Figure 1

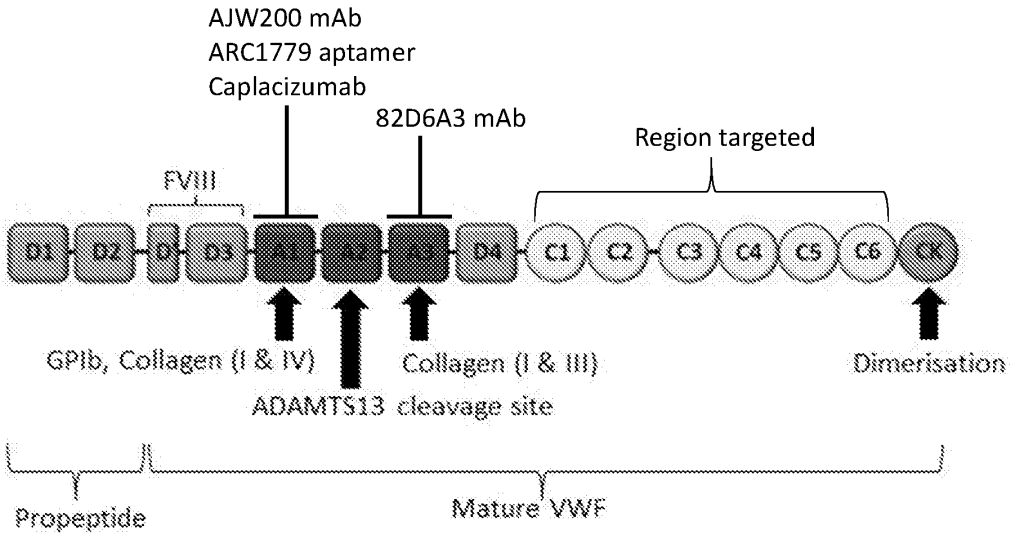

Figure 2

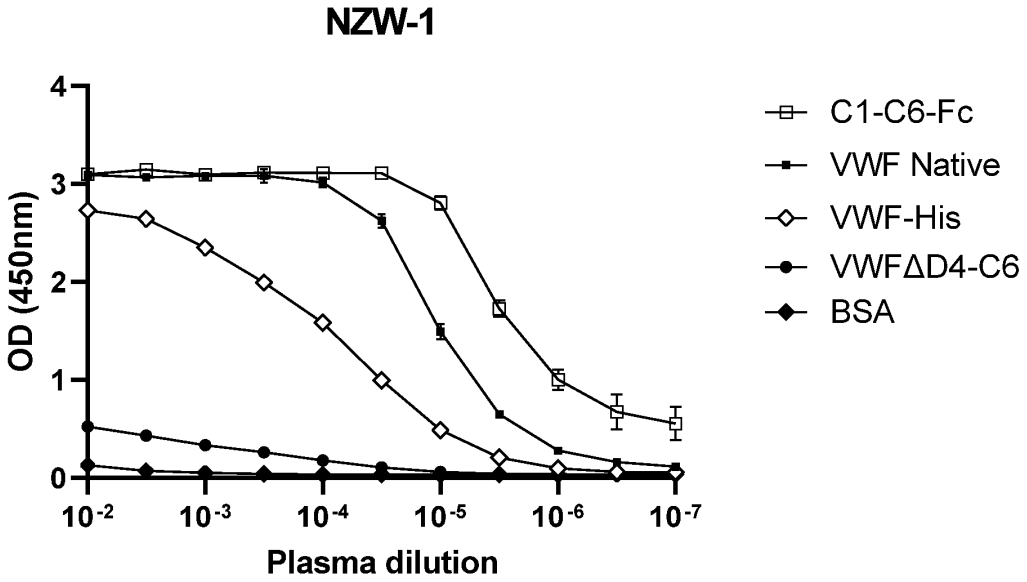

Figure 3A

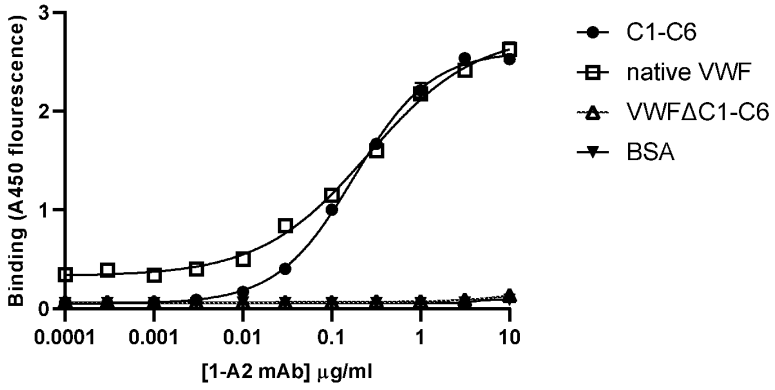

Figure 3B

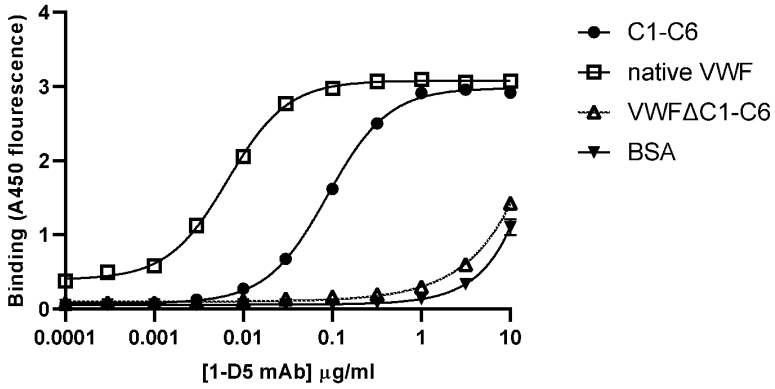

Figure 3C

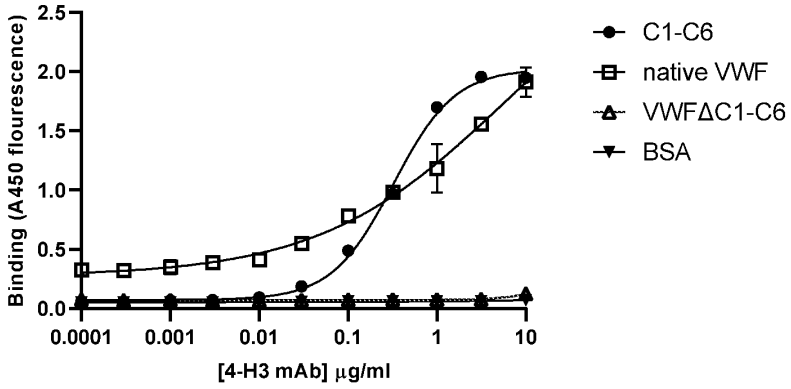

Figure 3D

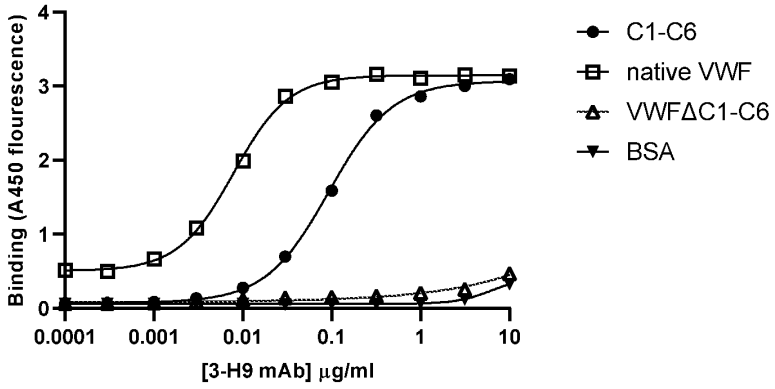

Figure 3E

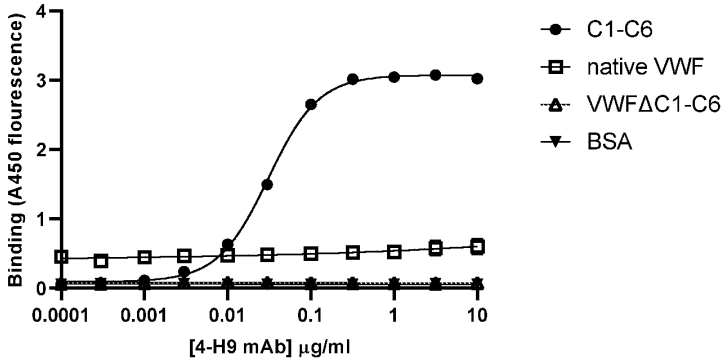

Figure 3F

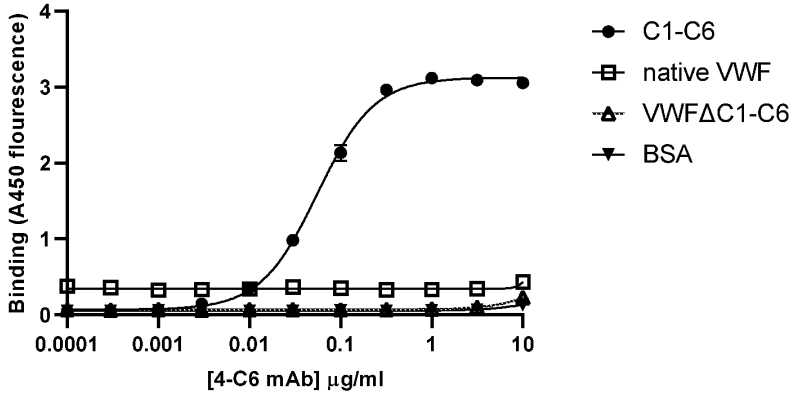

Figure 3G

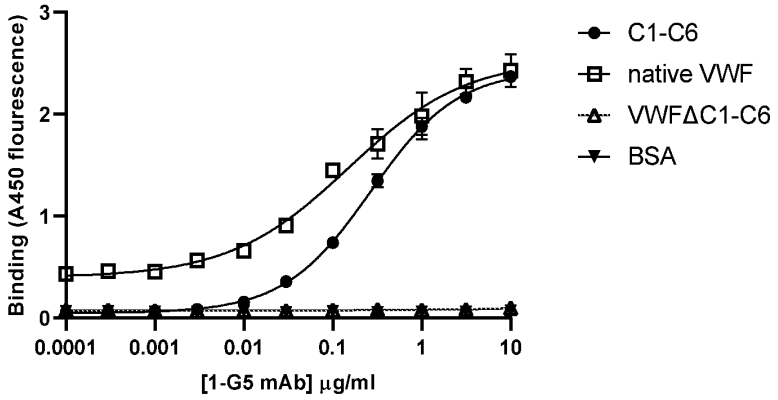

Figure 3H

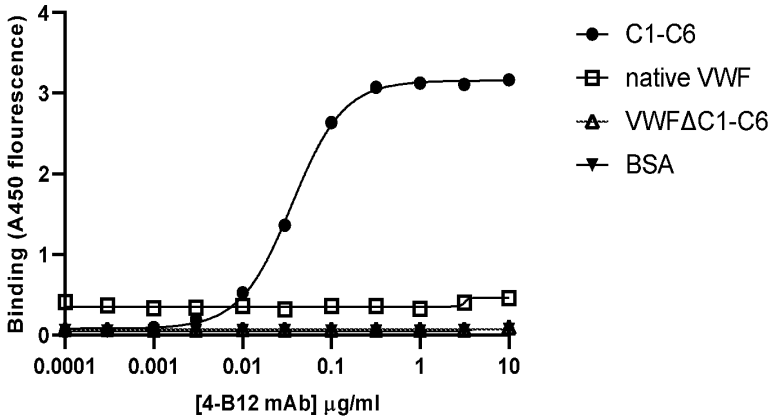

Figure 4

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

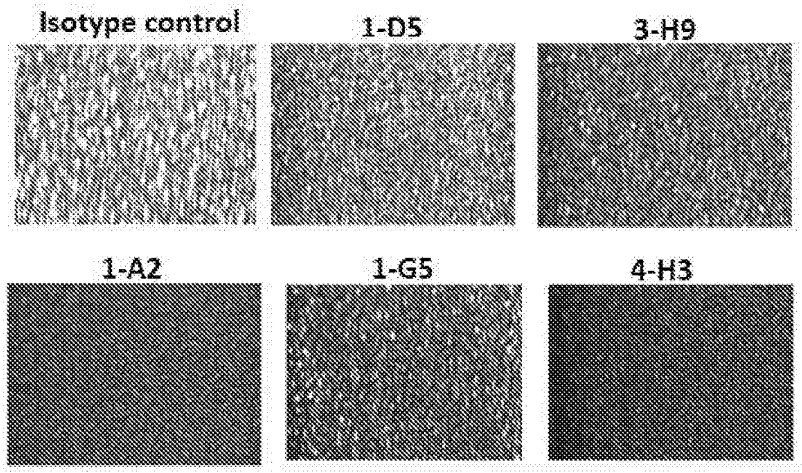

Figure 6A

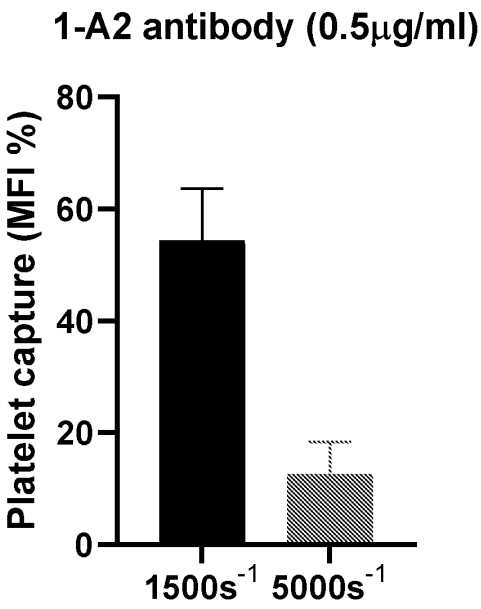

Figure 6B

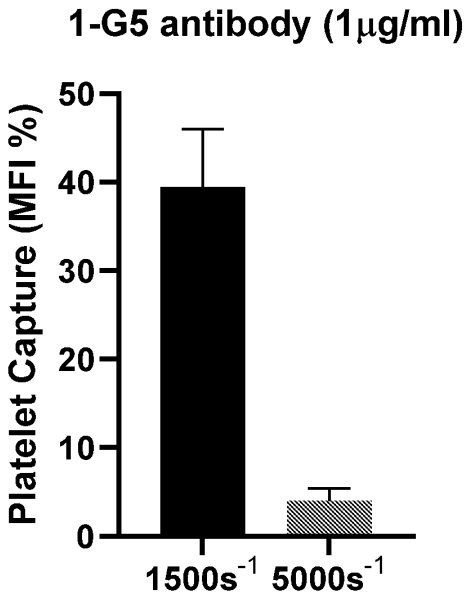

Figure 6C

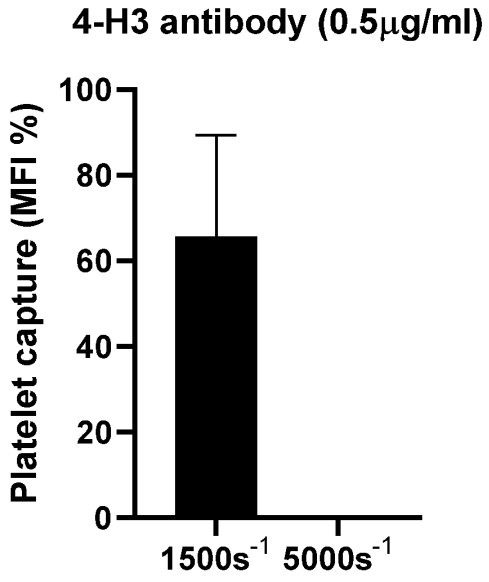

Figure 7A

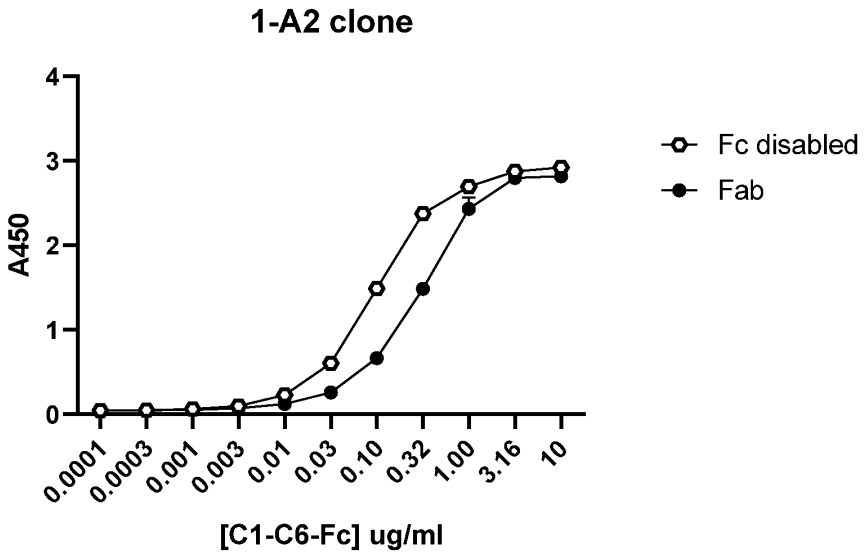

Figure 7B

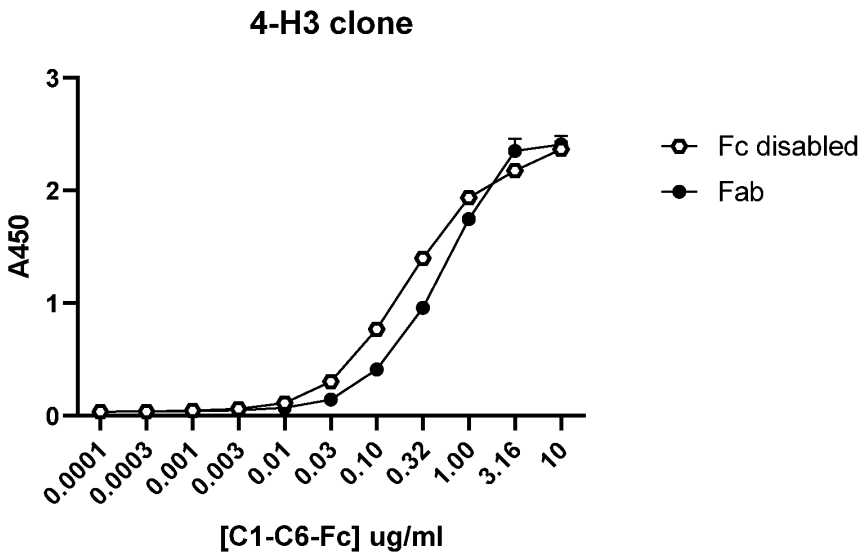

Figure 7C

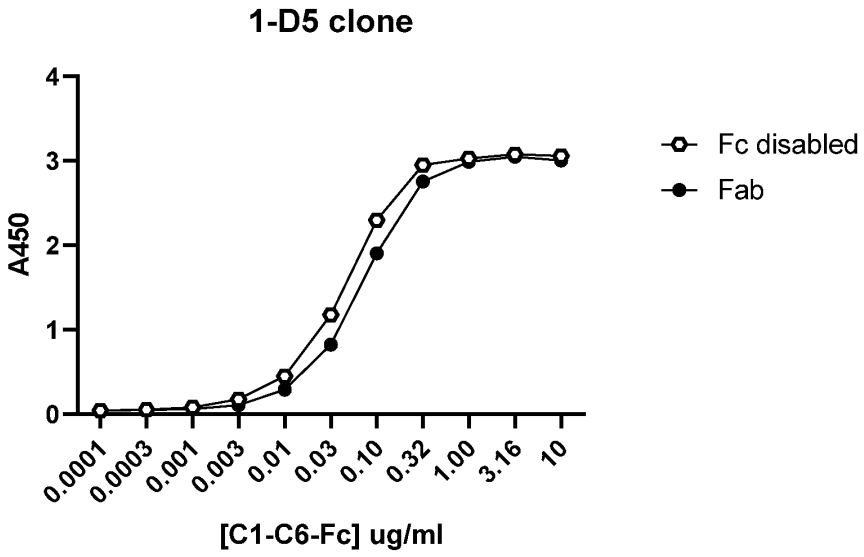

Figure 7D

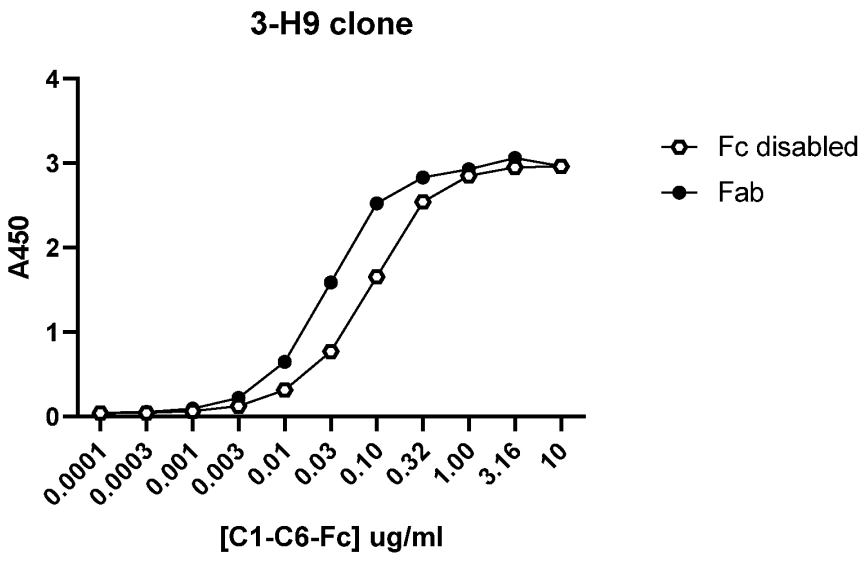

Figure 7E

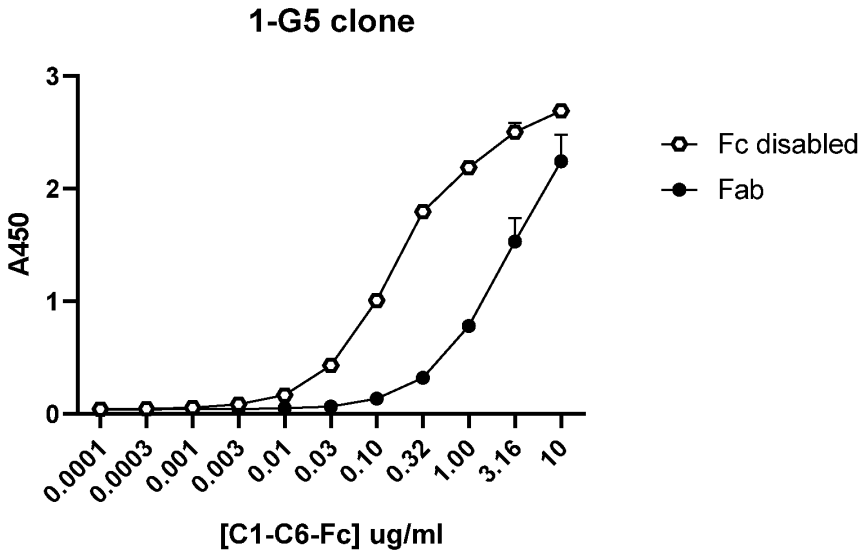

Figure 8

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

1-G5	SEQ ID NO: 81	SEQ ID NO: 82	SEQ ID NO: 83	SEQ ID NO: 84	SEQ ID NO: 85	SEQ ID NO: 86	SEQ ID NO: 87	SEQ ID NO: 90	SEQ ID NO: 91	SEQ ID NO: 92	SEQ ID NO: 93	SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 96	SEQ ID NO: 88	SEQ ID NO: 97
4-H9	SEQ ID NO: 99	SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 102	SEQ ID NO: 103	SEQ ID NO: 104	SEQ ID NO: 105	SEQ ID NO: 108	SEQ ID NO: 109	SEQ ID NO: 110	SEQ ID NO: 111	SEQ ID NO: 112	SEQ ID NO: 113	SEQ ID NO: 114	SEQ ID NO: 106	SEQ ID NO: 115
4-B12	SEQ ID NO: 117	SEQ ID NO: 118	SEQ ID NO: 119	SEQ ID NO: 120	SEQ ID NO: 121	SEQ ID NO: 122	SEQ ID NO: 123	SEQ ID NO: 126	SEQ ID NO: 127	SEQ ID NO: 128	SEQ ID NO: 129	SEQ ID NO: 130	SEQ ID NO: 131	SEQ ID NO: 132	SEQ ID NO: 124	SEQ ID NO: 133
4-C6	SEQ ID NO: 135	SEQ ID NO: 136	SEQ ID NO: 137	SEQ ID NO: 138	SEQ ID NO: 139	SEQ ID NO: 140	SEQ ID NO: 141	SEQ ID NO: 144	SEQ ID NO: 145	SEQ ID NO: 146	SEQ ID NO: 147	SEQ ID NO: 148	SEQ ID NO: 149	SEQ ID NO: 150	SEQ ID NO: 142	SEQ ID NO: 151

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 (hIgG1)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID No: 18)	GAS (SEQ ID No: 19)	LGGHSHSTTDLT (SEQ ID No: 20)	SQSVEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 156)	AIEMTQTPPSLSASVGETVRIRCLASEDIYSGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGHSHSTTDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_parental (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	SQSLEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 159)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_parental (hIgG1)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAGFNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANGAT (SEQ ID NO: 56)	QQQLVESGGRLVTPGTPLTLTCAVSGFSLNNYIMGWVRQAPGKGLEYIGIISTGGSTYYASWAKGRFTISRTSTTMDLKMTSLTTEDTATYFCARGGSSAGAGFNIWGPGTLVTVSS (SEQ ID NO: 52)	DIVMTQTPSSVSAAVGDTVTIQCQASQSINSGLAWYQQKPGQPPKRLIYKASTLASGVPSRFRGSGSGTDFTLTISDLECADAATYYCQSYHYISANGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_parental (hIgG1)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWYNT (SEQ ID NO: 74)	SQSLEESGGRLVTPGTPLTLTCSVSGFSLSNYDMSWVRQAPGKGLEWIGSIHAIGITYYANWAEGRFTISKTSTTVDLKMTSLTTEDTATYFCARGLVDLNMWGPGTLVTVSS (SEQ ID NO: 160)	AIKMTQTPSSVSVAVGGTVTINCQSSQSVYSNNLLSWYQQKPGQPPKLLIYDASTLESGVPSRFKGSGSGTQFTLTISGVQCEDAATYYCQGSYYSSGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-G5_parental (hIgG1)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	SQSLEESGGRLVTPGTPLTLTCSVSGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTISKTSTTVDLKMTSLTTEDTATYFCARGLVDLNMWGPGTLVTVSS (SEQ ID NO: 161)	DPVMTQTASSVSAAVGGTVTINCQASQSVYNNNYLSWYQQKPGQPPKLLIYDASTLASGVPSRFSGNGSGTQFTLTISGVQCDDAATYYCQGSYYSGGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_parental (hIgG1-L234A-L235A-P329G)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID No: 18)	GAS (SEQ ID No: 19)	LGGHSHSTTDLT (SEQ ID No: 20)	SQSVEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 156)	AIEMTQTPPSLSASVGETVRIRCLASEDIYSGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGHSHSTTDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 162)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_parental (hIgG1-L234A-L235A-P329G)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	SQSLEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 159)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 162)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_parental (hIgG1-L234A-L235A-P329G)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAGFNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANGAT (SEQ ID NO: 56)	QQQLVESGGRLVTPGTPLTLTCAVSGFSLNNYIMGWVRQAPGKGLEYIGIISTGGSTYYASWAKGRFTISRTSTTMDLKMTSLTTEDTATYFCARGGSSAGAGFNIWGPGTLVTVSS (SEQ ID NO: 52)	DIVMTQTPSSVSAAVGDTVTIQCQASQSINSGLAWYQQKPGQPPKRLIYKASTLASGVPSRFRGSGSGTDFTLTISDLECADAATYYCQSYHYISANGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 162)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_parental (hIgG1-L234A-L235A-P329G)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWYNT (SEQ ID NO: 74)	SQSLEESGGRLVTPGTPLTLTCSVSGFSLSNYDMSWVRQAPGKGLEWIGSIHAIGITYYANWAEGRFTISKTSTTVDLKMTSLTTEDTATYFCARGLVDLNMWGPGTLVTVSS (SEQ ID NO: 160)	AIKMTQTPSSVSVAVGGTVTINCQSSQSVYSNNLLSWYQQKPGQPPKLLIYDASTLESGVPSRFKGSGSGTQFTLTISGVQCEDAATYYCQGSYYSSGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKG	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 162)	
1-G5_parental (hIgG1-L234A-L235A-P329G)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	SQSLEESGGRLVTPGTPLTL TCTVSGFSLSSYDMTWVRQA PGKGLEWIGSIHATGITFYA NWAKGRFTTSKTSTTVDLKM TSLTTEDTATYFCARGLVDL NMWGPGTLVTVSS (SEQ ID NO: 161)	DPVMTQTASSVSAAVG GTVTINCQASQSVYNN NYLSWYQQKPGQPPKL LIYDASTLASGVPSRF SGNGSGTQFTLTISGV QCDDAATYYCQGSYYS GGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALGAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 162)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_parental (hIgG1-Fab)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	SQSVEESGGRLVPPGTPLTL TCTVSGIDLTSNAMNWVRQA PGKGLEWIGGIYGHDTSYYA AWAKGRFTISRTSTTVDLKM TRPTTDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 156)	AIEMTQTPPSLSASVG ETVRIRCLASEDIYSG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPSCGGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_parental (hIgG1-Fab)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	SQSLEESGGRLVPPGTPLTL TCTVSGIDLTSNAMNWVRQA PGKGLEWIGGIYGHDTSYYA AWAKGRFTISRTSTTVDLKM TRPTTDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 159)	AYDMTQTPPSLSASVG ETVRIRCLASEDIASG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPSCGGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_parental (hIgG1-Fab)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGRLVTPGTPLTL TCAVSGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRTSTTMDLKM TSLTTEDTATYFCARGGSSA GAGFNIWGPGTLVTVSS (SEQ ID NO: 52)	DIVMTQTPSSVSAAVG DTVTIQCQASQSINSG LAWYQQKPGQPPKRLI YKASTLASGVPSRFRG SGSGTDFTLTISDLEC ADAATYYCQSYHYISA NGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPSCGGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_parental (hIgG1-Fab)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	SQSLEESGGRLVTPGTPLTL TCSVSGFSLSNYDMSWVRQA PGKGLEWIGSIHAIGITYYA NWAEGRFTISKTSTTVDLKM TSLTTEDTATYFCARGLVDL NMWGPGTLVTVSS (SEQ ID NO: 160)	AIKMTQTPSSVSVAVG GTVTINCQSSQSVYSN NLLSWYQQKPGQPPKL LIYDASTLESGVPSRF KGSGSGTQFTLTISGV QCEDAATYYCQGSYYS SGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPSCGGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_parental (hIgG1-Fab)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	SQSLEESGGRLVTPGTPLTL TCSVSGFSLSSYDMTWVRQA PGKGLEWIGSIHATGITFYA NWAKGRFTTSKTSTTVDLKM TSLTTEDTATYFCARGLVDL NMWGPGTLVTVSS (SEQ ID NO: 161)	DPVMTQTASSVSAAVG GTVTINCQASQSVYNN NYLSWYQQKPGQPPKL LIYDASTLASGVPSRF SGNGSGTQFTLTISGV QCDDAATYYCQGSYYS GGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPSCGGGSK (SEQ ID NO: 163)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
4-H3_H0 (hIgG1)	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 165)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H1 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 194)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H2 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDSNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 166)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H3 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDNSKNTVYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 167)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H4 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDNSKNTLYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 168)	AYDMTQTPPSLSASVGETVRIRCLASEDIASGISWYQQKPGKPPTLLIYGASNLESGVPPRFSGSGSGTDYTLTIGGVQAEDAATYYCLGGYSFSSNGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
4-H3_H5 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWVAGIYGHDTSYYAA WAKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGFIY FDIWGQGTLVTVSS (SEQ ID NO: 169)	AYDMTQTPPSLSASVG ETVRIRCLASEDIASG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H6 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWVAGIYGHDTSYYAA WAKGRFTISRDSNTLYLQMN SLRAEDTAVYYCARGFIYFD IWGQGTLVTVSS (SEQ ID NO: 170)	AYDMTQTPPSLSASVG ETVRIRCLASEDIASG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H7 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWIGGIYGHDTSYYA AWAKGRFTISRDNSKNTVYL QMNSLRAEDTATYFCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 171)	AYDMTQTPPSLSASVG ETVRIRCLASEDIASG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H8 (hIgG1)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWIGGIYGHDTSYYAA WAKGRFTISRDSNTVYLQMN SLRAEDTATYFCARGFIYFD IWGQGTLVTVSS (SEQ ID NO: 172)	AYDMTQTPPSLSASVG ETVRIRCLASEDIASG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGYSFSS NGLTFGAGTKVEIK (SEQ ID NO: 43)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-D5_H0 (hIgG1)	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 174)	DIVMTQTPSSVSAAVG DTVTIQCQASQSINSG LAWYQQKPGQPPKRLI YKASTLASGVPSRFRG SGSGTDFTLTISDLEC ADAATYYCQSYHYISA NGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H1 (hIgG1)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 175)	DIVMTQTPSSVSAAVG DTVTIQCQASQSINSG LAWYQQKPGQPPKRLI YKASTLASGVPSRFRG SGSGTDFTLTISDLEC ADAATYYCQSYHYISA NGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H2 (hIgG1)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRDSNTMYLQM NSLRAEDTATYFCARGGSSA GAGFNIWGQGTLVTVSS (SEQ ID NO: 176)	DIVMTQTPSSVSAAVG DTVTIQCQASQSINSG LAWYQQKPGQPPKRLI YKASTLASGVPSRFRG SGSGTDFTLTISDLEC ADAATYYCQSYHYISA NGATFGGGTEVVVE (SEQ ID NO: 61)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_H0 (hIgG1)	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)	QGSYYSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSNYDMSWVRQA PGKGLEWVASIHAIGITYYA NWAEGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGLV DLNMWGQGTLVTVSS (SEQ ID NO: 178)	AIKMTQTPSSVSVAVG GTVTINCQSSQSVYSN NLLSWYQQKPGQPPKL LIYDASTLESGVPSRF KGSGSGTQFTLTISGV QCEDAATYYCQGSYYS SGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_H1 (hIgG1)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVVQPGRSLRL SCAASGFSLSNYDMSWVRQA PGKGLEWVASIHAIGITYYA NWAEGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGLV DLNMWGQGTLVTVSS (SEQ ID NO: 179)	AIKMTQTPSSVSVAVG GTVTINCQSSQSVYSN NLLSWYQQKPGQPPKL LIYDASTLESGVPSRF KGSGSGTQFTLTISGV QCEDAATYYCQGSYYS SGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
3-H9_H2 (hIgG1)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	QQLVESGGGVVQPGRSLRLS CAASGFSLSNYDMSWVRQAP GKGLEWIGSIHAIGITYYAN WAEGRFTISRDKNTVYLQMN SLRAEDTATYFCARGLVDLN MWGQGTLVTVSS (SEQ ID NO: 180)	AIKMTQTPSSVSVAVG GTVTINCQSSQSVYSN NLLSWYQQKPGQPPKL LIYDASTLESGVPSRF KGSGSGTQFTLTISGV QCEDAATYYCQGSYYS SGWYNTFGGGTEVVVE (SEQ ID NO: 79)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_Ho (hIgG1)	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 165)	AIEMTQTPPSLSASVG ETVRIRCLASEDIYSG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H1 (hIgG1)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 194)	AIEMTQTPPSLSASVG ETVRIRCLASEDIYSG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H2 (hIgG1)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWIGGIYGHDTSYYAA WAKGRFTISRDSNTVYLQMN SLRAEDTATYFCARGFIYFD IWGQGTLVTVSS (SEQ ID NO: 172)	AIEMTQTPPSLSASVG ETVRIRCLASEDIYSG ISWYQQKPGKPPTLLI YGASNLESGVPPRFSG SGSGTDYTLTIGGVQA EDAATYYCLGGHSHST TDLTFGAGTKVEIK (SEQ ID NO: 25)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-G5_H0 (hIgG1)	GFTFSSYD (SEQ ID NO: 181)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMTWVRQAPGKGLEWVASIHATGITFYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 182)	DPVMTQTASSVSAAVGGTVTINCQASQSVYNNNYLSWYQQKPGQPPKLLIYDASTLASGVPSRFSGNGSGTQFTLTISGVQCDDAATYYCQGSYYSGGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H1 (hIgG1)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWVASIHATGITFYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 183)	DPVMTQTASSVSAAVGGTVTINCQASQSVYNNNYLSWYQQKPGQPPKLLIYDASTLASGVPSRFSGNGSGTQFTLTISGVQCDDAATYYCQGSYYSGGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H2 (hIgG1)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTTSKDSNTVYLQMNSLRAEDTATYFCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 184)	DPVMTQTASSVSAAVGGTVTINCQASQSVYNNNYLSWYQQKPGQPPKLLIYDASTLASGVPSRFSGNGSGTQFTLTISGVQCDDAATYYCQGSYYSGGWDTAFGGGTKVVVK (SEQ ID NO: 97)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_L0 (hIgGK)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	SQSLEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 159)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_L1 (hIgGK)	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	SQSLEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 159)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
1-D5_L0 (hIgGK)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGRLVTPGTPLTL TCAVSGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRTSTTMDLKM TSLTTEDTATYFCARGGSSA GAGFNIWGPGTLVTVSS (SEQ ID NO: 52)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKLLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 187)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_L1 (hIgGK)	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGRLVTPGTPLTL TCAVSGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRTSTTMDLKM TSLTTEDTATYFCARGGSSA GAGFNIWGPGTLVTVSS (SEQ ID NO: 52)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKRLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 188)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_L0 (hIgGK)	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	SQSLEESGGRLVTPGTPLTL TCSVSGFSLSNYDMSWVRQA PGKGLEWIGSIHAIGITYYA NWAEGRFTISKTSTTVDLKM TSLTTEDTATYFCARGLVDL NMWGPGTLVTVSS (SEQ ID NO: 160)	DIQMTQSPSSLSASVG DRVTITCQSSQSVYSN NLLSWYQQKPGKAPKL LIYDASTLESGVPSRF SGSGSGTDFTLTISSL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_L0 (hIgGK)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	SQSVEESGGRLVPPGTPLTL TCTVSGIDLTSNAMNWVRQA PGKGLEWIGGIYGHDTSYYA AWAKGRFTISRTSTTVDLKM TRPTTDDTATYFCARGFIYF DIWGTGTLVTISS (SEQ ID NO: 156)	DIQMTQSPSSLSASVG DRVTITCLASEDIYSG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGHSHST TDLTFGGGTKVEIK (SEQ ID NO: 190)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-A2_L1 (hIgGK)	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID No: 18)	GAS (SEQ ID No: 19)	LGGHSHSTTDLT (SEQ ID No: 20)	SQSVEESGGRLVPPGTPLTLTCTVSGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRTSTTVDLKMTRPTTDDTATYFCARGFIYFDIWGTGTLVTISS (SEQ ID NO: 156)	DIQMTQSPSSLSASVGDRVTITCLASEDIYSGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGHSHSTTDLTFGGGTKVEIK (SEQ ID NO: 191)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_L0 (hIgGK)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	SQSLEESGGRLVTPGTPLTLTCSVSGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTTSKTSTTVDLKMTSLTTEDTATYFCARGLVDLNMWGPGTLVTVSS (SEQ ID NO: 161)	DIQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 192)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_L1 (hIgGK)	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	SQSLEESGGRLVTPGTPLTLTCSVSGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTTSKTSTTVDLKMTSLTTEDTATYFCARGLVDLNMWGPGTLVTVSS (SEQ ID NO: 161)	DPQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 193)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H2_L1	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID No: 18)	GAS (SEQ ID No: 19)	LGGHSHSTTDLT (SEQ ID No: 20)	QQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDSNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVGDRVTITCLASEDIYSGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGHSHSTTDLTFGGGTKVEIK (SEQ ID NO: 191)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H2_L0	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (SEQ ID NO: 10)	ARGFIYFDI (SEQ ID NO: 11)	EDIYSG (SEQ ID No: 18)	GAS (SEQ ID No: 19)	LGGHSHSTTDLT (SEQ ID No: 20)	QQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDSNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVGDRVTITCLASEDIYSGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGHSHSTTDLTFGGGTKVEIK (SEQ ID NO: 190)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
1-A2_H1_L1	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVTITCLASEDIYSG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGHSHST TDLTFGGGTKVEIK (SEQ ID NO: 191)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H1_L0	GIDLTSNA (SEQ ID NO: 9)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVTITCLASEDIYSG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGHSHST TDLTFGGGTKVEIK (SEQ ID NO: 190)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H0_L1	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVTITCLASEDIYSG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGHSHST TDLTFGGGTKVEIK (SEQ ID NO: 191)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-A2_H0_L0	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (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)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVTITCLASEDIYSG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGHSHST TDLTFGGGTKVEIK (SEQ ID NO: 190)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
4-H3_H8_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDSNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 172)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H8_L0	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDSNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 172)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H7_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDNSKNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 171)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H7_L0 rep	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDNSKNTVYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 171)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H6_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDSNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 170)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
4-H3_H6_L0	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWVAGIYGHDTSYYAA WAKGRFTISRDSNTLYLQMN SLRAEDTAVYYCARGFIYFD IWGQGTLVTVSS (SEQ ID NO: 170)	DIQMTQSPSSLSASVG DRVTITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H5_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWVAGIYGHDTSYYAA WAKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGFIY FDIWGQGTLVTVSS (SEQ ID NO: 169)	DYQMTQSPSSLSASVG DRVTITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H5_L0	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QQLVESGGGVVQPGRSLRLS CAASGIDLTSNAMNWVRQAP GKGLEWVAGIYGHDTSYYAA WAKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGFIY FDIWGQGTLVTVSS (SEQ ID NO: 169)	DIQMTQSPSSLSASVG DRVTITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H4_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTATYFCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 168)	DYQMTQSPSSLSASVG DRVTITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
4-H3_H4_Lo	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDNSKNTLYLQMNSLRAEDTATYFCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 168)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H3_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDNSKNTVYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 167)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H3_Lo	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWIGGIYGHDTSYYAAWAKGRFTISRDNSKNTVYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 167)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H2_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDSNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 166)	DYQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H2_Lo	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNGLT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRLSCAASGIDLTSNAMNWVRQAPGKGLEWVAGIYGHDTSYYAAWAKGRFTISRDSNTLYLQMNSLRAEDTAVYYCARGFIYFDIWGQGTLVTVSS (SEQ ID NO: 166)	DIQMTQSPSSLSASVGDRVTITCLASEDIASGISWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLGGYSFSSNGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
4-H3_H1_L1	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 194)	DYQMTQSPSSLSASVG DRVTIITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_H1_L0	GIDLTSNA (SEQ ID NO: 27)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGIDLTSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 194)	DIQMTQSPSSLSASVG DRVTIITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_Ho_L1 rep	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 165)	DYQMTQSPSSLSASVG DRVTIITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDYTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 186)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
4-H3_Ho_L0	GFTFSSNA (SEQ ID NO: 164)	IYGHDTS (SEQ ID NO: 28)	ARGFIYFDI (SEQ ID NO: 29)	EDIASG (SEQ ID NO: 36)	GAS (SEQ ID NO: 37)	LGGYSFSSNG LT (SEQ ID NO: 38)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSNAMNWVRQA PGKGLEWVAGIYGHDTSYYA AWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGFI YFDIWGQGTLVTVSS (SEQ ID NO: 165)	DIQMTQSPSSLSASVG DRVTIITCLASEDIASG ISWYQQKPGKAPKLLI YGASNLESGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCLGGYSFSS NGLTFGGGTKVEIK (SEQ ID NO: 185)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-D5_H2_L1	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRDSNTMYLQM NSLRAEDTATYFCARGGSSA GAGFNIWGQGTLVTVSS (SEQ ID NO: 176)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKRLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 188)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H2_L0	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QQQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEYIGIISTGGSTYYA SWAKGRFTISRDSNTMYLQM NSLRAEDTATYFCARGGSSA GAGFNIWGQGTLVTVSS (SEQ ID NO: 176)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKLLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 187)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H1_L1	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 175)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKRLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 188)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H1_L0	GFSLNNYI (SEQ ID NO: 45)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFSLNNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 175)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKLLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 187)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-D5_H0_L1	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 174)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKRLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 188)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
1-D5_H0_L0	GFTFSNYI (SEQ ID NO: 173)	ISTGGST (SEQ ID NO: 46)	ARGGSSAGAG FNI (SEQ ID NO: 47)	QSINSG (SEQ ID NO: 54)	KAS (SEQ ID NO: 55)	QSYHYISANG AT (SEQ ID NO: 56)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSNYIMGWVRQA PGKGLEWVAIISTGGSTYYA SWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGGS SAGAGFNIWGQGTLVTVSS (SEQ ID NO: 174)	DIQMTQSPSSLSASVG DRVTITCQASQSINSG LAWYQQKPGKAPKLLI YKASTLASGVPSRFSG SGSGTDFTLTISSLQP EDFATYYCQSYHYISA NGATFGGGTKVEIK (SEQ ID NO: 187)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_H2_L0	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	QQLVESGGGVVQPGRSLRLS CAASGFSLSNYDMSWVRQAP GKGLEWIGSIHAIGITYYAN WAEGRFTISRDKNTVYLQMN SLRAEDTATYFCARGLVDLN MWGQGTLVTVSS (SEQ ID NO: 180)	DIQMTQSPSSLSASVG DRVTITCQSSQSVYSN NLLSWYQQKPGKAPKL LIYDASTLESGVPSRF SGSGSGTDFTLTISSL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_H1_L0	GFSLSNYD (SEQ ID NO: 63)	IHAIGIT (SEQ ID NO: 64)	ARGLVDLNM (SEQ ID NO: 65)	QSVYSNNL (SEQ ID NO: 72)	DAS (SEQ ID NO: 73)	QGSYYSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVVQPGRSLRL SCAASGFSLSNYDMSWVRQA PGKGLEWVASIHAIGITYYA NWAEGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGLV DLNMWGQGTLVTVSS (SEQ ID NO: 179)	DIQMTQSPSSLSASVG DRVTITCQSSQSVYSN NLLSWYQQKPGKAPKL LIYDASTLESGVPSRF SGSGSGTDFTLTISSL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)
3-H9_H0_L0	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)	QGSYYSSGWY NT (SEQ ID NO: 74)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSNYDMSWVRQA PGKGLEWVASIHAIGITYYA NWAEGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGLV DLNMWGQGTLVTVSS (SEQ ID NO: 178)	DIQMTQSPSSLSASVG DRVTITCQSSQSVYSN NLLSWYQQKPGKAPKL LIYDASTLESGVPSRF SGSGSGTDFTLTISSL QPEDFATYYCQGSYYS SGWYNTFGGGTKVEIK (SEQ ID NO: 189)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
1-G5_H2_L1	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTTSKDSNTVYLQMNSLRAEDTATYFCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 184)	DPQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 193)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H2_L0	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWIGSIHATGITFYANWAKGRFTTSKDSNTVYLQMNSLRAEDTATYFCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 184)	DIQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 192)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H1_L1	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWVASIHATGITFYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 183)	DPQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 193)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H1_L0	GFSLSSYD (SEQ ID NO: 81)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRLSCAASGFSLSSYDMTWVRQAPGKGLEWVASIHATGITFYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 183)	DIQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 192)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLKSGTASWVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)
1-G5_H0_L1	GFTFSSYD (SEQ ID NO: 181)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWDTA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMTWVRQAPGKGLEWVASIHATGITFYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGLVDLNMWGQGTLVTVSS (SEQ ID NO: 182)	DPQMTQSPSSLSASVGDRVTITCQASQSVYNNNYLSWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQGSYYSGGWDTAFGGGTKVEIK (SEQ ID NO: 193)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Antibody	CDR-H1	CDR-H2	CDR-H3	CDR-L1	CDR-L2	CDR-L3	VH	VL	HC	LC
									KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	
1-G5_Ho_Lo	GFTFSSYD (SEQ ID NO: 181)	IHATGIT (SEQ ID NO: 82)	ARGLVDLNM (SEQ ID NO: 83)	QSVYNNNY (SEQ ID NO: 90)	DAS (SEQ ID NO: 91)	QGSYYSGGWD TA (SEQ ID NO: 92)	QVQLVESGGGVVQPGRSLRL SCAASGFTFSSYDMTWVRQA PGKGLEWVASIHATGITFYA NWAKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGLV DLNMWGQGTLVTVSS (SEQ ID NO: 182)	DIQMTQSPSSLSASVG DRVTITCQASQSVYNN NYLSWYQQKPGKAPKL LIYDASTLASGVPSRF SGSGSGTDFTLTISSL QPEDFATYYCQGSYYS GGWDTAFGGGTKVEIK (SEQ ID NO: 192)	ASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 157)	TVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTH 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
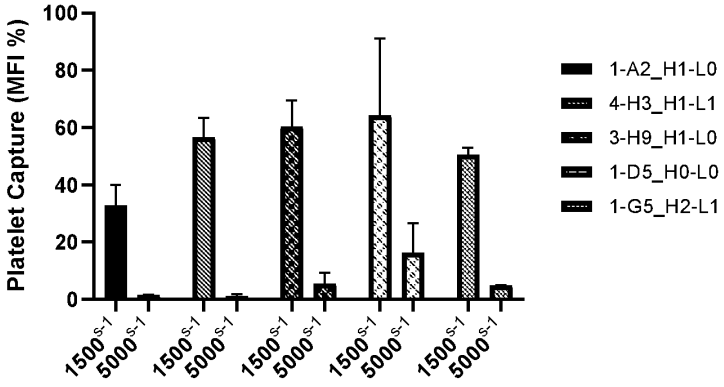
Figure 12