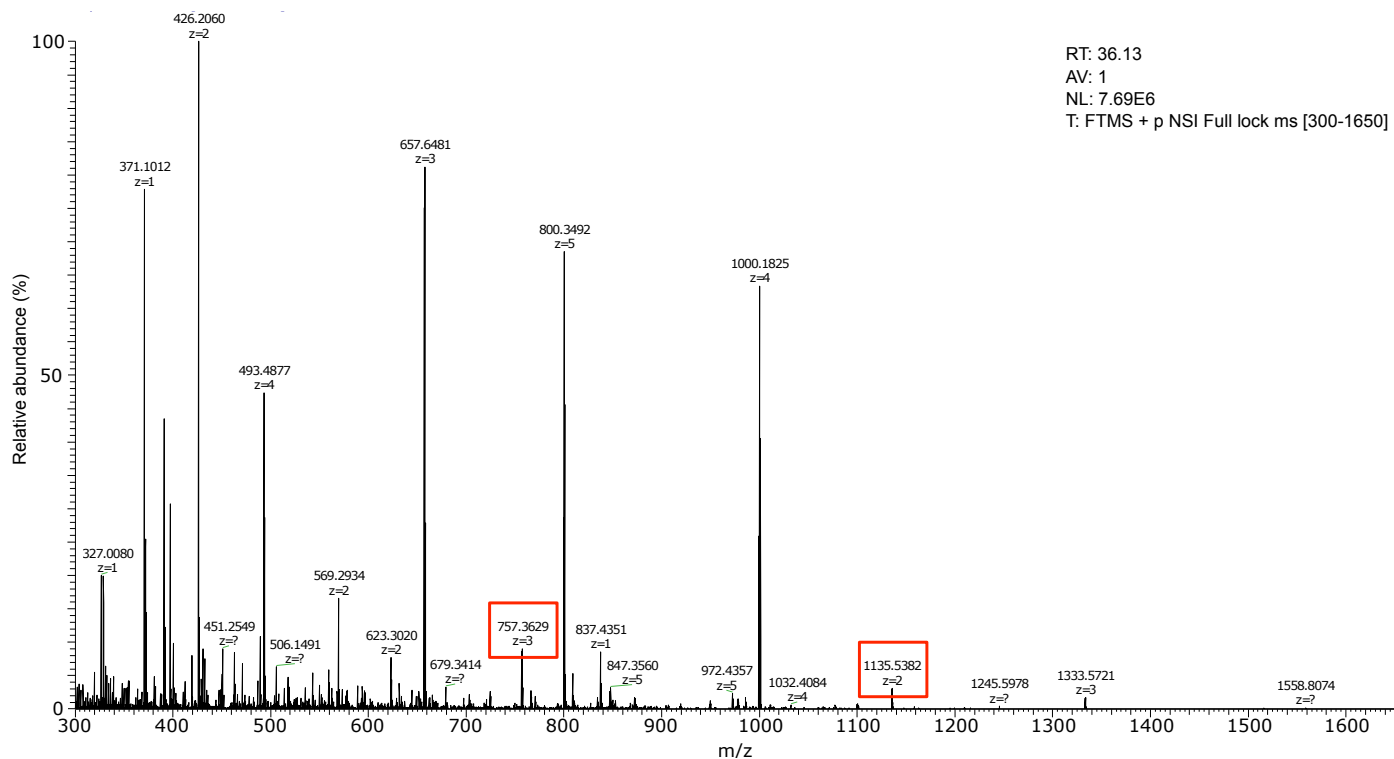
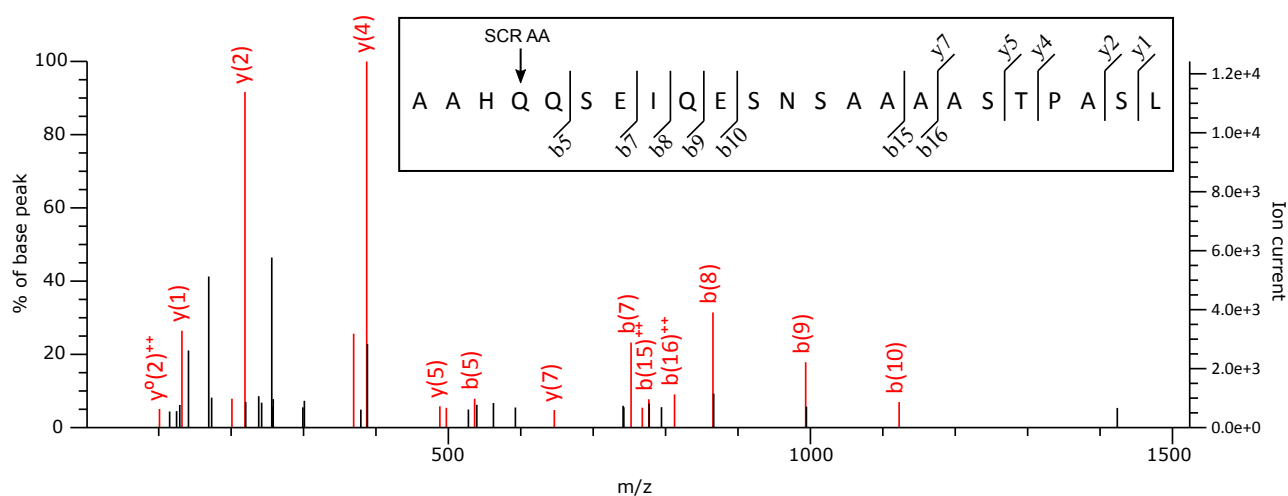


a



b



c

Dfr matched peptides	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique
F.KNMCKL.K	405.2039	808.3932	808.3935	-0.32	0	17	0.022	1	U
Y.MDPMRY.Q	422.6699	843.3252	843.3255	-0.3	0	20	0.01	1	U
W.SALHPDPW.M	461.7245	921.4344	921.4345	-0.02	1	22	0.006	1	U
Y.APTGGSPQLY.H	495.7487	989.4828	989.4818	1.05	1	28	0.0015	1	U
F.SQTTICRF.E	506.748	1011.4814	1011.4808	0.67	0	30	0.00095	1	U
F.GAAAAPGAVRHF.N	562.8019	1123.5892	1123.5887	0.52	0	22	0.0064	1	U
F.GAAAAPGAVRHF.N	375.5372	1123.5898	1123.5887	0.98	0	(14)	0.039	1	U
L.QLEKEVVRVW.F	429.2471	1284.7195	1284.719	0.36	1	22	0.0062	1	U
L.QLEKEVVRVW.F	478.271	1431.7912	1431.7874	2.61	2	11	0.081	1	U
F.HKQPKPSAQEITSL.A	521.955	1562.8432	1562.8416	0.99	0	18	0.016	1	U
W.HAPHAGHYAPTGGSP.L	523.9239	1568.7499	1568.7484	0.92	1	26	0.0027	1	U
Y.MTPPSGDLDMALGGGY.H	835.8563	1669.698	1669.6964	0.99	2	19	0.012	1	U
L.SQTRIQQGMASPHAAW.H	638.3087	1911.9043	1911.901	1.73	0	0	0.99	1	U
F.HKQPKPSAQEITSLADSL.Q	650.6819	1949.0239	1949.0218	1.08	1	11	0.074	1	U
L.AAHQQSEIQESNSAAAASTPASL.N	1135.0372	2268.0598	2268.0618	-0.85	0	(27)	0.0022	1	U
L.AAHQQSEIQESNSAAAASTPASL.N	757.0289	2268.0649	2268.0618	1.36	0	45	3E-05	1	U
Y.MDPMRY.Q +2 oxidation (M)	422.6699	843.3252	843.3255	-0.3	0	20	0.01	1	U