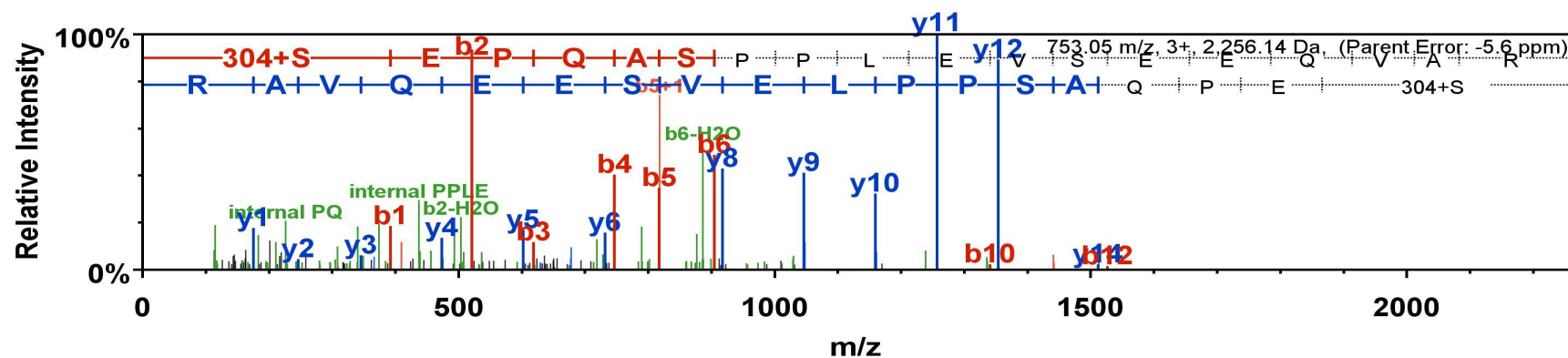


Supplementary Data 1: Information regarding protein assignments based on single-peptide assignments.

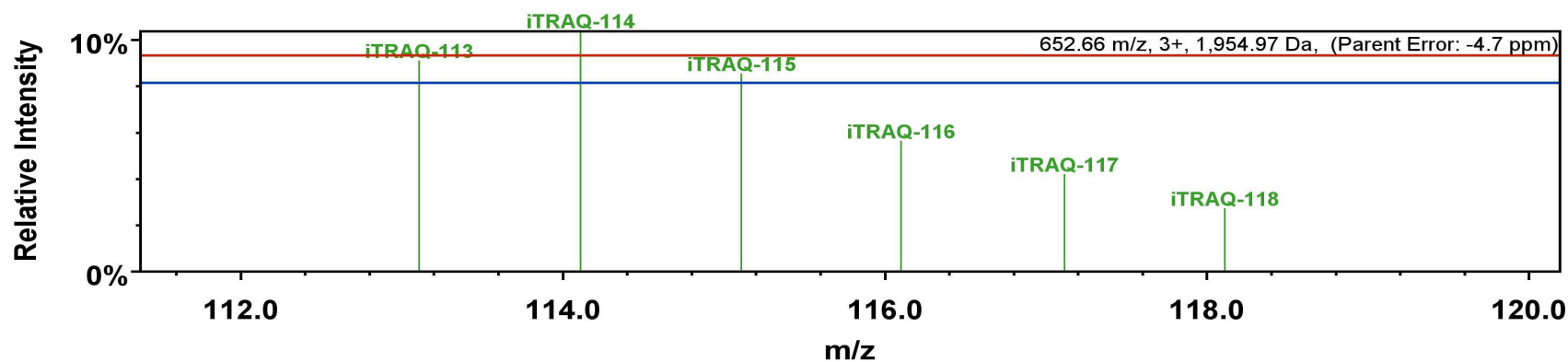
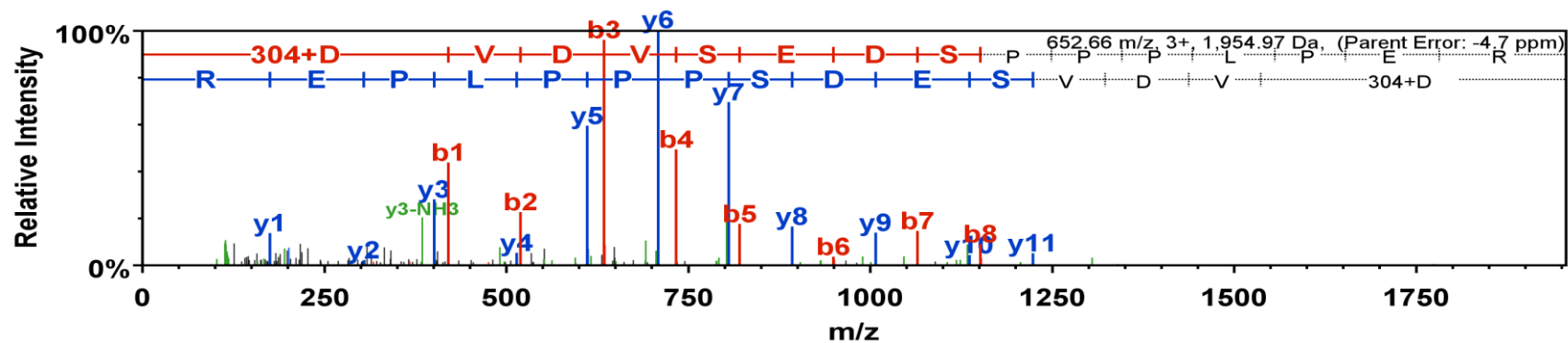
Each of the following pages contains the information of one of the 24 single-peptide assignment. The information includes sequence of the peptide, the precursor mass and charge, the Mascot ions score, expect value, labeled ms/ms spectrum of the peptide, and an expanded view of the reporter ion region for each spectrum.

Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350590018	hypothetical protein LOC100521745	(R)sEPQASPPLEVSEEQVAR(L)	70.93	iTRAQ8plex (+304)



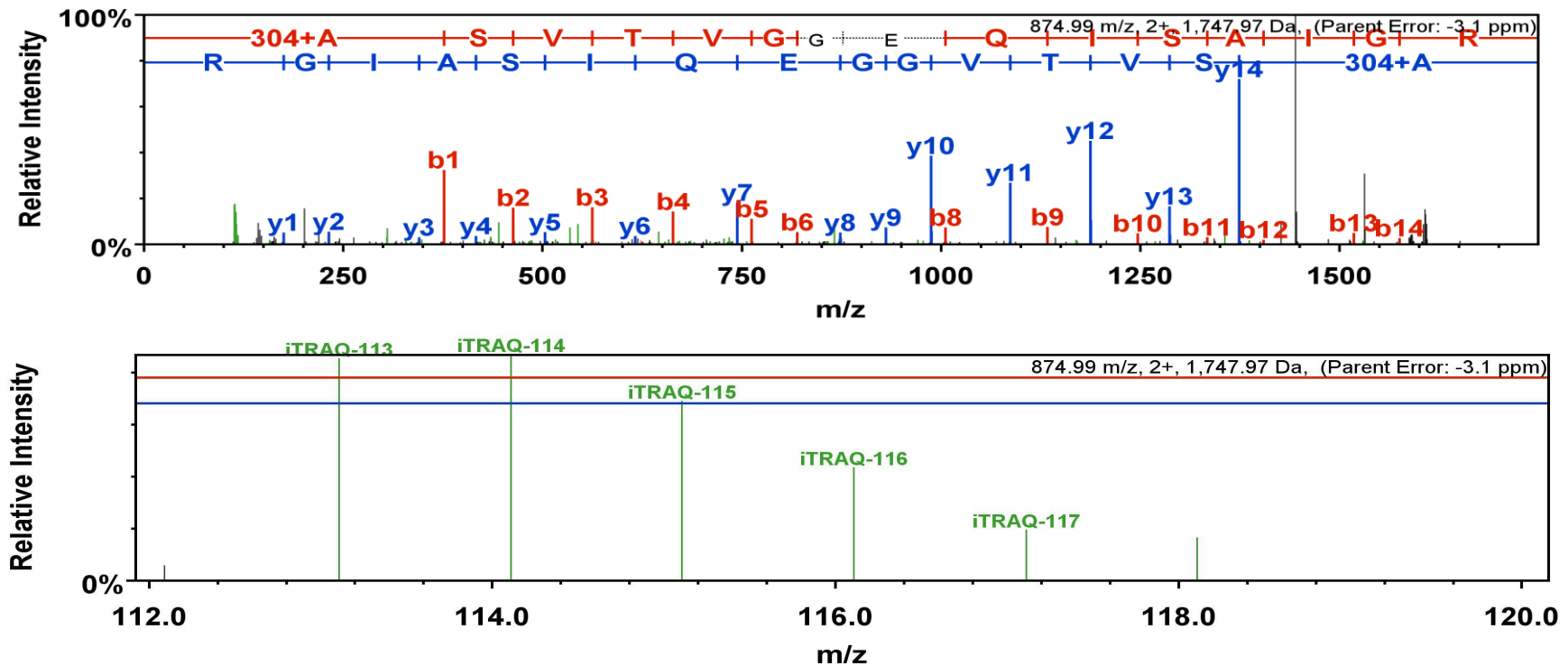
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 417515862	tyrosine-protein phosphatase non-receptor type 12	(K)dVDVSEDSPPPLPER(T)	57.5	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
652.664	1,954.97	3	0.000033	-4.694	1,016.00	57,004.00	670	Locus:1.1.1.1452.23	684



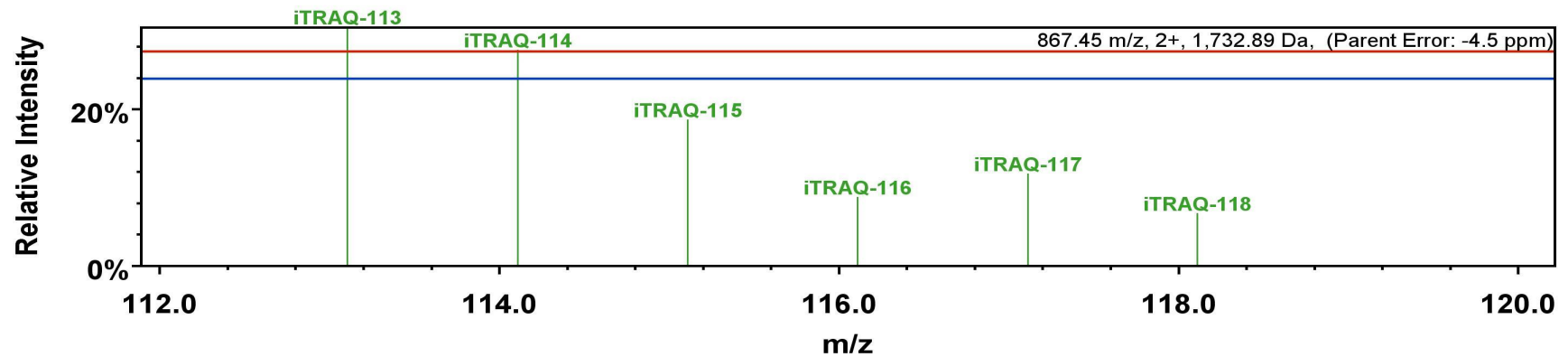
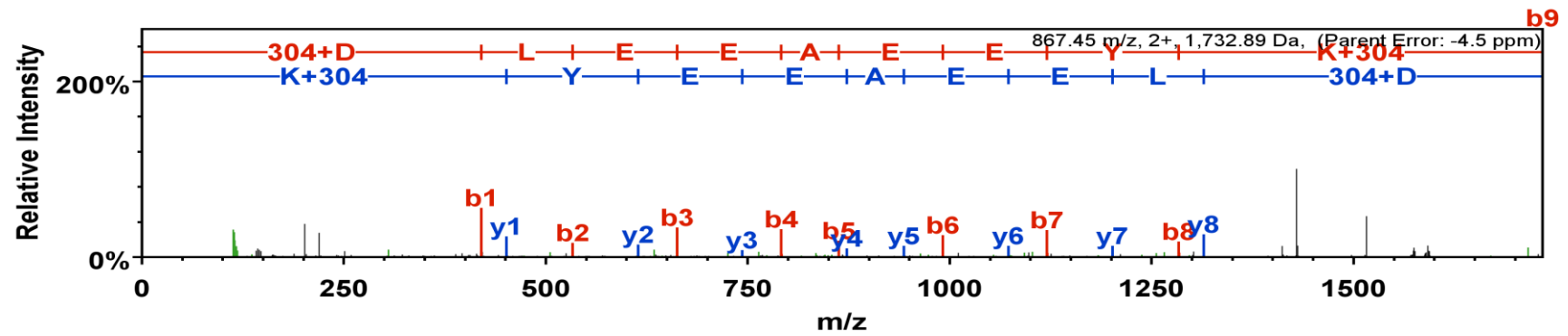
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350594682	D-tyrosyl-tRNA(Tyr) deacylase 1-like	(R)aSVTVGGEQISAIGR(G)	82.47	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
874.9914	1,747.97	2	0.000000028	-3.119	1,052.00	86,263.60	11	Locus:1.1.1.1367.29	25



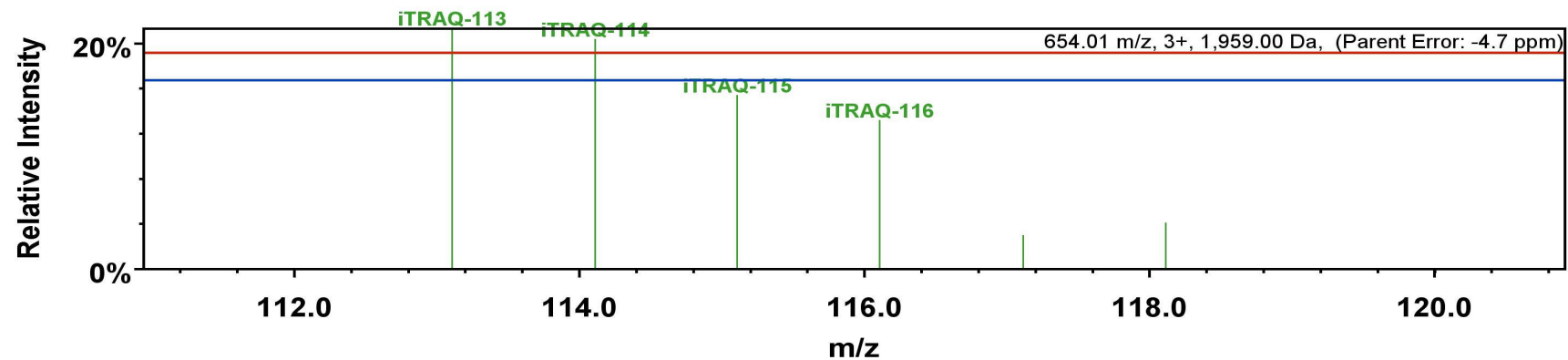
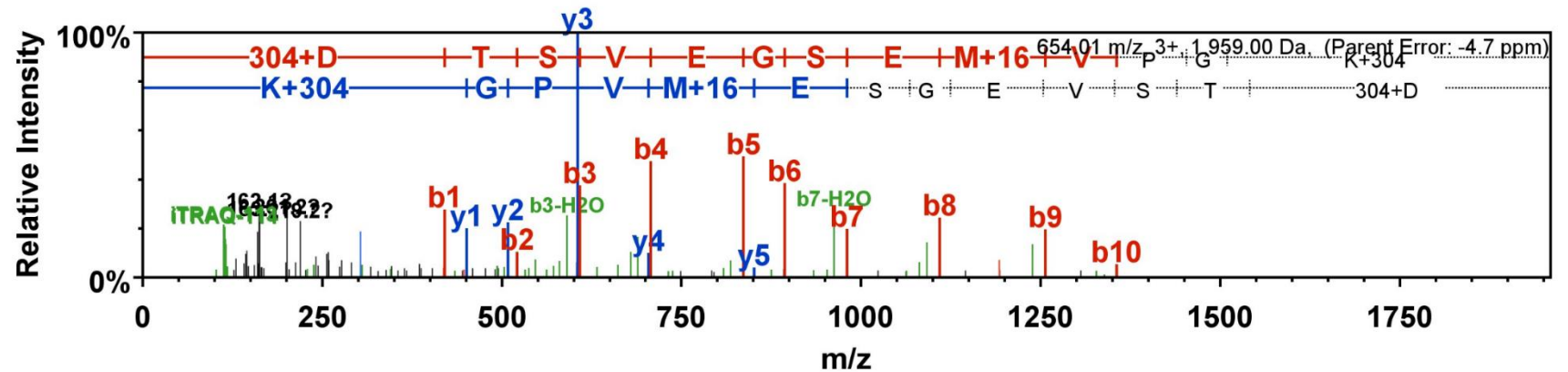
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350580865	tubulin-specific chaperone A-like	(K)dLEEAEYk(E)	62.72	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
867.4525	1,732.89	2	0.0000087	-4.491	960	94,762.20	83	Locus:1.1.1.1358.31	91



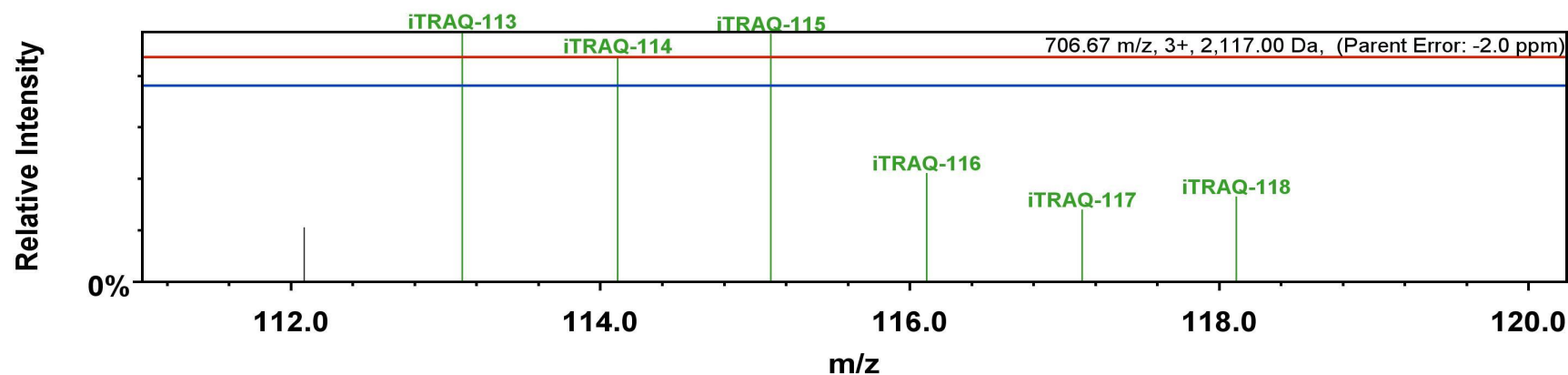
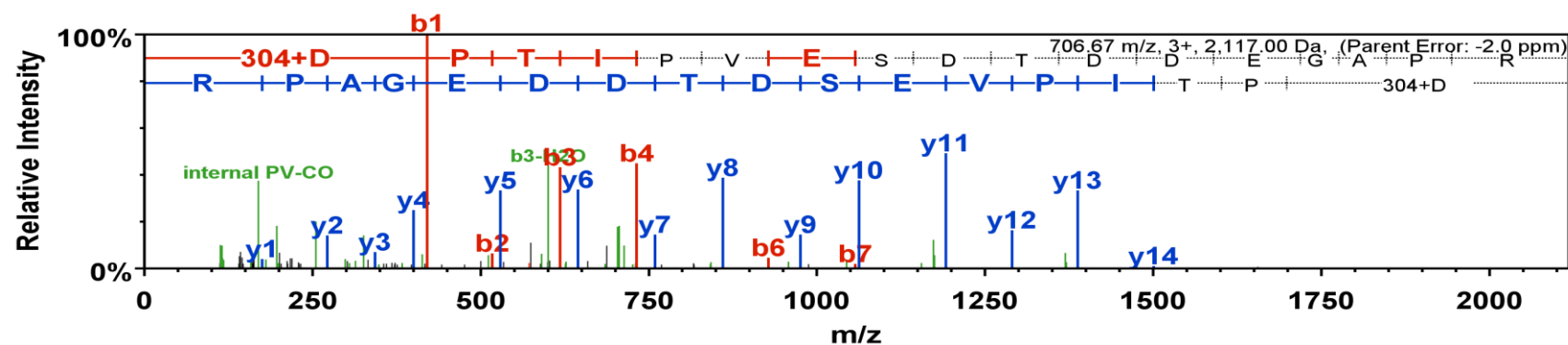
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350585800	regulator of chromosome condensation isoform 2	(R)dTSVEGSEmVPGk(V)	58.55	iTRAQ8plex (+304), Oxidation (+16), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
654.007	1,959.00	3	0.000034	-4.678	682	22,394.50	102	Locus:1.1.1.1282.22	114



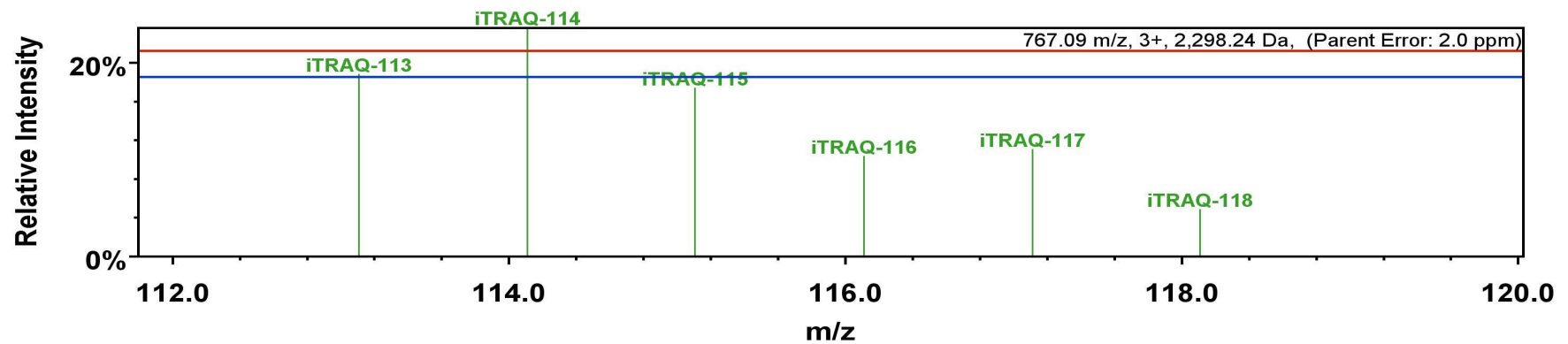
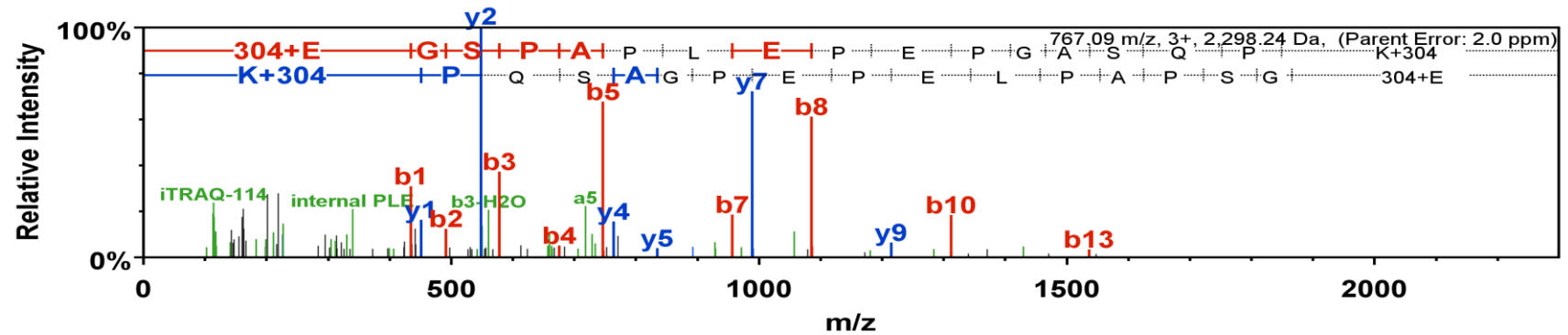
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350591690	60S ribosomal export protein NMD3-like	(R)dPTIPVESDTDDEGAPR(I)	92.56	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
706.6749	2,117.00	3	0.000000005	-1.993	891	33,292.40	461	Locus:1.1.1.1234.23	477



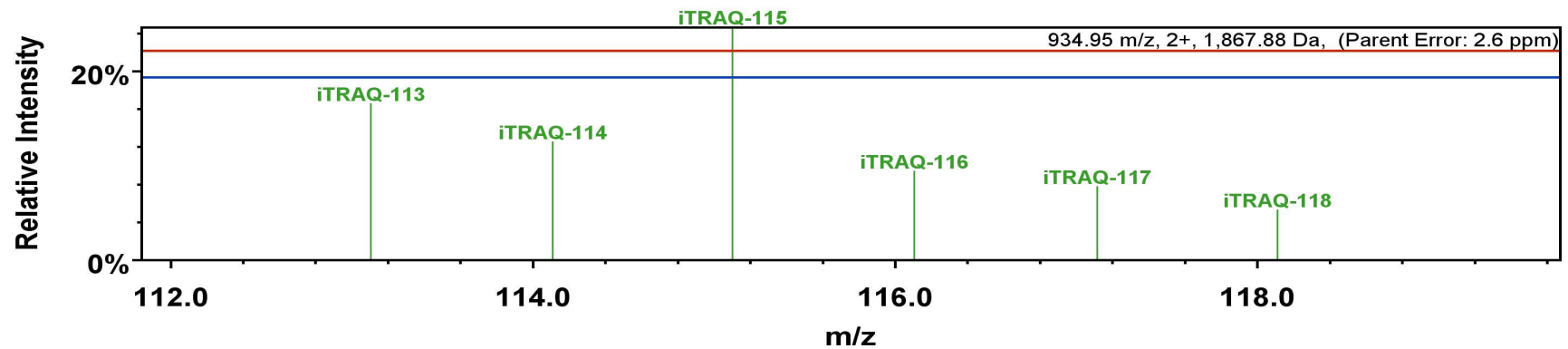
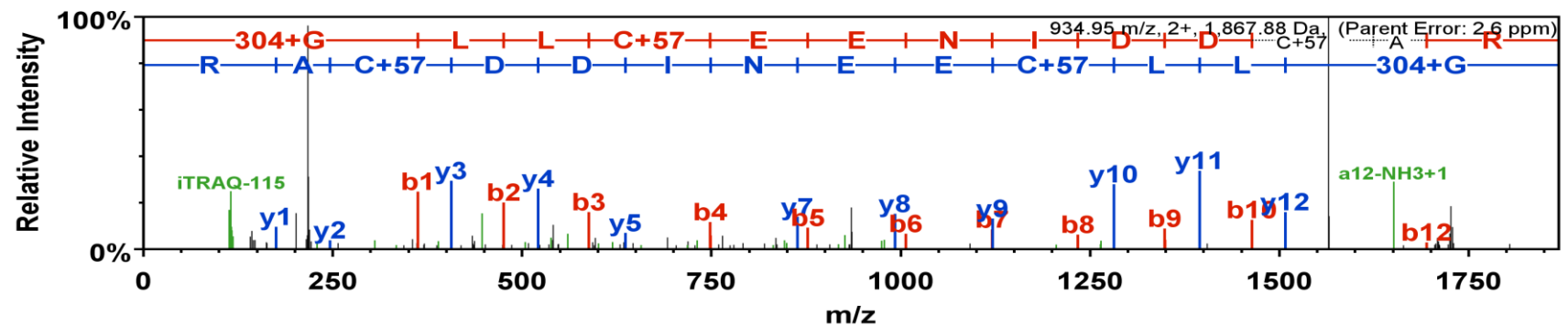
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 335297203	forkhead box protein K2-like	(R)eGSPAPLEPEPGASQPk(L)	37.47	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
767.0861	2,298.24	3	0.0078	1.995	776	17,264.00	394	Locus:1.1.1.1287.30	410



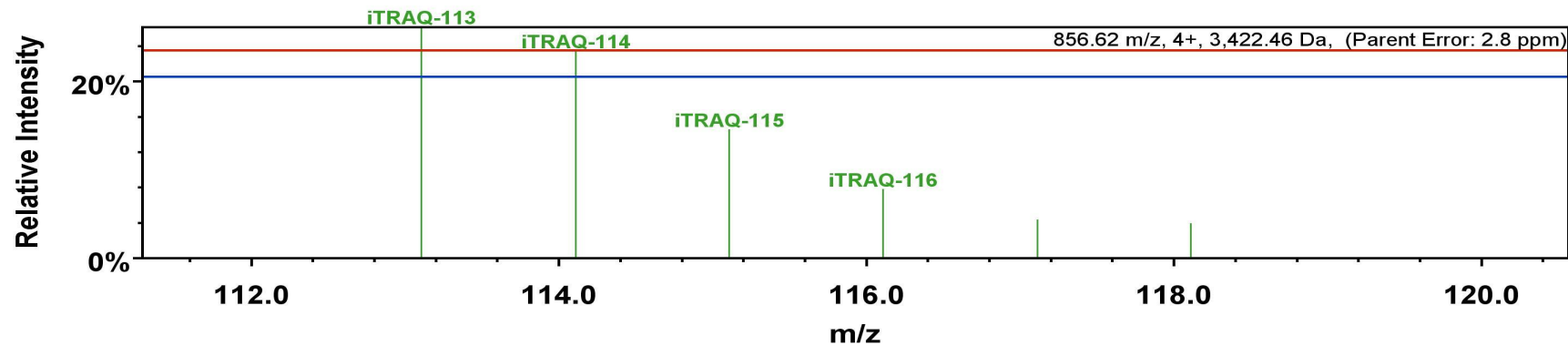
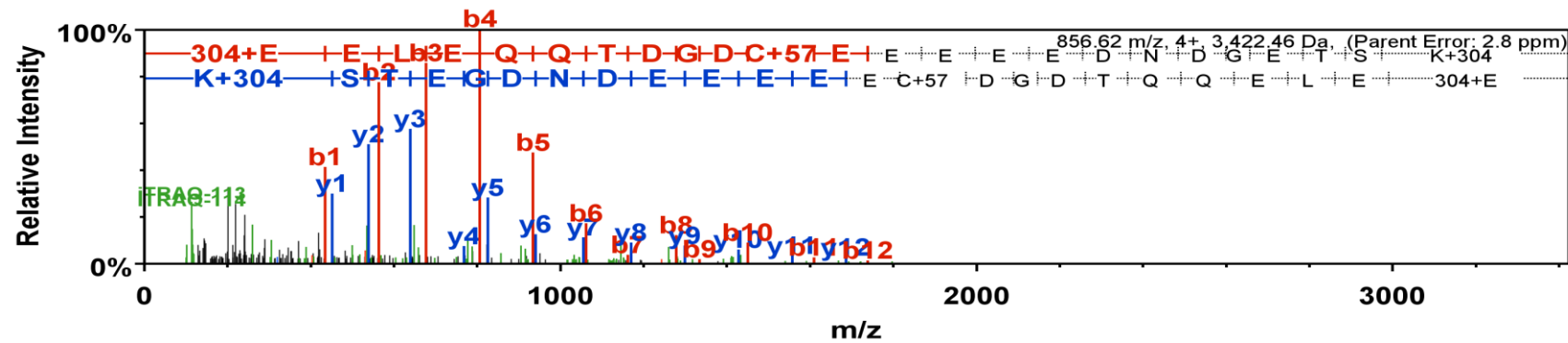
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 417515726	neurogenic locus notch-like protein 2	(R)gLLcEENIDDcAR(G)	61.04	iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
934.9454	1,867.88	2	0.0000095	2.63	1,026.00	33,196.00	923	Locus:1.1.1.1365.30	935



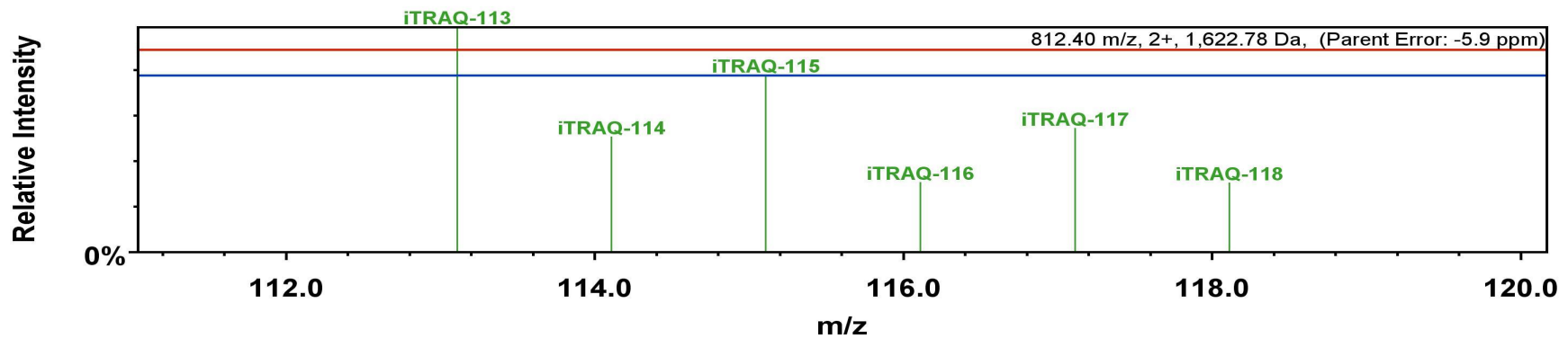
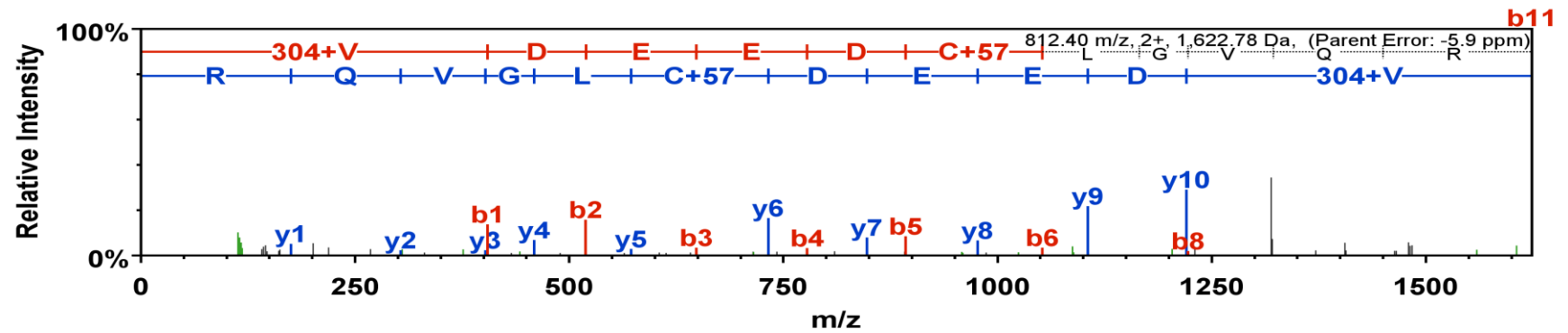
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 158635942	translocation protein SEC62	(K)eELEQQTDGDcEEEEEDN DGETSk(S)	104.56	iTRAQ8plex (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
856.6229	3,422.46	4	0.0000000000038	2.768	817	44,629.20	369	Locus:1.1.1.1398.18	392



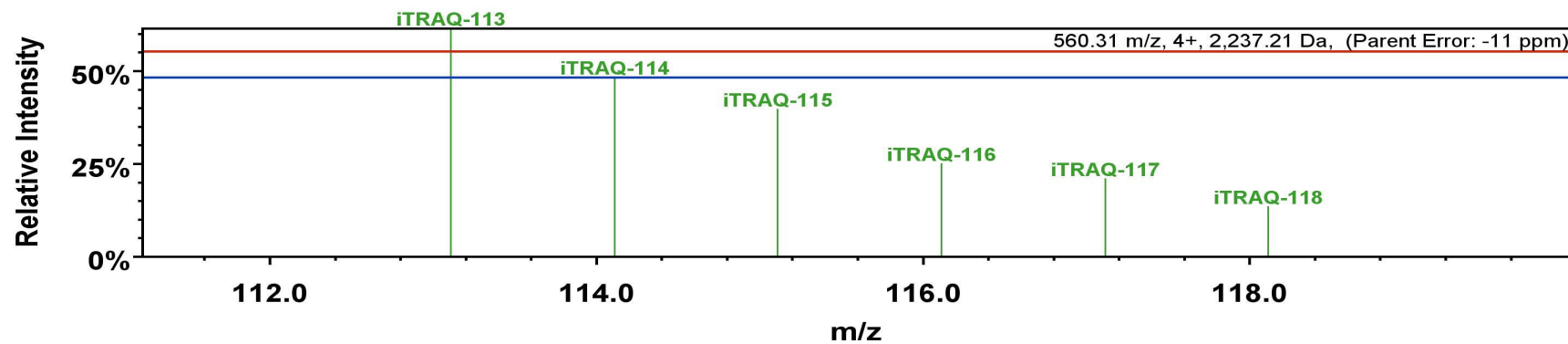
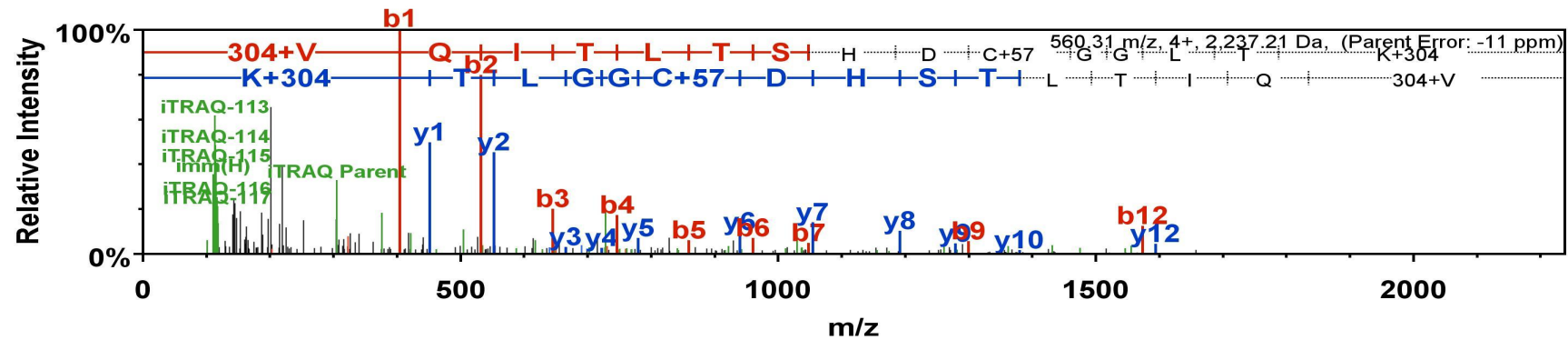
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 311258435	peroxisomal membrane protein PEX14 isoform 1	(R)vDEEDcLGVQR(E)	49.85	iTRAQ8plex (+304), Carbamidomethyl (+57)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
812.3964	1,622.78	2	0.000029	-5.912	847	12,421.50	334	Locus:1.1.1.1406.30	344



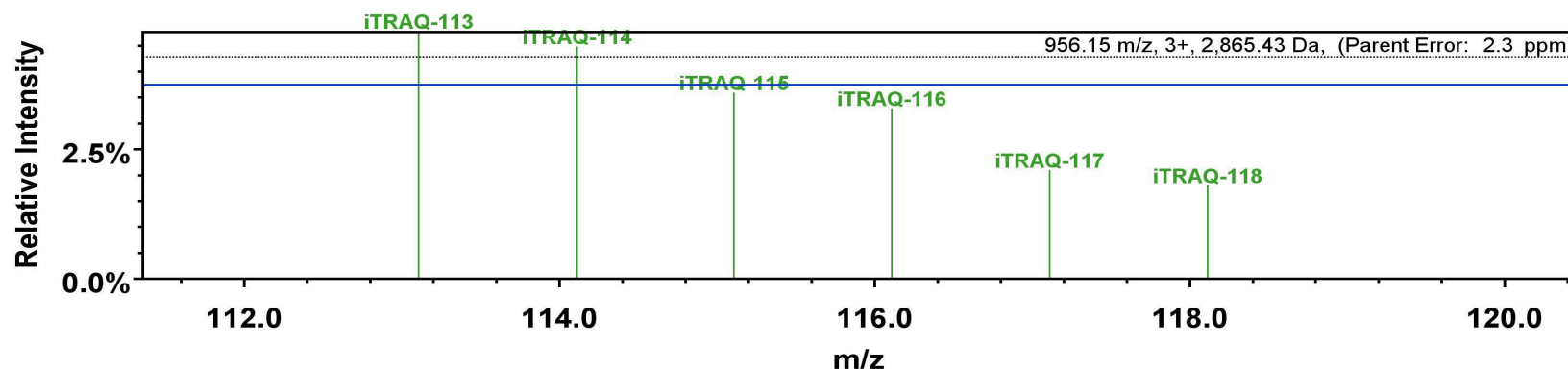
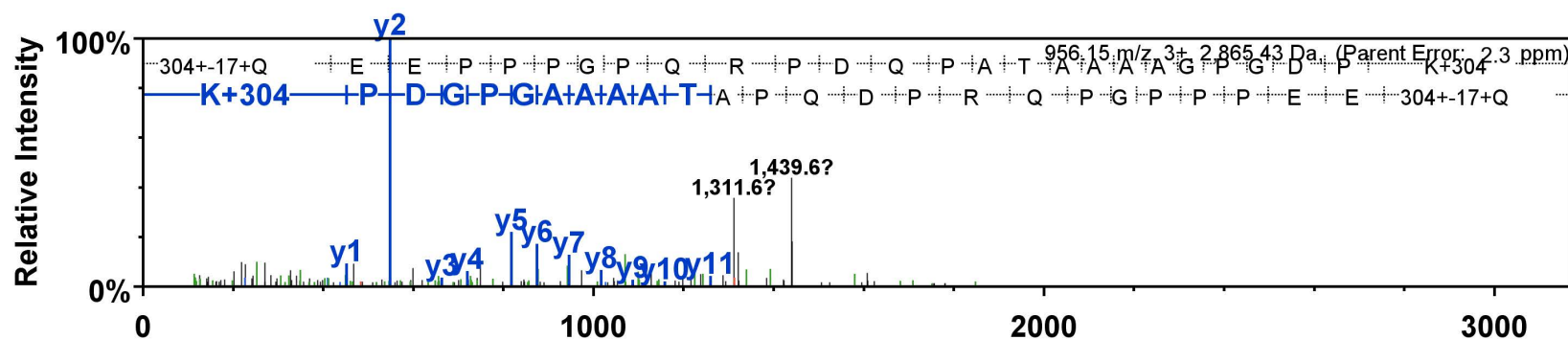
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 335309724	hypothetical protein LOC100624388	(K)vQITLTSHDcGGLTk(R)	44.92	iTRAQ8plex (+304), Carbamidomethyl (+57), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
560.3087	2,237.2059	4	0.00052	-10.89	1,034.00	142,722.00	100	Locus:1.1.1.1329.18	114



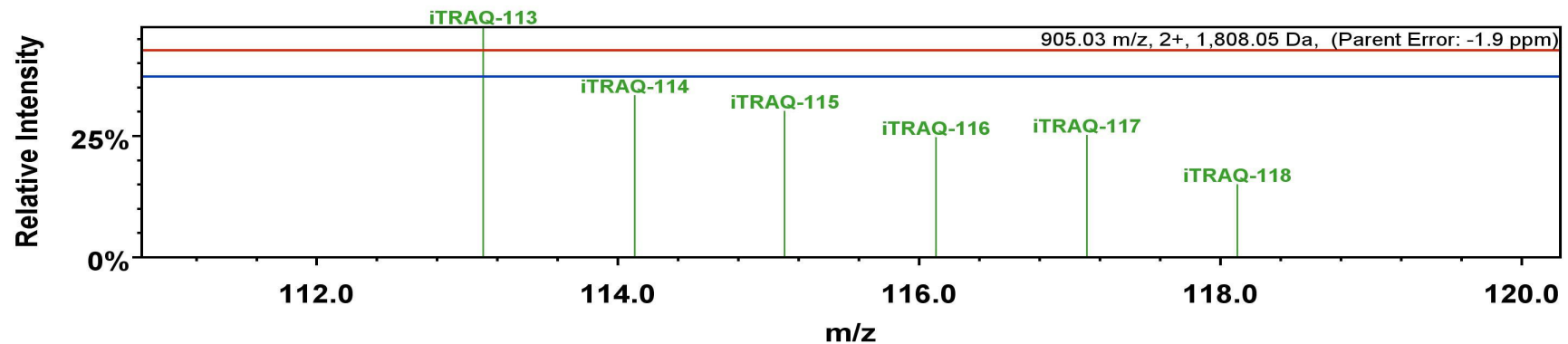
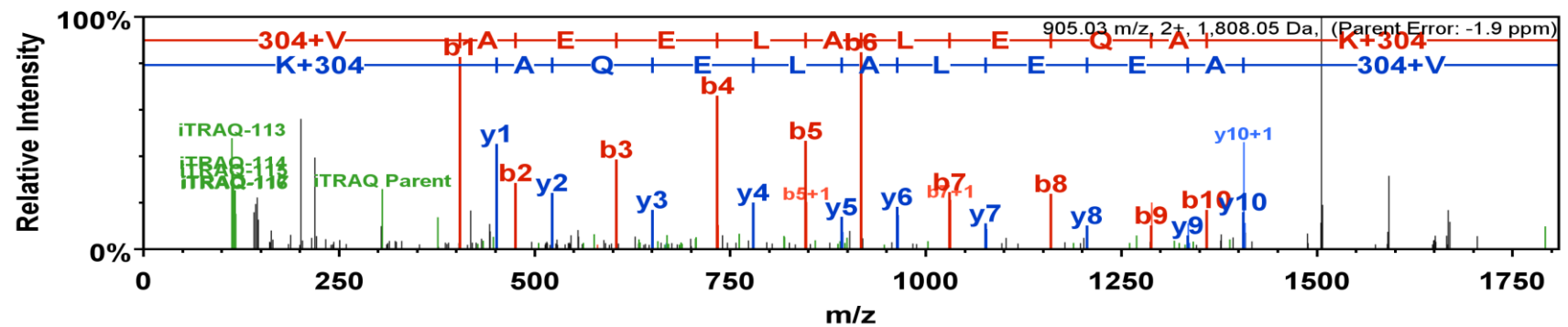
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 311248909	uncharacterized protein C19orf43-like	(R)qEEPPPGPQRPDQPATAA AAGPGDPk(R)	37.68	Gln->pyro-Glu (-17), iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
956.1495	2,865.43	3	0.0036	2.3	743	25,827.30	81	Locus:1.1.1.1299.31	106



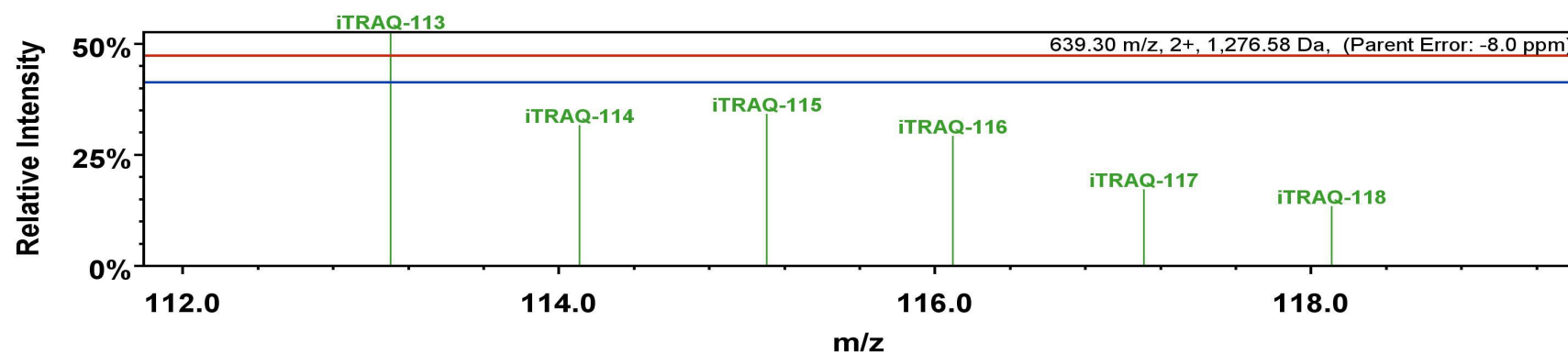
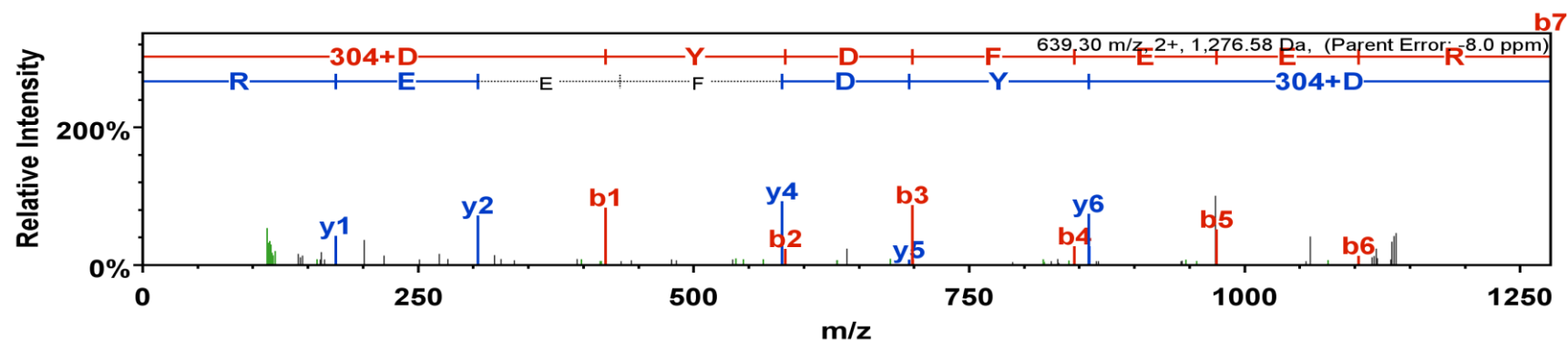
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 346644866	coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	(R)vAEELALEQAk(K)	54.73	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
905.0308	1,808.05	2	0.0002	-1.906	1,137.00	81,187.90	66	Locus:1.1.1.1385.31	76



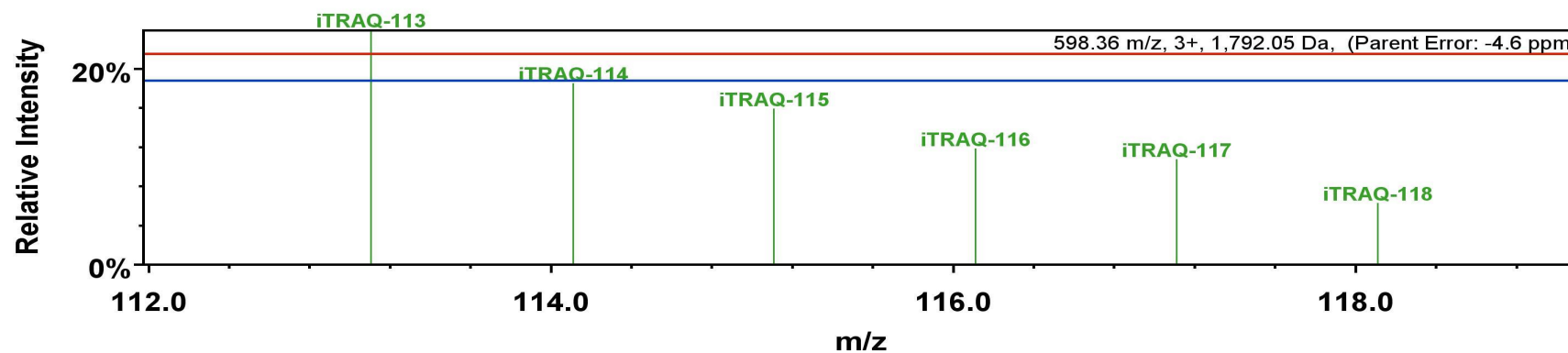
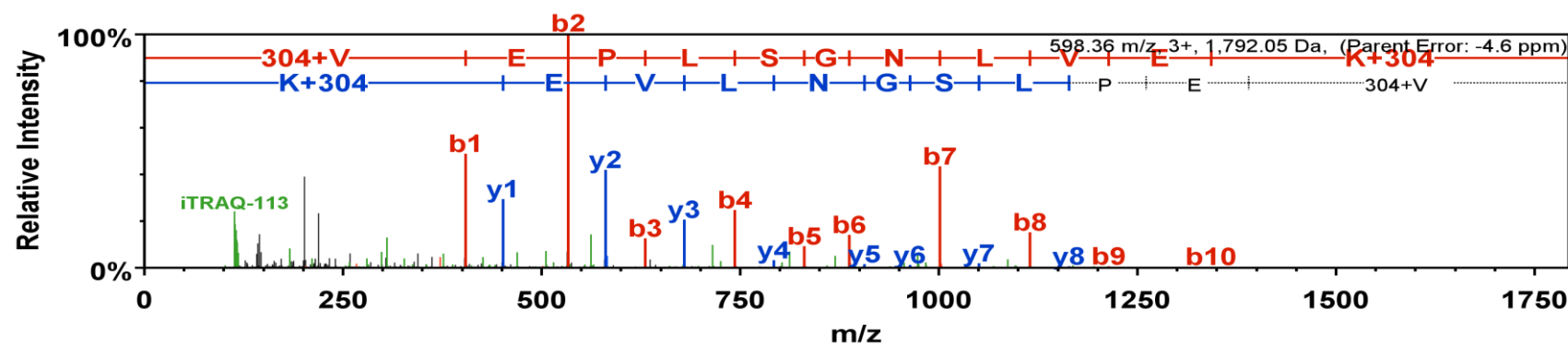
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350581181	zinc finger matrin-type protein 2-like isoform 2	(K)dYDFEER(M)	28.01	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
639.2961	1,276.58	2	0.0091	-8.011	812	15,274.40	139	Locus:1.1.1.1397.17	145



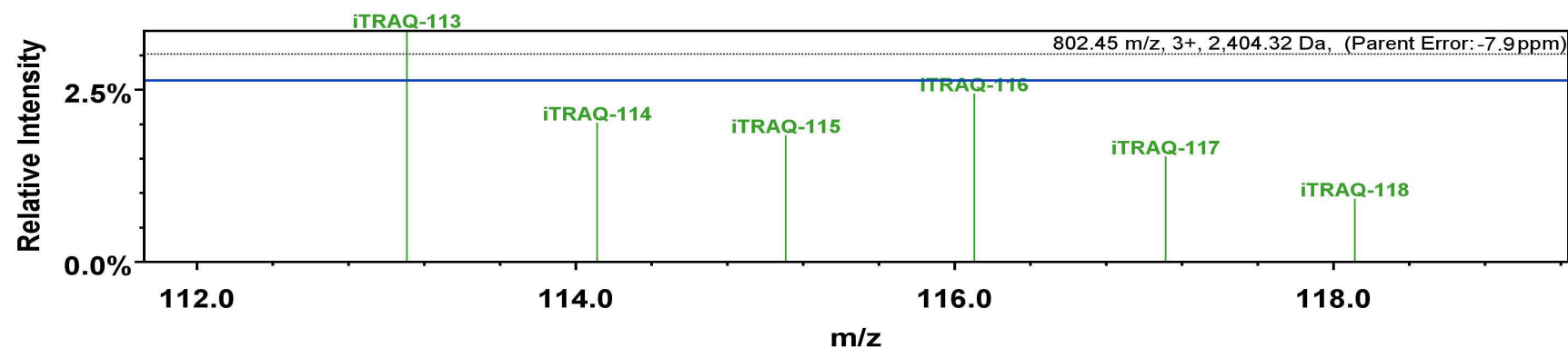
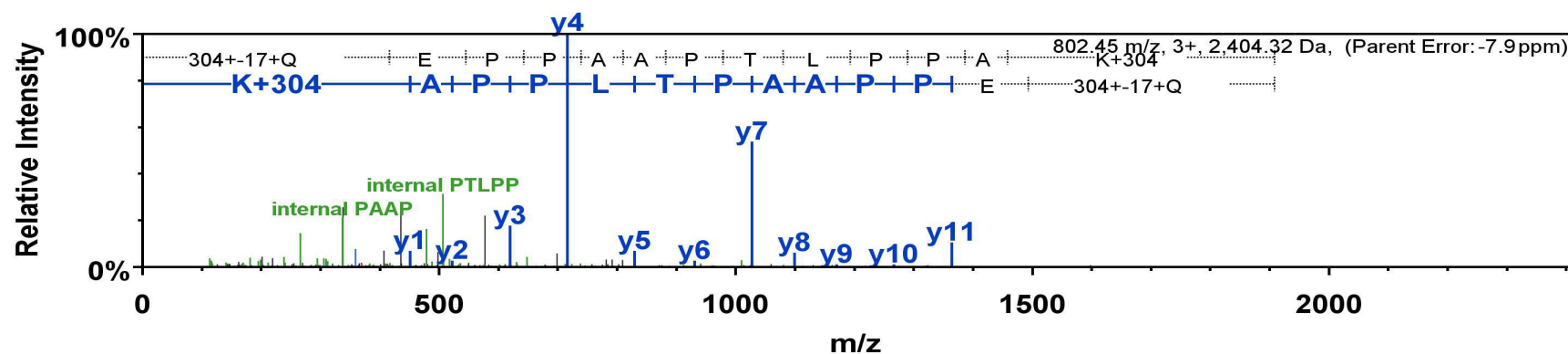
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 350596569	hypothetical protein LOC100623615	(K)vEPLSGNLVEk(D)	71.53	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
598.3564	1,792.05	3	0.00000033	-4.564	1,069.00	548160	202	Locus:1.1.1.1367.13	212



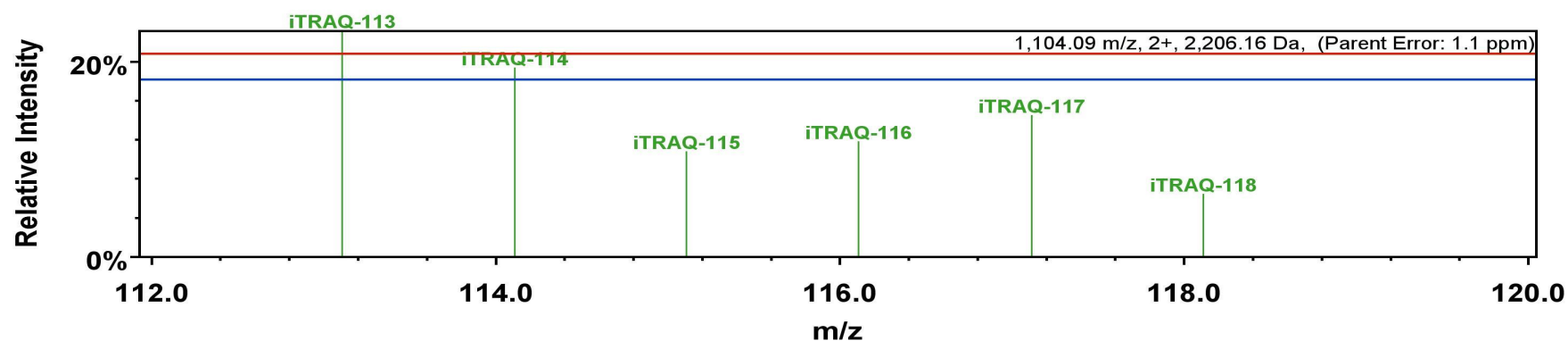
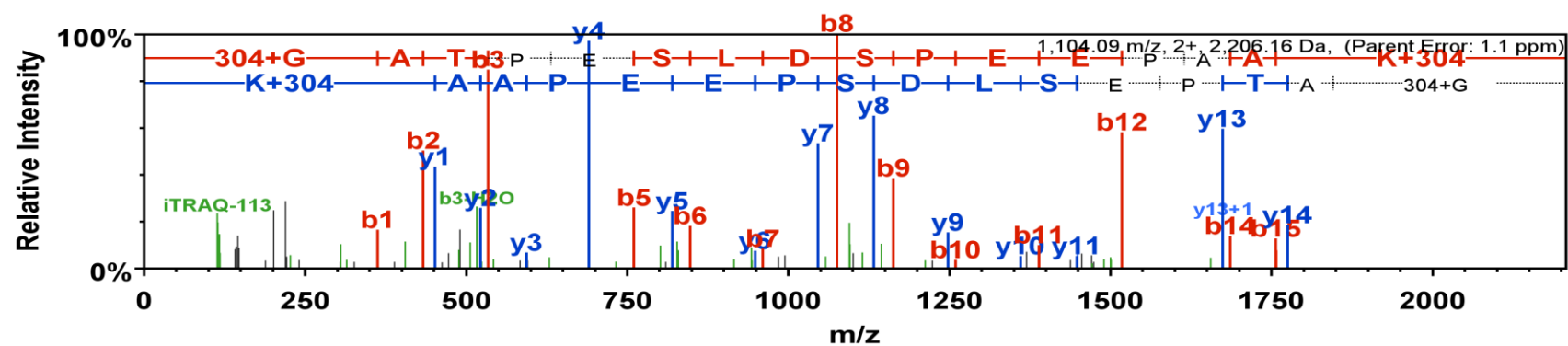
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 8134343	cell cycle exit and neuronal differentiation protein 1	(K)qEPPAAPTLPPAk(K)	55.16	Gln->pyro-Glu (-17), iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
802.4471	2,404.32	3	0.0004	-7.9	999	95,617.20	45	Locus:1.1.1.1301.31	57



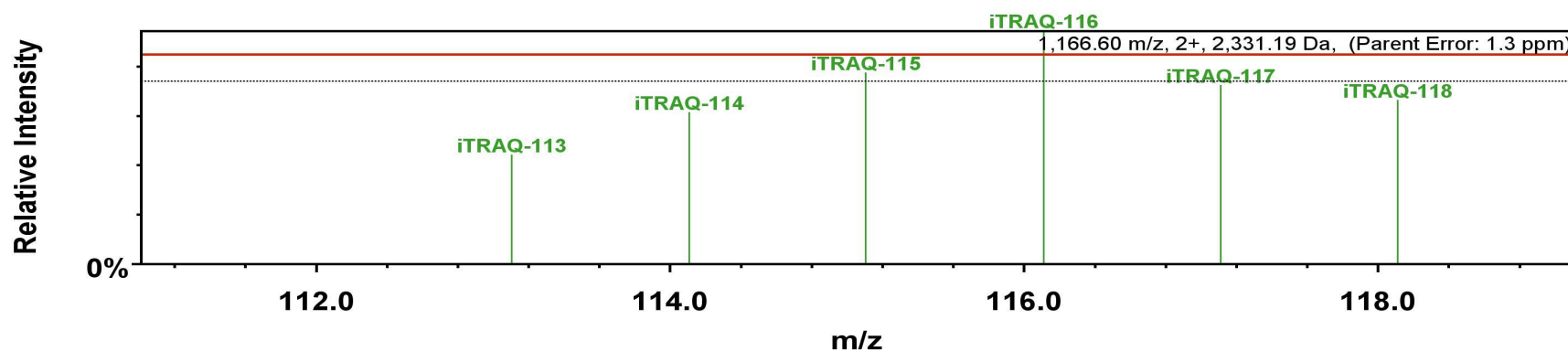
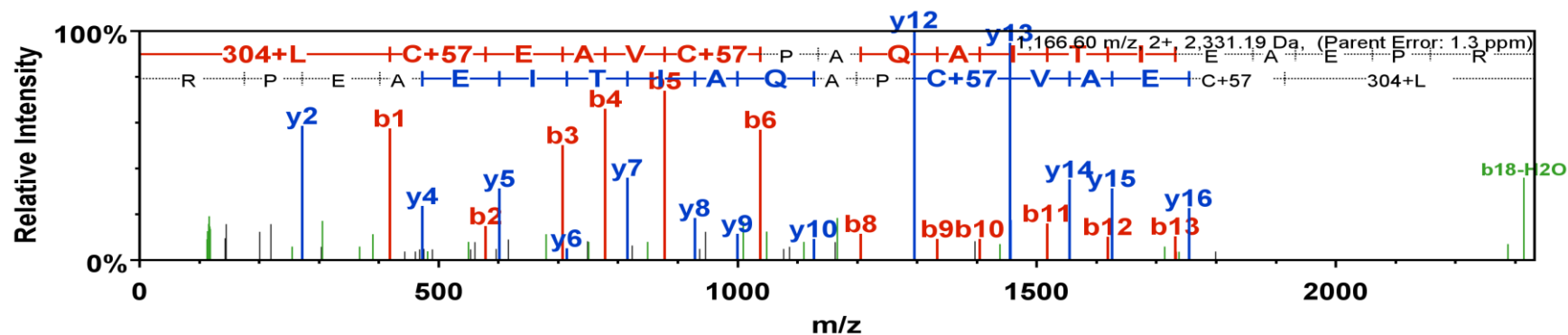
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 311268173	myb-binding protein 1A	(K)gATPESLDSPEEPAAk(K)	81.98	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
1,104.09	2,206.16	2	0.000000027	1.12	767	26,592.60	1278	Locus:1.1.1.1305.31	1293



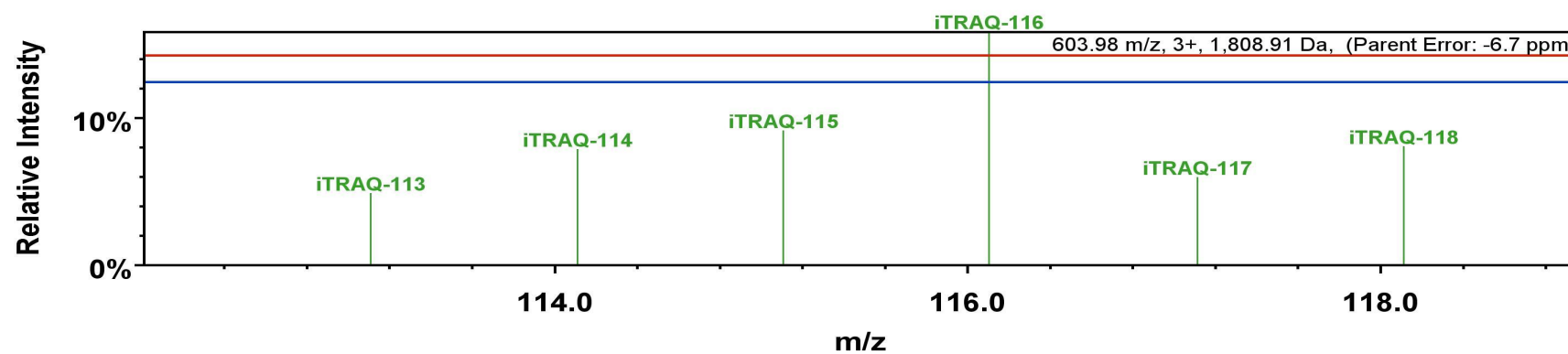
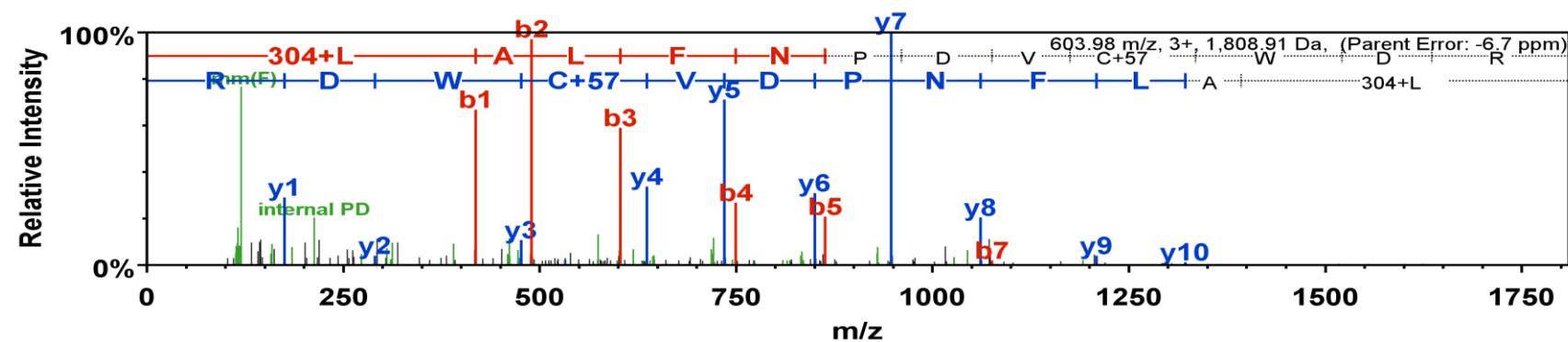
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 311247108	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial-like isoform 2	(K)lcEAVcPAQAITEAEPR(A)	86.51	iTRAQ8plex (+304), Carbamidomethyl (+57), Carbamidomethyl (+57)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
1,166.60	2,331.19	2	0.0000000099	1.258	1,478.00	12,751.90	145	Locus:1.1.1.1578.31	162



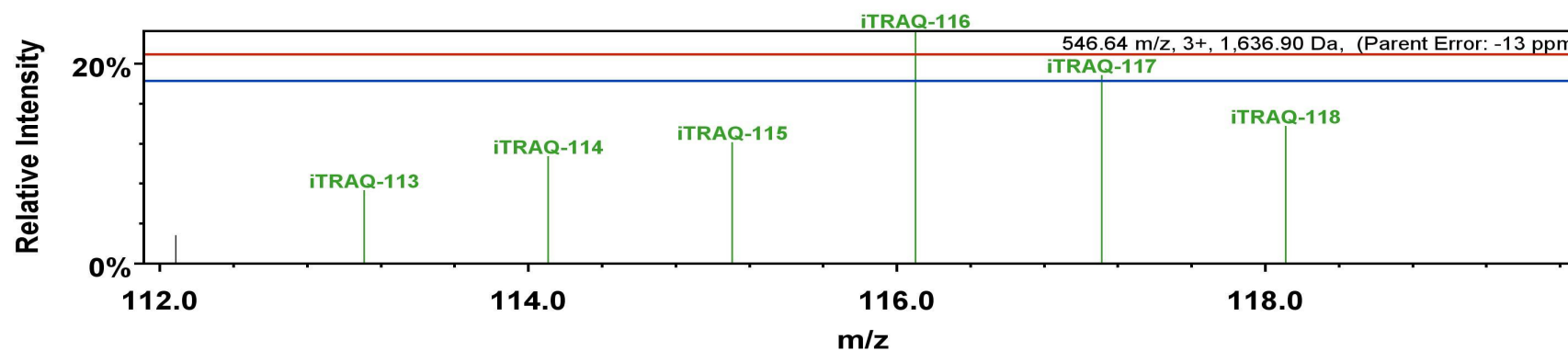
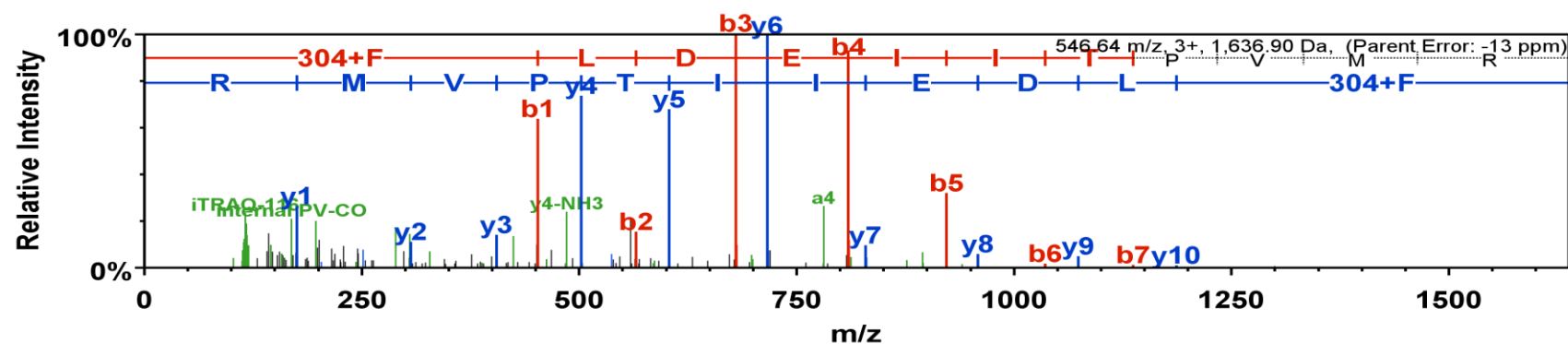
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 117660613	mitochondrial NDUFA4	(R)lALFNPDVcWDR(K)	47.59	iTRAQ8plex (+304), Carbamidomethyl (+57)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
603.9762	1,808.91	3	0.00045	-6.722	1,804.00	60,197.90	36	Locus:1.1.1.1573.6	47



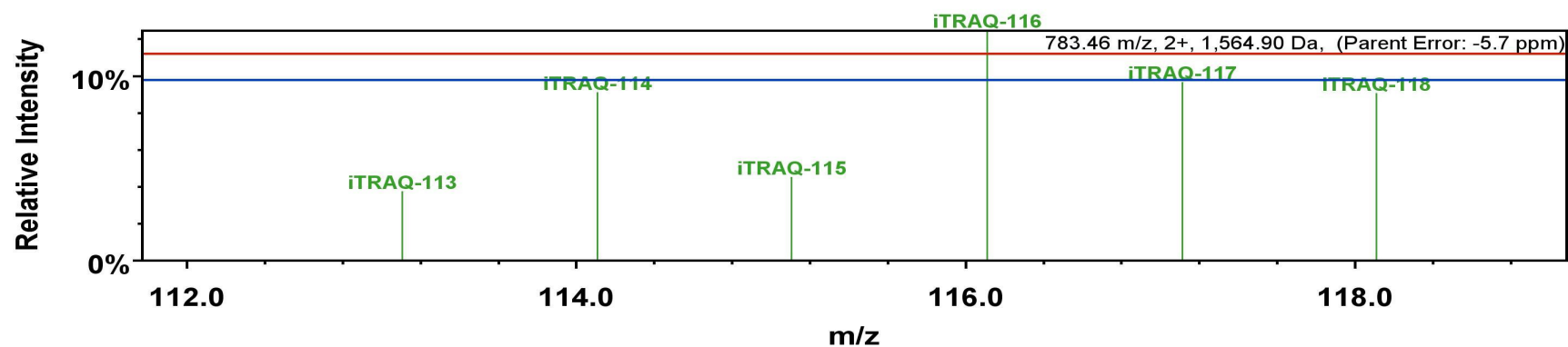
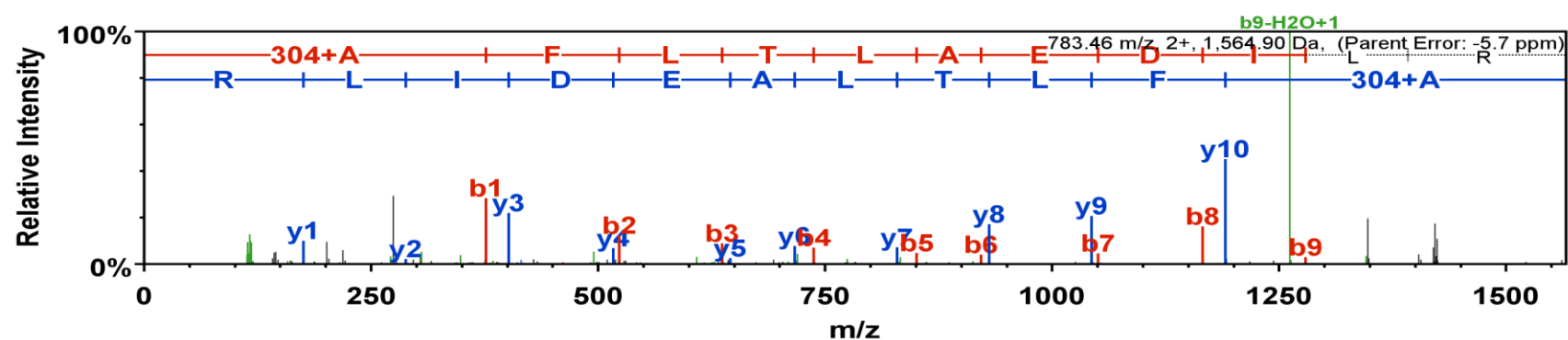
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 335285324	prenylcysteine oxidase-like	(K)fLDEIITPVMR(V)	71.36	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
546.639	1,636.90	3	0.0000013	-13.19	2,008.00	46,530.60	220	Locus:1.1.1.1634.2	230



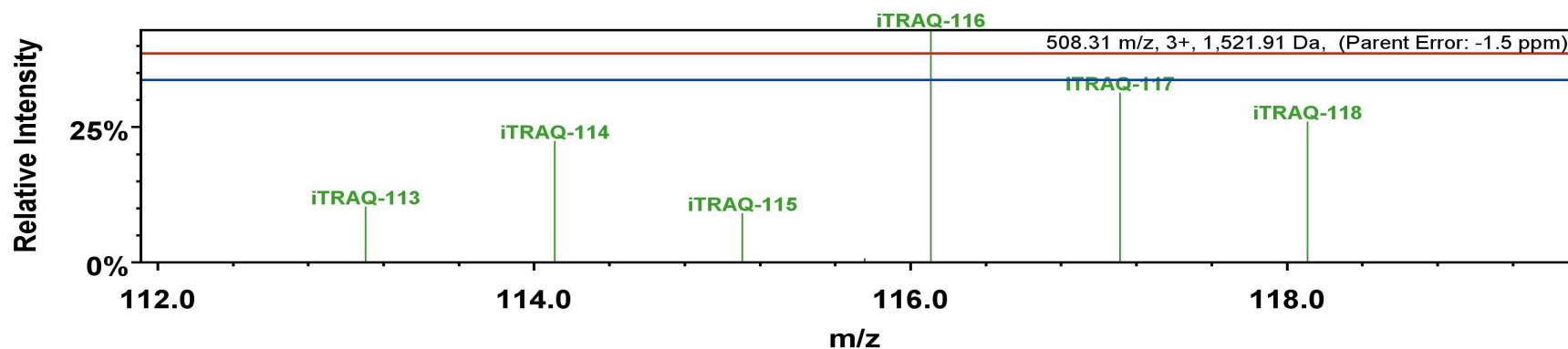
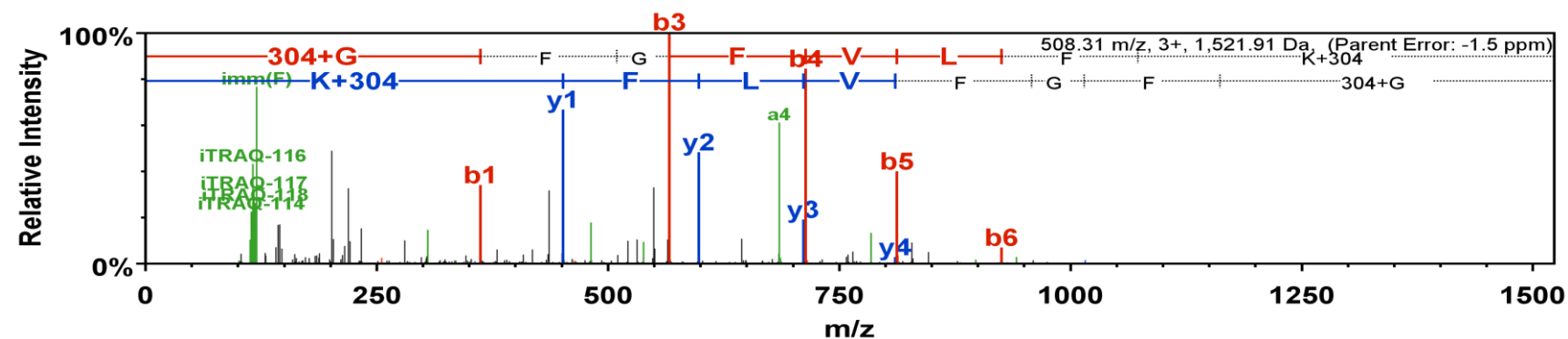
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 340007402	RAB10, member RAS oncogene family	(K)aFLTLAEDILR(K)	61.08	iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
783.4595	1,564.90	2	0.000044	-5.667	2,198.00	19,437.20	162	Locus:1.1.1.1684.2	172



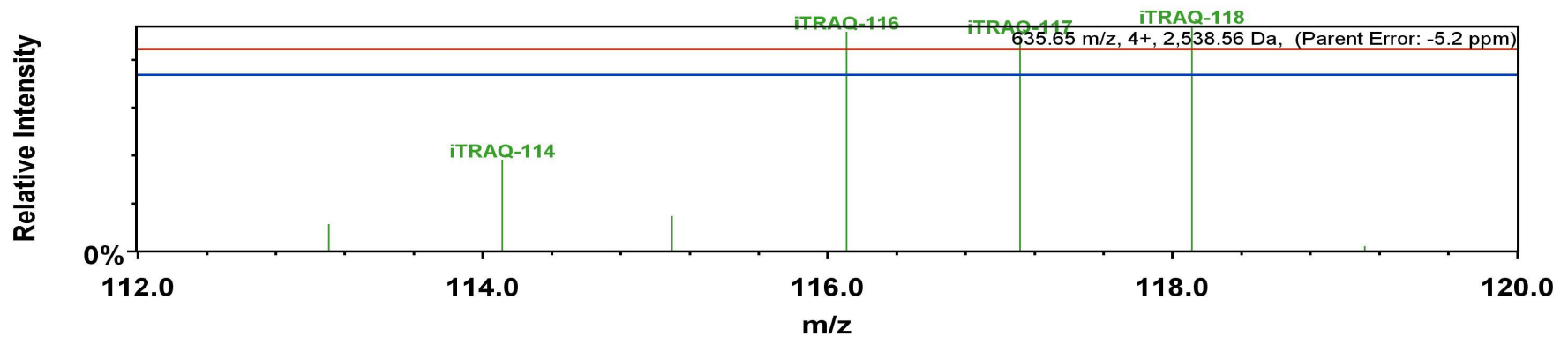
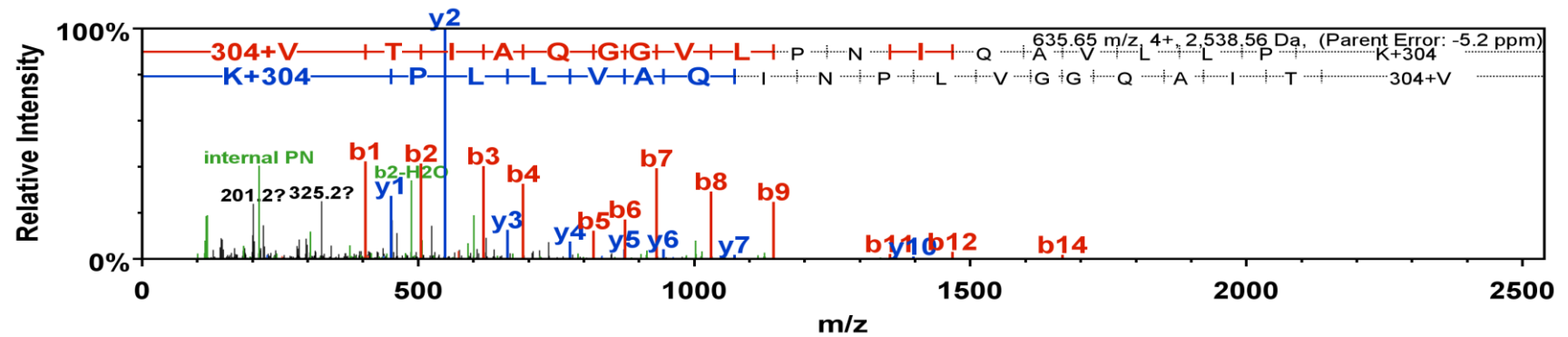
Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 311276597	hypothetical protein LOC100511612	(R)gFGFVLfK(D)	30.47	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
508.3122	1,521.91	3	0.043	-1.526	1,745.00	252108	75	Locus:1.1.1.1523.4	82



Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 335291882	histone H2A type 1-F-like	(K)vTIAQGGVLPNIQAVLLPk(K)	91.28	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
635.6471	2,538.56	4	0.0000000028	-5.229	1,897.00	1347340	101	Locus:1.1.1.1614.5	119



Accession no.	Protein name	Sequence	Mascot Ion score	Modifications
gi 335308216	60S ribosomal protein L31-like	(K)IYTLVTYVPVTTfK(N)	46.37	iTRAQ8plex (+304), iTRAQ8plex (+304)

Observed	Actual Mass	Charge	Expect	Delta PPM	Retention Time	TIC	Start	Spectrum ID	Stop
751.7817	2,252.32	3	0.00063	-2.287	2,111.00	74,754.60	102	Locus:1.1.1.1648.24	115

