

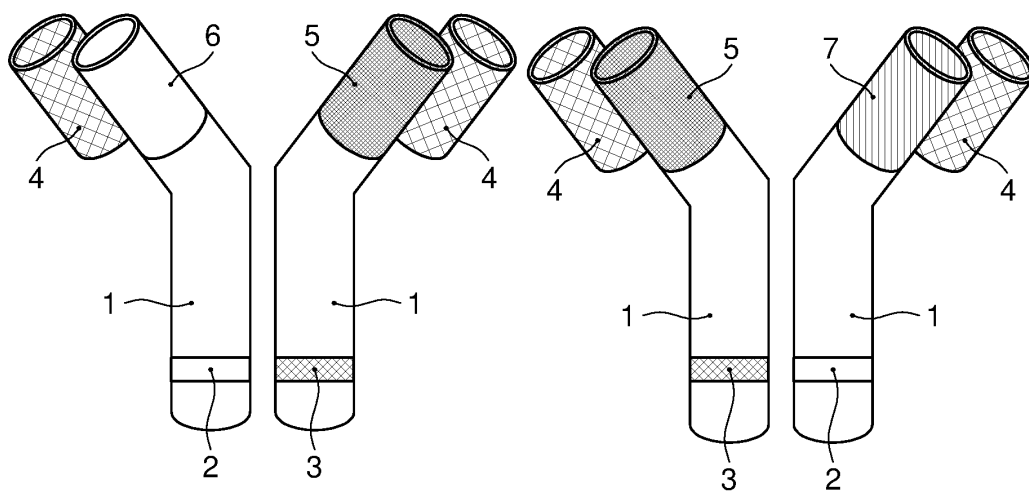


Fig. 1

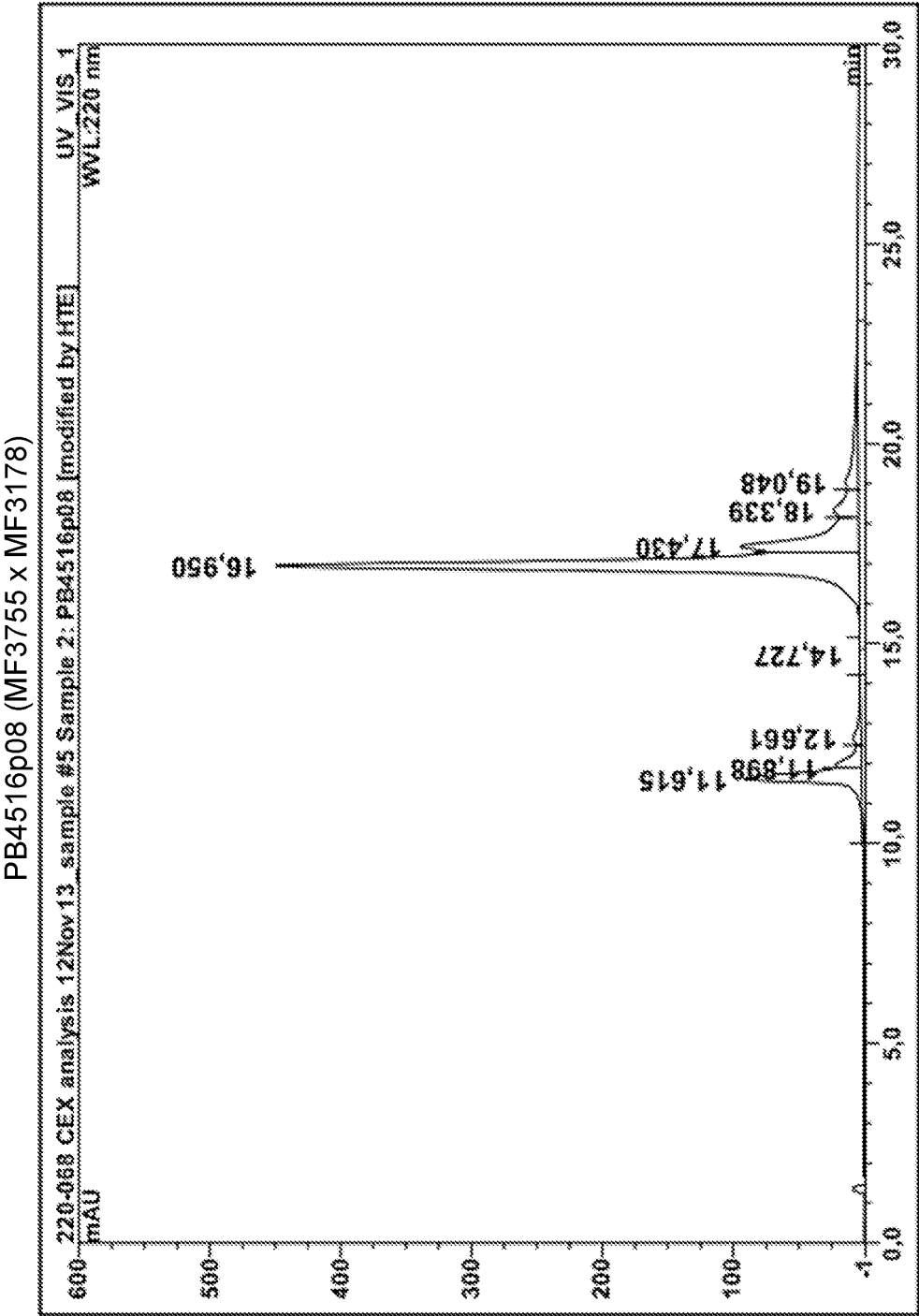


Fig. 2A

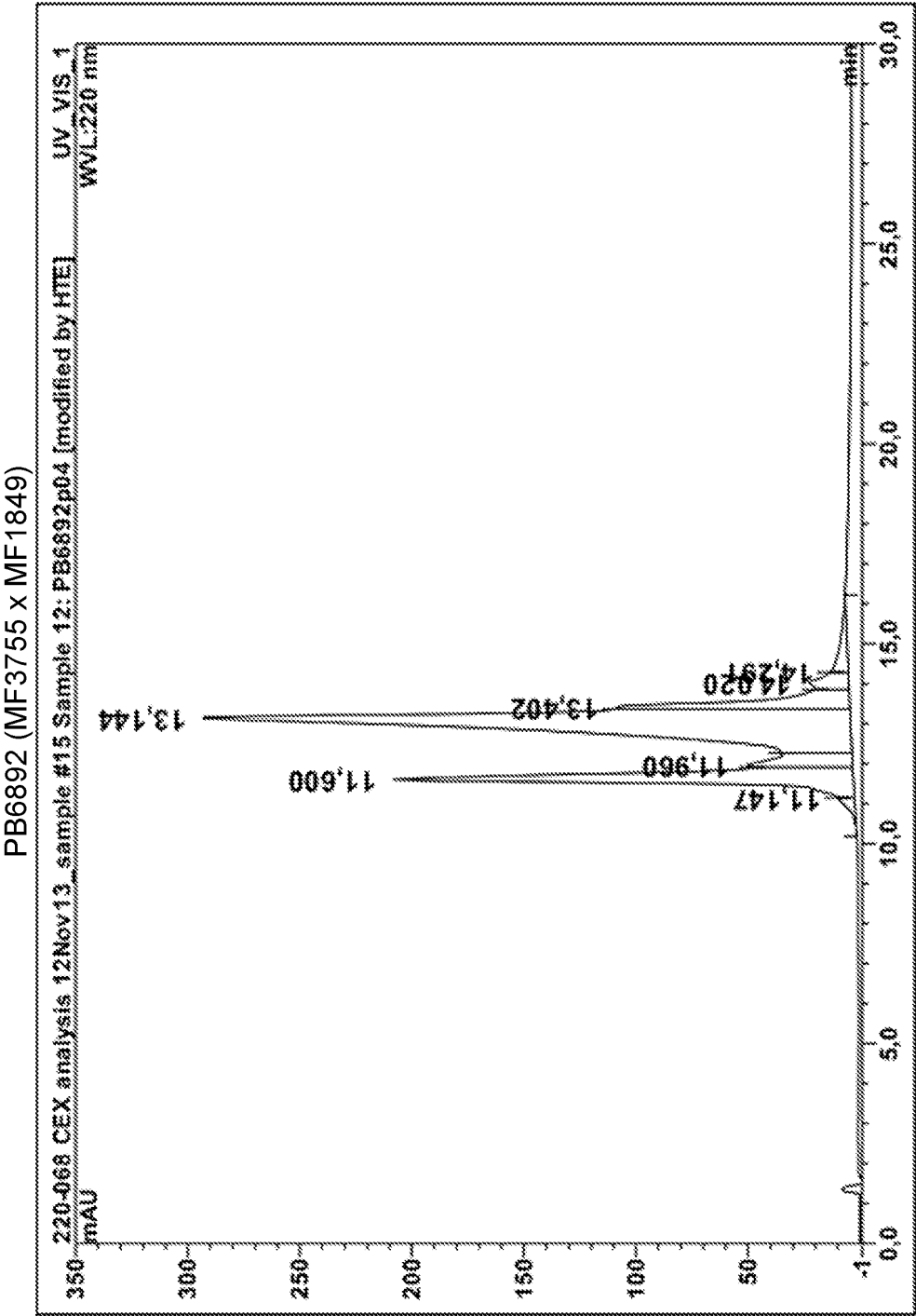


Fig. 2B

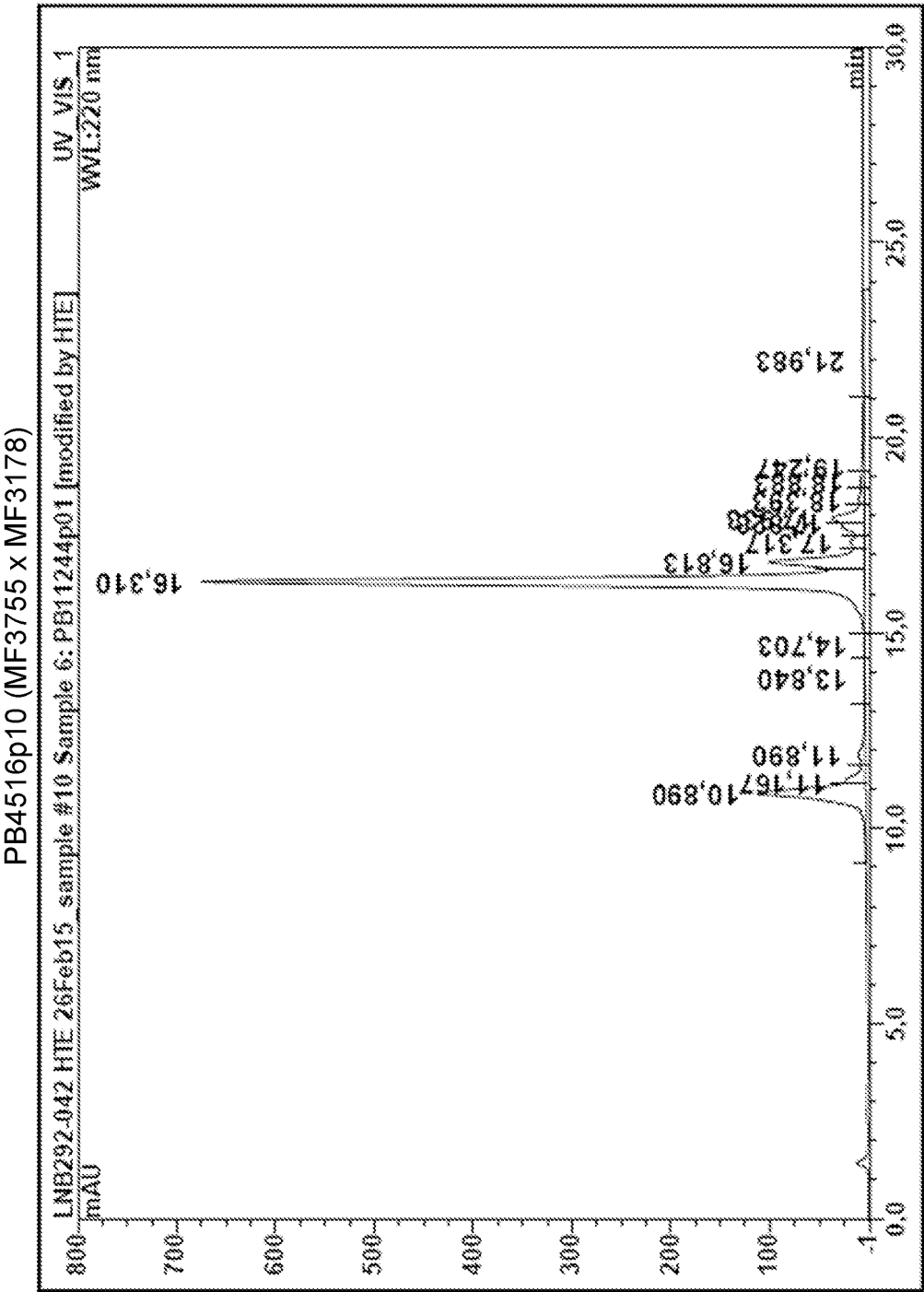


Fig. 3A

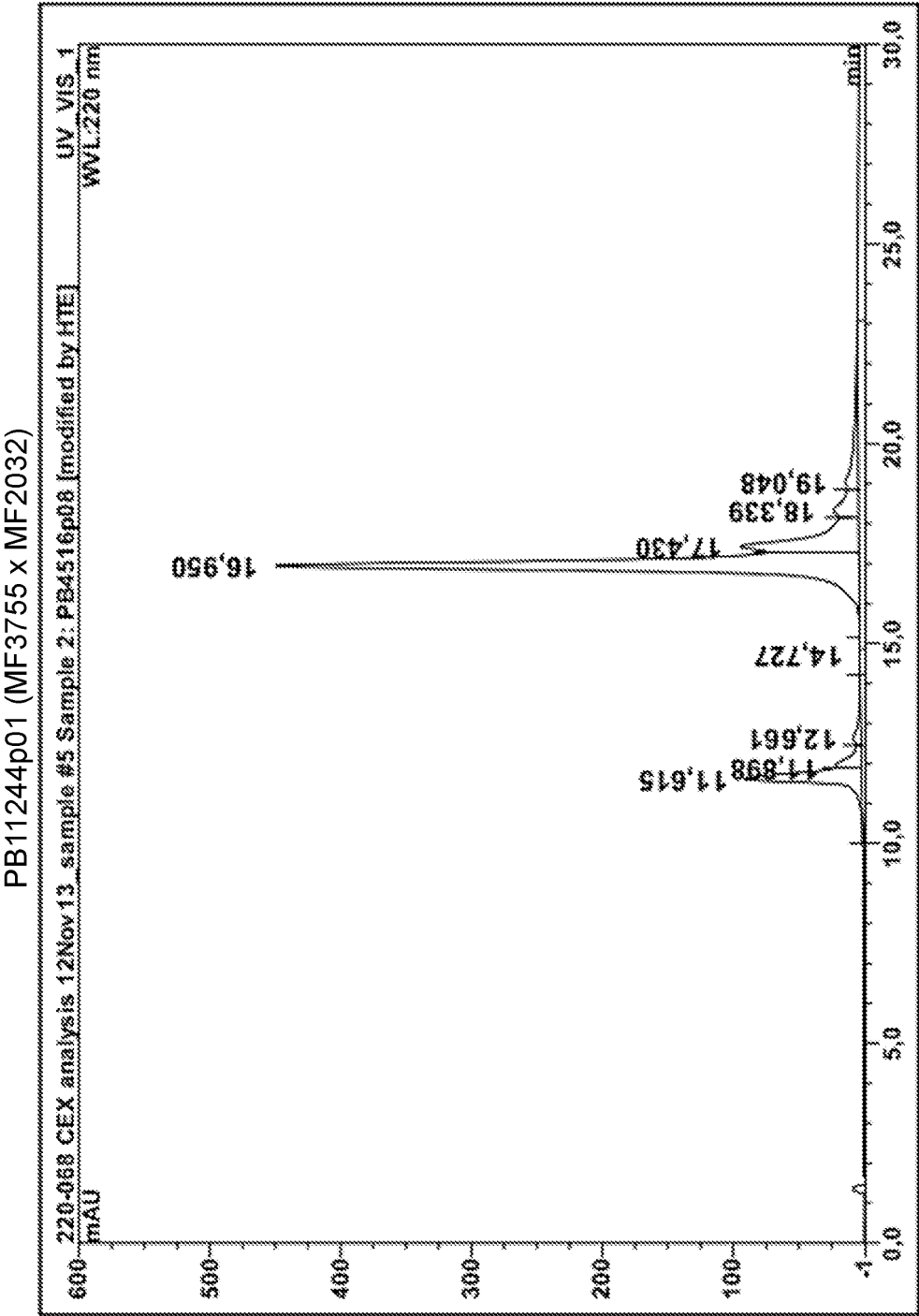


Fig. 3B

PB	Target 1	VH pl	Target 2	VH pl	Average VH pl T1, T2	Difference in VH pl between the pairs
PB11244	EGFR – MF3755-DE	6.09	HER2 – MF2032-KK	9.33	7.71	0.08
PB4516	EGFR – MF3755-DE	6.09	HER3 – MF3178-KK	9.17	7.63	

Fig. 3C

Co-elution of PB4516 and PB11244

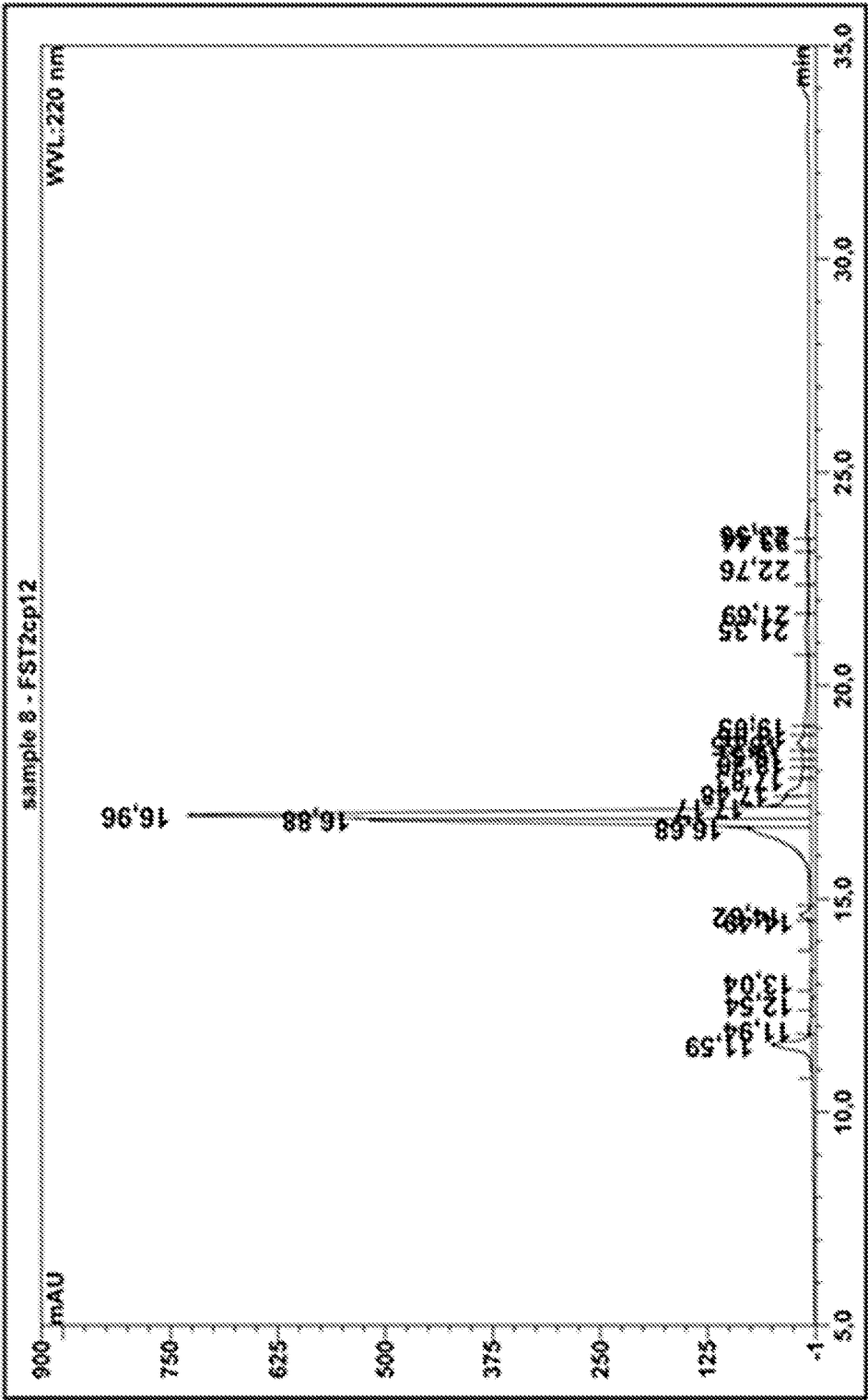


Fig. 4

Co-elution of PB4516 and PB11244

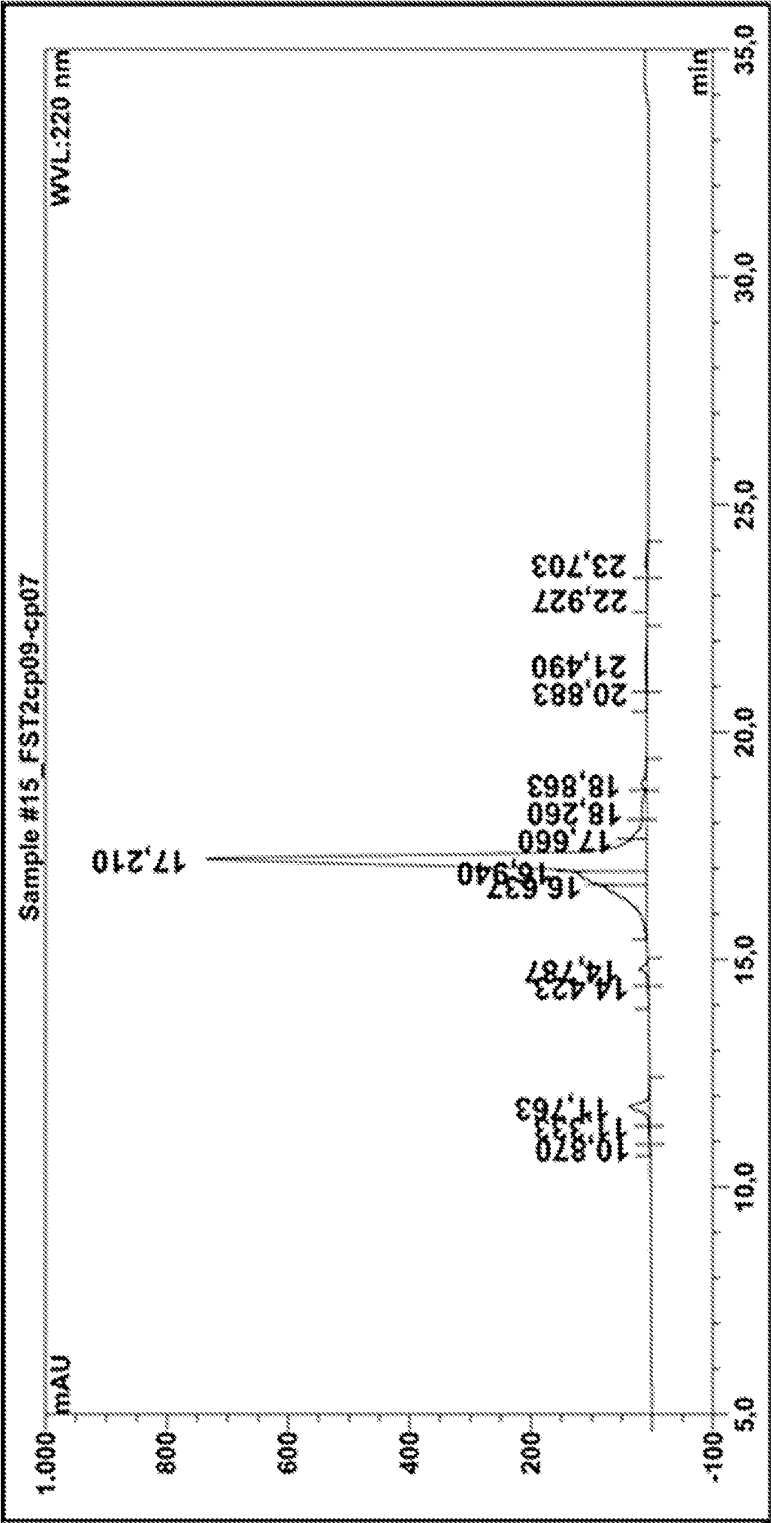


Fig. 5

MF	PG	Retention time
MF3178	PG3178	22.282
MF3958	PG3958	12.208
MF4003	PG4003	12.983
MF3163	PG3163	21.706
MF6061	PG6061	24.000
MF6930	PG6930	12.393
MF6256	PG6256	10.333
MF3755	PG3755	11.123
MF1898	PG1898	17.125
MF2032	PG2032	21.760

Fig. 6

PB	Target 1	VH pI	Target 2	VH pI	Average VH pI T1, T2	Total PB pI	Difference in VH pI between the pairs	Difference in total PB pI	Ret Time
PB4186	HER3 - MF3178-KK	9.17	HER2 - MF3958-DE	8.55	8.86	8.52	0.035	0.01	18.99
PB4528	HER3 - MF3178-KK	9.17	EGFR - MF4003-DE	8.62	8.895	8.59			19.53
PB4522	HER3 - MF3178-KK	9.17	EGFR - MF4280-DE	4.73	6.95	8.07	0.08	0.09	16.24
PB11003	HER3 - MF6061-KK	9.33	EGFR - MF4280-DE	4.73	7.03	8.16			16.48
PB14120	PD1 - MF6930-KK	6.54	TIM3 - MF6501-DE	5.21	5.875	8.07	0.01	0	11.37
PB14125	PD1 - MF6256-KK	6.52	TIM3 - MF6501-DE	5.21	5.865	8.07			11.4
PB6892	HER2 - MF1849-KK	8.55	EGFR - MF3755-DE	6.09	7.32	8.24	0.045	0	13.21
PB14063	LGR5 - MF7423-KK	8.64	EGFR - MF3755-DE	6.09	7.365	8.24			13.48
PB11243	EGFR - MF3755-DE	6.09	HER2 - MF1898-KK	9.2	7.645	8.37	0.625	0.21	13.9
PB14068	LGR5 - MF7423-KK	7.95	EGFR - MF3755-DE	6.09	7.0	8.16			13.98
PB11246	EGFR - MF3755-DE	6.09	HER2 - MF1898-KK	9.2	7.645	8.37	0.28	0.13	13.9
PB14063	LGR5 - MF7423-KK	8.64	EGFR - MF3755-DE	6.09	7.365	8.24			14.12
PB14323	LGR5 - MF7533-KK	9.01	EGFR - MF3755-DE	6.09	7.55	8.31	0.16	0.12	16.22
PB11244	EGFR - MF3755-DE	6.09	HER2 - MF2032-KK	9.32	7.71	8.43			16.31
PB6892	HER2 - MF1849-KK	8.55	EGFR - MF3755-DE	6.09	7.32	8.24	0.3	0.06	13.21
PB14068	LGR5 - MF7423-KK	7.95	EGFR - MF3755-DE	6.09	7.02	8.16			13.21

Fig. 7

Fig. 8

Amino acid sequences of the heavy chain variable regions of the various variable domains indicated by the MF number SEQ ID NO: 1-21 and the CDRs and light chain variable regions of SEQ ID NO: 22-27.

SEQUENCE LISTING SUMMARY

1	HER3-MF3178	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTMTDRDTSISTAYMELSLRSDDTAVYYCARDHGSRHFWSY WGFDYWGQGLTVTVSS
2	HER3-MF3163	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTMTDRDTSISTAYMELSLRSDDTAVYYCAKDSYSRHFYSW WAFDYWGQGLTVTVSS
3	HER3-MF6061	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVVRQAPGQGLEWMGWINPQ SGGTNYAQKFQGRVTMTDRDTSISTAYMELSLRSDDTAVYYCARDHGSRHFWSY WGFDYWGQGLTVTVSS
4	PD1-MF6930	EVQLVQSGAEVKKPGSSMKVSCASGGTFSSNYVISWVRQAPGQGLEWMGMIIIPV FETATYEKKFQGRVTIIADKSTSTVYELSSLRSEDAAVYYCARGTVEATLLFD YWGQGLTVTVSS
5	PD1-MF6256	EVQLVQSGAEVKKPGSSMKVSCASGGTFSSYVISWVRQAPGQGLEWMGMIIIPV FDTSSYEKKFQGRITIIADKSTSTVYLELSSLRSEDAAVYYCARGTVEATLLFD FWGQGLTVTVSS
6	HER2-MF1849	QVQLVSGSGGVVQPGSRSLRSCAASGFTFSSYGMHVVRQAPGKGLEWVAVISYD GSNKYYADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKGDYGSYSYA FDYWGQGLTVTVSS
7	LGR5-MF7423	QVQLVQSGAEVKKPGSSVKVSCASGGTFSSNYAISWVRQAPGQGLEWMGSIIP LGTTDHAQKFQDRVTITAGKSSNTAYMDLSSLRSDDTAVYYCARELIAARLDYF DSWGQGLTVTVSS
8	EGFR-MF3755	QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWRQAPGHGLEWMGWINAN TGDPTYAQGFTGRFVFLDTSVSTAYLQISSLKAEDSAVYYCTRERFLEWLHFD YWGQGLTVTVSS
9	LGR5-MF7428	QVQLVQSGAEVKKPGSSVKVSCASGGTFSSNYAISWVRQAPGQGLEWMGSIIP LGTTDHAQKFQDRVTITADKSSKTTYMELNSLRSDDTAVYYCARELIAARLDYF DSWGQGLTVTVSS
10	LGR5-MF7533	QVQLVQSGAEVKKPGSSVKVSCASGGTFSSNYAISWVRQAPGQGLEWMGSIIP LGTTDHAQKFQDRVTITAGKSSNTAYMDLSSLRSDDTAVYYCARELIAARLDYF DSWGRGTLTVTVSS
11	LGR5-MF7532	EVQLVQSGSKLKKPGASVKVSCASGYTFTSYTMNWRQAPGQGLEWMGWINTD TGDPTYAQGFTGRFVFLDTSVSTAFLQINSLKAEDTAVYYCARGDCDSTSCYR YSYGYEDYWGRTLVTVSS
12	EGFR-MF4280	QVQLVQSGAEVKKPGASVKVSGYTLTELSMHVVRQAPGKGLEWMGGFDPE YKTFFAQNFQGRVTMTEDTSADTAYMELSSLRSEDAVYYCATEGYETTTY YNLFDSWGQGLTVTVSS
13	HER2-MF3958	QVQLVQSGAEVKKPGASVKLSCKASGYTFTAYYINWVRQAPGQGLEWIGRIYPG SGYTSYAQKFQGRATLTAEESTTAYMELSSLRSEDAVYFCARPPVYYDSAWF AYWGQGLTVTVSS
14	EGFR-MF4003	QVQLVQSGSELKKPGASVKVSCASGYTFPSFAMNWLQAPGQGLEWMGWITTN TGDPTYAQGFSGRFVFLDTSVSTAYLQISSLKAEDTAVYYCARVYNWIRGFDY WGQGLTVTVSS
17	HER2-MF3025	QVQLKQSGAELVRPGTSVKLSCKASGYTFTGYINWVKQRPQGLEWIARIYPG SGYTYINEKFKGKATLTAEESSTAYMHLSSLTSEDAVYFCARPHYGYDDWYF AVWGTGTTTVTVSS
18	EGFR-MF4010	QVQLVQSGSELKKPGASVKVSCASGYTFTNNAMNWRQAPGQGLEWMGWINTI TGDPSYAQGFTGRFVFLDTSVNTAYLQISSLKAEDTAVYYCAREEFLEWLFFD YWGQGLTVTVSS

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Fig. 8, Cont'd

19	TIM3-MF6501	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNAWDSMAF DYWGQGTLVTVSS
20	HER2-MF1898	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYD GSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDGFRRTTSLG FDYWGQGTLVTVSS
21	HER2-MF2032	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYD GSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDYRRTARAG FDYWGQGTLVTVSS

22	VL CDR1	QSISSY
23	VL CDR2	AASSLQS
24	VL CDR3	QQSYSTP
25	IgVk1-39*01	DIQMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTP
26	Common Light Chain IgKV1*39/jk1	DIQMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ SYSTPPITFGQGTKVEIK
27	Common Light Chain IgKV1*39/jk5	DIQMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ SYSTPPITFGQGTKVEIK
28	IgG1 CH1 Hinge	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKHTHTCPPCP
29	IgG1 CH2	APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AK
30	IgG1 CH3 KK	GQPREPQVYTHPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
31	IgG1 CH3 DE	GQPREPQVYTHPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK