

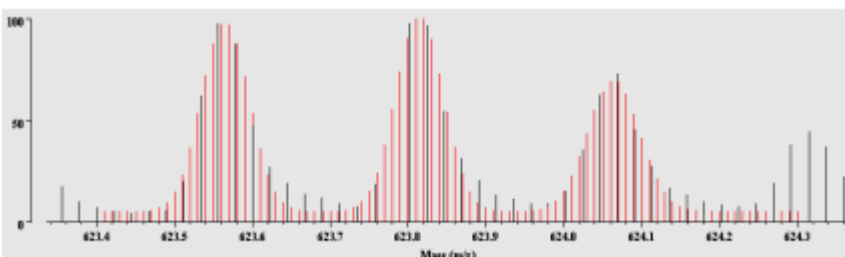
MS and MS/MS spectra for single
peptide reconstituted proteins

Manuscript:

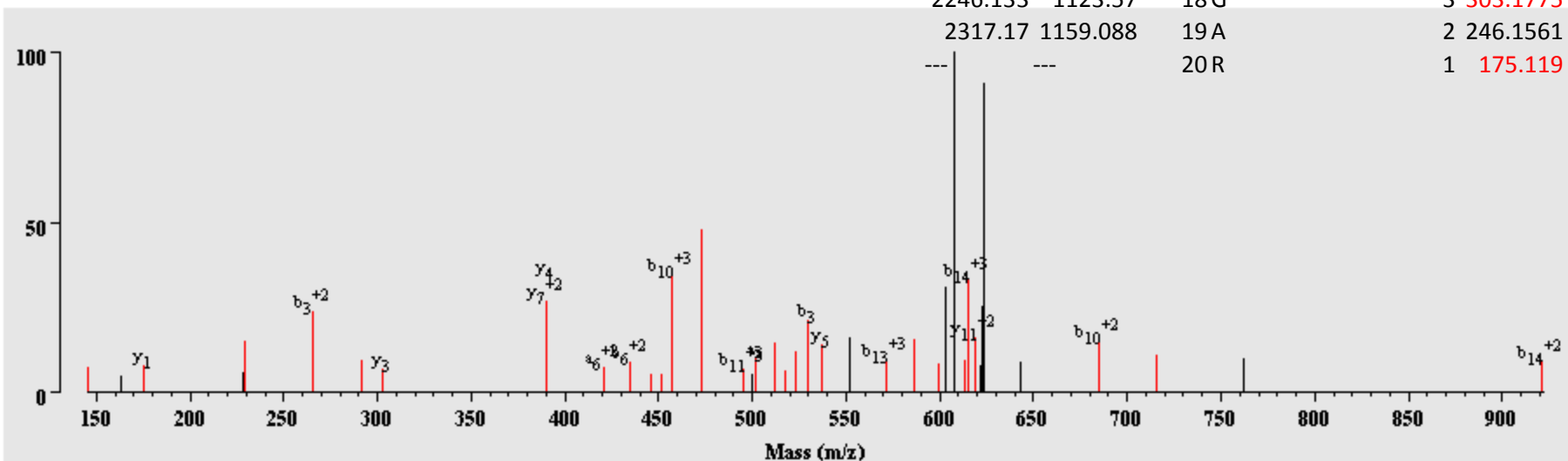
**Axonal Transport Proteomics in
Injured Sciatic Nerve**

Izhak Michaelevski^{1,*}, Katalin F.
Medzihradszky², Aenoch Lynn², Alma L.
Burlingame², and Mike Fainzilber^{1,*}

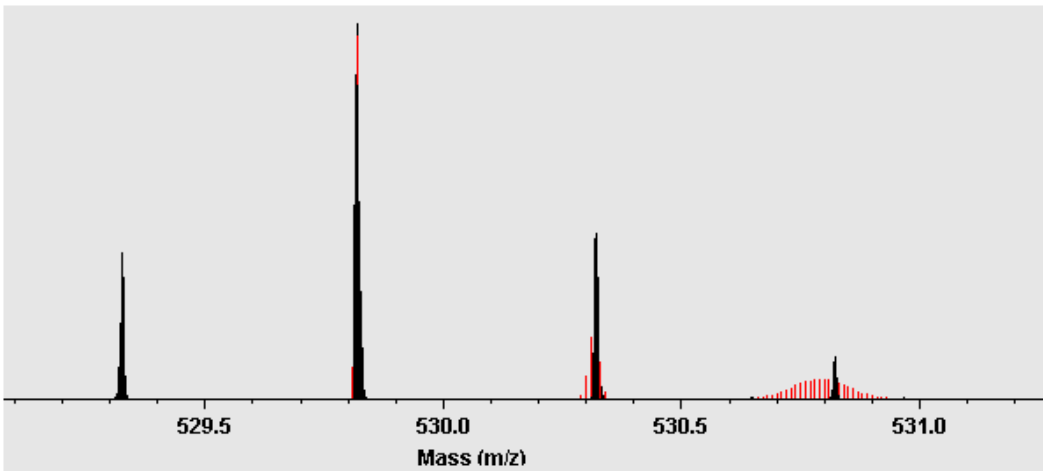
IRDPNQGGK(iTRAQ4plex)DITEEIM(Oxi)SGAR⁺⁴/(623.8693⁺⁴/ 2492.4549)/A0PJB5



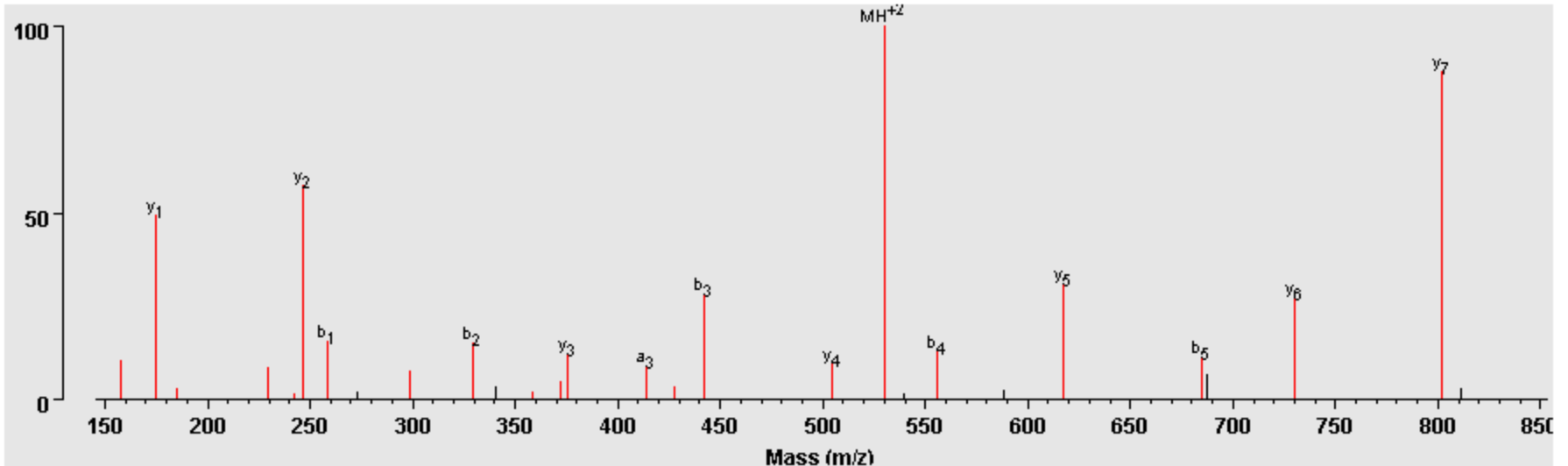
b	b+2	iTRAQ4plex	y	y+2
258.1934	---	1 I	20	---
414.2945	207.6509	2 R	19	2234.095 1117.551
529.3215	265.1644	3 D	18	2077.994 1039.501
626.3742	313.6907	4 P	17	1962.967 981.9872
740.4171	370.7122	5 N	16	1865.914 933.4608
868.4757	434.7415	6 Q	15	1751.871 876.4393
925.4972	463.2522	7 G	14	1623.813 812.4101
982.5187	491.763	8 G	13	1566.791 783.8993
1254.716	627.8615	9 K(iTRAQ4plex)	12	1509.77 755.3886
1369.743	685.3749	10 D	11	1237.573 619.2901
1482.827	741.917	11 I	10	1122.546 561.7766
1583.874	792.4408	12 T	9	1009.462 505.2346
1712.917	856.9621	13 E	8	908.4142 454.7107
1841.96	921.4834	14 E	7	779.3716 390.1894
1955.044	978.0254	15 I	6	650.329 325.6681
2102.079	1051.543	16 M(Oxidation)	5	537.245 269.1261
2189.111	1095.059	17 S	4	390.2096 195.6084
2246.133	1123.57	18 G	3	303.1775 152.0924
2317.17	1159.088	19 A	2	246.1561 123.5817
---	---	20 R	1	175.119 88.0631



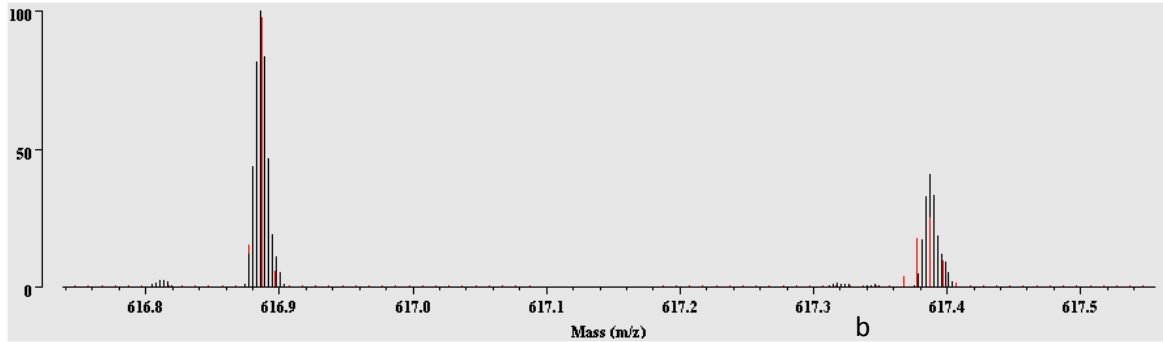
LALLEEAR⁺²/(530.1238⁺²/1059.2402)/A2AA80



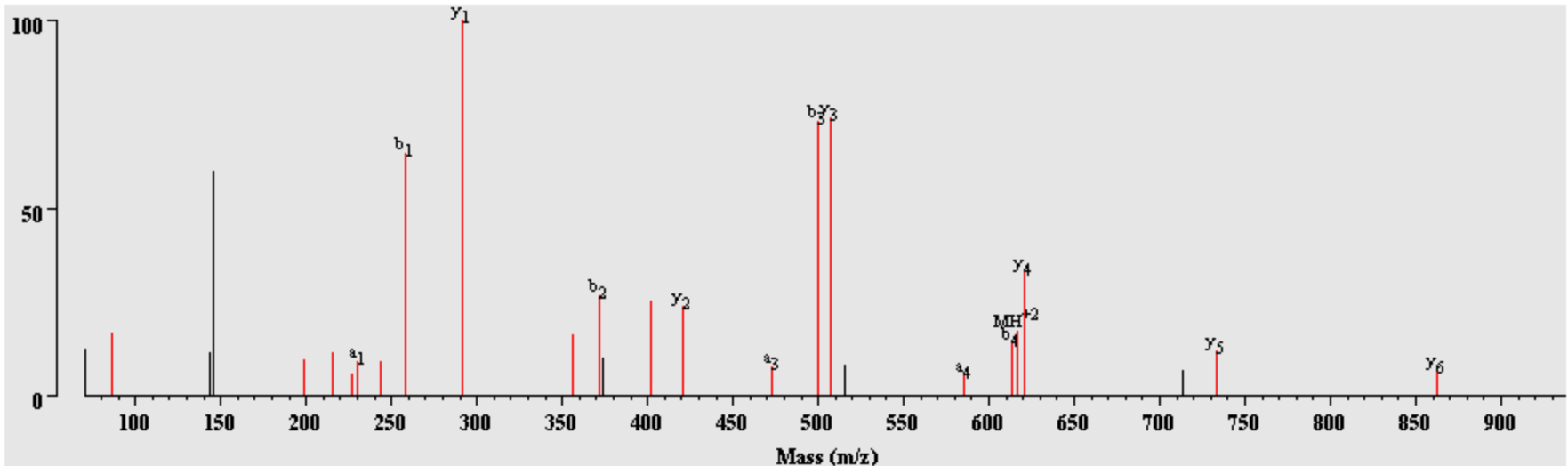
b	iTRAQ4plex	y	y+2
258.1934	1L	8---	---
329.2305	2A	7 801.4465	401.2269
442.3146	3L	6 730.4094	365.7083
555.3986	4L	5 617.3253	309.1663
684.4412	5E	4 504.2413	252.6243
813.4838	6E	3 375.1987	188.103
884.5209	7A	2 246.1561	123.5817
---	8R	1 175.119	88.0631



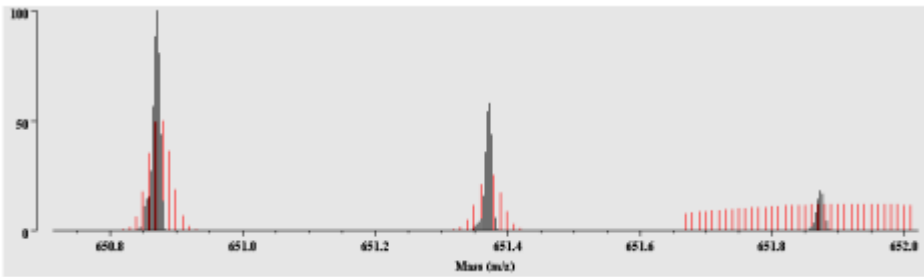
LIEILSEK(iTRAQ4)⁺²/(616.8871⁺²/1233.32)/A2AVJ7



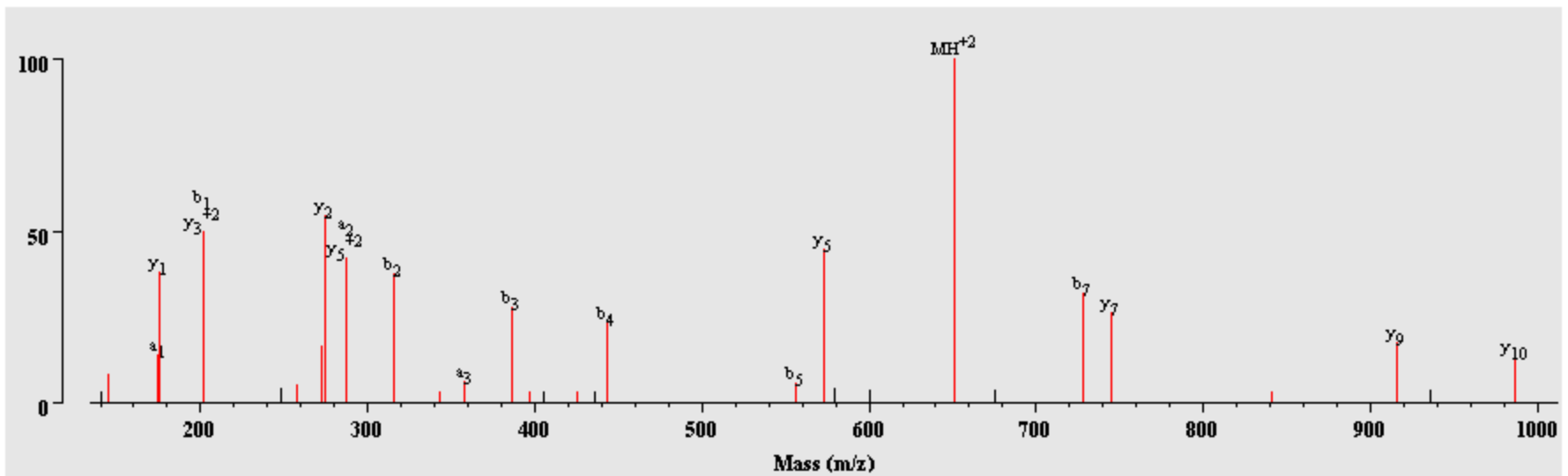
	b	iTRAQ4plex	y	y+2
	258.1934	1L	8---	---
	371.2775	2I	7 975.5843	488.2958
	500.3201	3E	6 862.5002	431.7537
	613.4041	4I	5 733.4576	367.2324
	726.4882	5L	4 620.3736	310.6904
	813.5202	6S	3 507.2895	254.1484
	942.5628	7E	2 420.2575	210.6324
	---	8K(iTRAQ4plex)	1 291.2149	146.1111



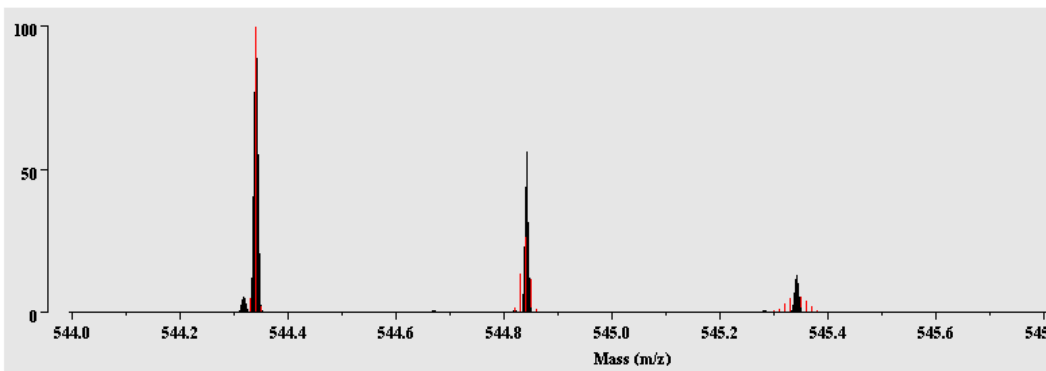
GIAGLG DVAEVR⁺²/(651.2418⁺²/1301.4762)/A2AWQ5



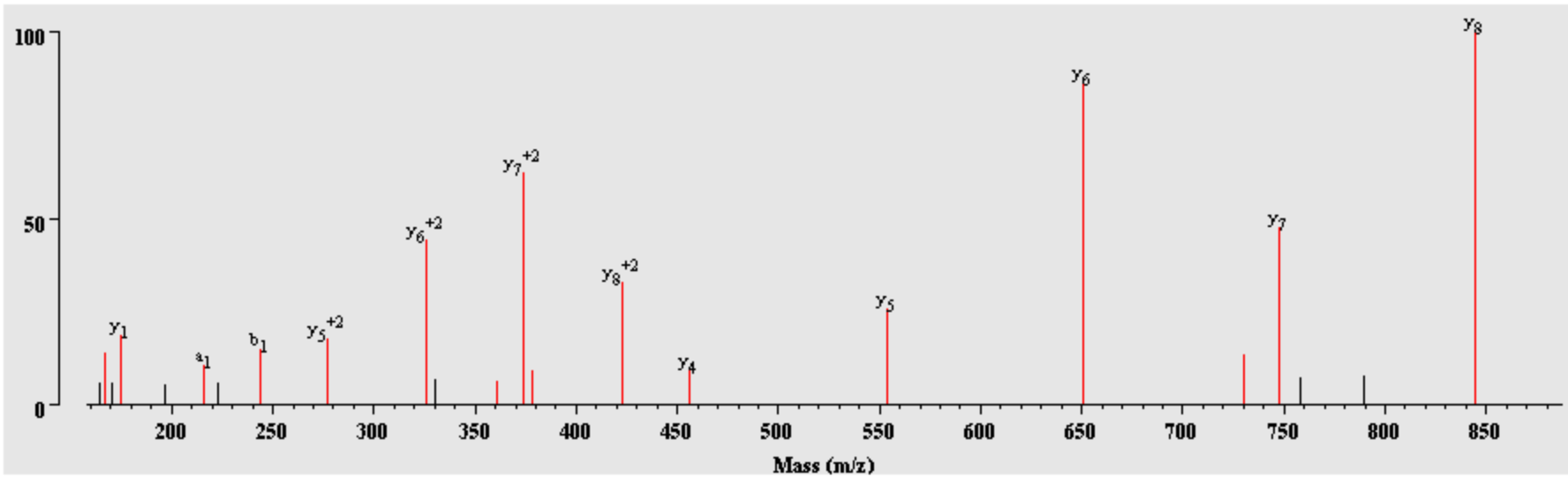
b	iTRAQ4plex	y	y+2
202.1308	1 G	12 ---	---
315.2149	2 I	11 1099.611	550.3089
386.252	3 A	10 986.5265	493.7669
443.2734	4 G	9 915.4894	458.2483
556.3575	5 L	8 858.468	429.7376
613.379	6 G	7 745.3839	373.1956
728.4059	7 D	6 688.3624	344.6849
827.4743	8 V	5 573.3355	287.1714
898.5114	9 A	4 474.2671	237.6372
1027.554	10 E	3 403.23	202.1186
1126.622	11 V	2 274.1874	137.5973
---	12 R	1 175.119	88.0631



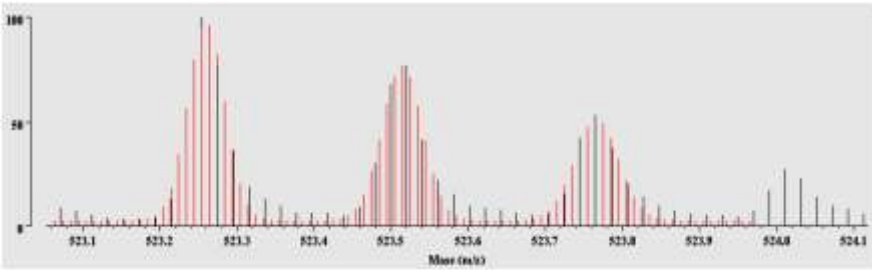
VPPPPLAPR⁺²/(544.6679⁺²/1088.3283)/A2BDX3



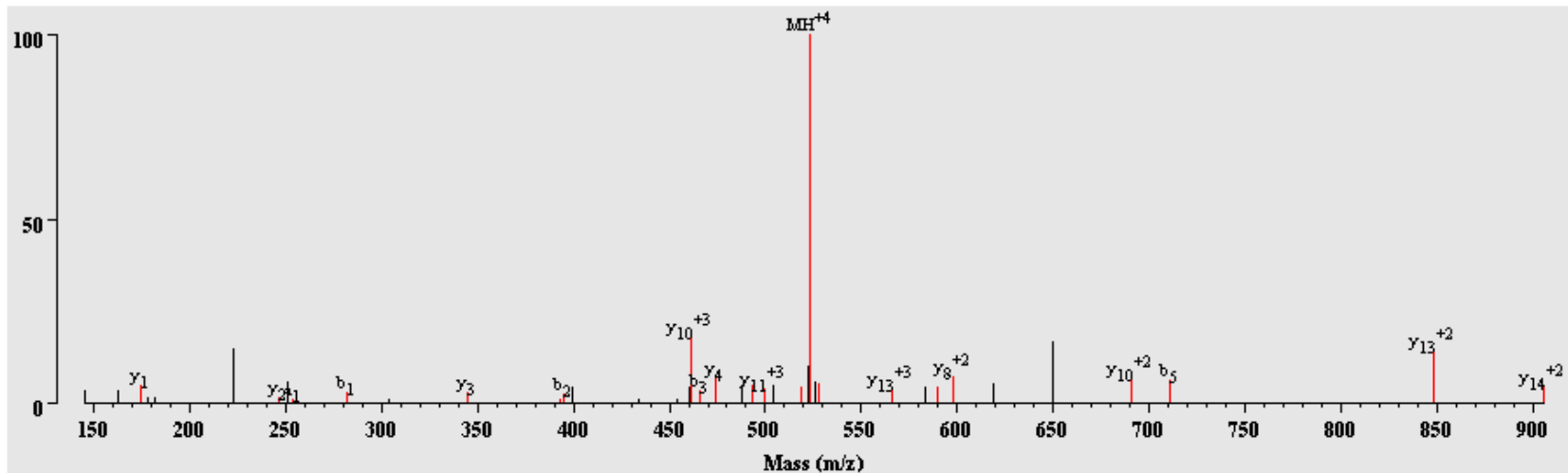
b	iTRAQ4plex	y	y+2
244.1778	1V	9---	---
341.2305	2P	8 844.5039	422.7556
438.2833	3P	7 747.4512	374.2292
535.336	4P	6 650.3984	325.7028
632.3888	5P	5 553.3457	277.1765
745.4729	6L	4 456.2929	228.6501
816.51	7A	3 343.2088	172.1081
913.5627	8P	2 272.1717	136.5895
---	9R	1 175.119	88.0631



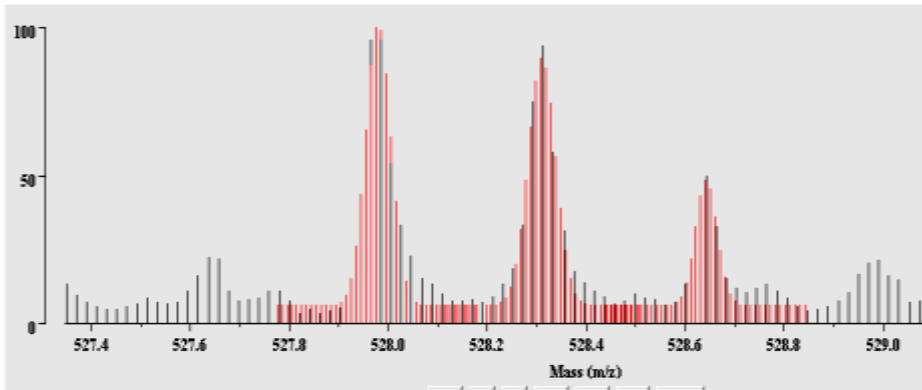
HIAEDADRK(iTRAQ4plex)YEEVAR⁴⁺/(523.5384⁴⁺/ 2091.1314)/A2RRI1



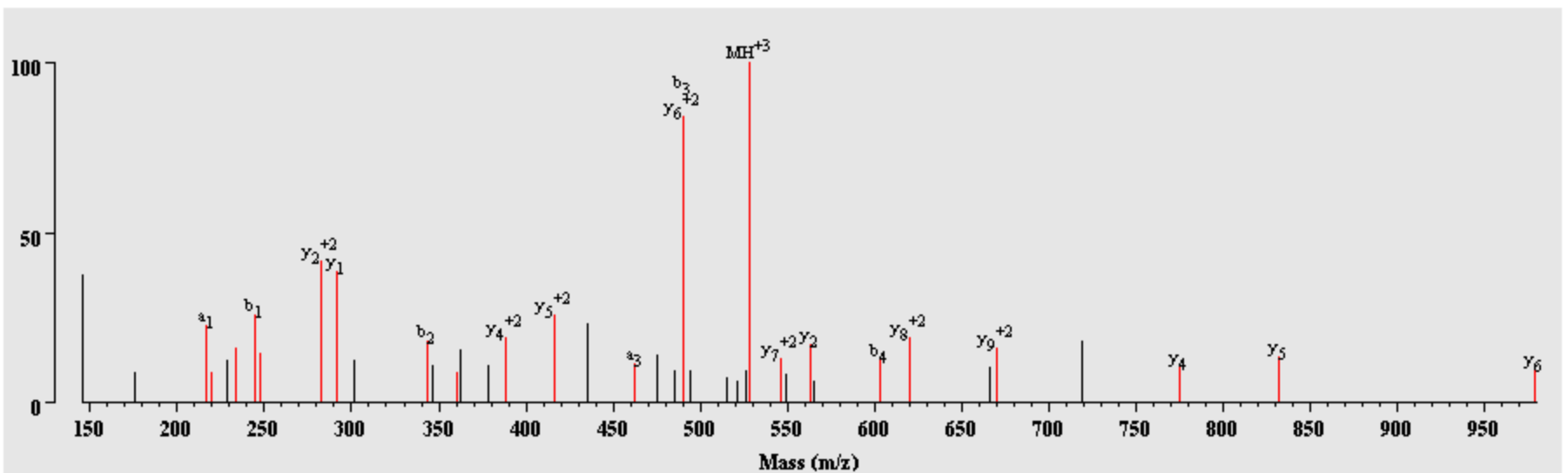
b	b+2	iTRAQ4plex	y	y+2
282.1683	141.5878	1 H	15 ---	---
395.2523	198.1298	2 I	14 1808.926	904.9666
466.2894	233.6484	3 A	13 1695.842	848.4246
595.332	298.1696	4 E	12 1624.805	812.906
710.359	355.6831	5 D	11 1495.762	748.3847
781.3961	391.2017	6 A	10 1380.735	690.8712
896.423	448.7151	7 D	9 1309.698	655.3527
1052.524	526.7657	8 R	8 1194.671	597.8392
1324.721	662.8642	9 K(iTRAQ4plex)	7 1038.57	519.7886
1487.785	744.3959	10 Y	6 766.373	383.6901
1616.827	808.9172	11 E	5 603.3097	302.1585
1745.87	873.4385	12 E	4 474.2671	237.6372
1844.938	922.9727	13 V	3 345.2245	173.1159
1915.975	958.4912	14 A	2 246.1561	123.5817
---	---	15 R	1 175.119	88.0631



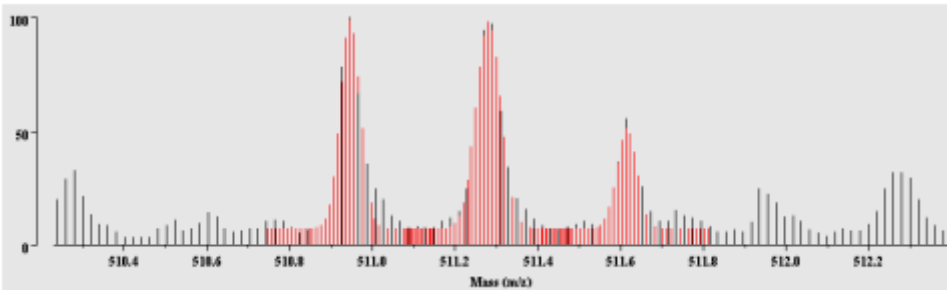
VVFIFGPDK(iTRAQ4plex)K(iTRAQ4plex)⁺³/(528.21+3/1582.61) /O08709



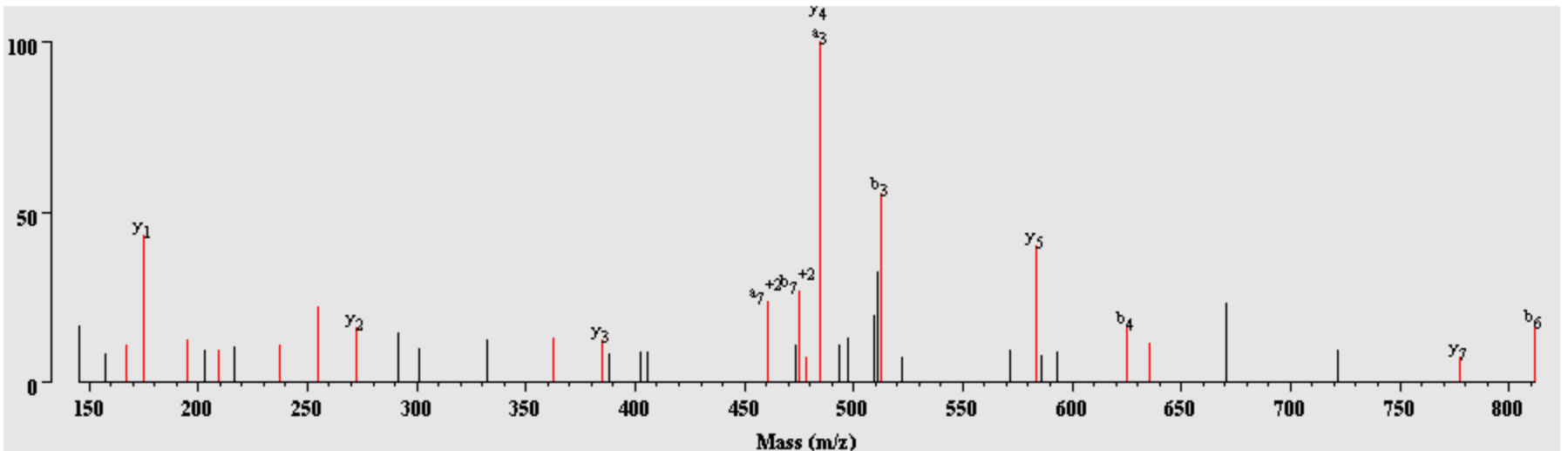
b	b+2	iTRAQ4plex	y	y+2
244.1778	---	1 V	10	---
343.2462	---	2 V	9	1338.802 669.9048
490.3146	---	3 F	8	1239.734 620.3706
603.3986	---	4 I	7	1092.666 546.8364
750.4671	---	5 F	6	979.5815 490.2944
807.4885	---	6 G	5	832.5131 416.7602
904.5413	---	7 P	4	775.4916 388.2494
1019.568	---	8 D	3	678.4388 339.7231
1291.765	646.3863	9 K(iTRAQ4plex)	2	563.4119 282.2096
---	---	10 K(iTRAQ4plex)	1	291.2149 146.1111



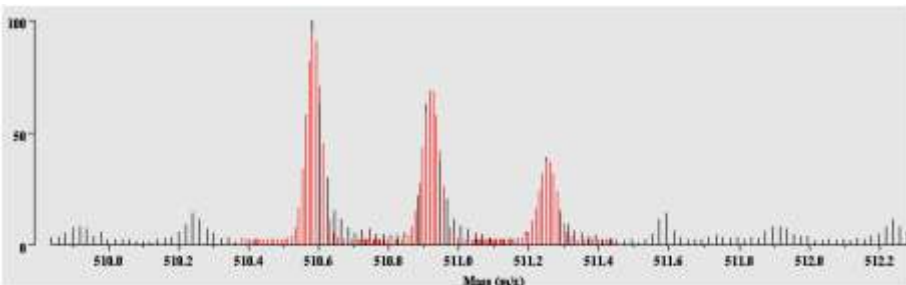
YGFIEGHVVIPR⁺³/(511.2686⁺³/1531.79)/O08779



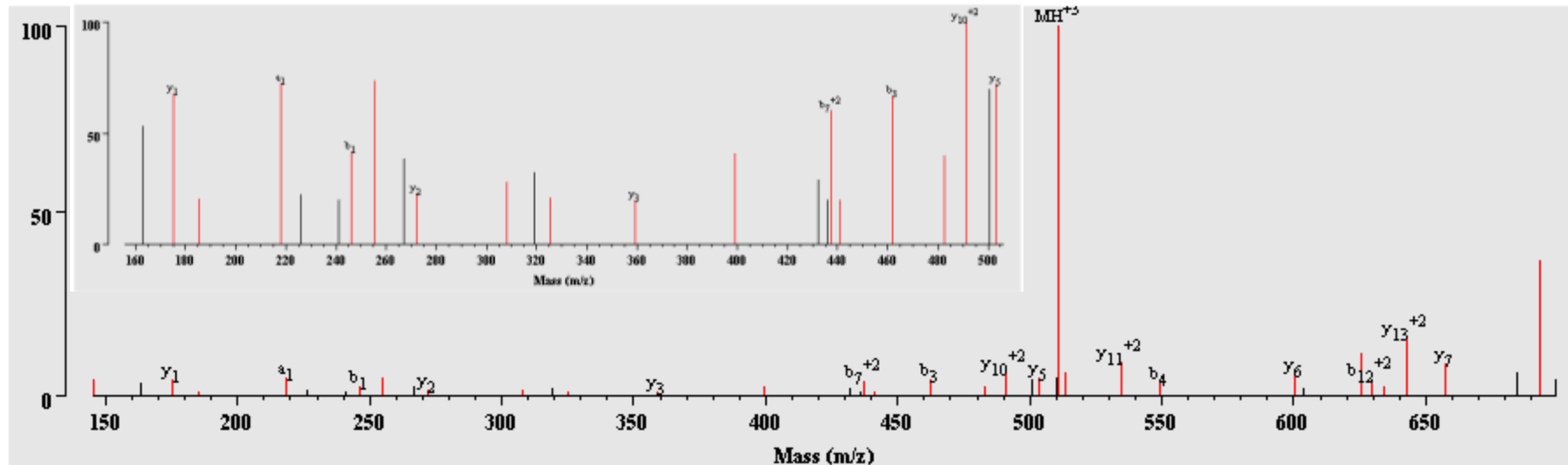
b	b+2	iTRAQ4plex	y	y+2
308.1727	---	1 Y	12	---
365.1941	---	2 G	11	1223.69 612.3484
512.2625	---	3 F	10	1166.668 583.8377
625.3466	---	4 I	9	1019.6 510.3035
754.3892	---	5 E	8	906.5156 453.7614
811.4107	---	6 G	7	777.473 389.2401
948.4696	474.7384	7 H	6	720.4515 360.7294
1047.538	524.2726	8 V	5	583.3926 292.1999
1146.606	573.8068	9 V	4	484.3242 242.6657
1259.691	630.3489	10 I	3	385.2558 193.1315
1356.743	678.8753	11 P	2	272.1717 136.5895
---	---	12 R	1	175.119 88.0631



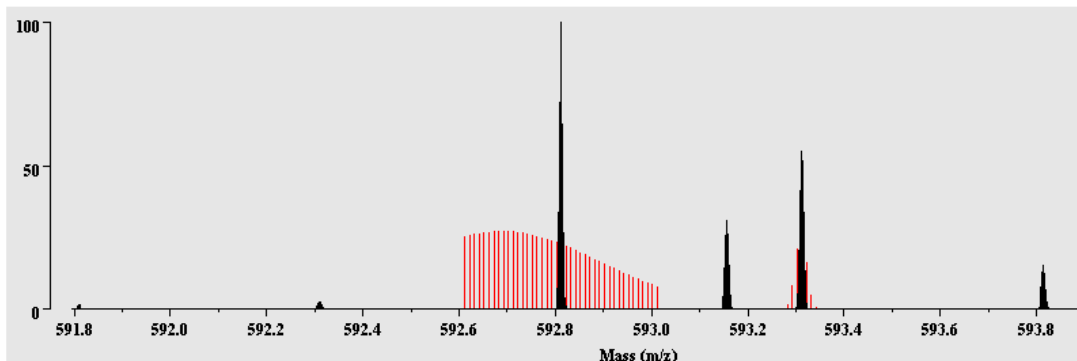
TSESPARGPSGR³/(510.8814³/1530.6295)/O35108



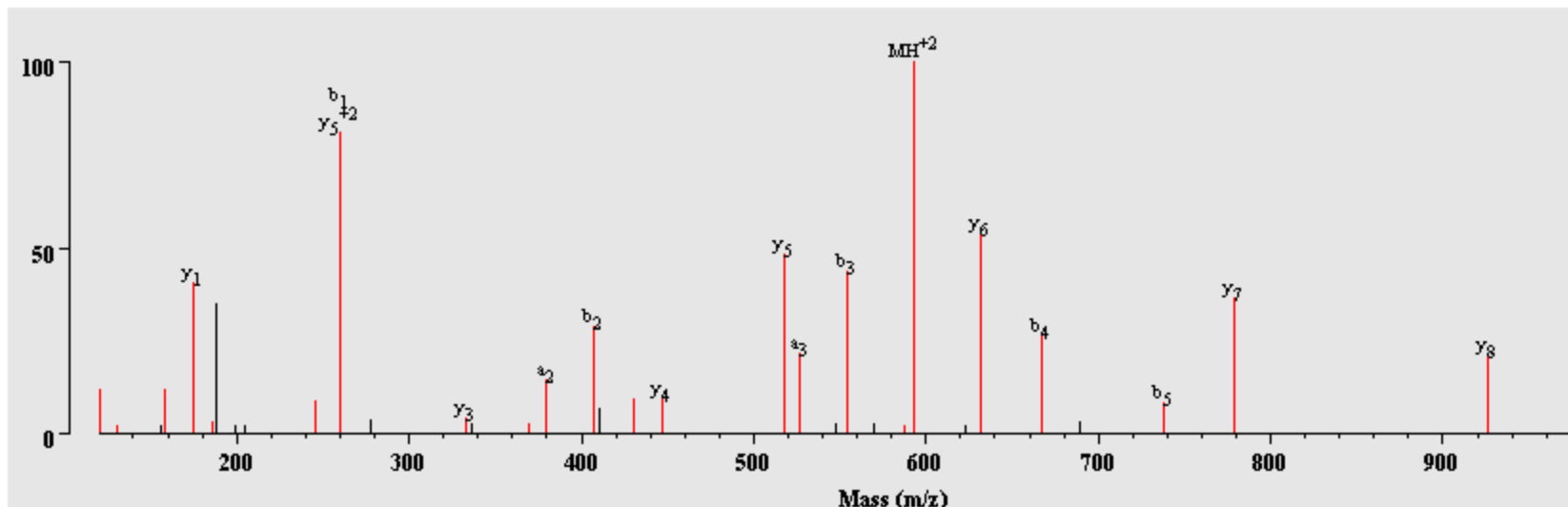
b	b+2	iTRAQ4plex	y	y+2
246.157	---	1 T	14	---
333.189	---	2 S	13	1284.629 642.8182
462.2316	---	3 E	12	1197.597 599.3022
549.2637	---	4 S	11	1068.555 534.7809
646.3164	---	5 P	10	981.5225 491.2649
717.3535	---	6 A	9	884.4697 442.7385
873.4547	437.231	7 R	8	813.4326 407.2199
930.4761	465.7417	8 G	7	657.3315 329.1694
1027.529	514.2681	9 P	6	600.31 300.6586
1114.561	557.7841	10 S	5	503.2572 252.1323
1171.582	586.2948	11 G	4	416.2252 208.6162
1258.614	629.8108	12 S	3	359.2037 180.1055
1355.667	678.3372	13 P	2	272.1717 136.5895
---	---	14 R	1	175.119 88.0631



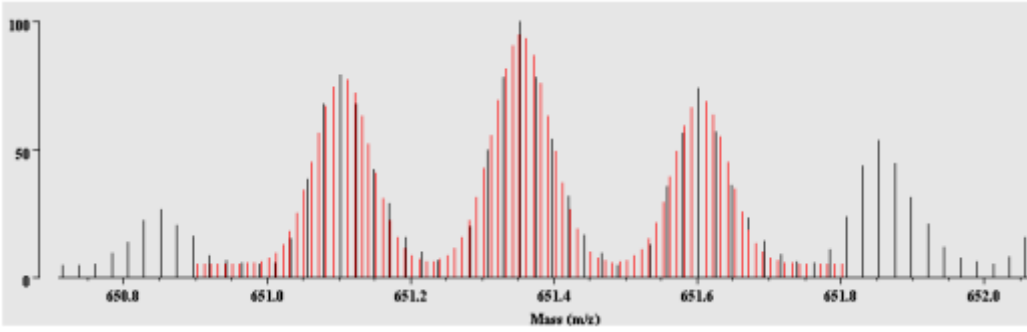
DFFLANASR⁺²/(593.1611⁺²/1185.3148)/O35350



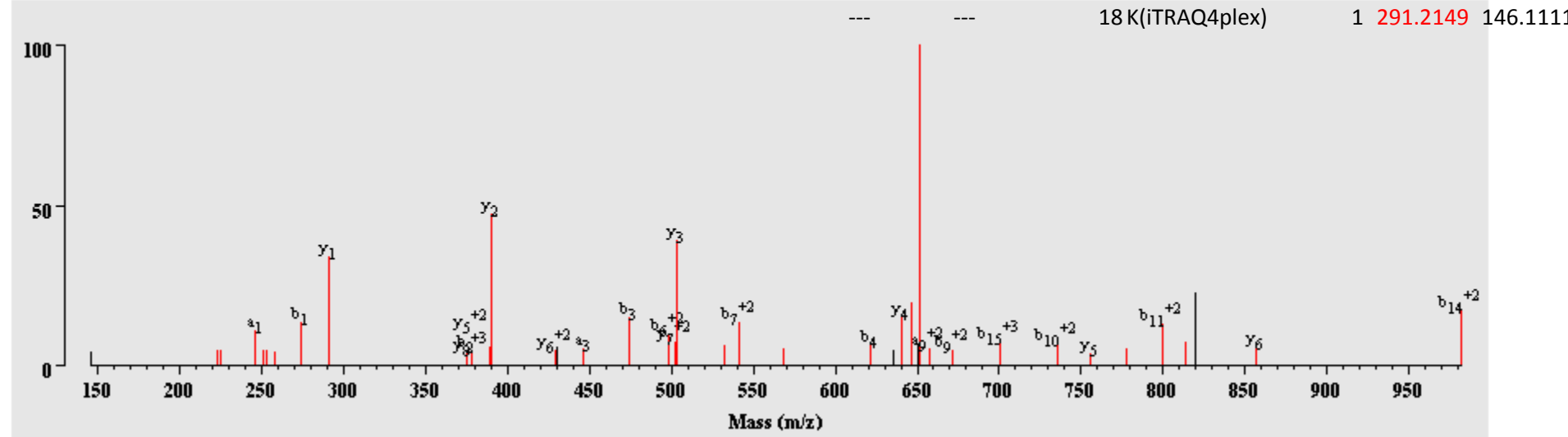
b	iTRAQ4plex	y	y+2
260.1363	1 D	9 ---	---
407.2047	2 F	8 925.489	463.2482
554.2731	3 F	7 778.4206	389.7139
667.3572	4 L	6 631.3522	316.1797
738.3943	5 A	5 518.2681	259.6377
852.4372	6 N	4 447.231	224.1191
923.4743	7 A	3 333.1881	167.0977
1010.506	8 S	2 262.151	131.5791
---	9 R	1 175.119	88.0631



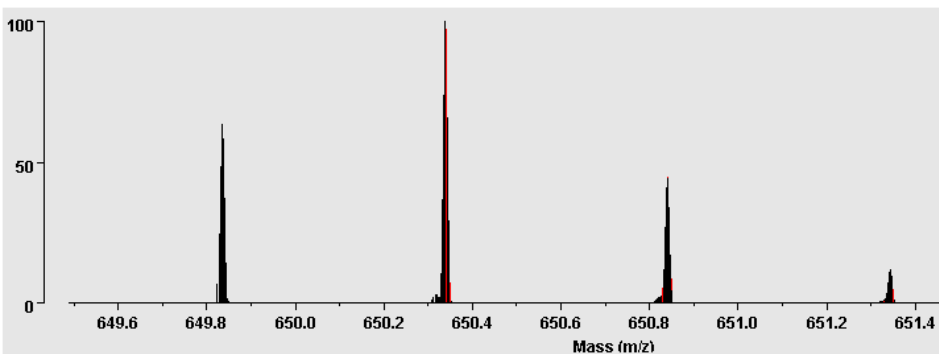
ETVFTK(iTRAQ4plex)SPYQEFTDHLVK(iTRAQ4plex)⁺⁴/(651.416⁺⁴ /2602.6419)/O55211



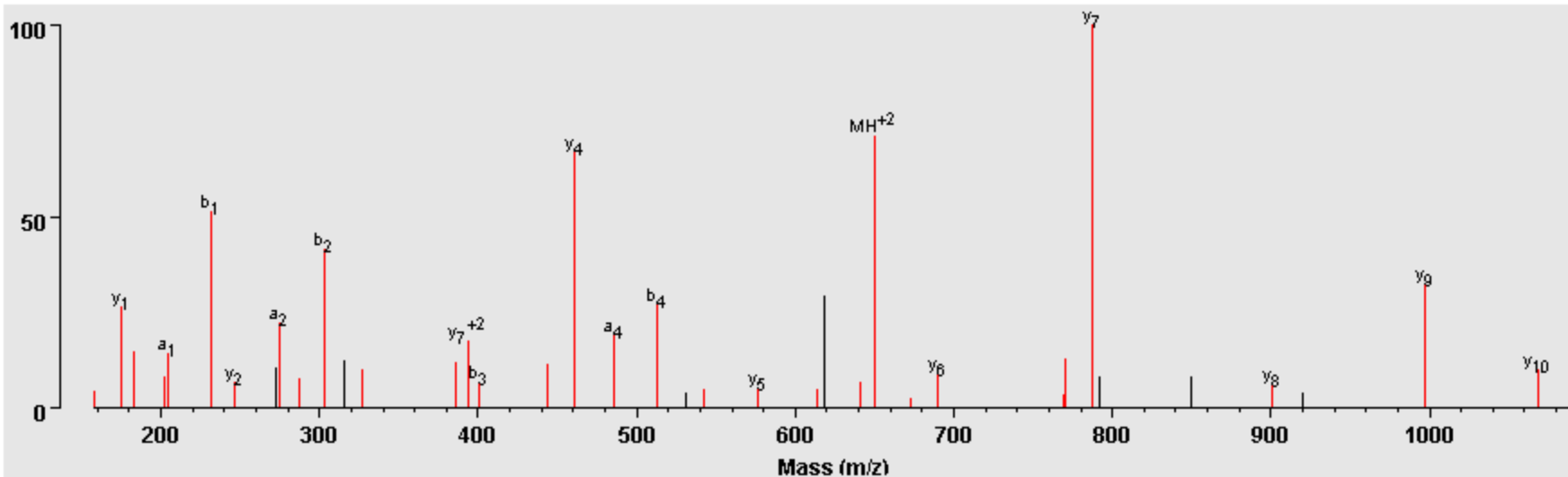
b	b+2	iTRAQ4plex	y	y+2
274.1519	---	1 E	18	---
375.1996	---	2 T	17	2328.248 1164.628
474.268	---	3 V	16	2227.2 1114.104
621.3364	---	4 F	15	2128.132 1064.57
722.3841	---	5 T	14	1981.063 991.0353
994.5811	497.7942	6 K(iTRAQ4plex)	13	1880.016 940.5114
1081.613	541.3102	7 S	12	1607.819 804.4129
1178.666	589.8366	8 P	11	1520.787 760.8969
1341.729	671.3683	9 Y	10	1423.734 712.3705
1469.788	735.3976	10 Q	9	1260.671 630.8389
1598.83	799.9189	11 E	8	1132.612 566.8096
1745.899	873.4531	12 F	7	1003.569 502.2883
1846.947	923.9769	13 T	6	856.5009 428.7541
1961.974	981.4904	14 D	5	755.4532 378.2302
2099.032	1050.02	15 H	4	640.4263 320.7168
2212.116	1106.562	16 L	3	503.3673 252.1873
2311.185	1156.096	17 V	2	390.2833 195.6453
---	---	18 K(iTRAQ4plex)	1	291.2149 146.1111



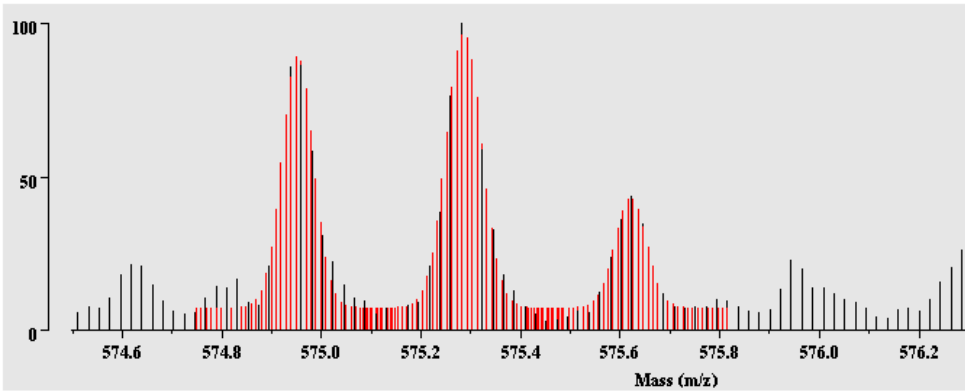
SAPLPNDSQAR⁺²/(650.7059⁺²/1300.4043)/O70172



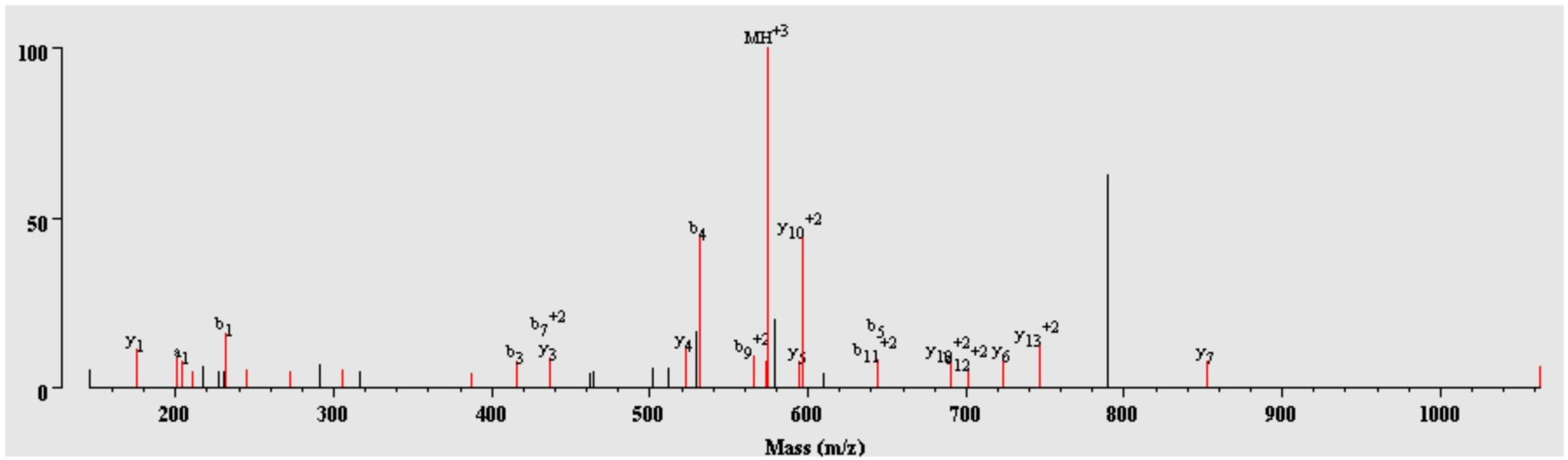
b	iTRAQ4plex	y	y+2
232.1414	1S	11 ---	---
303.1785	2A	10 1068.543	534.7753
400.2312	3P	9 997.5061	499.2567
513.3153	4L	8 900.4534	450.7303
610.3681	5P	7 787.3693	394.1883
724.411	6N	6 690.3165	345.6619
839.4379	7D	5 576.2736	288.6404
926.47	8S	4 461.2467	231.127
1054.529	9Q	3 374.2146	187.611
1125.566	10A	2 246.1561	123.5817
---	11R	1 175.119	88.0631



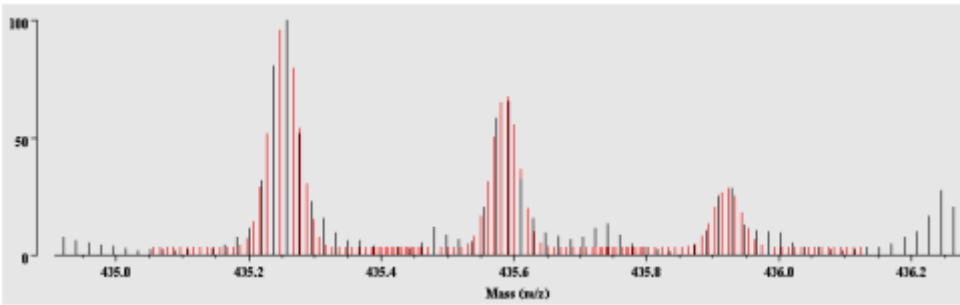
SLADIAREEASNFR⁺³/(575.2971⁺³/1723.8765)/O70435



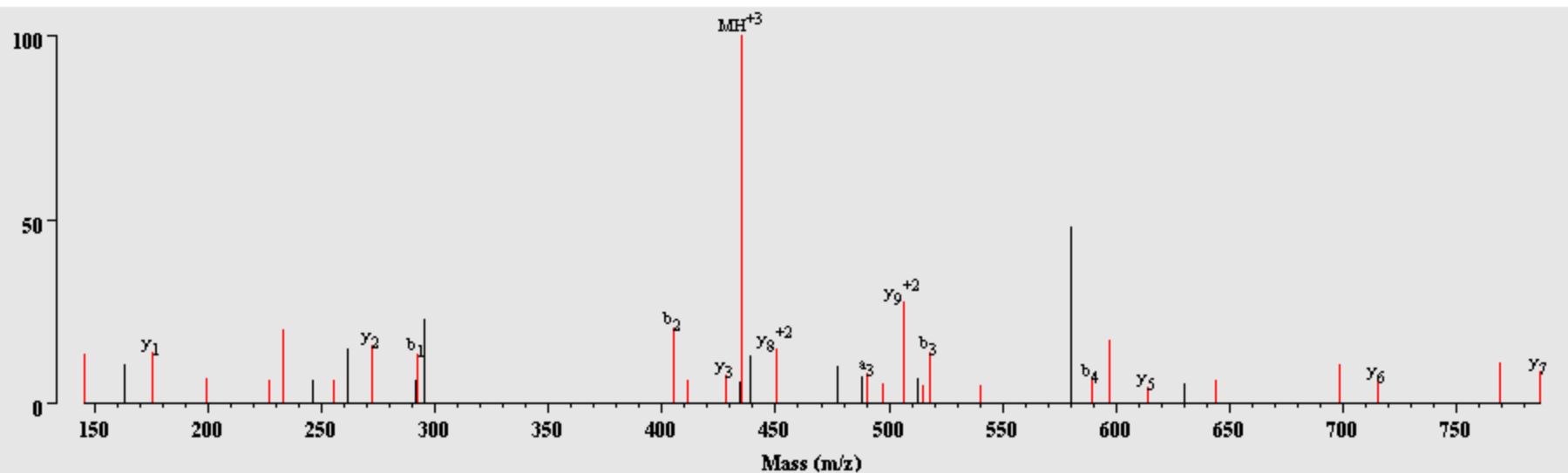
b	b+2	iTRAQ4plex	y	y+2
232.1414	---	1 S	14	---
345.2254	---	2 L	13	1491.755 746.3812
416.2625	---	3 A	12	1378.671 689.8391
531.2895	---	4 D	11	1307.634 654.3206
644.3736	---	5 I	10	1192.607 596.8071
715.4107	---	6 A	9	1079.523 540.2651
871.5118	436.2595	7 R	8	1008.486 504.7465
1000.554	500.7808	8 E	7	852.3846 426.6959
1129.597	565.3021	9 E	6	723.342 362.1747
1200.634	600.8207	10 A	5	594.2994 297.6534
1287.666	644.3367	11 S	4	523.2623 262.1348
1401.709	701.3582	12 N	3	436.2303 218.6188
1548.777	774.8924	13 F	2	322.1874 161.5973
---	---	14 R	1	175.119 88.0631



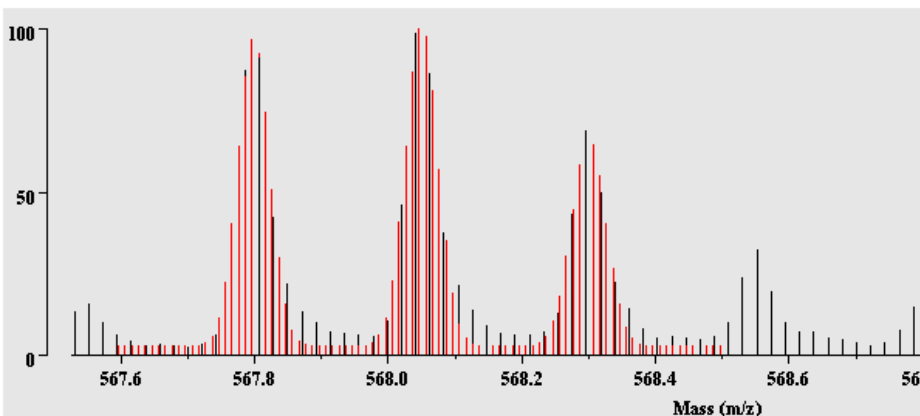
FLIATGERPR⁺³/(455.137⁺³/1304.5262)/O89049



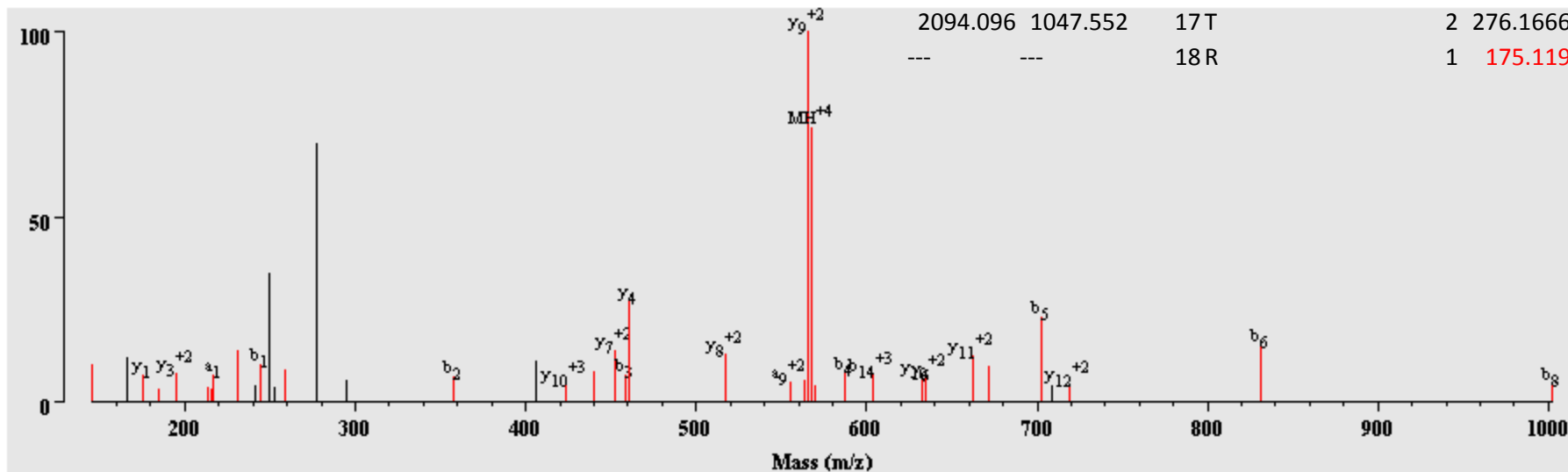
b	b+2	iTRAQ4plex	y	y+2
292.1778	---	1 F	10	---
405.2618	---	2 L	9	1012.59 506.7985
518.3459	---	3 I	8	899.5057 450.2565
589.383	---	4 A	7	786.4217 393.7145
690.4307	---	5 T	6	715.3846 358.1959
747.4521	---	6 G	5	614.3369 307.6721
876.4947	---	7 E	4	557.3154 279.1613
1032.596	516.8016	8 R	3	428.2728 214.6401
1129.649	565.3279	9 P	2	272.1717 136.5895
---	---	10 R	1	175.119 88.0631



VLTEDELGHPEK(iTRAQ4plex)GDAITR⁺⁴/(568.0959⁺⁴/2269.361) /P05369

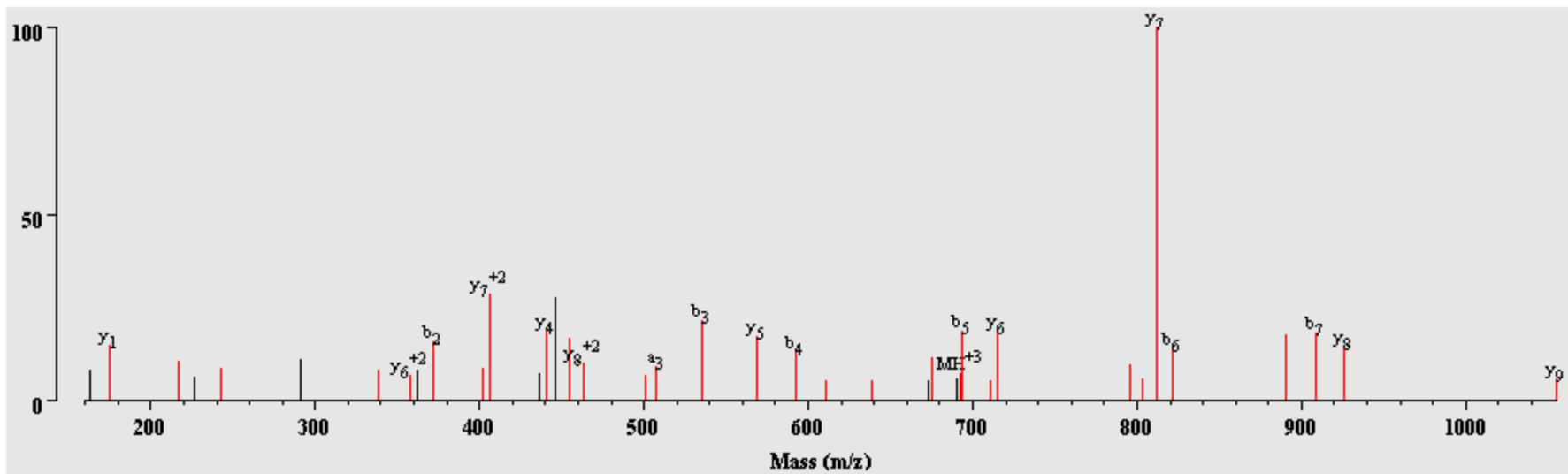
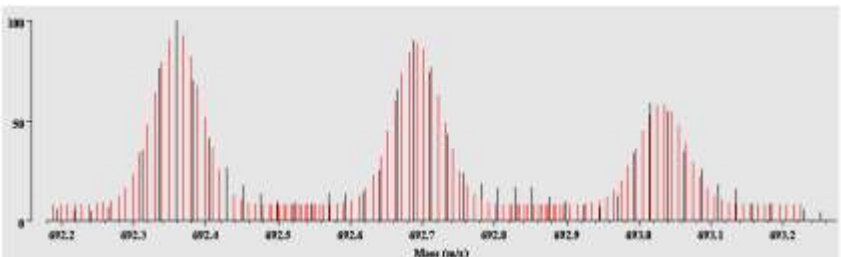


b	b+2	iTRAQ4plex	y	y+2
244.1778	---	1V	18	---
357.2618	---	2L	17	2025.037 1013.022
458.3095	---	3T	16	1911.953 956.4801
587.3521	---	4E	15	1810.905 905.9562
702.379	---	5D	14	1681.863 841.4349
831.4216	---	6E	13	1566.836 783.9215
944.5057	---	7L	12	1437.793 719.4002
1001.527	---	8G	11	1324.709 662.8581
1138.586	569.7967	9H	10	1267.688 634.3474
1235.639	618.3231	10P	9	1130.629 565.8179
1364.681	682.8443	11E	8	1033.576 517.2916
1636.878	818.9429	12 K(iTRAQ4plex)	7	904.5332 452.7703
1693.9	847.4536	13 G	6	632.3362 316.6717
1808.927	904.9671	14 D	5	575.3148 288.161
1879.964	940.4856	15 A	4	460.2878 230.6475
1993.048	997.0277	16 I	3	389.2507 195.129
2094.096	1047.552	17 T	2	276.1666 138.587
---	---	18 R	1	175.119 88.0631



NLYGTQSLELPFQGAHR⁺³/(692.7769⁺³/2076.3157)/P07722

b	b+2	iTRAQ4plex	y	y+2
259.1523	---	1 N	17	---
372.2363	---	2 L	16	1816.934 908.9707
535.2997	---	3 Y	15	1703.85 852.4286
592.3211	---	4 G	14	1540.787 770.897
693.3688	---	5 T	13	1483.765 742.3862
821.4274	---	6 Q	12	1382.718 691.8624
908.4594	---	7 S	11	1254.659 627.8331
1021.544	---	8 L	10	1167.627 584.3171
1150.586	---	9 E	9	1054.543 527.7751
1263.67	---	10 L	8	925.5003 463.2538
1360.723	---	11 P	7	812.4162 406.7117
1507.791	---	12 F	6	715.3634 358.1854
1635.85	---	13 Q	5	568.295 284.6511
1692.871	---	14 G	4	440.2364 220.6219
1763.909	---	15 A	3	383.215 192.1111
1900.967	950.9873	16 H	2	312.1779 156.5926
---	---	17 R	1	175.119 88.0631



IIAEGANGPTTPEADK(iTRAQ4)IFLER⁺⁴/(633.6845⁺⁴/2531.7156)

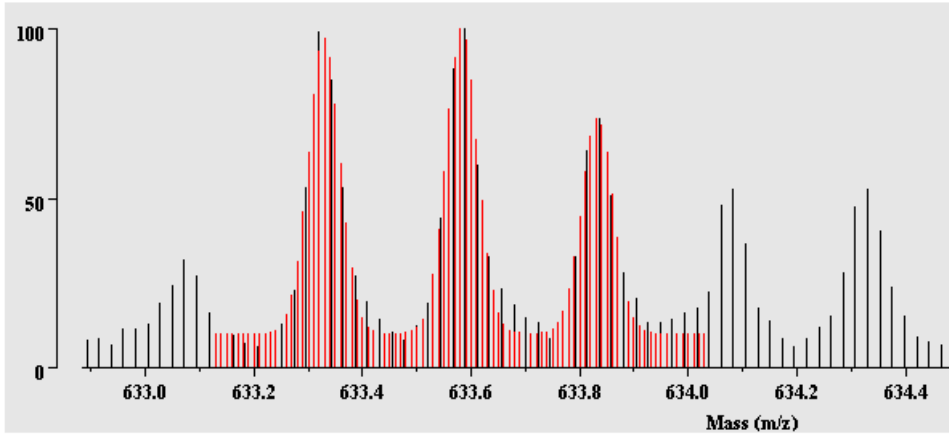
/P10860^b

b+2

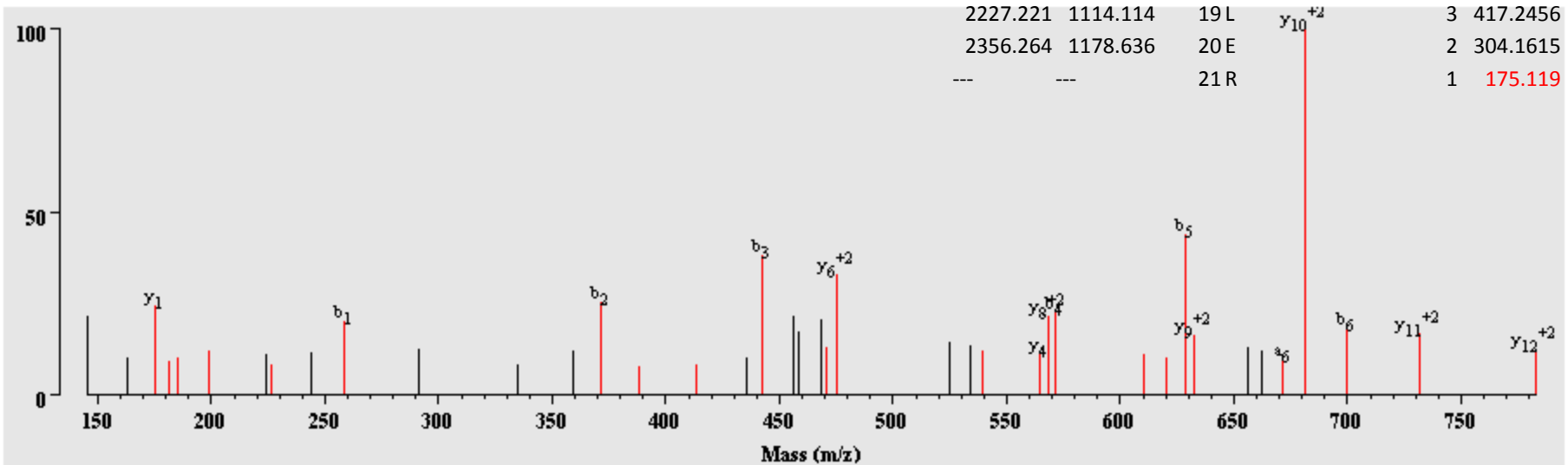
y

y+2

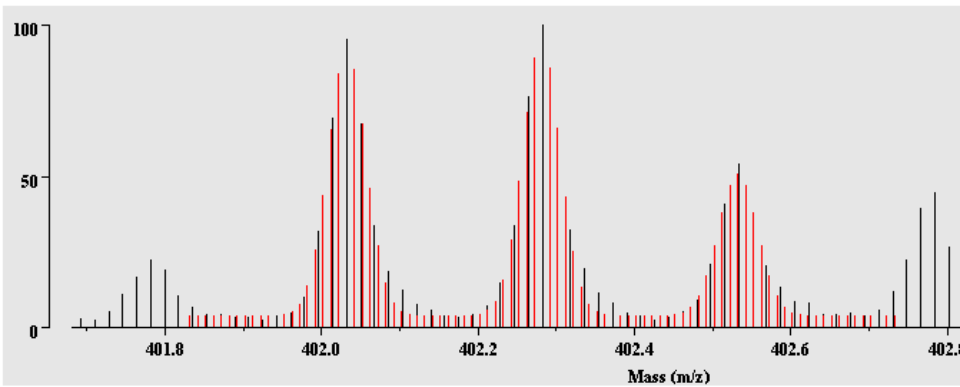
iTRAQ4plex



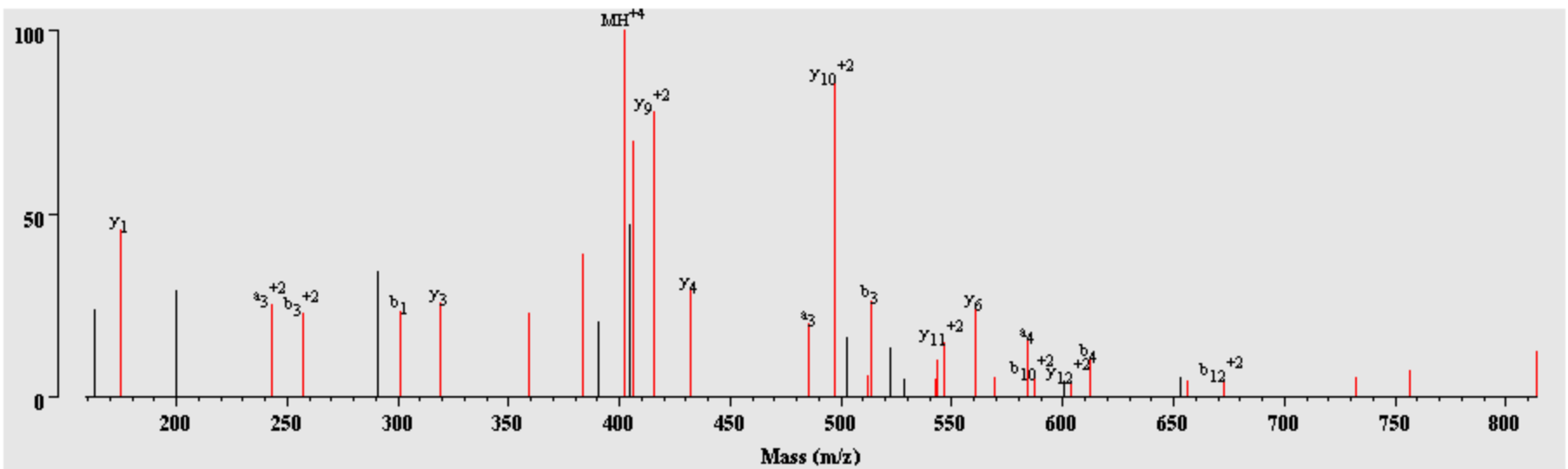
258.1934	---	1 I	21	---	---
371.2775	---	2 I	20	2273.189	1137.098
442.3146	---	3 A	19	2160.105	1080.556
571.3572	---	4 E	18	2089.068	1045.038
628.3786	---	5 G	17	1960.026	980.5164
699.4158	---	6 A	16	1903.004	952.0057
813.4587	---	7 N	15	1831.967	916.4872
870.4801	---	8 G	14	1717.924	859.4657
967.5329	---	9 P	13	1660.903	830.955
1068.581	---	10 T	12	1563.85	782.4286
1169.628	---	11 T	11	1462.802	731.9047
1266.681	---	12 P	10	1361.755	681.3809
1395.724	---	13 E	9	1264.702	632.8545
1466.761	---	14 A	8	1135.659	568.3332
1581.788	---	15 D	7	1064.622	532.8147
1853.985	927.496	16 K(iTRAQ4plex)	6	949.5951	475.3012
1967.069	984.038	17 I	5	677.3981	339.2027
2114.137	1057.572	18 F	4	564.314	282.6606
2227.221	1114.114	19 L	3	417.2456	209.1264
2356.264	1178.636	20 E	2	304.1615	152.5844
---	---	21 R	1	175.119	88.0631



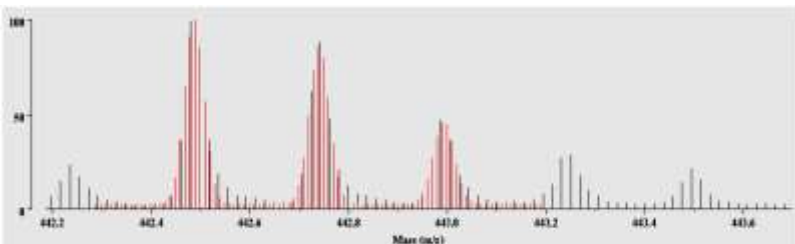
RVLVYGGRGALGSR⁺⁴/(402.2248⁺⁴/1605.877)/P11348



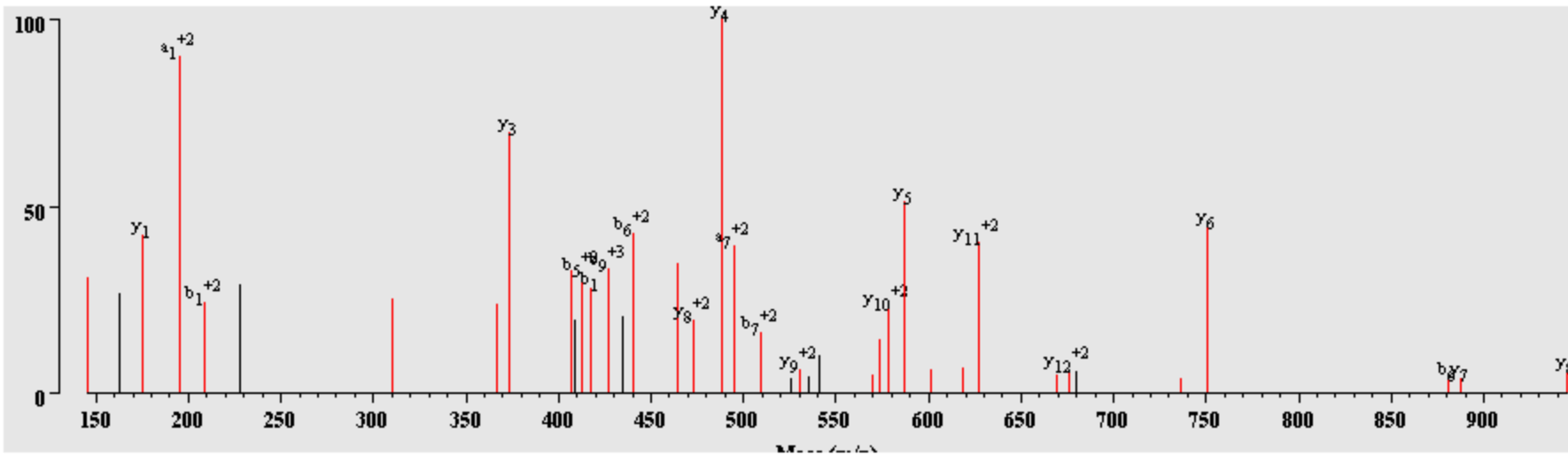
b	b+2	iTRAQ4plex	y	y+2
301.2104	151.1089	1 R	14 ---	---
400.2789	200.6431	2 V	13 1304.743	652.8753
513.3629	257.1851	3 L	12 1205.675	603.3411
612.4313	306.7193	4 V	11 1092.591	546.7991
775.4947	388.251	5 Y	10 993.5225	497.2649
832.5161	416.7617	6 G	9 830.4591	415.7332
889.5376	445.2724	7 G	8 773.4377	387.2225
1045.639	523.323	8 R	7 716.4162	358.7117
1102.66	551.8337	9 G	6 560.3151	280.6612
1173.697	587.3523	10 A	5 503.2936	252.1504
1286.781	643.8943	11 L	4 432.2565	216.6319
1343.803	672.405	12 G	3 319.1724	160.0899
1430.835	715.9211	13 S	2 262.151	131.5791
---	---	14 R	1 175.119	88.0631



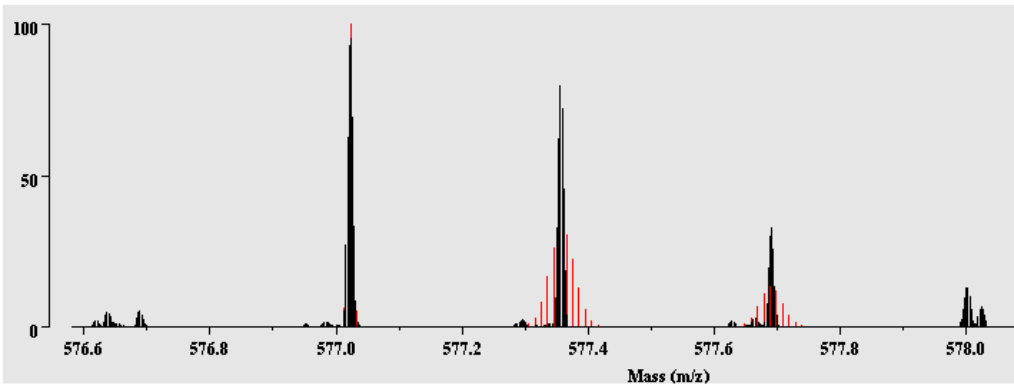
K(iTRAQ4plex)PPPDGHYVDVVR⁺⁴/(442.7224⁺⁴/1767.8672) /P14942



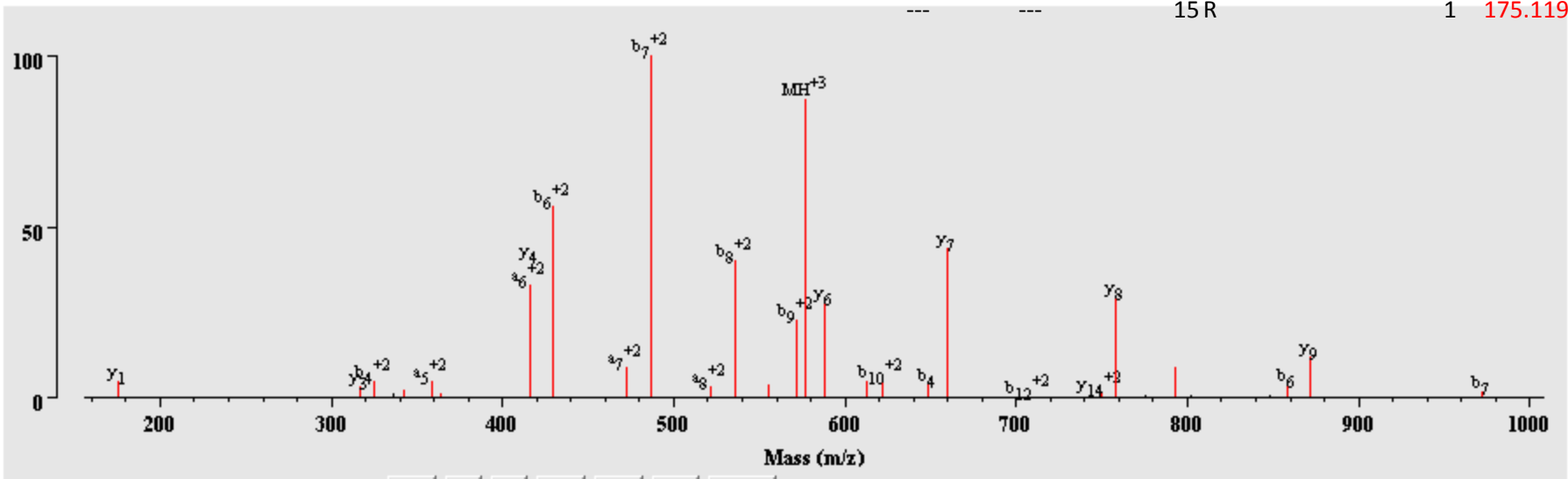
b	b+2	iTRAQ4plex	y	y+2
417.3064	209.1568	1 K(iTRAQ4plex)	13---	---
514.3591	257.6832	2 P	12	1350.68 675.8437
611.4119	306.2096	3 P	11	1253.627 627.3173
708.4647	354.736	4 P	10	1156.575 578.7909
823.4916	412.2494	5 D	9	1059.522 530.2645
880.5131	440.7602	6 G	8	944.4948 472.7511
1017.572	509.2896	7 H	7	887.4734 444.2403
1180.635	590.8213	8 Y	6	750.4145 375.7109
1279.704	640.3555	9 V	5	587.3511 294.1792
1394.731	697.869	10 D	4	488.2827 244.645
1493.799	747.4032	11 V	3	373.2558 187.1315
1592.868	796.9374	12 V	2	274.1874 137.5973
---	---	13 R	1	175.119 88.0631



SGK(iTRAQ4plex)SPILVATAVAAR⁺³/(577.3058⁺³/1729.9026) /P16381

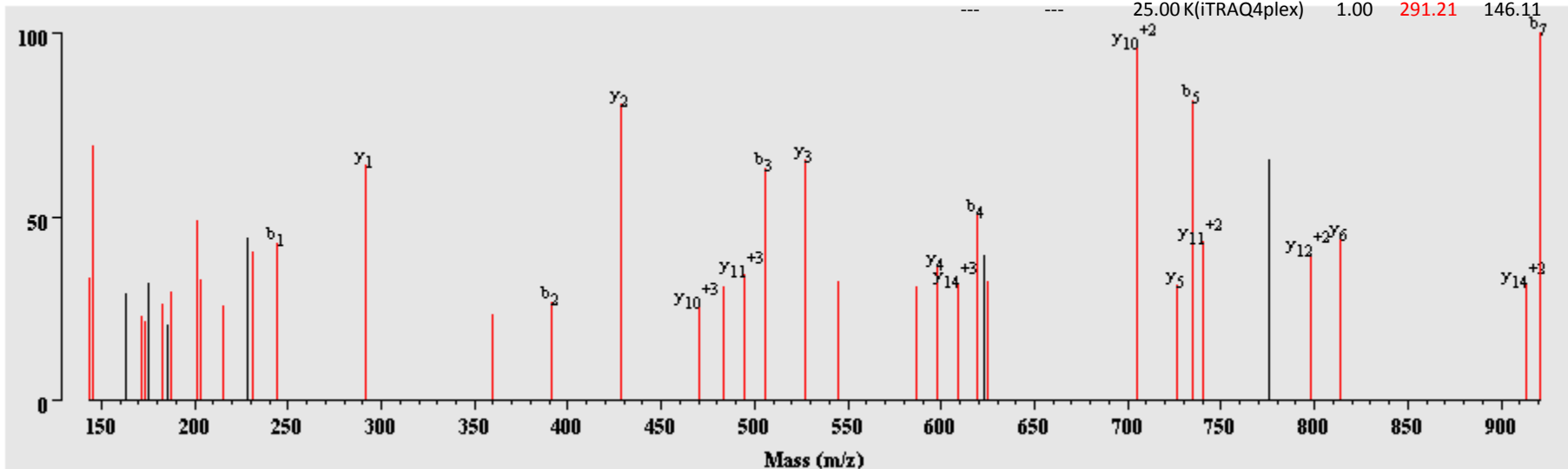
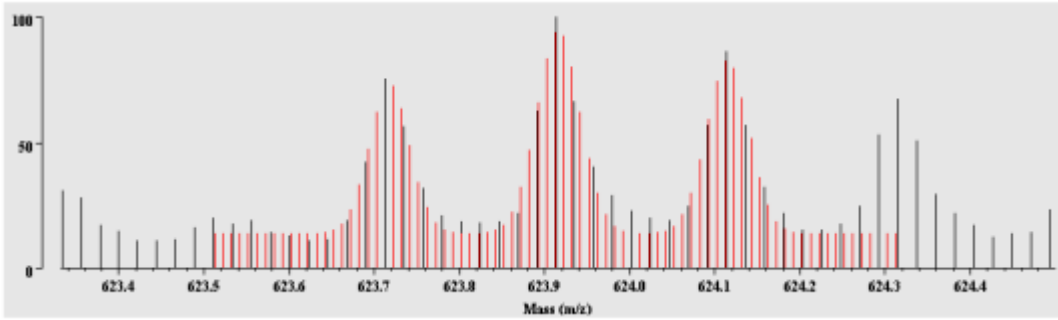


b	b+2	iTRAQ4plex	y	y+2
232.1414	---	1 S	15	---
289.1628	---	2 G	14	1497.923 749.4653
561.3599	281.1836	3 K(iTRAQ4plex)	13	1440.902 720.9546
648.3919	324.6996	4 S	12	1168.705 584.8561
745.4446	373.226	5 P	11	1081.673 541.34
858.5287	429.768	6 I	10	984.62 492.8137
971.6128	486.31	7 L	9	871.536 436.2716
1070.681	535.8442	8 V	8	758.4519 379.7296
1141.718	571.3628	9 A	7	659.3835 330.1954
1242.766	621.8866	10 T	6	588.3464 294.6768
1313.803	657.4052	11 A	5	487.2987 244.153
1412.872	706.9394	12 V	4	416.2616 208.6344
1483.909	742.458	13 A	3	317.1932 159.1002
1554.946	777.9765	14 A	2	246.1561 123.5817
---	---	15 R	1	175.119 88.0631

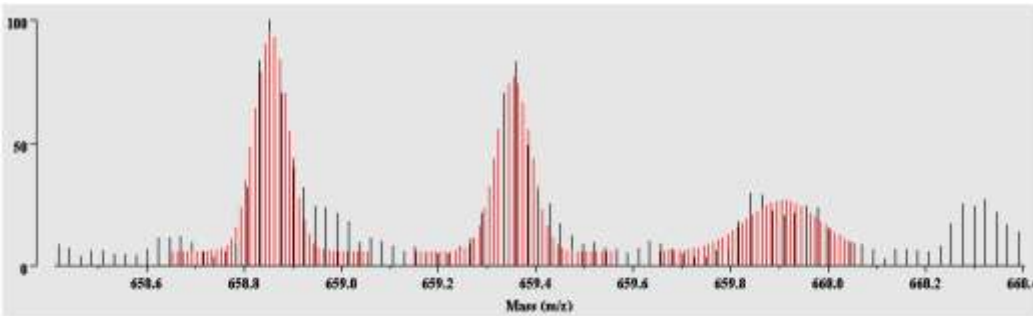


VFNNDADLSGITEDAPLK(iTRAQ4)LSQAVHK(iTRAQ4)⁺⁵/ (624.0453⁺⁵/3116.1966)/P17475

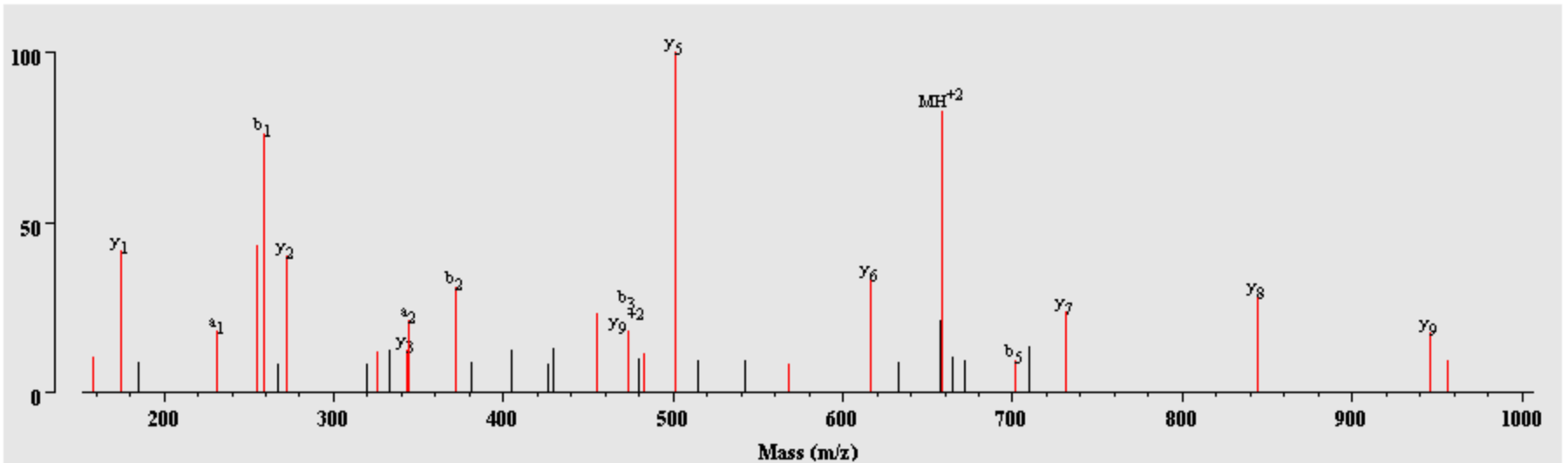
b	b+2	iTRAQ4plex	y	y+2
244.18	---	1.00 V	25.00	---
391.25	---	2.00 F	24.00	2871.51 1436.26
505.29	---	3.00 N	23.00	2724.44 1362.72
619.33	---	4.00 N	22.00	2610.40 1305.70
734.36	---	5.00 D	21.00	2496.35 1248.68
805.40	---	6.00 A	20.00	2381.33 1191.17
920.42	---	7.00 D	19.00	2310.29 1155.65
1033.51	---	8.00 L	18.00	2195.26 1098.14
1120.54	---	9.00 S	17.00	2082.18 1041.59
1177.56	---	10.00 G	16.00	1995.15 998.08
1290.64	---	11.00 I	15.00	1938.13 969.57
1391.69	---	12.00 T	14.00	1825.04 913.02
1520.73	---	13.00 E	13.00	1723.99 862.50
1635.76	---	14.00 D	12.00	1594.95 797.98
1706.80	---	15.00 A	11.00	1479.92 740.47
1803.85	---	16.00 P	10.00	1408.89 704.95
1916.94	---	17.00 L	9.00	1311.84 656.42
2189.13	1095.07	18.00 K(iTRAQ4plex)	8.00	1198.75 599.88
2302.22	1151.61	19.00 L	7.00	926.55 463.78
2389.25	1195.13	20.00 S	6.00	813.47 407.24
2517.31	1259.16	21.00 Q	5.00	726.44 363.72
2588.34	1294.68	22.00 A	4.00	598.38 299.69
2687.41	1344.21	23.00 V	3.00	527.34 264.17
2824.47	1412.74	24.00 H	2.00	428.27 214.64
---	---	25.00 K(iTRAQ4plex)	1.00	291.21 146.11



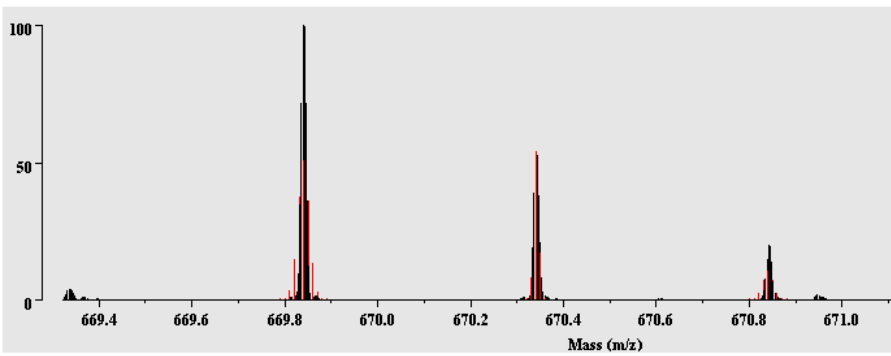
NITLDDASAPR⁺²/(659.2197⁺²/1317.432)/P18395



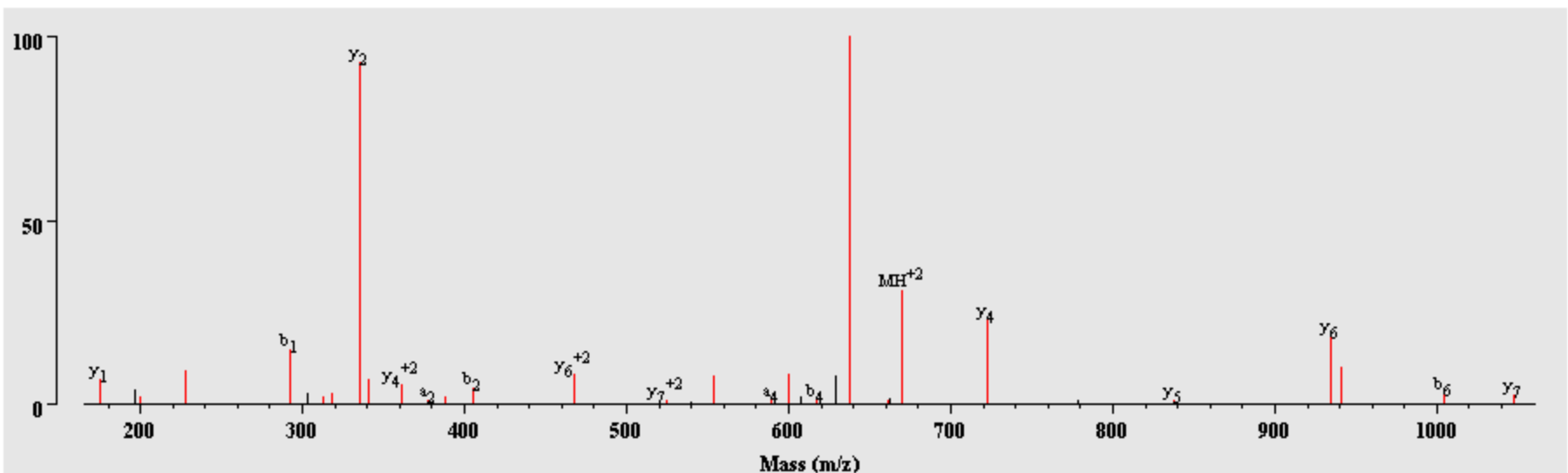
b	iTRAQ4plex	y	y+2
259.1523	1N	11---	---
372.2363	2I	10	1058.548 529.7775
473.284	3T	9	945.4636 473.2354
586.3681	4L	8	844.4159 422.7116
701.395	5D	7	731.3319 366.1696
816.422	6D	6	616.3049 308.6561
887.4591	7A	5	501.278 251.1426
974.4911	8S	4	430.2409 215.6241
1045.528	9A	3	343.2088 172.1081
1142.581	10P	2	272.1717 136.5895
---	11R	1	175.119 88.0631



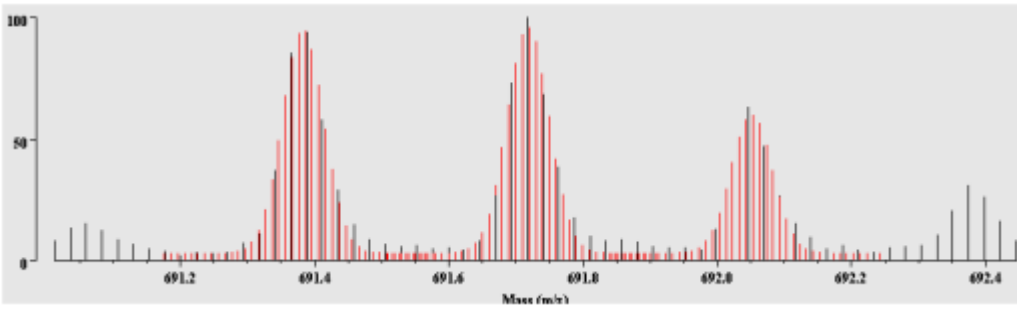
M(Ox)LPDK(iTRAQ4)DC(Carbamidomethyl)R⁺²/ (670.0473⁺²/1339.0871)/P18760



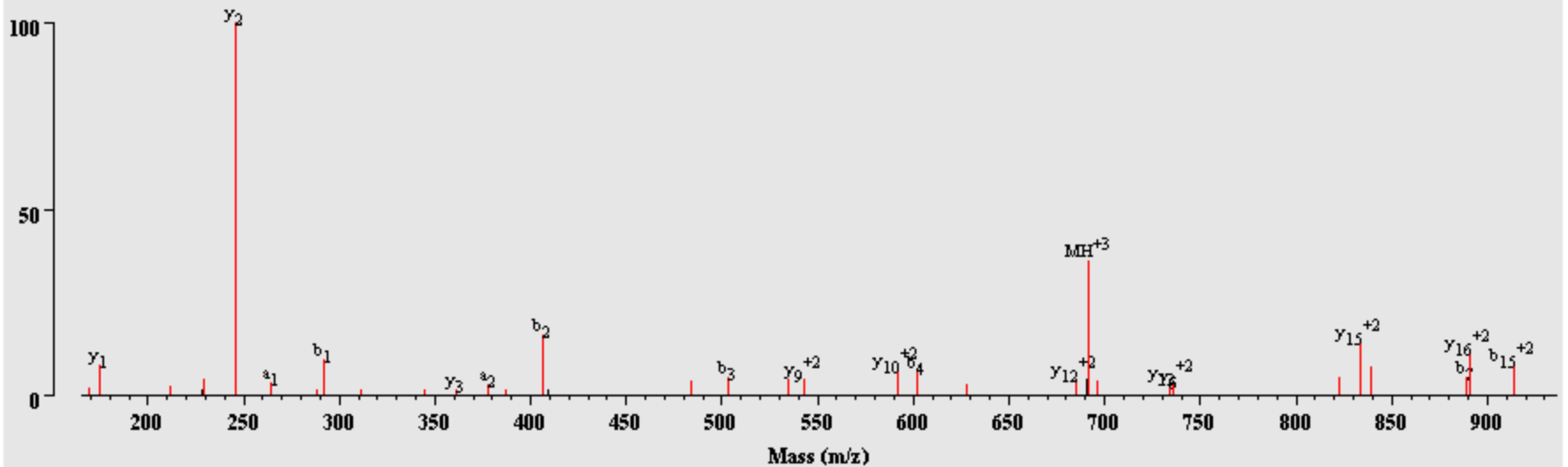
b	b+2	iTRAQ4plex	y	y+2
292.1447	---	1 M(Oxidation)	8	---
405.2288	---	2 L	7	1047.537 524.2723
502.2816	---	3 P	6	934.4533 467.7303
617.3085	---	4 D	5	837.4005 419.2039
889.5055	445.2564	5 K(iTRAQ4plex)	4	722.3736 361.6904
1004.533	502.7699	6 D	3	450.1765 225.5919
		C(Carbamidome		
1164.563	582.7852	7 thyl)	2	335.1496 168.0784
---	---	8 R	1	175.119 88.0631



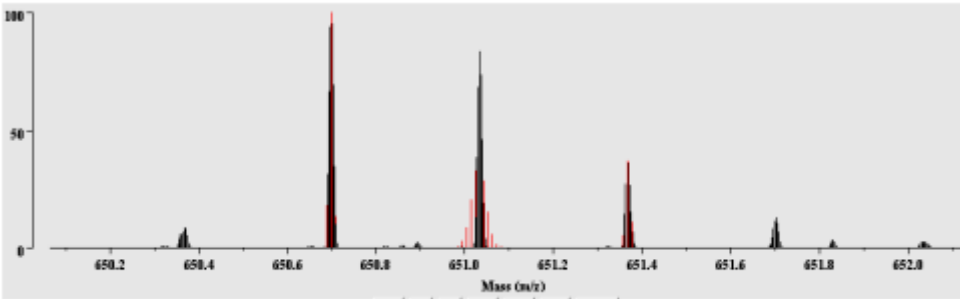
FNPVTGEVPPRYPLDAR⁺³/(691.7902⁺³/2073.3557)/P20059



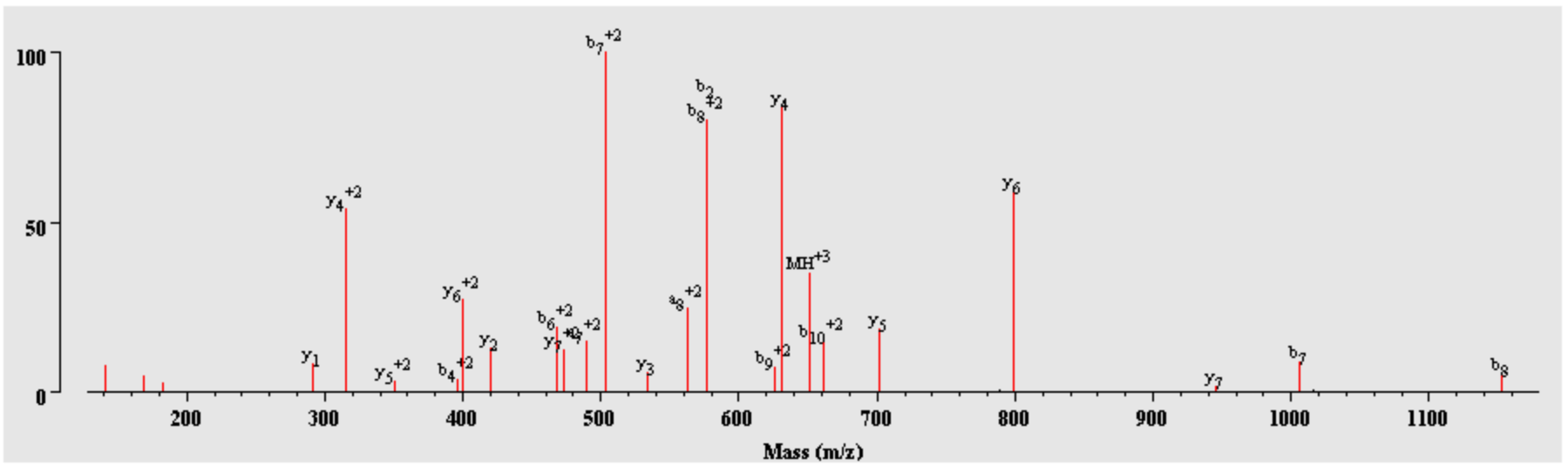
b	b+2	iTRAQ4plex	y	y+2
292.1778	---	1 F	17	---
406.2207	---	2 N	16	1780.934 890.9707
503.2734	---	3 P	15	1666.891 833.9492
602.3419	---	4 V	14	1569.838 785.4228
703.3895	---	5 T	13	1470.77 735.8886
760.411	---	6 G	12	1369.722 685.3648
889.4536	---	7 E	11	1312.701 656.854
988.522	---	8 V	10	1183.658 592.3327
1085.575	---	9 P	9	1084.59 542.7985
1182.628	---	10 P	8	987.537 494.2722
1338.729	669.868	11 R	7	890.4843 445.7458
1501.792	751.3996	12 Y	6	734.3832 367.6952
1598.845	799.926	13 P	5	571.3198 286.1636
1711.929	856.468	14 L	4	474.2671 237.6372
1826.956	913.9815	15 D	3	361.183 181.0951
1897.993	949.5001	16 A	2	246.1561 123.5817
---	---	17 R	1	175.119 88.0631



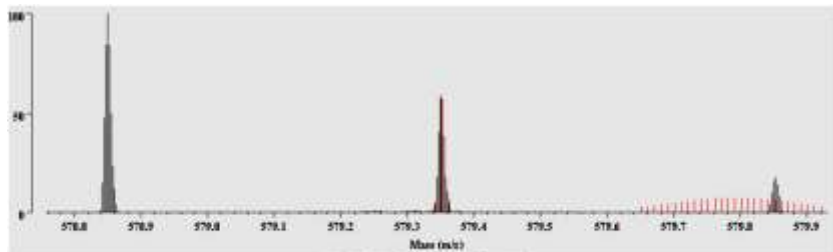
C(Carbamidomethyl)K(iTRAQ4)VNSGAFPAPIEK(iTRAQ4)⁺³ /(650.9452⁺³/1950.8207)/P20760



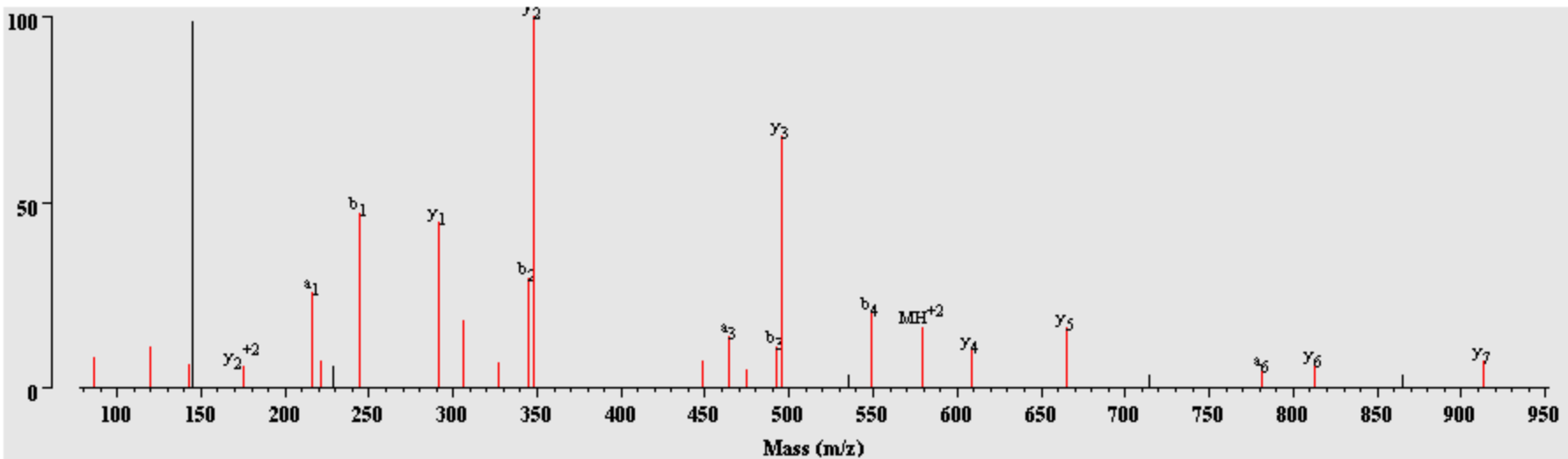
b	b+2	iTRAQ4plex C(Carbamidome thyl)	y	y+2
305.14	---	1	14	---
577.337	289.1721	2	13	1645.952 823.4794
676.4054	338.7064	3	12	1373.755 687.3809
790.4484	395.7278	4	11	1274.686 637.8467
877.4804	439.2438	5	10	1160.643 580.8252
934.5018	467.7546	6	9	1073.611 537.3092
1005.539	503.2731	7	8	1016.59 508.7985
1152.607	576.8073	8	7	945.5526 473.2799
1249.66	625.3337	9	6	798.4842 399.7457
1320.697	660.8523	10	5	701.4314 351.2193
1417.75	709.3786	11	4	630.3943 315.7008
1530.834	765.9207	12	3	533.3415 267.1744
1659.877	830.442	13	2	420.2575 210.6324
---	---	14	1	291.2149 146.1111



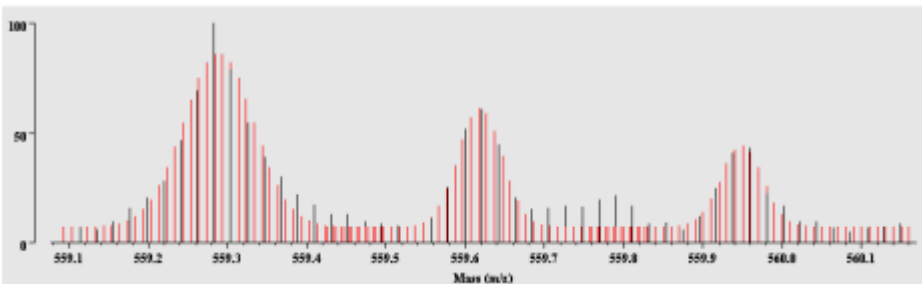
VTFGLFGK(iTRAQ4)⁺²/(579.1217⁺²/1157.236)/P24368



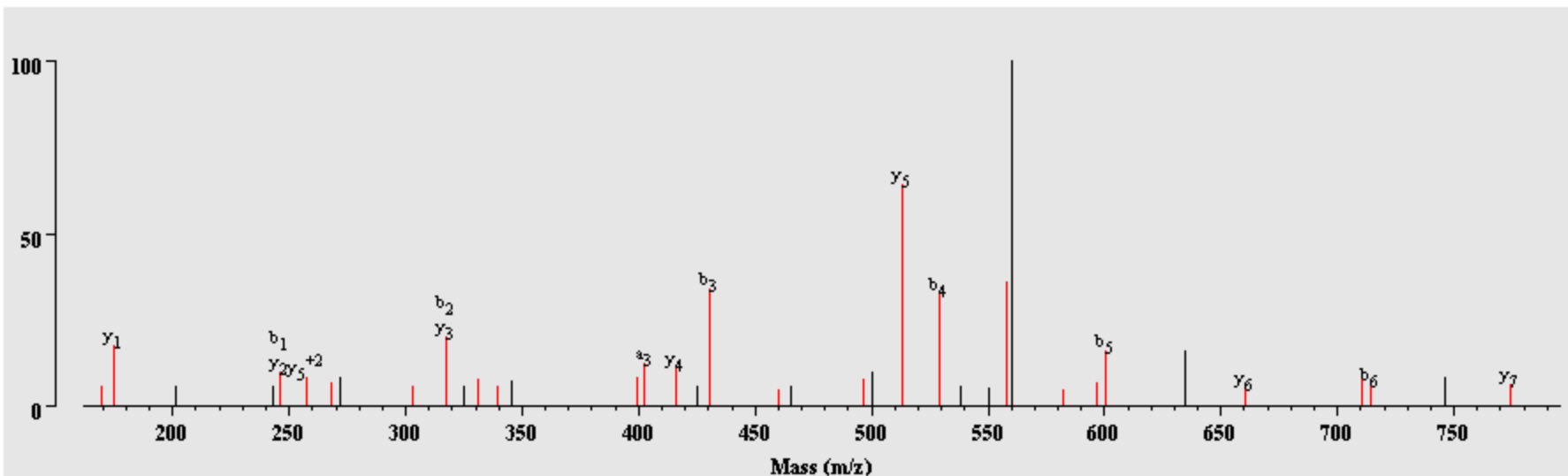
b	iTRAQ4plex	y	y+2
244.1778	1 V	8---	---
345.2254	2 T	7 913.5264	457.2668
492.2938	3 F	6 812.4787	406.743
549.3153	4 G	5 665.4103	333.2088
662.3994	5 L	4 608.3888	304.698
809.4678	6 F	3 495.3047	248.156
866.4893	7 G	2 348.2363	174.6218
---	8 K(iTRAQ4plex)	1 291.2149	146.1111



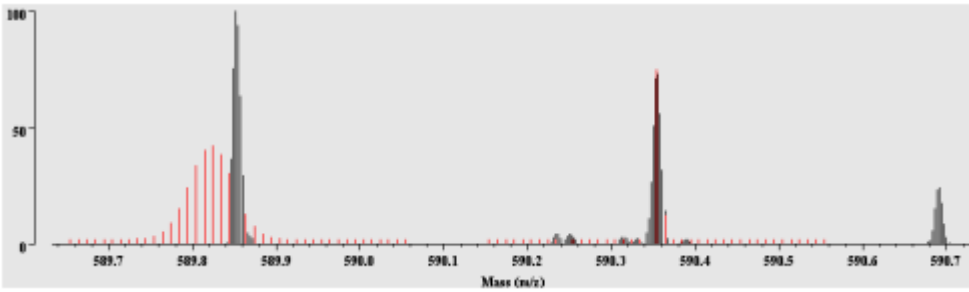
TALVANTSNM(Ox)PVAAR⁺³/(559.593⁺³/1676.7642)/P50516



b	iTRAQ4plex	y	y+2
246.157	1 T	15 ---	---
317.1941	2 A	14 1430.742	715.8747
430.2782	3 L	13 1359.705	680.3561
529.3466	4 V	12 1246.621	623.8141
600.3837	5 A	11 1147.552	574.2799
714.4267	6 N	10 1076.515	538.7613
815.4743	7 T	9 962.4724	481.7398
902.5064	8 S	8 861.4247	431.216
1016.549	9 N	7 774.3927	387.7
1163.585	10 M(Oxidation)	6 660.3498	330.6785
1260.637	11 P	5 513.3144	257.1608
1359.706	12 V	4 416.2616	208.6344
1430.743	13 A	3 317.1932	159.1002
1501.78	14 A	2 246.1561	123.5817
---	15 R	1 175.119	88.0631

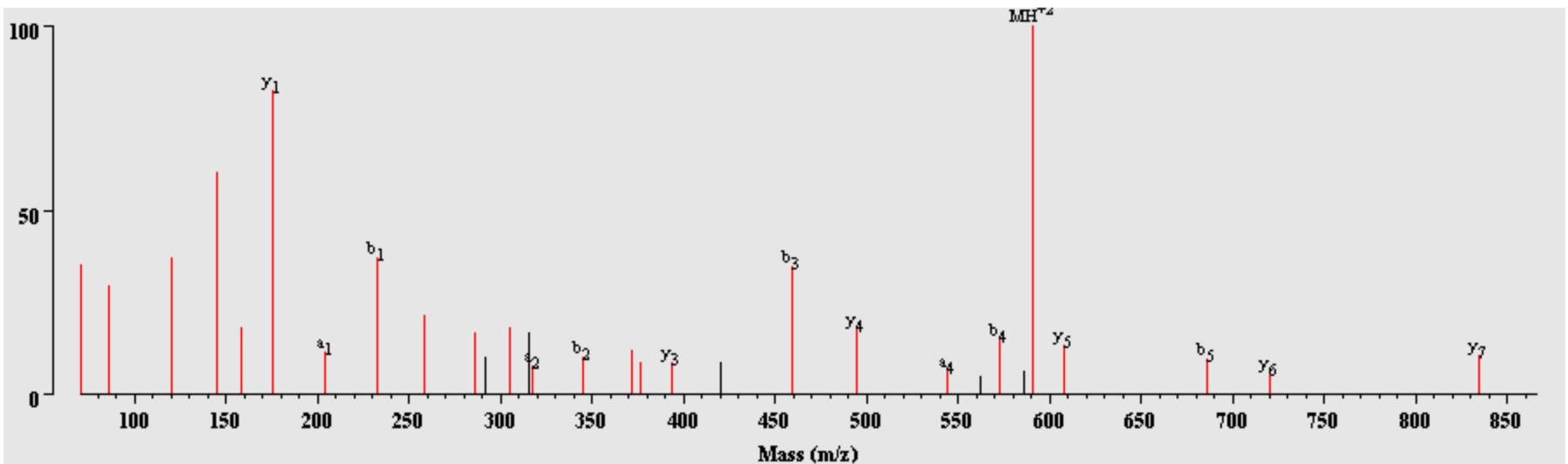


SLNILTAFR⁺²/(589.2013⁺²/1179.3952/P52555)

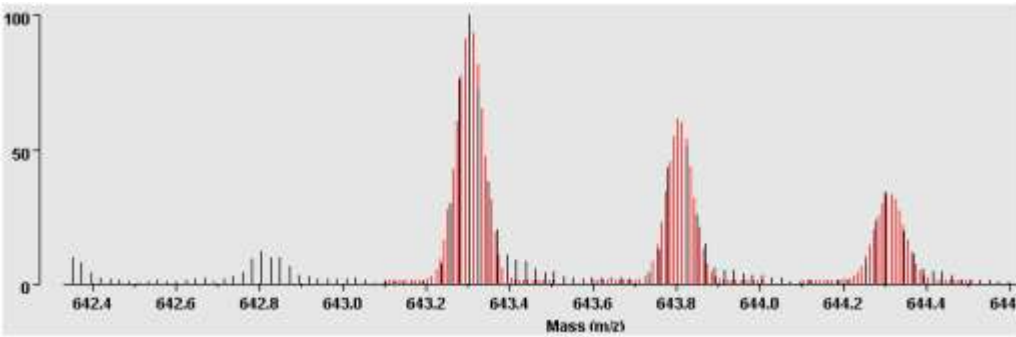


b

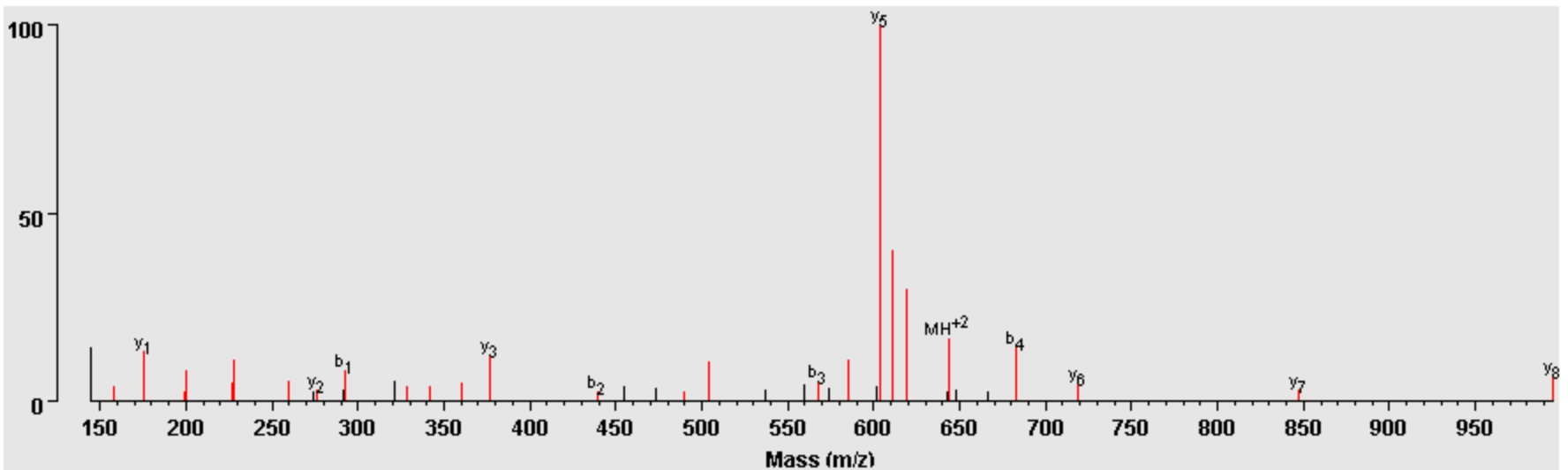
	iTRAQ4plex	y	y+2
232.1414	1S	9---	---
345.2254	2L	8 947.5673	474.2873
459.2684	3N	7 834.4832	417.7452
572.3524	4I	6 720.4403	360.7238
685.4365	5L	5 607.3562	304.1817
786.4842	6T	4 494.2722	247.6397
857.5213	7A	3 393.2245	197.1159
1004.59	8F	2 322.1874	161.5973
---	9R	1 175.119	88.0631



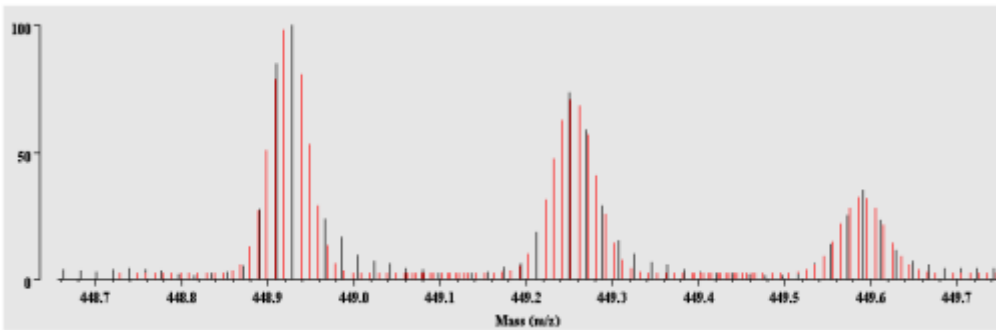
M(Ox)FEDPETTR⁺²/(643.6195⁺²/1286.2315)/P60229



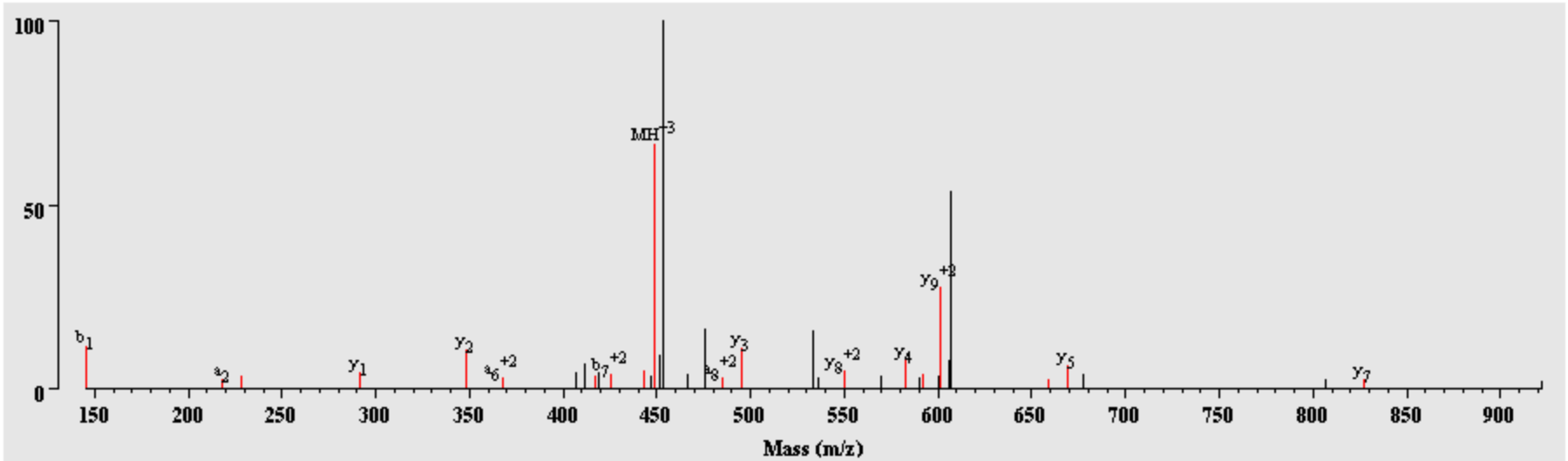
b	iTRAQ4plex M(Oxidati	y	y+2
292.1447	1 on)	9---	---
439.2132	2 F	8 994.4476	497.7274
568.2557	3 E	7 847.3792	424.1932
683.2827	4 D	6 718.3366	359.6719
780.3355	5 P	5 603.3097	302.1585
909.378	6 E	4 506.2569	253.6321
1010.426	7 T	3 377.2143	189.1108
1111.473	8 T	2 276.1666	138.587
---	9 R	1 175.119	88.0631



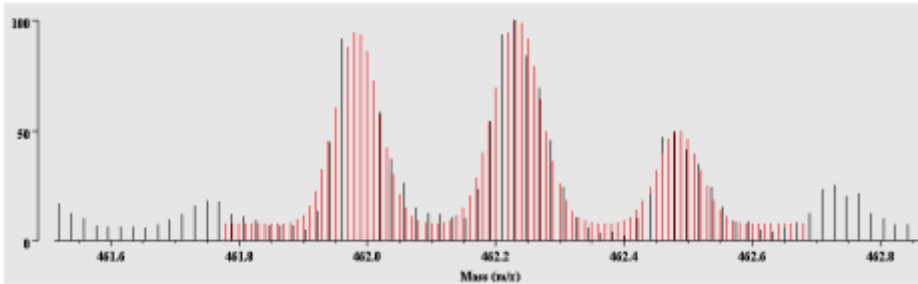
M(Met-loss)TK(iTRAQ4)GTSSFGK(iTRAQ4)⁺³/ (449.0797⁺³/1345.2243)/P61928



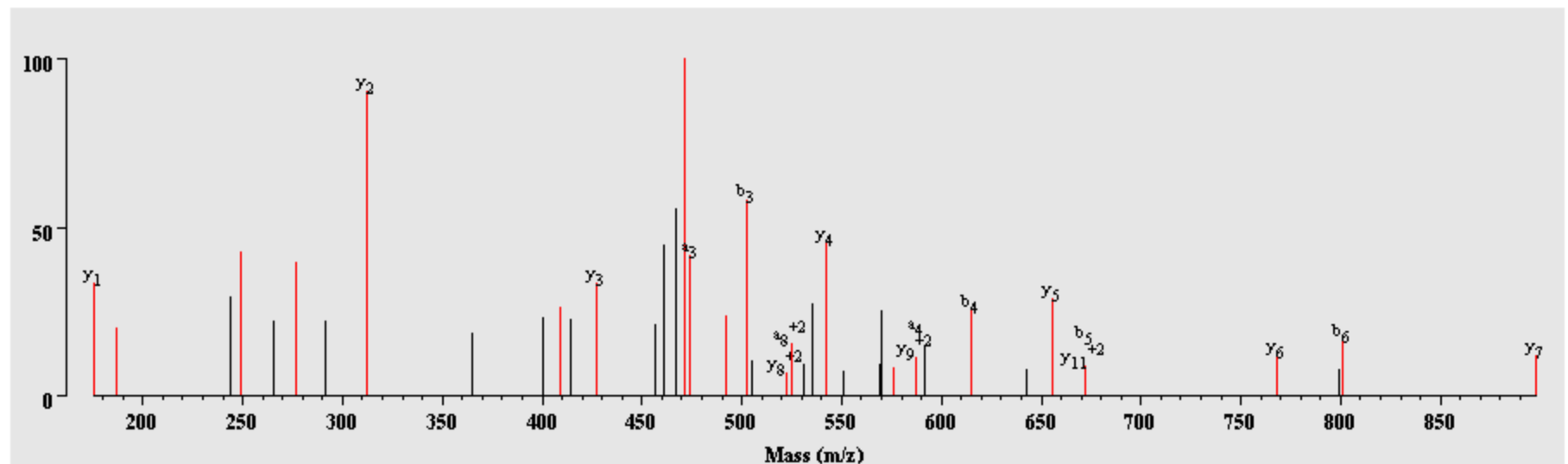
b	b+2	iTRAQ4plex	y	y+2
145.1093	---	1 M(Met-loss)	10	---
246.157	---	2 T	9	1200.683 600.845
518.354	259.6807	3 K(iTRAQ4plex)	8	1099.635 550.3211
575.3755	288.1914	4 G	7	827.4379 414.2226
676.4232	338.7152	5 T	6	770.4165 385.7119
763.4552	382.2312	6 S	5	669.3688 335.188
850.4872	425.7473	7 S	4	582.3368 291.672
997.5557	499.2815	8 F	3	495.3047 248.156
1054.577	527.7922	9 G	2	348.2363 174.6218
---	---	10 K(iTRAQ4plex)	1	291.2149 146.1111



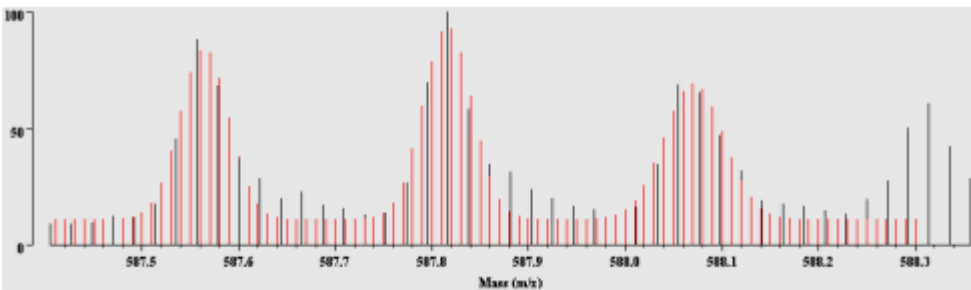
HGYIGEFEIIDDHR⁺⁴/(462.2564⁺⁴/1846.0035)/P62245



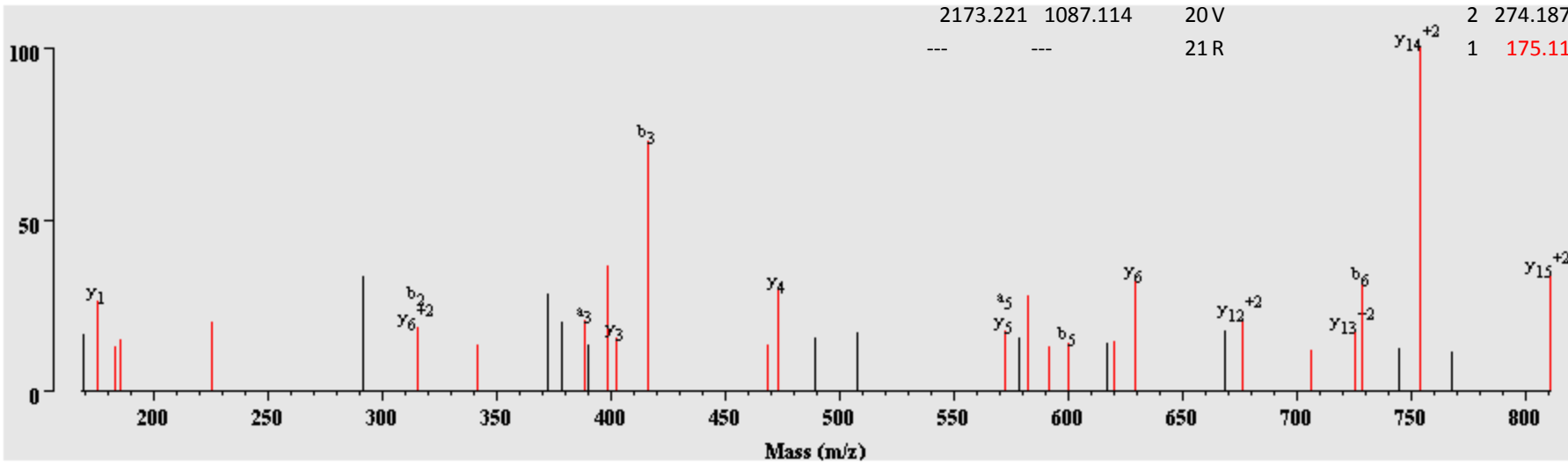
b	b+2	iTRAQ4plex	y	y+2
282.1683	141.5878	1 H	14 ---	---
339.1897	170.0985	2 G	13 1563.744	782.3755
502.253	251.6302	3 Y	12 1506.722	753.8648
615.3371	308.1722	4 I	11 1343.659	672.3331
672.3586	336.6829	5 G	10 1230.575	615.7911
801.4012	401.2042	6 E	9 1173.554	587.2804
948.4696	474.7384	7 F	8 1044.511	522.7591
1077.512	539.2597	8 E	7 897.4425	449.2249
1190.596	595.8018	9 I	6 768.3999	384.7036
1303.68	652.3438	10 I	5 655.3158	328.1615
1418.707	709.8573	11 D	4 542.2318	271.6195
1533.734	767.3707	12 D	3 427.2048	214.106
1670.793	835.9002	13 H	2 312.1779	156.5926
---	---	14 R	1 175.119	88.0631



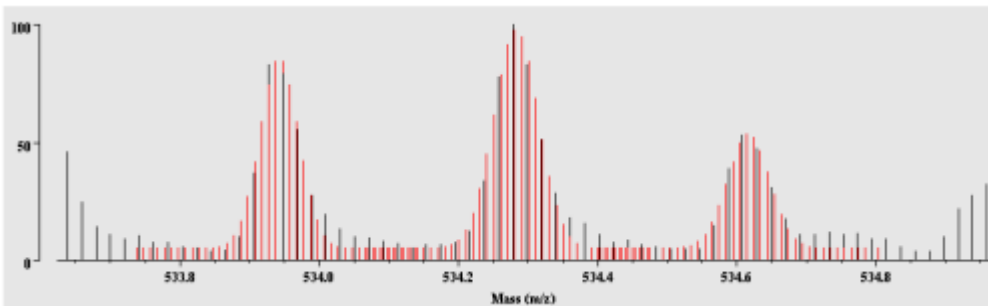
GLTPSQIGVILRDSHGVAQVR+4/(587.9329+4/2348.7094/P62278)



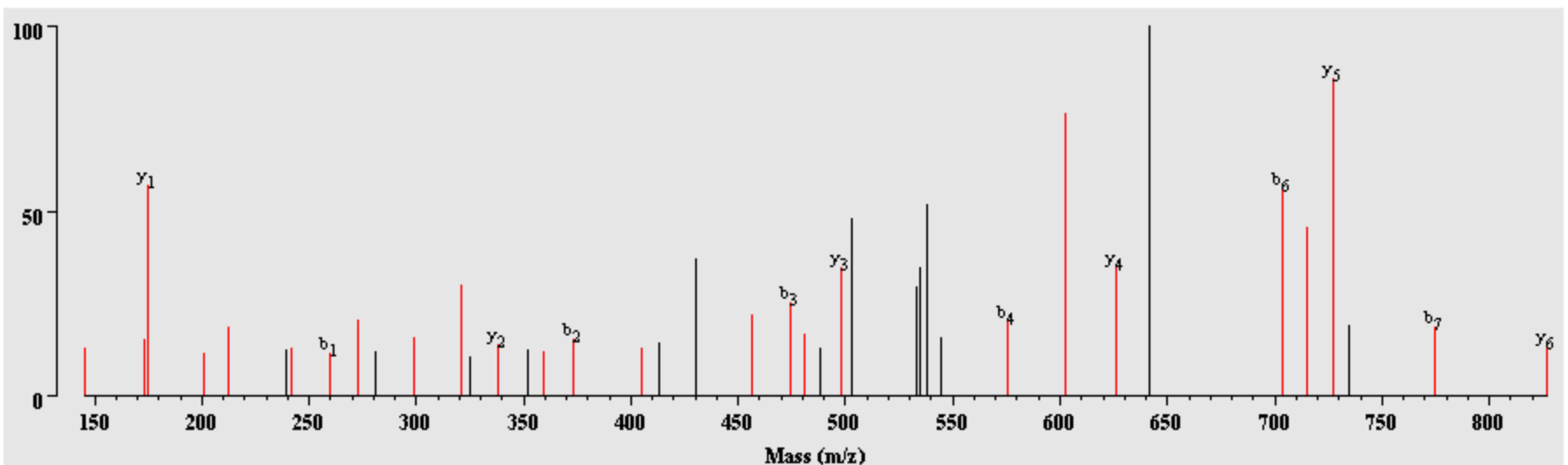
b	b+2	iTRAQ4plex	y	y+2
202.1308---		1 G	21---	---
315.2149---		2 L	20	2146.209 1073.608
416.2625---		3 T	19	2033.125 1017.066
513.3153---		4 P	18	1932.077 966.5423
600.3473---		5 S	17	1835.025 918.0159
728.4059---		6 Q	16	1747.993 874.4999
841.49---		7 I	15	1619.934 810.4706
898.5114---		8 G	14	1506.85 753.9286
997.5799---		9 V	13	1449.829 725.4179
1110.664---		10 I	12	1350.76 675.8837
1223.748---		11 L	11	1237.676 619.3416
1379.849	690.4282	12 R	10	1124.592 562.7996
1494.876	747.9417	13 D	9	968.4908 484.749
1581.908	791.4577	14 S	8	853.4639 427.2356
1718.967	859.9871	15 H	7	766.4318 383.7196
1775.988	888.4979	16 G	6	629.3729 315.1901
1875.057	938.0321	17 V	5	572.3515 286.6794
1946.094	973.5506	18 A	4	473.2831 237.1452
2074.153	1037.58	19 Q	3	402.2459 201.6266
2173.221	1087.114	20 V	2	274.1874 137.5973
---	---	21 R	1	175.119 88.0631



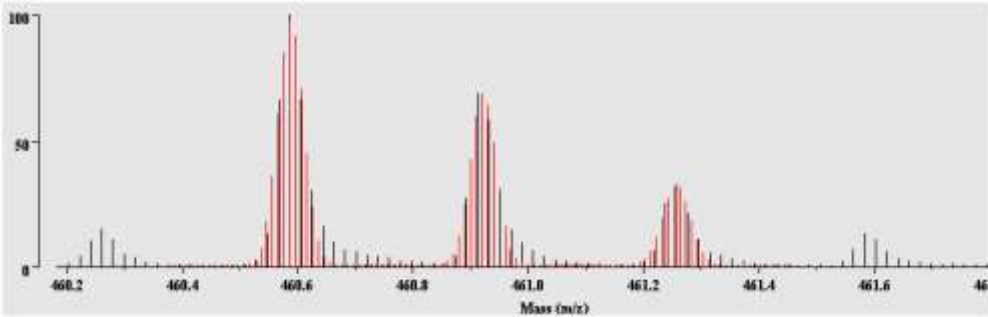
DLTTAGAVTQC(Carbamidomethyl)YR⁺³/ (534.211⁺³/1600.6183)/P62717



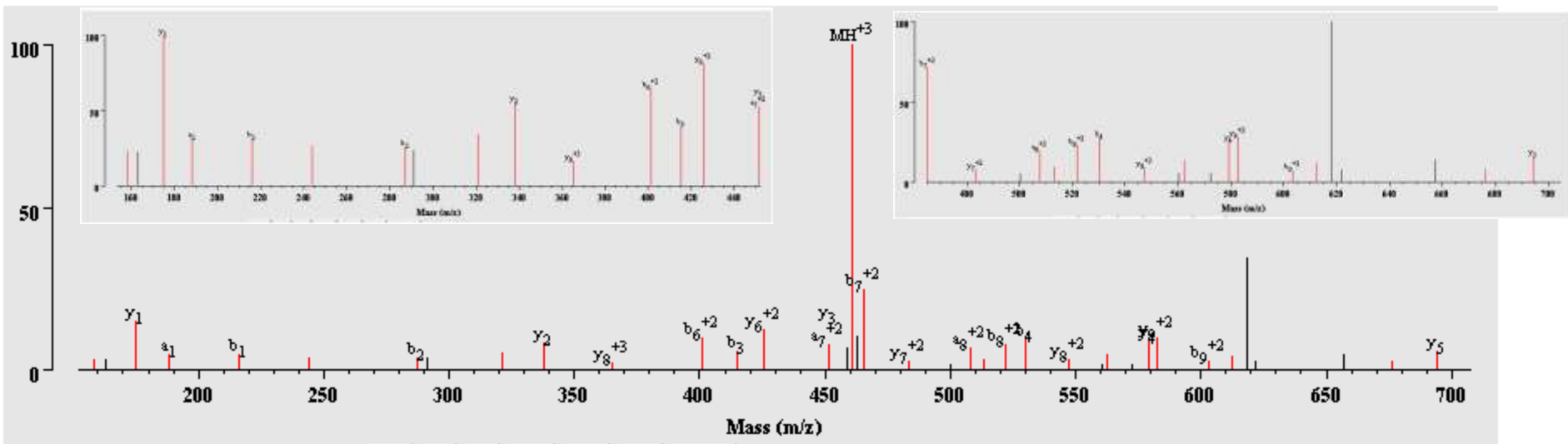
b	iTRAQ4plex	y	y+2
260.1363	1D	13 ---	---
373.2203	2L	12 1340.663	670.835
474.268	3T	11 1227.579	614.293
575.3157	4T	10 1126.531	563.7691
646.3528	5A	9 1025.483	513.2453
703.3743	6G	8 954.4462	477.7267
774.4114	7A	7 897.4247	449.216
873.4798	8V	6 826.3876	413.6974
974.5275	9T	5 727.3192	364.1632
1102.586	10Q	4 626.2715	313.6394
	C(Carbamidome		
1262.617	11 thyl)	3 498.2129	249.6101
1425.68	12 Y	2 338.1823	169.5948
---	13 R	1 175.119	88.0631



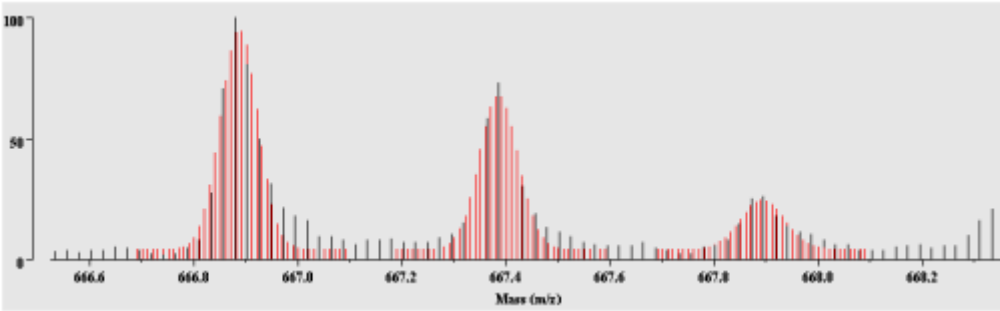
AAQDRDQIYR⁺³/(460.8363⁺³/1380.4941)/P62996



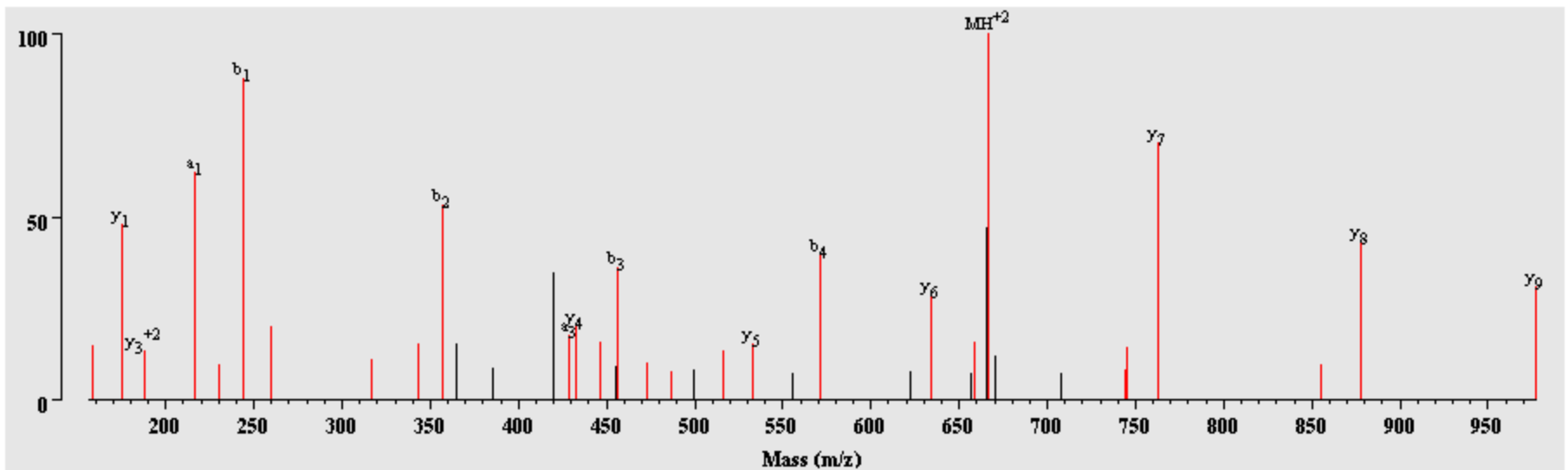
b	b+2	iTRAQ4plex	y	y+2
216.1465	---	1A	10	---
287.1836	---	2A	9	1164.576 582.7914
415.2421	---	3Q	8	1093.539 547.2729
530.2691	---	4D	7	965.4799 483.2436
686.3702	343.6887	5R	6	850.453 425.7301
801.3971	401.2022	6D	5	694.3519 347.6796
929.4557	465.2315	7Q	4	579.3249 290.1661
1042.54	521.7735	8I	3	451.2663 226.1368
1205.603	603.3052	9Y	2	338.1823 169.5948
---	---	10R	1	175.119 88.0631



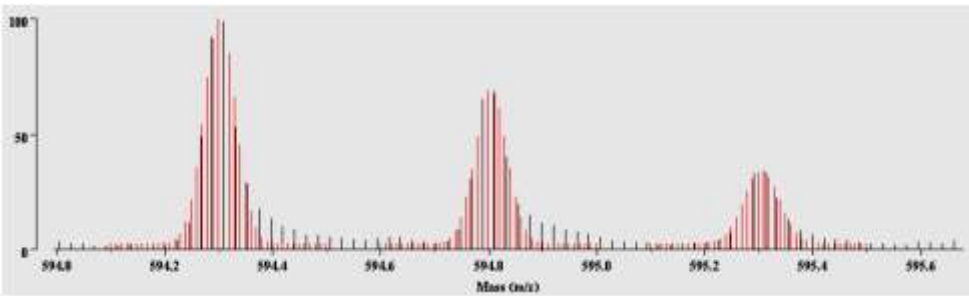
VLVDQTTGLSR⁺²/(667.263⁺²/1333.5186)/P70372



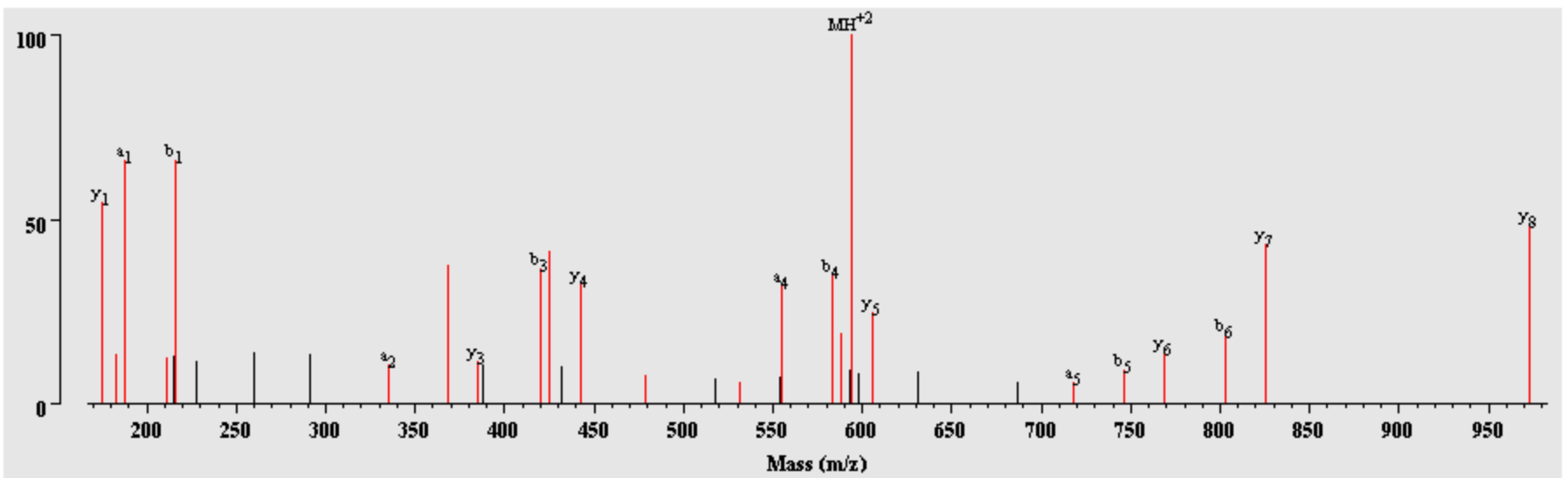
b	iTRAQ4plex	y	y+2
244.1778	1V	11---	---
357.2618	2L	10	1089.59 545.2986
456.3302	3V	9	976.5058 488.7565
571.3572	4D	8	877.4374 439.2223
699.4158	5Q	7	762.4104 381.7089
800.4634	6T	6	634.3519 317.6796
901.5111	7T	5	533.3042 267.1557
958.5326	8G	4	432.2565 216.6319
1071.617	9L	3	375.235 188.1212
1158.649	10S	2	262.151 131.5791
---	11R	1	175.119 88.0631



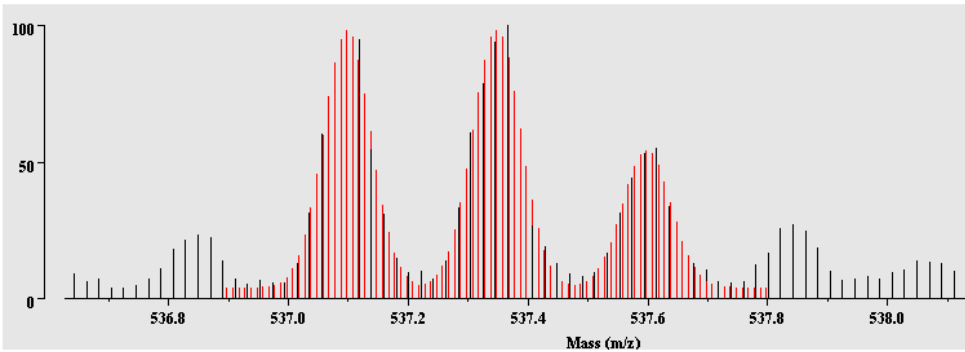
AFGYGPLR⁺²/(594.6846⁺²/1188.3618)/P84104



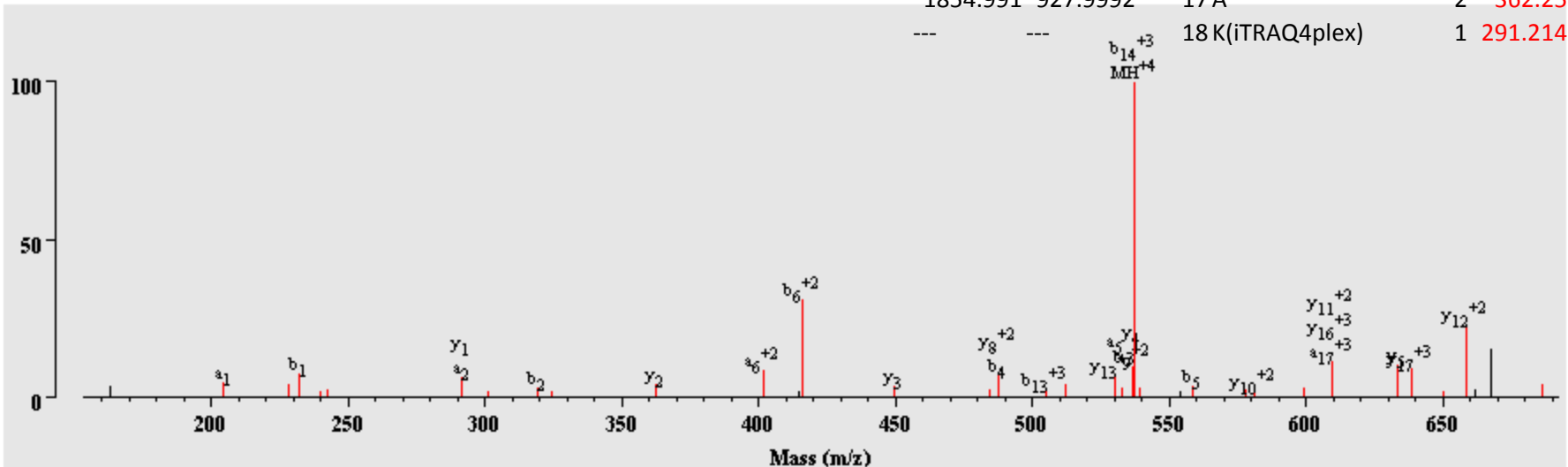
b	iTRAQ4plex	y	y+2
216.1465	1A	9---	---
363.2149	2F	8	972.4938 486.7505
420.2363	3G	7	825.4254 413.2163
583.2997	4Y	6	768.4039 384.7056
746.363	5Y	5	605.3406 303.1739
803.3845	6G	4	442.2772 221.6423
900.4372	7P	3	385.2558 193.1315
1013.521	8L	2	288.203 144.6051
---	9R	1	175.119 88.0631



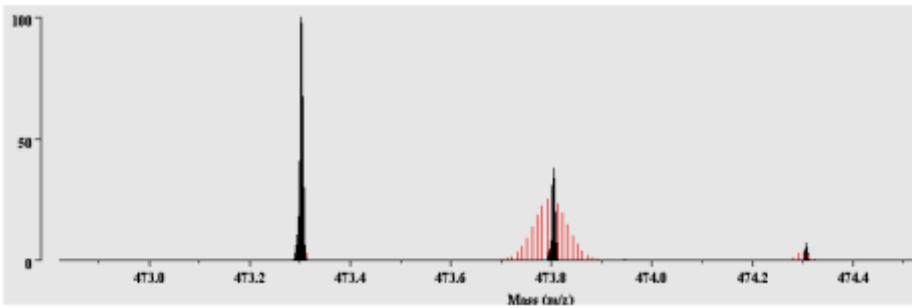
SSPAAK(iTRAQ4)PGSTPSRPSSAK(iTRAQ4)⁺⁴/(537.2805⁺⁴ /2146.0996)/Q3B8Q0



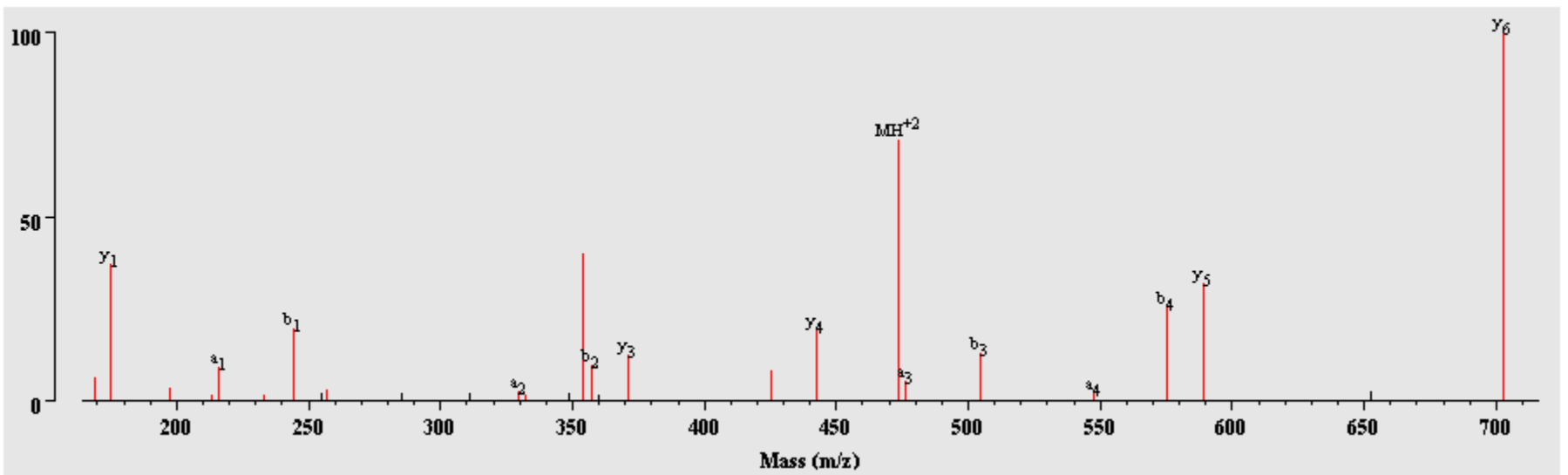
b	b+2	iTRAQ4plex	y	y+2
232.1414	---	1 S	18	---
319.1734	---	2 S	17	1914.065 957.536
416.2262	---	3 P	16	1827.033 914.02
487.2633	---	4 A	15	1729.98 865.4936
558.3004	---	5 A	14	1658.943 829.975
830.4974	415.7523	6 K(iTRAQ4plex)	13	1587.906 794.4565
927.5502	464.2787	7 P	12	1315.709 658.358
984.5716	492.7895	8 G	11	1218.656 609.8316
1071.604	536.3055	9 S	10	1161.634 581.3208
1172.651	586.8293	10 T	9	1074.602 537.8048
1269.704	635.3557	11 P	8	973.5547 487.281
1356.736	678.8717	12 S	7	876.5019 438.7546
1512.837	756.9223	13 R	6	789.4699 395.2386
1609.89	805.4486	14 P	5	633.3688 317.188
1696.922	848.9647	15 S	4	536.316 268.6617
1783.954	892.4807	16 S	3	449.284 225.1456
1854.991	927.9992	17 A	2	362.252 181.6296
---	---	18 K(iTRAQ4plex)	1	291.2149 146.1111



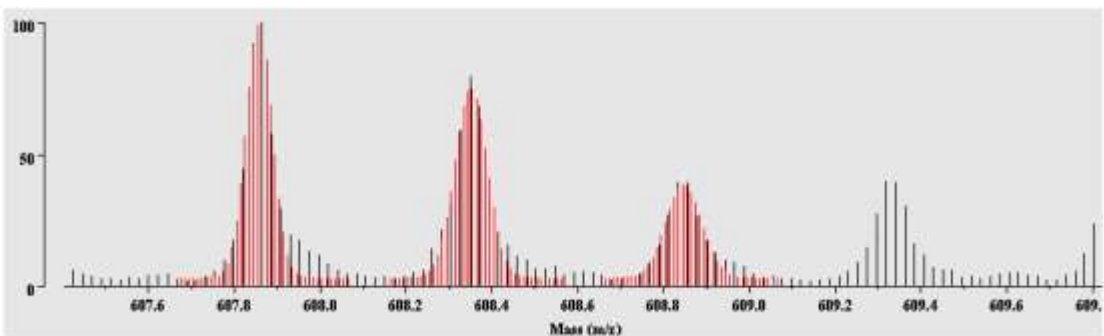
VLFAPVR⁺²/(473.5856⁺²/946.1697)/Q3THX5



b	iTRAQ4plex	y	y+2
244.1778	1 V	7 ---	---
357.2618	2 L	6 702.4297	351.7185
504.3302	3 F	5 589.3457	295.1765
575.3673	4 A	4 442.2772	221.6423
672.4201	5 P	3 371.2401	186.1237
771.4885	6 V	2 274.1874	137.5973
---	7 R	1 175.119	88.0631

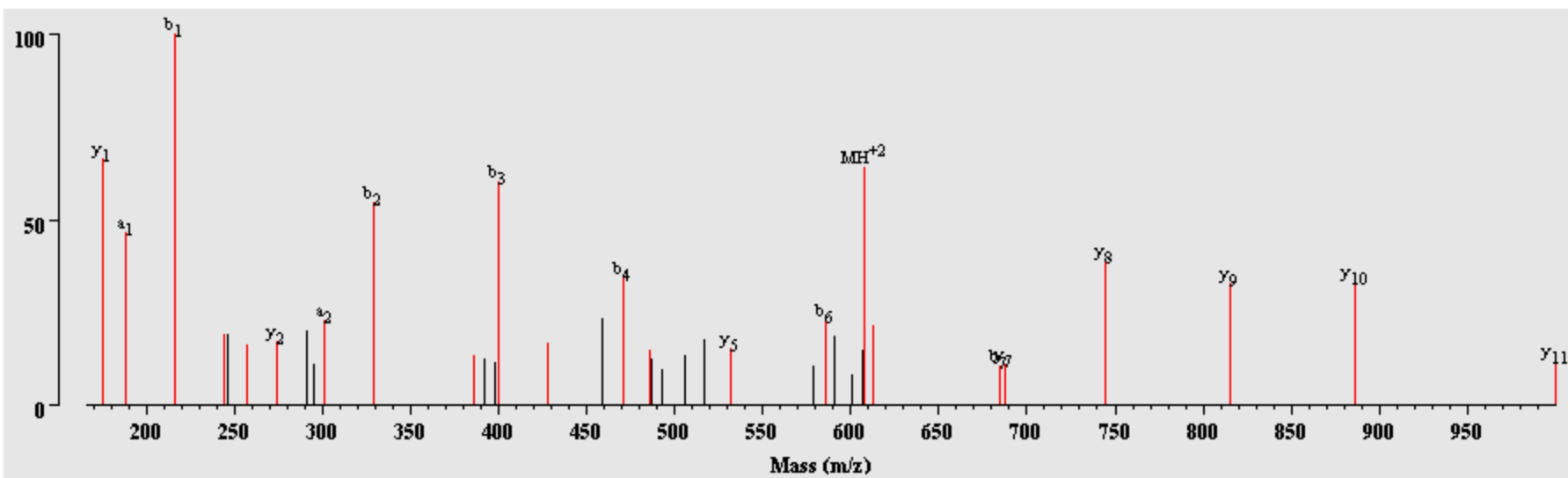


ALAAGGVGSIVR⁺²/(608.2181⁺²/1215.4289)/Q3TK56

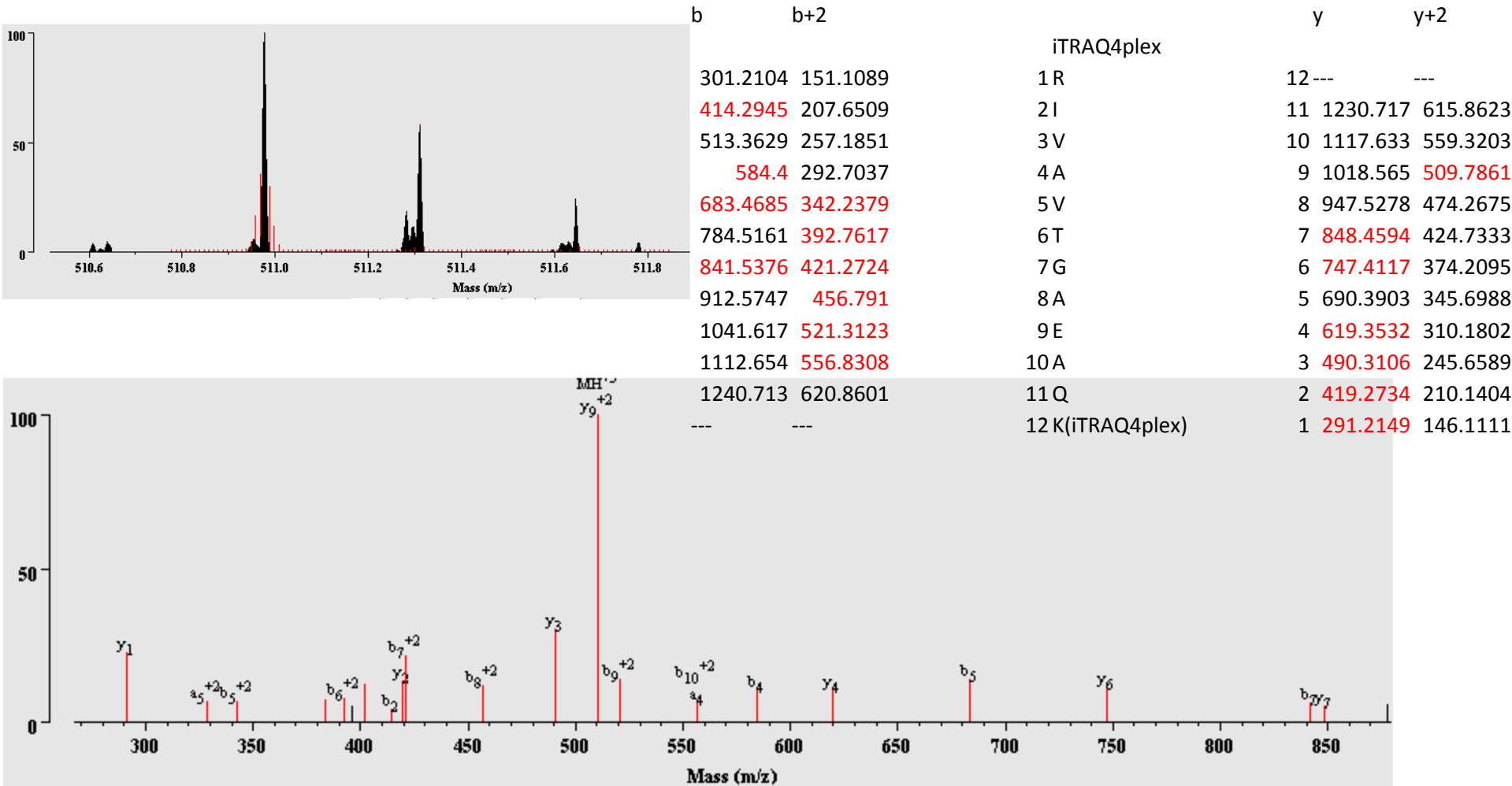


b

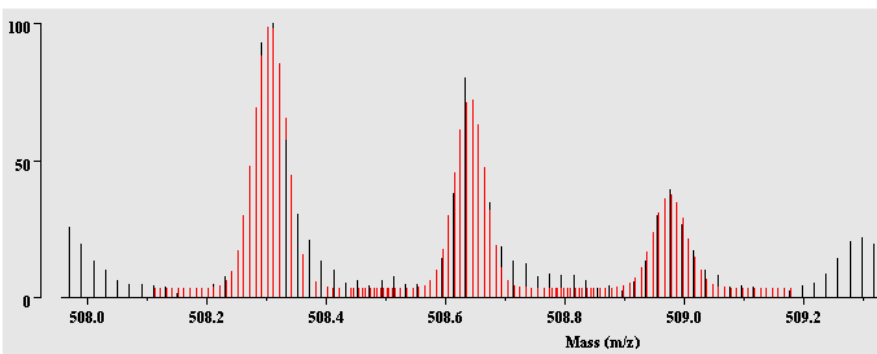
	iTRAQ4plex	y	y+2
216.1465	1A	12 ---	---
329.2305	2L	11 999.5946	500.3009
400.2676	3A	10 886.5105	443.7589
471.3047	4A	9 815.4734	408.2403
528.3262	5G	8 744.4363	372.7218
585.3477	6G	7 687.4148	344.211
684.4161	7V	6 630.3933	315.7003
741.4375	8G	5 531.3249	266.1661
828.4696	9S	4 474.3035	237.6554
941.5536	10I	3 387.2714	194.1394
1040.622	11V	2 274.1874	137.5973
---	12R	1 175.119	88.0631



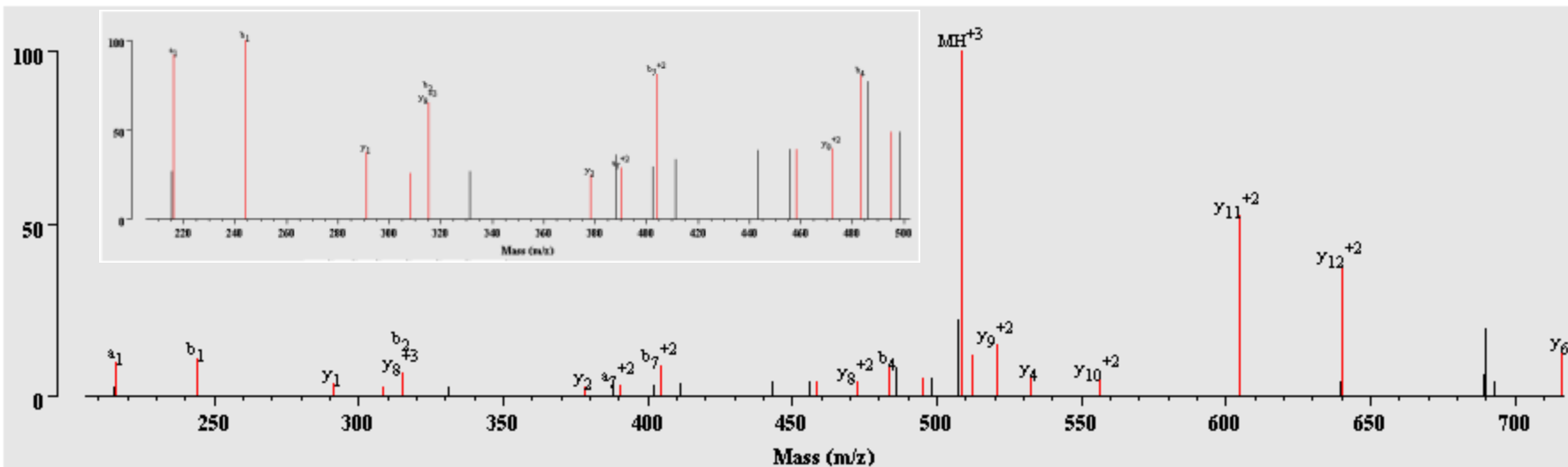
RIVAVTGAEAQK(iTRAQ4plex)⁺³/(511.2169⁺³/1531.6357)/ Q3TZ32



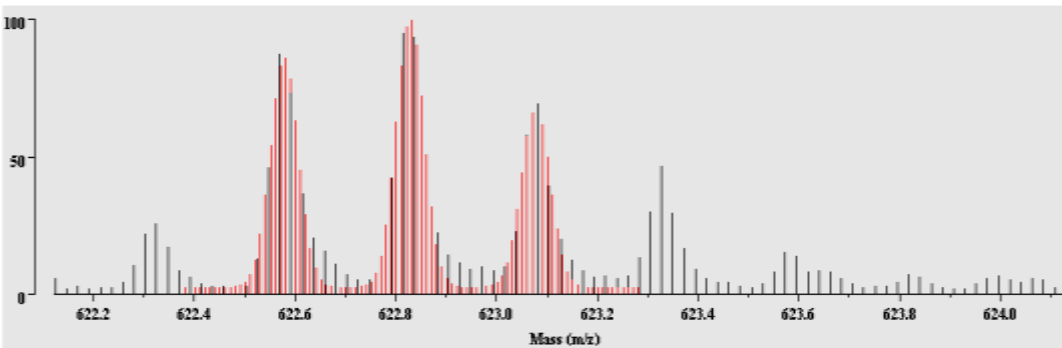
VAPAPARPSGPK(iTRAQ4)⁺³/(508.5435⁺³/1523.6156)/Q3U4S9



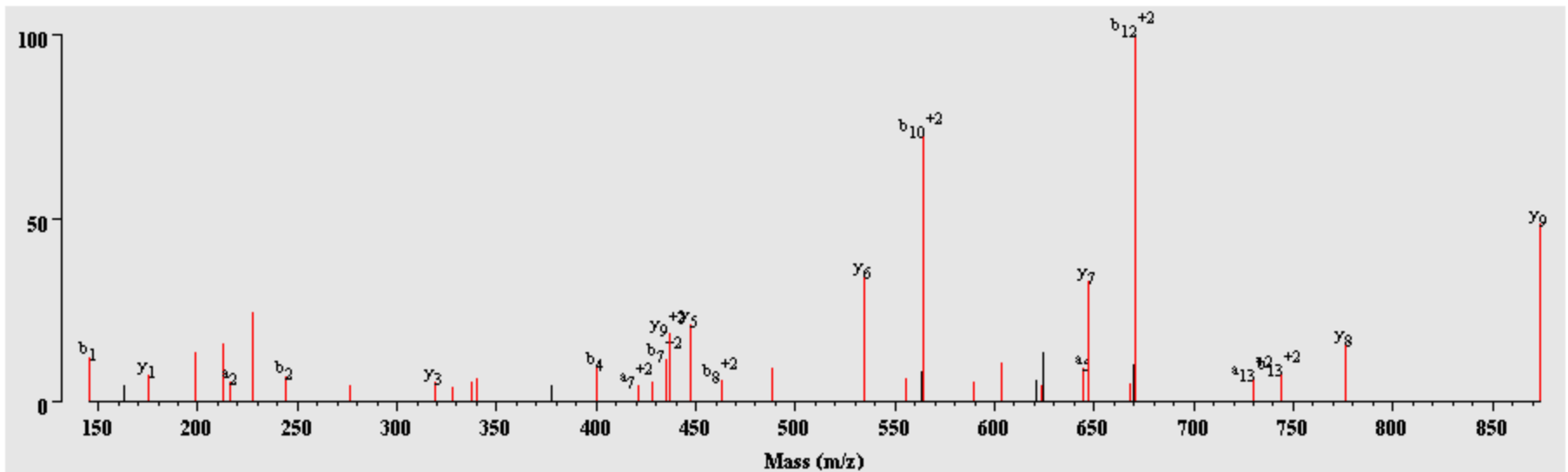
b	b+2	iTRAQ4plex	y	y+2
244.1778	---	1 V	13	---
315.2149	---	2 A	12	1279.724 640.3656
412.2676	---	3 P	11	1208.687 604.847
483.3047	---	4 A	10	1111.634 556.3206
580.3575	---	5 P	9	1040.597 520.8021
651.3946	---	6 A	8	943.5441 472.2757
807.4957	404.2515	7 R	7	872.507 436.7572
904.5485	452.7779	8 P	6	716.4059 358.7066
991.5805	496.2939	9 S	5	619.3532 310.1802
1048.602	524.8046	10 G	4	532.3211 266.6642
1145.655	573.331	11 P	3	475.2997 238.1535
1232.687	616.847	12 S	2	378.2469 189.6271
---	---	13 K(iTRAQ4plex)	1	291.2149 146.1111



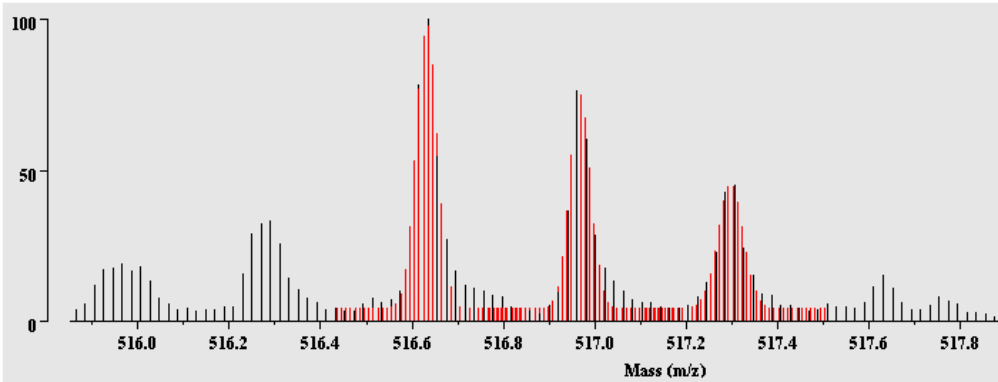
M(Met-loss)VGVK(iTRAQ4)PVGSDPDFQPELSGAGSR⁺⁴/ (829.207⁺⁴/2488.6061)/Q3U8R9



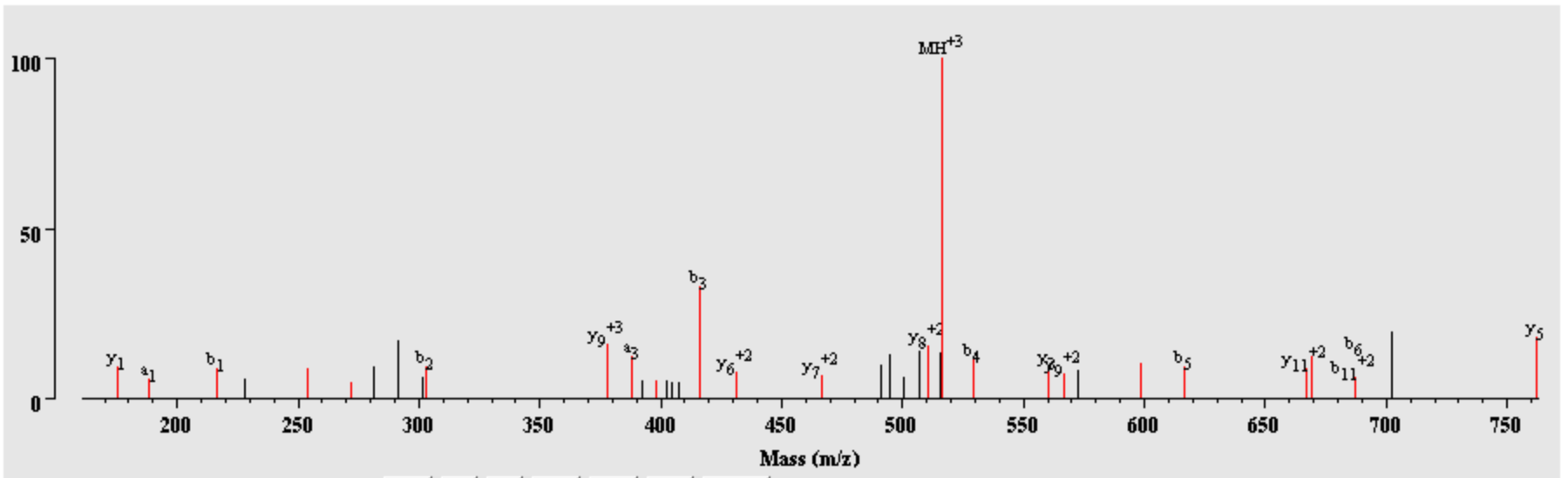
b	b+2	iTRAQ4plex	y	y+2
145.1093	---	1 M(Met-loss)	23	---
244.1778	---	2 V	22	2343.206 1172.107
301.1992	---	3 G	21	2244.138 1122.573
400.2676	---	4 V	20	2187.116 1094.062
672.4647	336.736	5 K(iTRAQ4plex)	19	2088.048 1044.528
769.5174	385.2623	6 P	18	1815.851 908.429
868.5858	434.7966	7 V	17	1718.798 859.9026
925.6073	463.3073	8 G	16	1619.73 810.3684
1012.639	506.8233	9 S	15	1562.708 781.8577
1127.666	564.3368	10 D	14	1475.676 738.3417
1224.719	612.8632	11 P	13	1360.649 680.8282
1339.746	670.3766	12 D	12	1263.596 632.3018
1486.814	743.9108	13 F	11	1148.57 574.7884
1614.873	807.9401	14 Q	10	1001.501 501.2542
1711.926	856.4665	15 P	9	873.4425 437.2249
1840.968	920.9878	16 E	8	776.3897 388.6985
1954.052	977.5298	17 L	7	647.3471 324.1772
2041.084	1021.046	18 S	6	534.2631 267.6352
2098.106	1049.557	19 G	5	447.231 224.1191
2169.143	1085.075	20 A	4	390.2096 195.6084
2226.165	1113.586	21 G	3	319.1724 160.0899
2313.197	1157.102	22 S	2	262.151 131.5791
---	---	23 R	1	175.119 88.0631



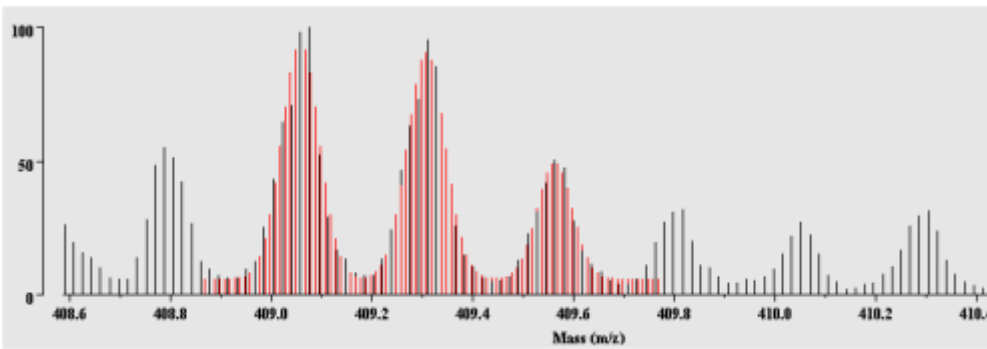
ASLISAVSDK(iTRAQ4)LR⁺³/(516.8928⁺³/1548.6634)/Q3UCW0



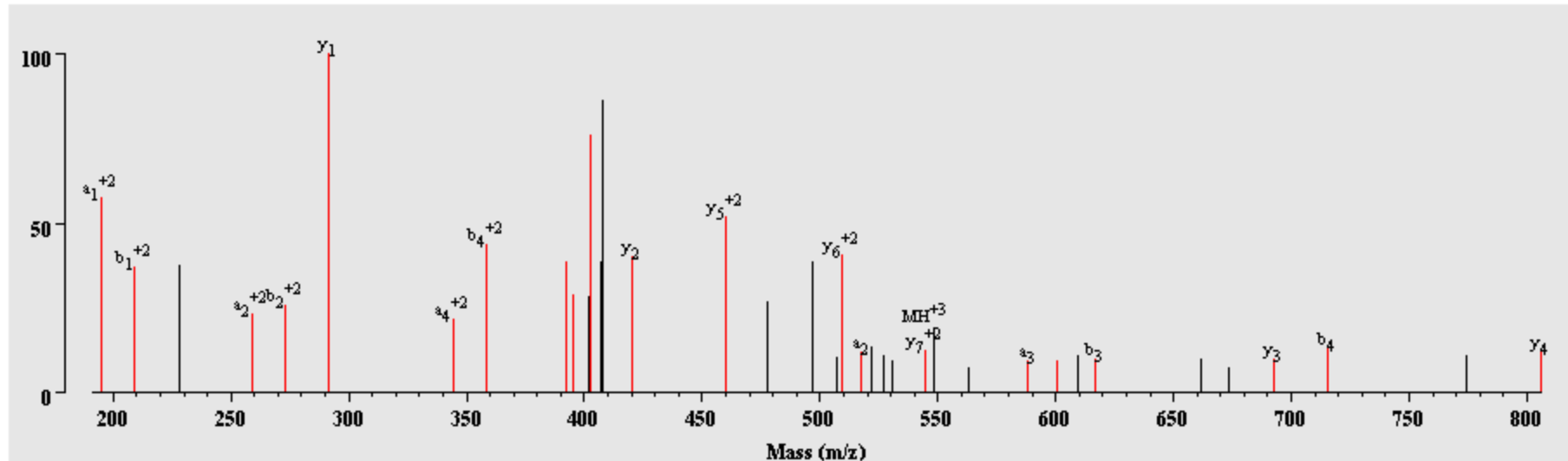
b	b+2	iTRAQ4plex	y	y+2
216.1465	---	1 A	12	---
303.1785	---	2 S	11	1332.797 666.902
416.2625	---	3 L	10	1245.765 623.386
529.3466	---	4 I	9	1132.681 566.844
616.3786	---	5 S	8	1019.597 510.3019
687.4158	---	6 A	7	932.5645 466.7859
786.4842	---	7 V	6	861.5274 431.2674
873.5162	---	8 S	5	762.459 381.7331
988.5431	---	9 D	4	675.427 338.2171
1260.74	630.8737	10 K(iTRAQ4plex)	3	560.4 280.7037
1373.824	687.4158	11 L	2	288.203 144.6051
---	---	12 R	1	175.119 88.063



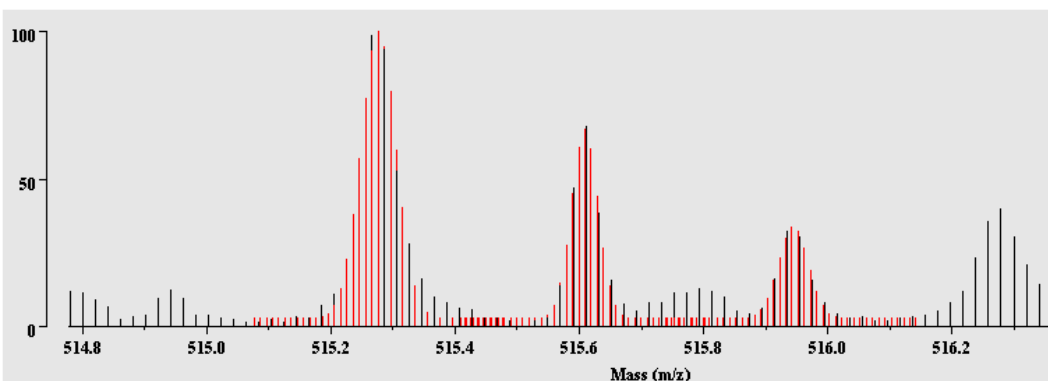
K(iTRAQ4)QAVLLK(iTRAQ4)EK(iTRAQ4)⁺⁴/ (409.1435⁺⁴/1633.5516)/Q5BKC4



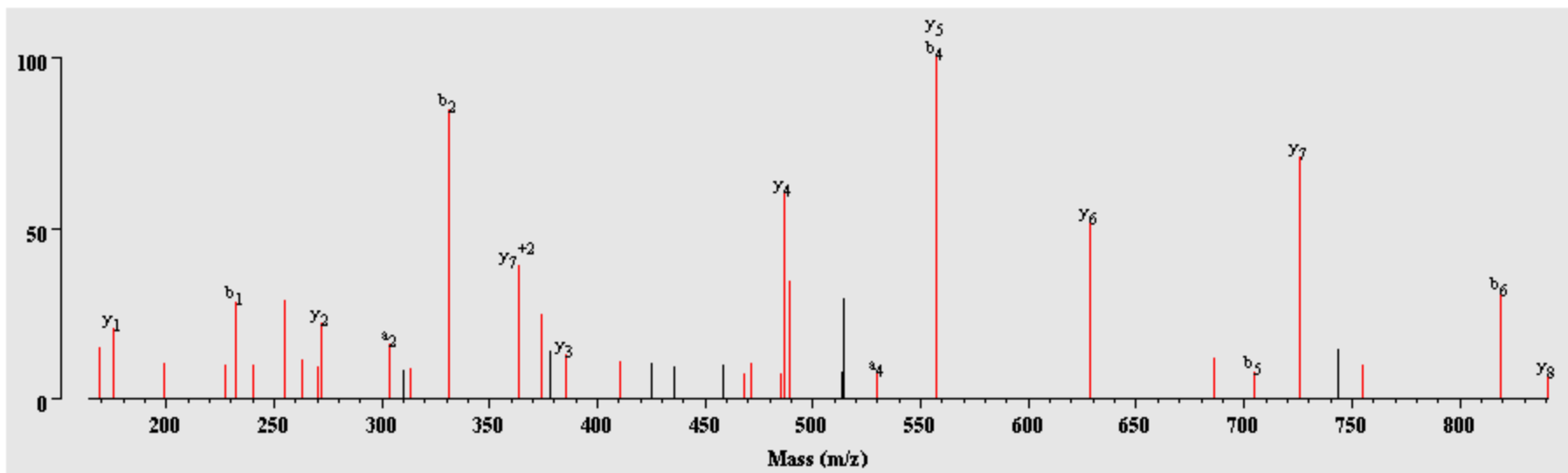
b	b+2	iTRAQ4plex	y	y+2
417.3064	209.1568	1 K(iTRAQ4plex)	9 ---	---
545.3649	273.1861	2 Q	8 1216.787	608.897
616.4021	308.7047	3 A	7 1088.728	544.8677
715.4705	358.2389	4 V	6 1017.691	509.3492
828.5545	414.7809	5 L	5 918.6226	459.8149
941.6386	471.3229	6 L	4 805.5385	403.2729
1213.836	607.4214	7 K(iTRAQ4plex)	3 692.4545	346.7309
1342.878	671.9427	8 E	2 420.2575	210.6324
---	---	9 K(iTRAQ4plex)	1 291.2149	146.1111



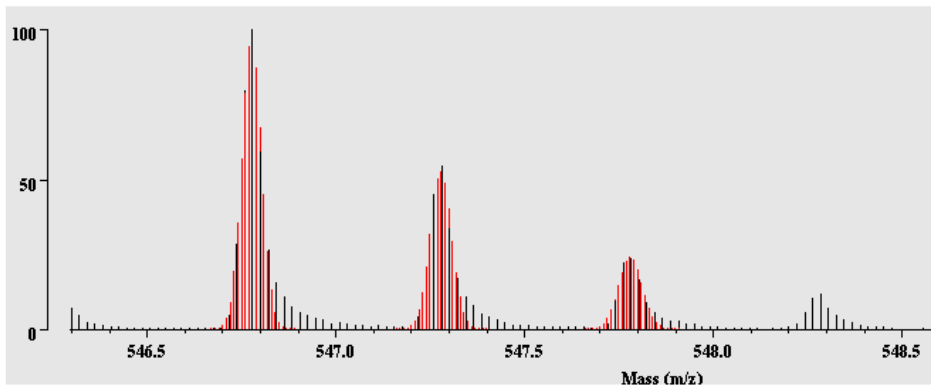
SVPEM(Ox)DPAATIPR⁺³/(515.5376⁺³/1544.5978)/Q5SRX1



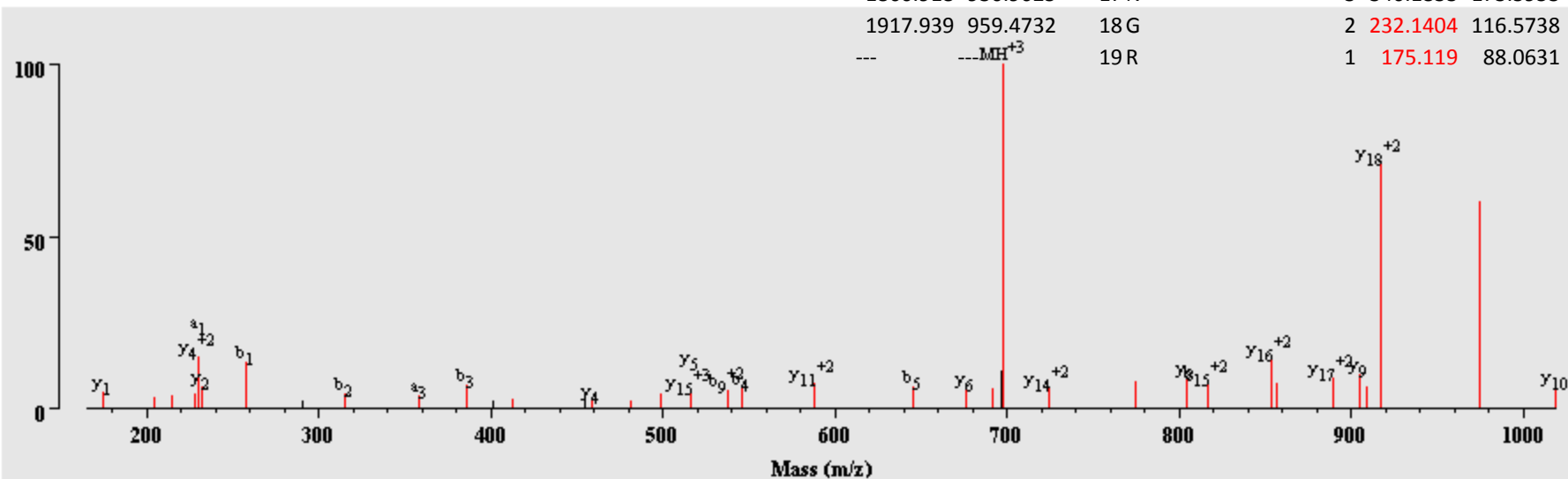
b	iTRAQ4plex	y	y+2
232.1414	1S	13---	---
331.2098	2V	12	1312.657 656.8319
428.2625	3P	11	1213.588 607.2977
557.3051	4E	10	1116.535 558.7713
704.3405	5M(Oxidation)	9	987.4928 494.25
819.3675	6D	8	840.4574 420.7323
916.4202	7P	7	725.4304 363.2189
987.4574	8A	6	628.3777 314.6925
1058.495	9A	5	557.3406 279.1739
1159.542	10T	4	486.3035 243.6554
1272.626	11I	3	385.2558 193.1315
1369.679	12P	2	272.1717 136.5895
---	13R	1	175.119 88.0631



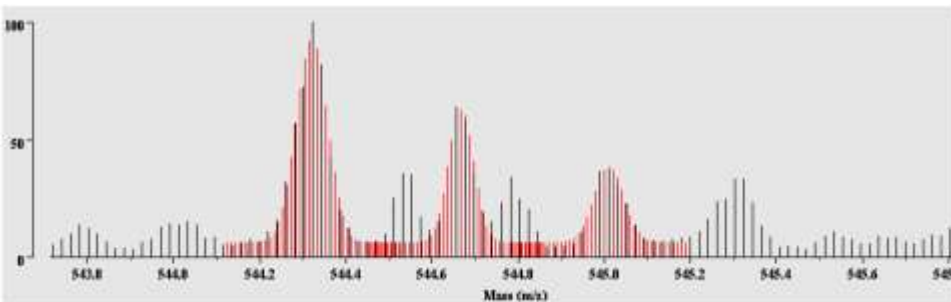
IGAC(Carbamidomethyl)VSGERLTGAC(Carbamidomethyl)GLNGR⁺³/ (698.3574⁺³/2093.0574)/Q62714



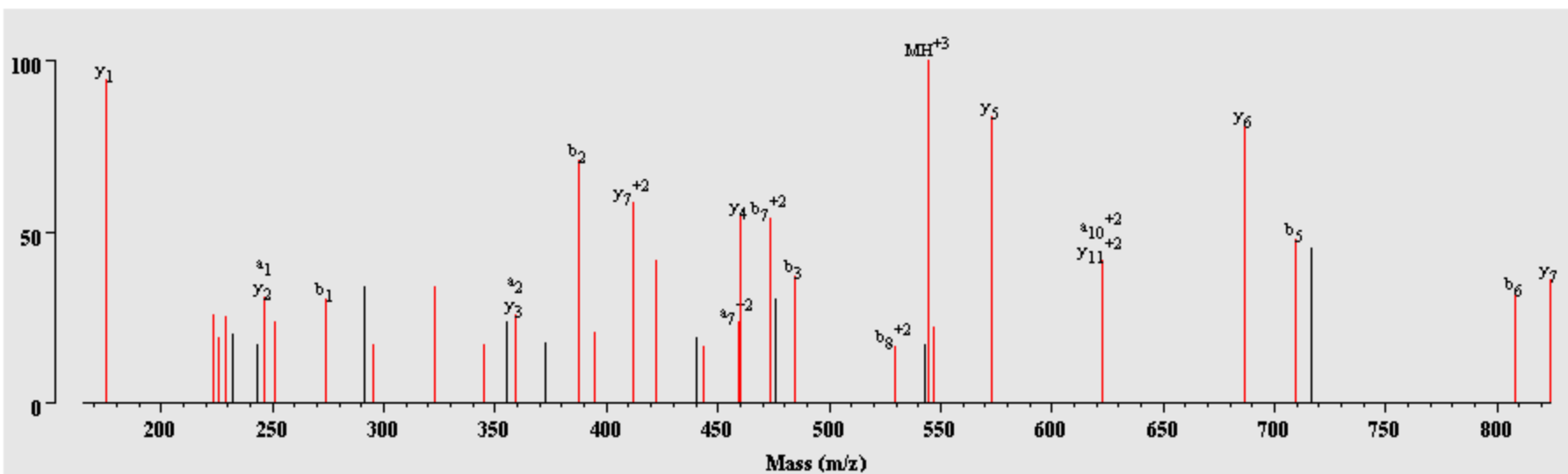
b	b+2	iTRAQ4plex	y	y+2
258.1934	---	1I	19	---
315.2149	---	2G	18	1834.865 917.936
386.252	---	3A	17	1777.843 889.4252
546.2826	---	C(Carbamidome 4 thyl)	16	1706.806 853.9067
645.351	---	5V	15	1546.775 773.8914
732.3831	---	6S	14	1447.707 724.3572
789.4045	---	7G	13	1360.675 680.8411
918.4471	---	8E	12	1303.654 652.3304
1074.548	537.7778	9R	11	1174.611 587.8091
1187.632	594.3198	10L	10	1018.51 509.7586
1288.68	644.8436	11T	9	905.4258 453.2165
1345.701	673.3544	12G	8	804.3781 402.6927
1416.739	708.8729	13A	7	747.3566 374.182
1576.769	788.8882	C(Carbamidome 14 thyl)	6	676.3195 338.6634
1633.791	817.399	15G	5	516.2889 258.6481
1746.875	873.941	16L	4	459.2674 230.1373
1860.918	930.9625	17N	3	346.1833 173.5953
1917.939	959.4732	18G	2	232.1404 116.5738
---	MH ⁺³	19R	1	175.119 88.0631



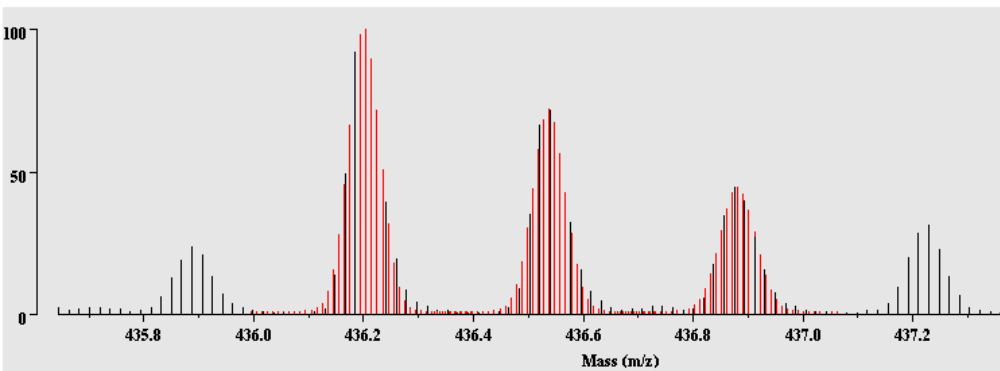
ELPPQVHLLTLAR⁺³/(544.6559⁺³/1631.9528)/Q6P762



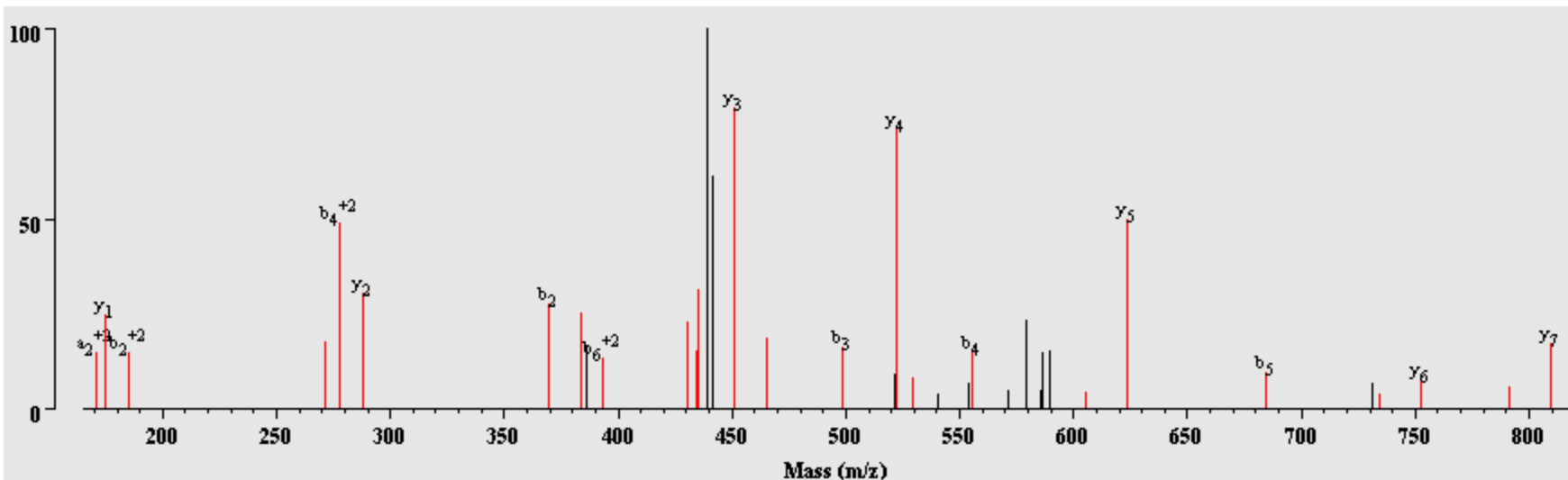
b	b+2	iTRAQ4plex	y	y+2
274.1519	---	1 E	13	---
387.236	---	2 L	12	1357.831 679.4194
484.2888	---	3 P	11	1244.747 622.8773
581.3415	---	4 P	10	1147.695 574.3509
709.4001	---	5 Q	9	1050.642 525.8246
808.4685	---	6 V	8	922.5833 461.7953
945.5274	473.2674	7 H	7	823.5148 412.2611
1058.612	529.8094	8 L	6	686.4559 343.7316
1171.696	586.3514	9 L	5	573.3719 287.1896
1272.743	636.8753	10 T	4	460.2878 230.6475
1385.827	693.4173	11 L	3	359.2401 180.1237
1456.864	728.9358	12 A	2	246.1561 123.5817
---	---	13 R	1	175.119 88.0631



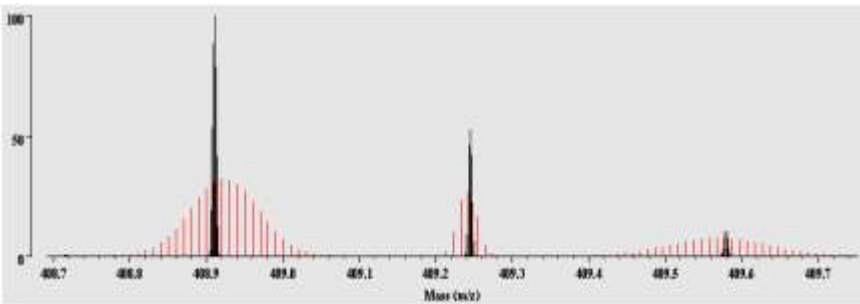
SHEGETAYIR³/(436.4702³/1307.3959)/Q6PDM2



b	b+2	iTRAQ4plex	y	y+2
232.1414	---	1S	10	---
369.2003	185.1038	2H	9	1075.517 538.262
498.2429	249.6251	3E	8	938.4578 469.7325
555.2643	278.1358	4G	7	809.4152 405.2112
684.3069	342.6571	5E	6	752.3937 376.7005
785.3546	393.1809	6T	5	623.3511 312.1792
856.3917	428.6995	7A	4	522.3035 261.6554
1019.455	510.2312	8Y	3	451.2663 226.1368
1132.539	566.7732	9I	2	288.203 144.6051
---	---	10R	1	175.119 88.0631



TLAGDVHIVR+3/(409.1463+3/1225.422)/Q9QZ88



b	b+2	iTRAQ4plex	y	y+2
246.157	---	1T	10	---
359.2411	---	2L	9	979.5683 490.2878
430.2782	---	3A	8	866.4843 433.7458
487.2997	---	4G	7	795.4472 398.2272
602.3266	---	5D	6	738.4257 369.7165
701.395	---	6V	5	623.3988 312.203
838.4539	419.7306	7H	4	524.3303 262.6688
951.538	476.2726	8I	3	387.2714 194.1394
1050.606	525.8068	9V	2	274.1874 137.5973
---	---	10R	1	175.119 88.0631

