTKNQVSLTCLV KGFFYSDIAVEMESNQEPENNYKTIPTFV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTKQSLSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIPTFSDEQLK SGTASVVCCLNNFIPREA KYQWKVDNALQSGNSQES VTEQDSKSTYISLSITL LQKADTEKHKVYACEVTH QGLSGSPVTKFSFNRGEC (SEQ ID NO: 158)
3-Ho_Lo (hlgGK)		GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDNNM (SEQ ID NO: 65)	QSYVNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QSYTSGWY NT (SEQ ID NO: 74)	SQSLESGRGLVPTGPTLTL TCVSVSGSLNNVIMGWRRQA PGKLGLEIGGIISGTYTAA NMAEGFTIISRTSITVLKRM TSLTIEDTATYFCARGIVDL NMWQFGTIVTVSS (SEQ ID NO: 160)	DIQMTQSPFSLASVSG DVTITTCQASQSVIN LAWYQKPKGAPKRLI YKASTLASGFSRFG SSGGIDFTLITLSLQF EDPALTTCGSHIISA NGATFFGGGKVEIK (SEQ ID NO: 189)	ASTKGSVFPEFLAPSSKSTSGGTAALGCL VKDTFFPEVTVSMNSGALITSGVHITFFAV LQSSGLSLSSVTVFSSSGIGTIYICN VNHKFSNTKVKDKVEPKSCDKTHICPPC FAPELLLGGSVFLEFPPEKPKTILMLSRPT EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPEQYNSTYAVSVLVTLHQDW LNKREYKCKVSNKALPAFIEKTIISKAG QFREFQVYTLPEPSROBLTKNQVSLTCLV KGFFYSDIAVEMESNQEPENNYKTIPTFV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTKQSLSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIPTFSDEQLK SGTASVVCCLNNFIPREA KYQWKVDNALQSGNSQES VTEQDSKSTYISLSITL LQKADTEKHKVYACEVTH QGLSGSPVTKFSFNRGEC (SEQ ID NO: 158)
1-A2_Lo (hlgGK)	GDLTSNA (SEQ ID NO: 9)	TYGHGTS (SEQ ID NO: 10)	ARGFTIYDI (SEQ ID NO: 11)	EDTYGG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGHSHSTID LT (SEQ ID NO: 20)	SQSVESGRGLVPTGPTLTL TCTVSGDLITSNAMWRRQA PGKLGLEIGGIYGHGHTSYTAA AWAKGFTIISRTSITVLKRM TRPTIDTATYFCARGEIYF DIWGTGTLIVTS (SEQ ID NO: 156)	DIQMTQSPFSLASVSG DVTITTCLEASEDTYSG ISWYQKPKGAPKRLI YGASNLDESVPKSRFG SSGGIDFTLITLSLQF EDPALTTCGSHIISA NGATFFGGGKVEIK (SEQ ID NO: 190)	ASTKGSVFPEFLAPSSKSTSGGTAALGCL VKDTFFPEVTVSMNSGALITSGVHITFFAV LQSSGLSLSSVTVFSSSGIGTIYICN VNHKFSNTKVKDKVEPKSCDKTHICPPC FAPELLLGGSVFLEFPPEKPKTILMLSRPT EVTCVVDVSHDEPDEVKNWYVDGVGVH NAKTRPEQYNSTYAVSVLVTLHQDW LNKREYKCKVSNKALPAFIEKTIISKAG QFREFQVYTLPEPSROBLTKNQVSLTCLV KGFFYSDIAVEMESNQEPENNYKTIPTFV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHNHYTKQSLSLSFEGK (SEQ ID NO: 157)	TVAAPSVFIPTFSDEQLK SGTASVVCCLNNFIPREA KYQWKVDNALQSGNSQES VTEQDSKSTYISLSITL LQKADTEKHKVYACEVTH QGLSGSPVTKFSFNRGEC (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_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 TCTVSGIDLTSMAMWRQA YKQWLEWIGSIHATGTFYA AMAKGRTIISRTISYVLQNM TRPTIDDTATYFCARGFIYFD DIWGTGLTVTSS (SEQ ID NO: 156)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLSSGVSRFSG SGSGTDYTLTISSLOP EDFATYICLGGHSHIT TDLTPGGTKVEIK (SEQ ID NO: 191)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
	GFSLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVLDNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWMD TA (SEQ ID NO: 92)	SQSLEESGRLVFGTEPLTL TCTSVSFFLSLSYVMTWRQA YKQWLEWIGSIHATGTFYA NNAKGRFTISKTSTVGLQNM TSLTIEDTATYFCARGLVLD NNAWGPGLTVTSS (SEQ ID NO: 161)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG NLYLWYQKPKGKAPKLLI LYLDASTLASGVSRF SGSGTDFTLTISL QPEDFATYICGGSYIS GMDTAFGGTKVEIK (SEQ ID NO: 192)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
1-G5_L1 (hlgGK)	GFSLSYD (SEQ ID NO: 81)	IHAIGT (SEQ ID NO: 82)	ARGLVLDNM (SEQ ID NO: 83)	QSVYNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYSGWMD TA (SEQ ID NO: 92)	SQSLEESGRLVFGTEPLTL TCTSVSFFLSYVMTWRQA YKQWLEWIGSIHATGTFYA NNAKGRFTISKTSTVGLQNM TSLTIEDTATYFCARGLVLD NNAWGPGLTVTSS (SEQ ID NO: 161)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG NLYLWYQKPKGKAPKLLI LYLDASTLASGVSRF SGSGTDFTLTISL QPEDFATYICGGSYIS GMDTAFGGTKVEIK (SEQ ID NO: 193)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (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 YKQWLEWIGSIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLSSGVSRFSG SGSGTDYTLTISSLOP EDFATYICLGGHSHIT TDLTPGGTKVEIK (SEQ ID NO: 191)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (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 YKQWLEWIGSIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLSSGVSRFSG SGSGTDYTLTISSLOP EDFATYICLGGHSHIT TDLTPGGTKVEIK (SEQ ID NO: 190)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (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 YKQWLEWIGSIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLSSGVSRFSG SGSGTDYTLTISSLOP EDFATYICLGGHSHIT TDLTPGGTKVEIK (SEQ ID NO: 190)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (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 YKQWLEWIGSIHATGTFYA WAKGRTISRDNTVYLQNM SIRAEDTATYFCARGFIYFD IWGGTGLTVTSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVG DRVTITCLASDEDYSG ISWYQKQPKGKAPKLLI YGASNLSSGVSRFSG SGSGTDYTLTISSLOP EDFATYICLGGHSHIT TDLTPGGTKVEIK (SEQ ID NO: 190)	ASTKGESVFELAPSSKTSISGTAALGCL VKDYFPEVTVSNWNGALTISGVHIFPAV LQSSGLVSLSSVTVFSSSLGTQYICN VNHKFSNTKVDKVEKSKCKTHICPC FAPELLGGPSVFLPPEKFKDTLMISRT EVTCVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSVLTVLHQDW LNKREYKCKVSKALPAFIKTIISKAG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFFPSDIAVEMESNGQFENNYKTIPEV LSDSGSFELYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDQRLK SGTASVVCCLINNFYREA KQWKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYERKHYACAEVTH QGLSSPVTIKSNRGEIC (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	GIDLTSSNA (SEQ ID NO: 9)	IYGHDTIS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGILTSSNANWVRQA PGKLEWVAGIYGHDTISYA AMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYICARGEI YFDLWGQGITLVYSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLSLOP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 191)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSDHEDPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	RVAAESVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWQKVDNALQSGNSQES VTEQDSKDSITYSLSLT LQKADYEKHKVYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
	GIDLTSSNA (SEQ ID NO: 9)	IYGHDTIS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGILTSSNANWVRQA PGKLEWVAGIYGHDTISYA AMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYICARGEI YFDLWGQGITLVYSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLSLOP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 190)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSDHEDPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	RVAAESVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWQKVDNALQSGNSQES VTEQDSKDSITYSLSLT LQKADYEKHKVYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
1-A2_Ho_L1	GFTFSSNA (SEQ ID NO: 164)	IYGHDTIS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGFTFSSNANWVRQA PGKLEWVAGIYGHDTISYA AMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYICARGEI YFDLWGQGITLVYSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLSLOP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 191)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSDHEDPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	RVAAESVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWQKVDNALQSGNSQES VTEQDSKDSITYSLSLT LQKADYEKHKVYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
	GFTFSSNA (SEQ ID NO: 164)	IYGHDTIS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID NO: 18)	GAS (SEQ ID NO: 19)	LGGHSHSTTD LT (SEQ ID NO: 20)	QVQLVESGGGVQPGSRRL SCAASGFTFSSNANWVRQA PGKLEWVAGIYGHDTISYA AMAKGRFTISRDNKNTLYL QMSLSRAEDTAVYICARGEI YFDLWGQGITLVYSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVITITCLASEDIYSG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLSLOP EDFATYICLGGHSHST TDLTFGGGTKEIK (SEQ ID NO: 190)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNWNGSGLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEPKSCDKTHCPCC PAPELLGGPSVFLPPEPKKOTLMISRT EVTCVVDVSDHEDPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QRFEPQVTVLPFSSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	RVAAESVFIFFPPSDQQLK SGTASVVCLLNNFYREA KQWQKVDNALQSGNSQES VTEQDSKDSITYSLSLT LQKADYEKHKVYACEVTH QGLSSPVTKSNRGC (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_H8_L1	GIDLT _{SN} A (SEQ ID NO: 27)	IYGHDT _S (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDI _{ASG} (SEQ ID NO: 36)	G _{AS} (SEQ ID NO: 37)	LG _{GY} FS _{SSNG} LT (SEQ ID NO: 38)	QQLVESGGGVQ _F GRSIL _{RS} CAASGDI _L T _S NAMNW _{RQ} AP GKGL _{EW} IG _Y I _G HDT _S Y _{AA} WAK _{GR} FT _I SR _Q NT _S YL _Q MN SLRA _{ED} T _{AT} Y _F C _{ARG} FI _{YD} I _{WQ} Q _{GT} L _{IV} T _{VS} (SEQ ID NO: 172)	DY _Q MTQ _S PS _S LS _{AS} V _G D _{RV} LT _I CL _{AS} D _{IT} AS _G IS _W Y _Q K _R CP _K AP _K LI _L Y _{GA} N _{LE} S _{GV} PS _{RF} SG SG _S GT _D Y _L T _I LS _{LO} P ED _F AT _I Y _C LG _Y FS _{SS} NGL _I FG _{GT} K _Y E _{IK} (SEQ ID NO: 186)	ASTK _{GP} SV _{TF} LP _{AF} SS _K ST _S GG _T AA _L G _{CL} VK _Q Y _F FP _{FT} V _Y MN _{SG} AL _T SG _V H _T FP _{AF} LQ _{SS} GL _Y SL _{SV} Y _{TF} VS _{SS} IG _Y Q _Y IC _N V _N H _K ES _{NT} K _Y Q _K VE _K SC _{DK} TH _{CP} PC PA _{EL} LL _{GG} SV _Y FL _{FF} PK _R Q _L IM _L SR _{TP} E _{VT} CV _{VD} VS _{HE} DP _{EV} FN _W Y _{VD} GV _{EH} N _{AK} T _{PR} EQ _Y NT _S Y _{RV} VS _L VL _{TH} Q _{DM} LN _K G _{EY} K _Y CK _N K _{AL} PA _F IE _K T _I SK _{AK} O _{PR} EQ _Y VL _{TP} PS _{RD} EL _T KN _Q VS _L TL _{CL} K _{GF} Y _S DI _{AV} EW _{ES} NG _Q FN _Y KT _{TP} L _{SD} SG _S FF _L Y _{SK} LT _Y V _K SR _{WQ} Q _{GN} V _{FS} C SV _M HE _{AL} HN _{HT} Y _T Q _K SL _S LS _{PS} FG (SEQ ID NO: 157)	ASTK _{GP} SV _{TF} LP _{AF} SS _K ST _S GG _T AA _L G _{CL} VK _Q Y _F FP _{FT} V _Y MN _{SG} AL _T SG _V H _T FP _{AF} LQ _{SS} GL _Y SL _{SV} Y _{TF} VS _{SS} IG _Y Q _Y IC _N V _N H _K ES _{NT} K _Y Q _K VE _K SC _{DK} TH _{CP} PC PA _{EL} LL _{GG} SV _Y FL _{FF} PK _R Q _L IM _L SR _{TP} E _{VT} CV _{VD} VS _{HE} DP _{EV} FN _W Y _{VD} GV _{EH} N _{AK} T _{PR} EQ _Y NT _S Y _{RV} VS _L VL _{TH} Q _{DM} LN _K G _{EY} K _Y CK _N K _{AL} PA _F IE _K T _I SK _{AK} O _{PR} EQ _Y VL _{TP} PS _{RD} EL _T KN _Q VS _L TL _{CL} K _{GF} Y _S DI _{AV} EW _{ES} NG _Q FN _Y KT _{TP} L _{SD} SG _S FF _L Y _{SK} LT _Y V _K SR _{WQ} Q _{GN} V _{FS} C SV _M HE _{AL} HN _{HT} Y _T Q _K SL _S LS _{PS} FG (SEQ ID NO: 157)	TV _{AA} PS _{VF} IP _{FF} SD _{EQ} LK SG _T AS _Y VC _{LL} LN _{FN} Y _P REA K _Y Q _K W _Y D _N AL _Q SG _{NS} Q _{ES} V _{TE} Q _D SK _{OS} T _Y SL _{AS} TL _T L _{SK} AD _Y E _K H _K V _Y ACE _{VT} H Q _{GL} SS _P VT _K SF _{NR} G _{EC} (SEQ ID NO: 158)
	4-H3_H7_L1	GIDLT _{SN} A (SEQ ID NO: 27)	IYGHDT _S (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDI _{ASG} (SEQ ID NO: 36)	G _{AS} (SEQ ID NO: 37)	LG _{GY} FS _{SSNG} LT (SEQ ID NO: 38)	QQLVESGGGVQ _F GRSIL _{RS} SCAASGDI _L T _S NAMNW _{RQ} A P _K G _K GLEW _I G _Y I _G HDT _S Y _{AA} A _{MA} K _{GR} FT _I SR _Q NS _K NT _Y L Q _M N _S LR _{AD} E _{AT} Y _F C _{ARG} I Y _F D _I W _Q Q _{GT} L _{IV} T _{VS} (SEQ ID NO: 171)	DY _Q MTQ _S PS _S LS _{AS} V _G D _{RV} LT _I CL _{AS} D _{IT} AS _G IS _W Y _Q K _R CP _K AP _K LI _L Y _{GA} N _{LE} S _{GV} PS _{RF} SG SG _S GT _D Y _L T _I LS _{LO} P ED _F AT _I Y _C LG _Y FS _{SS} NGL _I FG _{GT} K _Y E _{IK} (SEQ ID NO: 186)	ASTK _{GP} SV _{TF} LP _{AF} SS _K ST _S GG _T AA _L G _{CL} VK _Q Y _F FP _{FT} V _Y MN _{SG} AL _T SG _V H _T FP _{AF} LQ _{SS} GL _Y SL _{SV} Y _{TF} VS _{SS} IG _Y Q _Y IC _N V _N H _K ES _{NT} K _Y Q _K VE _K SC _{DK} TH _{CP} PC PA _{EL} LL _{GG} SV _Y FL _{FF} PK _R Q _L IM _L SR _{TP} E _{VT} CV _{VD} VS _{HE} DP _{EV} FN _W Y _{VD} GV _{EH} N _{AK} T _{PR} EQ _Y NT _S Y _{RV} VS _L VL _{TH} Q _{DM} LN _K G _{EY} K _Y CK _N K _{AL} PA _F IE _K T _I SK _{AK} O _{PR} EQ _Y VL _{TP} PS _{RD} EL _T KN _Q VS _L TL _{CL} K _{GF} Y _S DI _{AV} EW _{ES} NG _Q FN _Y KT _{TP} L _{SD} SG _S FF _L Y _{SK} LT _Y V _K SR _{WQ} Q _{GN} V _{FS} C SV _M HE _{AL} HN _{HT} Y _T Q _K SL _S LS _{PS} FG (SEQ ID NO: 157)	TV _{AA} PS _{VF} IP _{FF} SD _{EQ} LK SG _T AS _Y VC _{LL} LN _{FN} Y _P REA K _Y Q _K W _Y D _N AL _Q SG _{NS} Q _{ES} V _{TE} Q _D SK _{OS} T _Y SL _{AS} TL _T L _{SK} AD _Y E _K H _K V _Y ACE _{VT} H Q _{GL} SS _P VT _K SF _{NR} G _{EC} (SEQ ID NO: 158)
4-H3_H7_Lo rep	GIDLT _{SN} A (SEQ ID NO: 27)	IYGHDT _S (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDI _{ASG} (SEQ ID NO: 36)	G _{AS} (SEQ ID NO: 37)	LG _{GY} FS _{SSNG} LT (SEQ ID NO: 38)	QQLVESGGGVQ _F GRSIL _{RS} SCAASGDI _L T _S NAMNW _{RQ} AP P _K G _K GLEW _I G _Y I _G HDT _S Y _{AA} A _{MA} K _{GR} FT _I SR _Q NS _K NT _Y L Q _M N _S LR _{AD} E _{AT} Y _F C _{ARG} I Y _F D _I W _Q Q _{GT} L _{IV} T _{VS} (SEQ ID NO: 171)	DY _Q MTQ _S PS _S LS _{AS} V _G D _{RV} LT _I CL _{AS} D _{IT} AS _G IS _W Y _Q K _R CP _K AP _K LI _L Y _{GA} N _{LE} S _{GV} PS _{RF} SG SG _S GT _D Y _L T _I LS _{LO} P ED _F AT _I Y _C LG _Y FS _{SS} NGL _I FG _{GT} K _Y E _{IK} (SEQ ID NO: 185)	ASTK _{GP} SV _{TF} LP _{AF} SS _K ST _S GG _T AA _L G _{CL} VK _Q Y _F FP _{FT} V _Y MN _{SG} AL _T SG _V H _T FP _{AF} LQ _{SS} GL _Y SL _{SV} Y _{TF} VS _{SS} IG _Y Q _Y IC _N V _N H _K ES _{NT} K _Y Q _K VE _K SC _{DK} TH _{CP} PC PA _{EL} LL _{GG} SV _Y FL _{FF} PK _R Q _L IM _L SR _{TP} E _{VT} CV _{VD} VS _{HE} DP _{EV} FN _W Y _{VD} GV _{EH} N _{AK} T _{PR} EQ _Y NT _S Y _{RV} VS _L VL _{TH} Q _{DM} LN _K G _{EY} K _Y CK _N K _{AL} PA _F IE _K T _I SK _{AK} O _{PR} EQ _Y VL _{TP} PS _{RD} EL _T KN _Q VS _L TL _{CL} K _{GF} Y _S DI _{AV} EW _{ES} NG _Q FN _Y KT _{TP} L _{SD} SG _S FF _L Y _{SK} LT _Y V _K SR _{WQ} Q _{GN} V _{FS} C SV _M HE _{AL} HN _{HT} Y _T Q _K SL _S LS _{PS} FG (SEQ ID NO: 157)	TV _{AA} PS _{VF} IP _{FF} SD _{EQ} LK SG _T AS _Y VC _{LL} LN _{FN} Y _P REA K _Y Q _K W _Y D _N AL _Q SG _{NS} Q _{ES} V _{TE} Q _D SK _{OS} T _Y SL _{AS} TL _T L _{SK} AD _Y E _K H _K V _Y ACE _{VT} H Q _{GL} SS _P VT _K SF _{NR} G _{EC} (SEQ ID NO: 158)	
4-H3_H6_L1	GIDLT _{SN} A (SEQ ID NO: 27)	IYGHDT _S (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDI _{ASG} (SEQ ID NO: 36)	G _{AS} (SEQ ID NO: 37)	LG _{GY} FS _{SSNG} LT (SEQ ID NO: 38)	QQLVESGGGVQ _F GRSIL _{RS} CAASGDI _L T _S NAMNW _{RQ} AP GKGL _{EW} IG _Y I _G HDT _S Y _{AA} WAK _{GR} FT _I SR _Q NT _S YL _Q MN SLRA _{ED} T _{AT} Y _F C _{ARG} FI _{YD} I _{WQ} Q _{GT} L _{IV} T _{VS} (SEQ ID NO: 170)	DY _Q MTQ _S PS _S LS _{AS} V _G D _{RV} LT _I CL _{AS} D _{IT} AS _G IS _W Y _Q K _R CP _K AP _K LI _L Y _{GA} N _{LE} S _{GV} PS _{RF} SG SG _S GT _D Y _L T _I LS _{LO} P ED _F AT _I Y _C LG _Y FS _{SS} NGL _I FG _{GT} K _Y E _{IK} (SEQ ID NO: 186)	ASTK _{GP} SV _{TF} LP _{AF} SS _K ST _S GG _T AA _L G _{CL} VK _Q Y _F FP _{FT} V _Y MN _{SG} AL _T SG _V H _T FP _{AF} LQ _{SS} GL _Y SL _{SV} Y _{TF} VS _{SS} IG _Y Q _Y IC _N V _N H _K ES _{NT} K _Y Q _K VE _K SC _{DK} TH _{CP} PC PA _{EL} LL _{GG} SV _Y FL _{FF} PK _R Q _L IM _L SR _{TP} E _{VT} CV _{VD} VS _{HE} DP _{EV} FN _W Y _{VD} GV _{EH} N _{AK} T _{PR} EQ _Y NT _S Y _{RV} VS _L VL _{TH} Q _{DM} LN _K G _{EY} K _Y CK _N K _{AL} PA _F IE _K T _I SK _{AK} O _{PR} EQ _Y VL _{TP} PS _{RD} EL _T KN _Q VS _L TL _{CL} K _{GF} Y _S DI _{AV} EW _{ES} NG _Q FN _Y KT _{TP} L _{SD} SG _S FF _L Y _{SK} LT _Y V _K SR _{WQ} Q _{GN} V _{FS} C SV _M HE _{AL} HN _{HT} Y _T Q _K SL _S LS _{PS} FG (SEQ ID NO: 157)	TV _{AA} PS _{VF} IP _{FF} SD _{EQ} LK SG _T AS _Y VC _{LL} LN _{FN} Y _P REA K _Y Q _K W _Y D _N AL _Q SG _{NS} Q _{ES} V _{TE} Q _D SK _{OS} T _Y SL _{AS} TL _T L _{SK} AD _Y E _K H _K V _Y ACE _{VT} H Q _{GL} SS _P VT _K SF _{NR} G _{EC} (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_H6_Lo			ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQGRSLRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYFCARGFIYFD IWGGGLTVTVSS (SEQ ID NO: 170)	DIQMTQSPSSLSASVG DRVITITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	RGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPSEDLK STGASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
									ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	RGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)
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)	QQLVESGGGVQGRSLRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYFCARGFIYFD IWGGGLTVTVSS (SEQ ID NO: 169)	DYQMTQSPSSLSASVG DRVITITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPSEDLK STGASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
									ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	RGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)
4-H3_H5_Lo			ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYFSNSG LT (SEQ ID NO: 38)	QQLVESGGGVQGRSLRLS CAASGIDITSNAMMWVRQAP GKGLRWAGIYGHDTSYAA WAKGRFTISRDNKNTLYLQAN SLRAEDTAVYFCARGFIYFD IWGGGLTVTVSS (SEQ ID NO: 169)	DIQMTQSPSSLSASVG DRVITITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPSEDLK STGASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
									ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	RGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)
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)	QQLVESGGGVQGRSLRLS SCAASGIDITSNAMMWVRQA FGKGLRWAGIYGHDTSYAA AWAKGRFTISRDNKNTLYLQAN SLRAEDTAVYFCARGFIYFD IWGGGLTVTVSS (SEQ ID NO: 168)	DYQMTQSPSSLSASVG DRVITITCLASEDTASG ISWYQQKPKAPKLLI YGASNLDSGVSRFSG SGSGDTFTLTISLQIP EDFATYICLGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPSEDLK STGASVCLLNINFPREA KQWKVDNALQSGNSQES VTEQDSKDSITYSLSTLT LQKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
									ASTKGPVFPLAEFSKSTSGGTAALGCL VKDYFPEPVTVSNWNSGALTSGVHTFPAV LQSSGLYSLSSVTVFPSSSLGTQYICN VNHKFSNTKVKRVEPKSCDKRTHCTPCPC PAPELLGGESVFLFPPEKDKTLMISRTPT EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTRPREEQYNSTYRVVSVLTVLHQDW LNKGKRYKCKVSKALPAFTEKTIISKAGK QPREPQVYTLTPSRDELITKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)	RGFYFSDIAVEMESNGQFENNYKITFPV LSDSGSFFLYSKLTVDKSRWQQGNVFSC SYMHEALHHYTKQSLSLSPGK (SEQ ID NO: 157)

[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-D5_Ho_Lo	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	ARGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSHYISANG AI (SEQ ID NO: 56)	QVQLVESGGGVQVQPSRLRL SCAASGFTFSNYIMGWVRA PCKGLEWASIIHAIGIYYA QWASGKRFITSRDNKNTLYL QMSLSRAEDTAVYICARGGS SAGAGENIWQQGTLVTSS (SEQ ID NO: 174)	DIQMTQSPSSLSASVG DRVLTITCQSSQSYIN LAWYQQKPKAPKLII YKASTLASGVSRFSG SGSGTDFTLTISSLQF EDFATYYCQSHYISA NGATPFGGGTKVEIK (SEQ ID NO: 187)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNMNGSLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKESCKDTHCPCC FAPPELLGGPSVFLPEPKKOTLMISRTIP EVTCVVDVSDHDEPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	KGTFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)
										TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKRVNDALOSNGSQS VTEQSKDSTYSLSSTLT LGRADYEKKHYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
3-H9_H2_Lo	GFTLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSGWY NT (SEQ ID NO: 74)	QQLVESGGGVQVQPSRLRL SCAASGFTFSNYIMGWVRA PCKGLEWASIIHAIGIYYA QWASGKRFITSRDNKNTLYL QMSLSRAEDTAVYICARGLV DLNMQQGITLVTVSS (SEQ ID NO: 180)	DIQMTQSPSSLSASVG DRVLTITCQSSQSYIN NLLSWYQQKPKAPKL LTYDASTLTLESVSRF SGSGTDFTLTISL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNMNGSLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKESCKDTHCPCC FAPPELLGGPSVFLPEPKKOTLMISRTIP EVTCVVDVSDHDEPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKRVNDALOSNGSQS VTEQSKDSTYSLSSTLT LGRADYEKKHYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
3-H9_H1_Lo	GFTLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVQVQPSRLRL SCAASGFTFSNYIMGWVRA PCKGLEWASIIHAIGIYYA QWASGKRFITSRDNKNTLYL QMSLSRAEDTAVYICARGLV DLNMQQGITLVTVSS (SEQ ID NO: 179)	DIQMTQSPSSLSASVG DRVLTITCQSSQSYIN NLLSWYQQKPKAPKL LTYDASTLTLESVSRF SGSGTDFTLTISL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNMNGSLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKESCKDTHCPCC FAPPELLGGPSVFLPEPKKOTLMISRTIP EVTCVVDVSDHDEPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKRVNDALOSNGSQS VTEQSKDSTYSLSSTLT LGRADYEKKHYACEVTH QGLSSPVTKSNRGC (SEQ ID NO: 158)
3-H9_Ho_Lo	GFTFSNYD (SEQ ID NO: 177)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVQVQPSRLRL SCAASGFTFSNYIMGWVRA PCKGLEWASIIHAIGIYYA QWASGKRFITSRDNKNTLYL QMSLSRAEDTAVYICARGLV DLNMQQGITLVTVSS (SEQ ID NO: 178)	DIQMTQSPSSLSASVG DRVLTITCQSSQSYIN LAWYQQKPKAPKL LTYDASTLTLESVSRF SGSGTDFTLTISL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGSEVFLEAPSSKSTSGGTAALGCL VKDYFEFVTVSNMNGSLTISGHTFPFV LQSSGLYSLSSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKESCKDTHCPCC FAPPELLGGPSVFLPEPKKOTLMISRTIP EVTCVVDVSDHDEPEVKRWYVDGVEVH NAKTREREQYHSTYRVSVLTVLHQDW LNKREYKCKVSKALPAFIEKTIISKARG QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKITPEV LQSDGSFFLYSKLTVDKSRWQQGNVFSC SVMEHALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFFPPSDQQLK SGTASVCLLNINFYREA KQWKRVNDALOSNGSQS VTEQSKDSTYSLSSTLT LGRADYEKKHYACEVTH QGLSSPVTKSNRGC (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-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 DLNMWQQGTLIVTSS	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSCDKTHTCPCP FAPELLGGPSVFLPPEPKKDTLMISRTPE EVTCCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSIVLVHLQDW LNGKEYKCKVSKALFAPIEKTIISKAGK QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK	TVAAPSVFIFFPDSBQALK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
							(SEQ ID NO: 184)	(SEQ ID NO: 193)	(SEQ ID NO: 157)	(SEQ ID NO: 158)
1-G ₅ _H ₂ _L ₀	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 DLNMWQQGTLIVTSS	DIQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSCDKTHTCPCP FAPELLGGPSVFLPPEPKKDTLMISRTPE EVTCCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSIVLVHLQDW LNGKEYKCKVSKALFAPIEKTIISKAGK QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK	TVAAPSVFIFFPDSBQALK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
							(SEQ ID NO: 184)	(SEQ ID NO: 192)	(SEQ ID NO: 157)	(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 DLNMWQQGTLIVTSS	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSCDKTHTCPCP FAPELLGGPSVFLPPEPKKDTLMISRTPE EVTCCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSIVLVHLQDW LNGKEYKCKVSKALFAPIEKTIISKAGK QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK	TVAAPSVFIFFPDSBQALK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
							(SEQ ID NO: 183)	(SEQ ID NO: 193)	(SEQ ID NO: 157)	(SEQ ID NO: 158)
1-G ₅ _H ₁ _L ₀	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 DLNMWQQGTLIVTSS	DIQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSCDKTHTCPCP FAPELLGGPSVFLPPEPKKDTLMISRTPE EVTCCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSIVLVHLQDW LNGKEYKCKVSKALFAPIEKTIISKAGK QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK	TVAAPSVFIFFPDSBQALK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
							(SEQ ID NO: 183)	(SEQ ID NO: 192)	(SEQ ID NO: 157)	(SEQ ID NO: 158)
1-G ₅ _H ₀ _L ₁	GFTFSSYD (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 CAASGFTFSYSDMTWVRQA PGKLEWVASIHATGIIIFYA WAKRGFTTISRDNKNTLLYL SLRAEDTATVYCARGLV DLNMWQQGTLIVTSS	DPQMTQSPFSSLSASVG DRVTITLCOASQSYNN NYLSWYQQKPKGKAPKL LYDASTLASGVFSR SGSGGDTFTLTISLL QPEDFATYYCGGSIYS GMDTAFGGGTVEIK	ASTKGSEVFLEAPSSKTSGGTAALGCL VKDYFPEVTVSWNSGALTISGHTFPFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKVDKVEKSCDKTHTCPCP FAPELLGGPSVFLPPEPKKDTLMISRTPE EVTCCVVVDVSHEDPEVKENWYVDGVEVH NAKTREREQYNTSYRVSIVLVHLQDW LNGKEYKCKVSKALFAPIEKTIISKAGK QPREPQVTLTPPSRDELTKNQVSLTCLV KGFYFSDIAVEMESNGQFENNYKTIPEV LQSDGSFFLYSKLTVDKGRWQQGNVFSC SVMEHALHNHYTKQSLSLSPFGK	TVAAPSVFIFFPDSBQALK SGTASVVCILLINFIYFREA KYQMKVDNALQSGNSQES VTEQDSKDSYISLSSTLT LQKADYEKHKVYACEVTH QGLSSPVTIKSNRGEIC (SEQ ID NO: 158)
							(SEQ ID NO: 182)	(SEQ ID NO: 193)	(SEQ ID NO: 157)	(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
									RGFYFSDIAVEWESNGQFENNYKTIPEV 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 SCAASGFTFSYDMTWQRA PGKGLWVASIHATGIIFYA NNAKGRTISRDNKNTLYL QWNSLRADTAVYICARGLV DLNHWGGTILTVGS (SEQ ID NO: 182)	DIQMTQSPFSSLSASVG DRVLTITCQASQSYNN NYLSWYQQKPGKAPKL LIYDASTCLASGVFSRP SGSGSDFTLTITSSL QPEDFATYYCQGSYYS GGMDTAFGGGKVEIK (SEQ ID NO: 192)	ASTKGFSVFELAPSSKSTSGGTAALGCL VKDYFEEVTVSMNSGALTISGVHFFAV LQSSGLYSLSVTVFSSSLGTQTYICN VNHKFSNTKYDKKVEKSCDKTHICPC PAPELLGGPSVFLFPPKPKDTLMISRTPE EVTCVVVDVSHEDPEVKFNWYVDGVEYH NAKTREDEQYNSTYRVSVLTVVLHQDW LNGKREYKVKSKALPAPIETLSKAKG QPREPOVYTLPPSRDELTKNQVSLTCLV KGFYFSDIAVEWESNGQFENNYKTIPEV LSDSGSFFLYSKLTVDKSRWQQGNFSC SYMHEALHNHYTKQSLSLSPGK (SEQ ID NO: 157)	TVAAFSVFIFFPSDRLK SGTASVVCLLNNFYREA KVQWKVDNALQSGNSQES VTEQDSKDSSTYSLSSTLT LGRADYEKKYVJACEVTH QGLSSPVTKSFNGEC (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