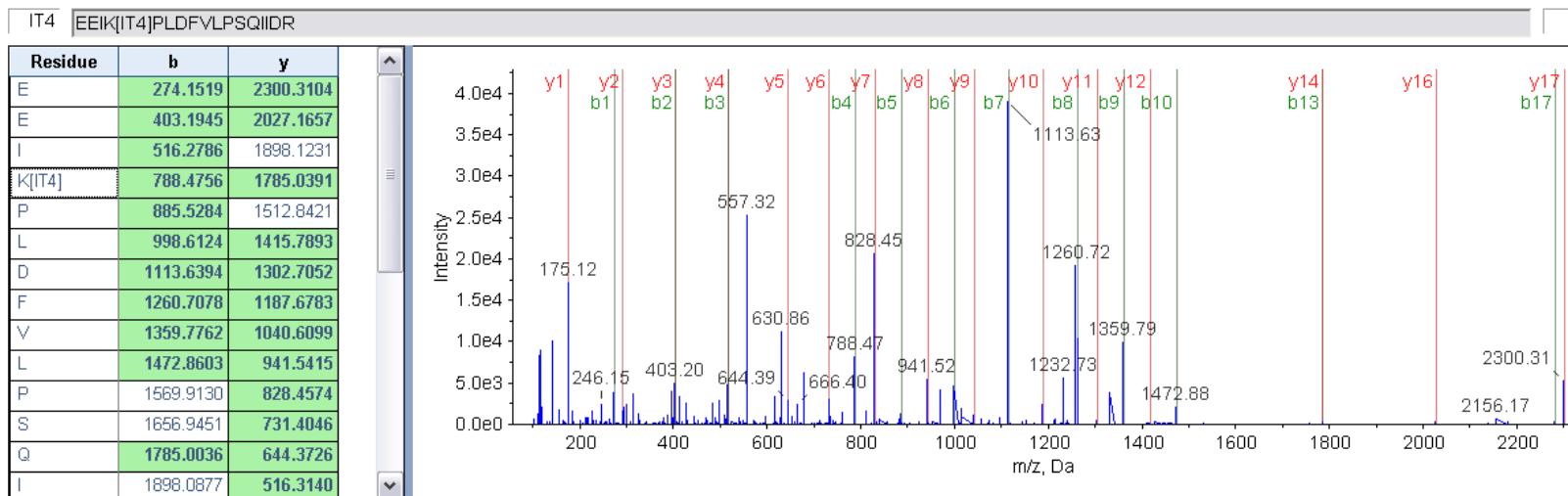
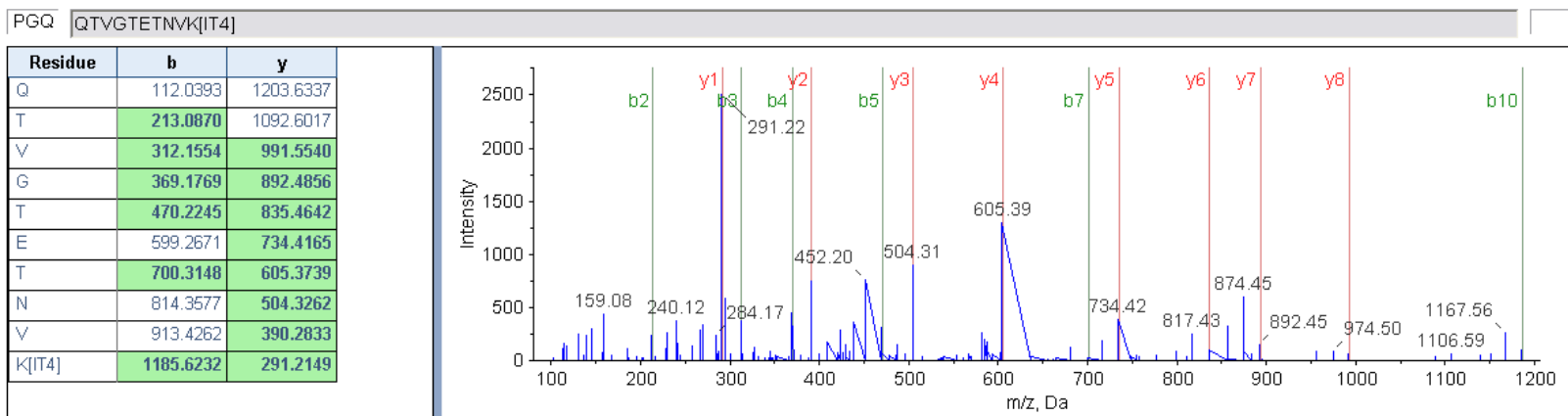


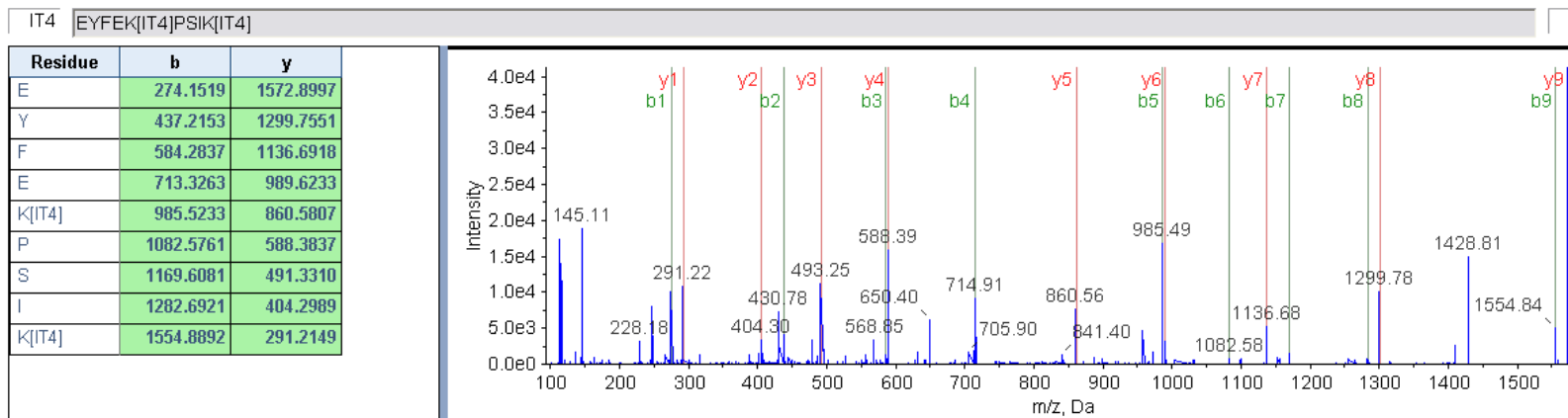
Q72LZ4



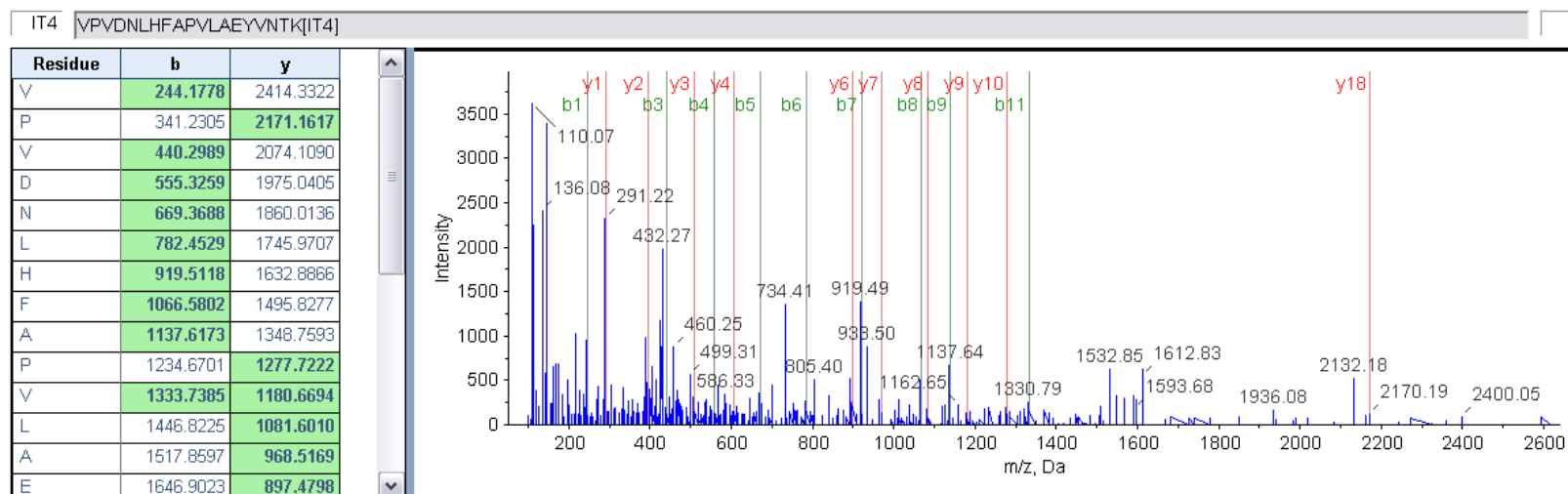
Q72MX9\_LEPIC



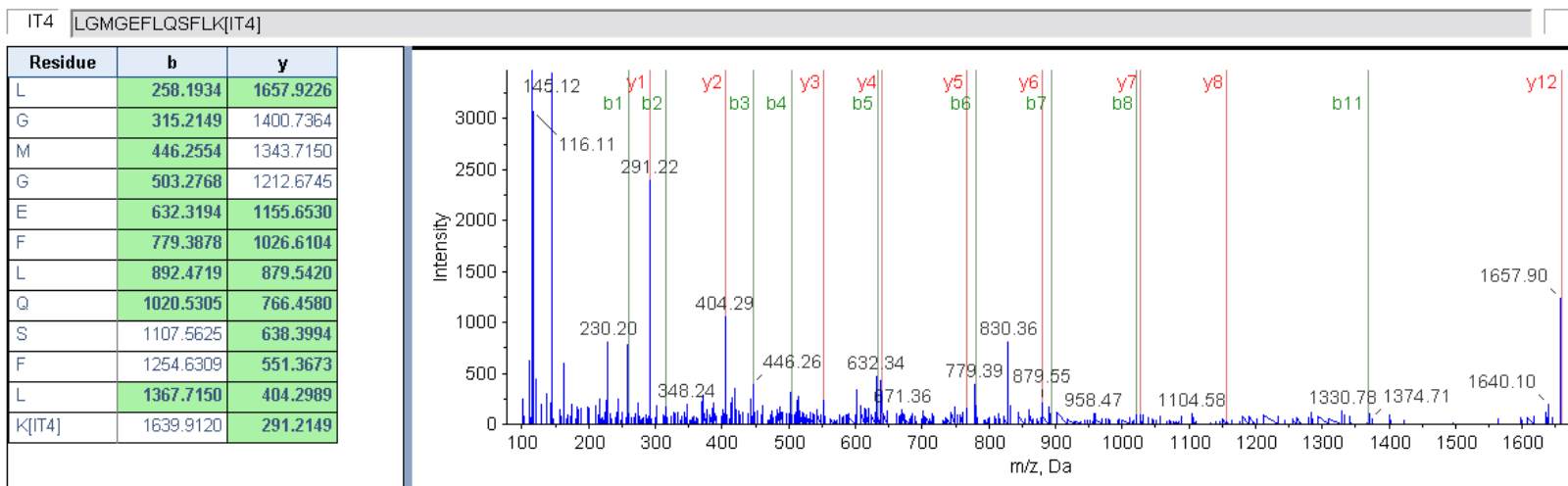
### Q72RP1



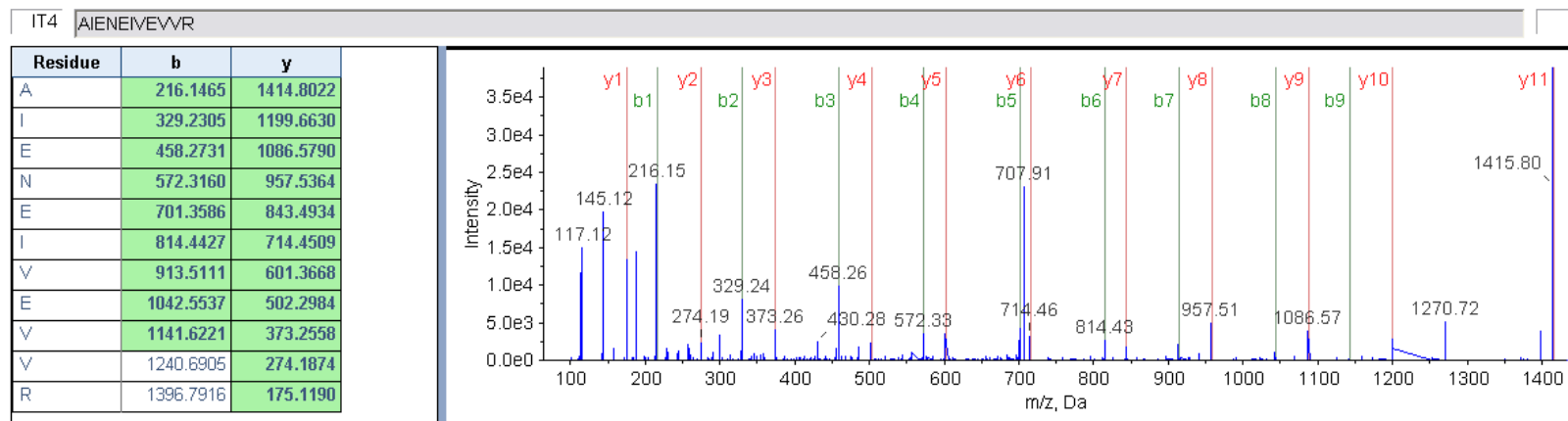
### Q72V73



LIC2\_SPN3857



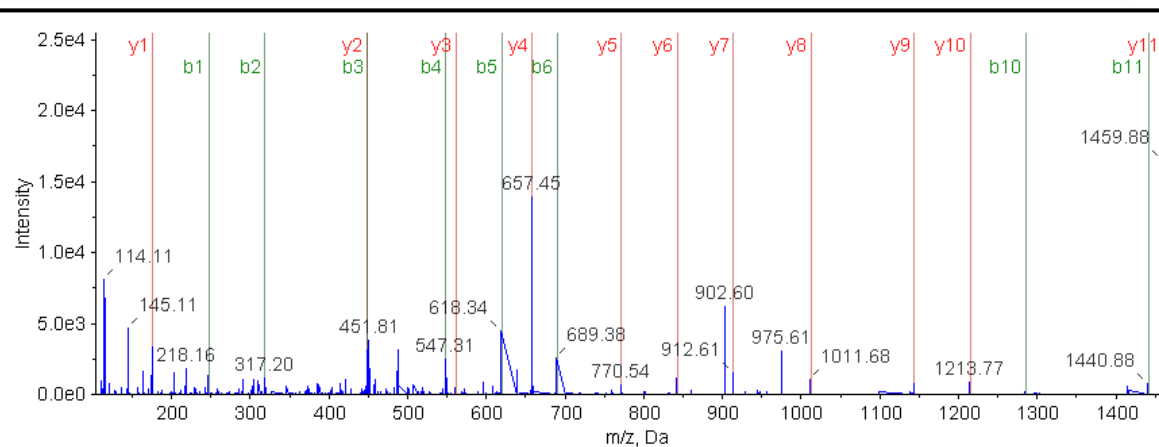
Q75G27



### Q75FW7

IT4 | TAMVAAIPLK[IT4]R

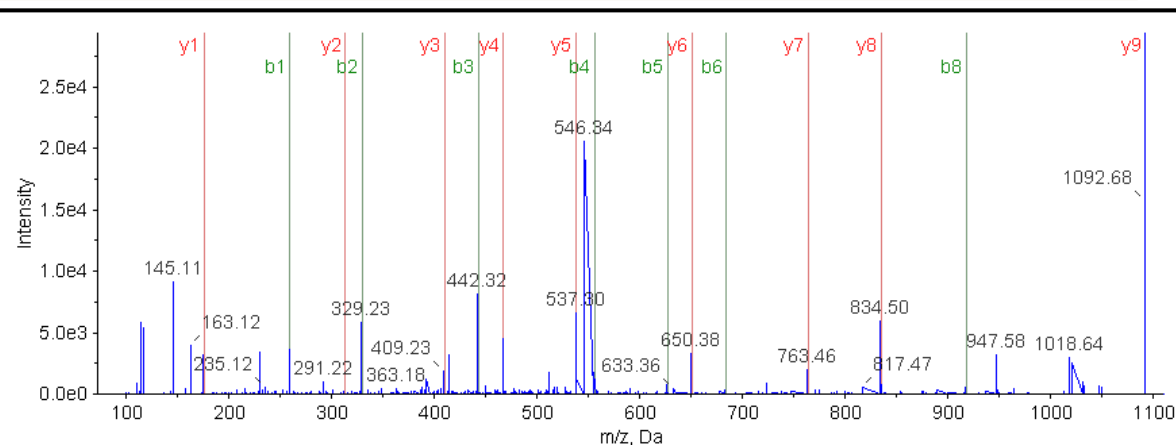
Residue	b	y
T	246.1570	1458.9069
A	317.1941	1213.7571
M	448.2346	1142.7200
V	547.3030	1011.6795
A	618.3401	912.6111
A	689.3773	841.5740
I	802.4613	770.5369
P	899.5141	657.4528
L	1012.5981	560.4000
K[IT4]	1284.7952	447.3160
R	1440.8963	175.1190



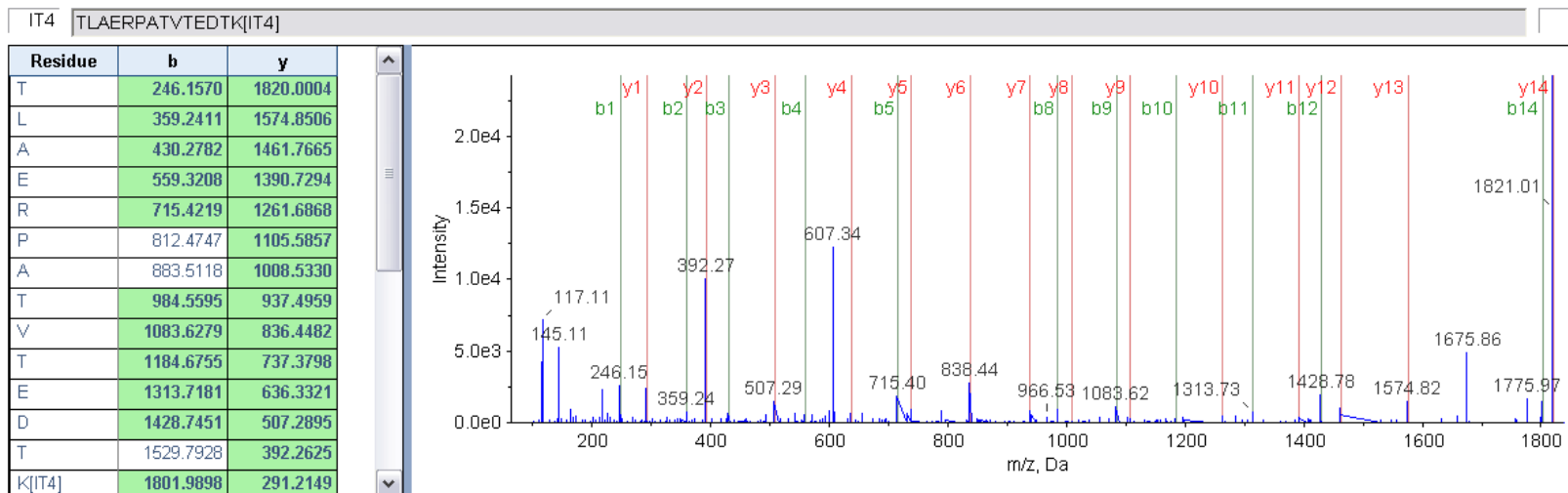
### Q75F18

IT4 | IAIAGPHR

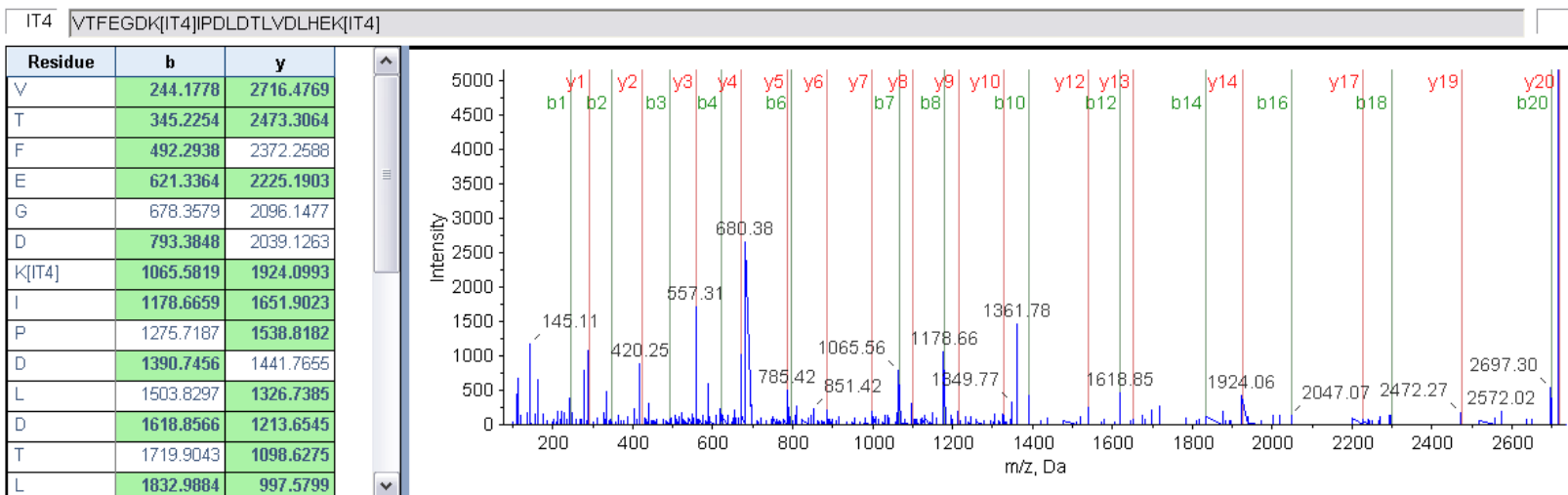
Residue	b	y
I	258.1934	1091.6806
A	329.2305	834.4944
I	442.3146	763.4573
I	555.3986	650.3733
A	626.4358	537.2892
G	683.4572	466.2521
P	780.5100	409.2306
H	917.5689	312.1779
R	1073.6700	175.1190



### Q72VT5



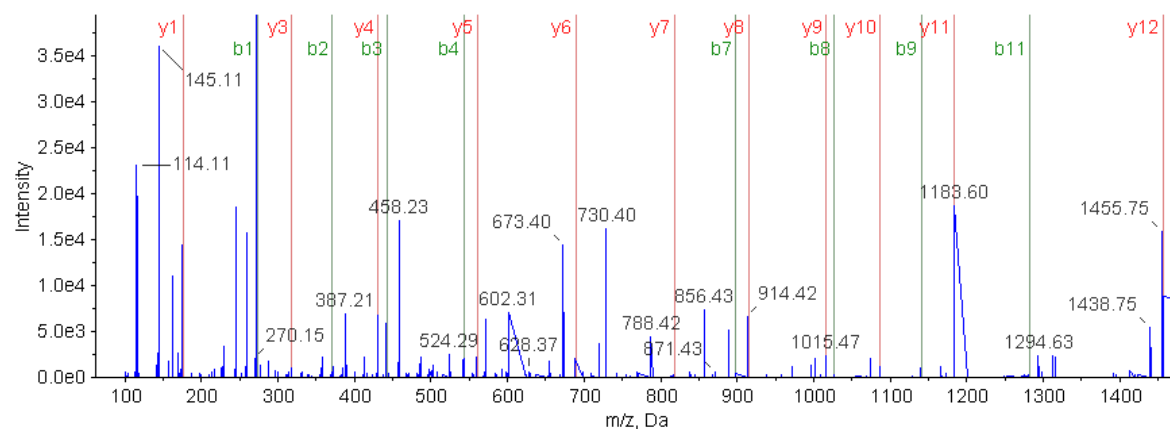
### Q72VD6



Q72VC1

IT4 QPATPEEEIAR

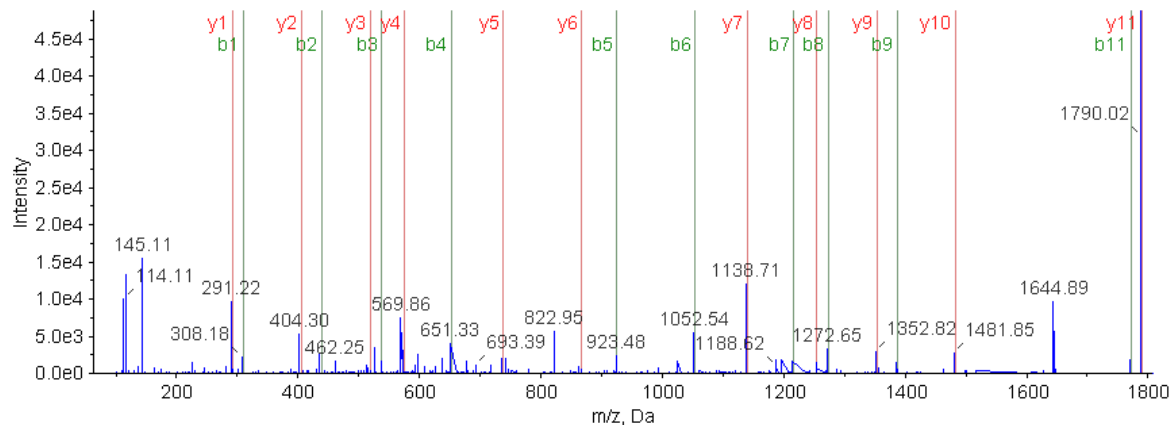
Residue	b	y
Q	273.1679	1455.7560
P	370.2207	1183.5953
A	441.2578	1086.5426
T	542.3055	1015.5055
P	639.3582	914.4578
E	768.4008	817.4050
E	897.4434	688.3624
E	1026.4860	559.3198
I	1139.5701	430.2772
A	1210.6072	317.1932
A	1281.6443	246.1561
R	1437.7454	175.1190



Q72V61

IT4 YEVDK[IT4]EYGILK[IT4]

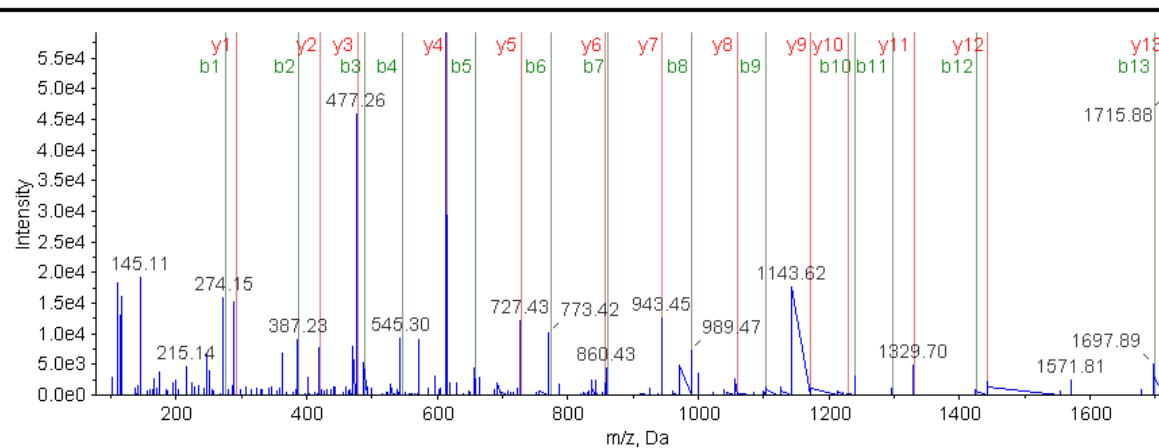
Residue	b	y
Y	308.1727	1789.0107
E	437.2153	1481.8454
V	536.2837	1352.8028
D	651.3106	1253.7343
K[IT4]	923.5076	1138.7074
E	1052.5502	866.5104
Y	1215.6136	737.4678
G	1272.6350	574.4045
I	1385.7191	517.3830
L	1498.8032	404.2989
K[IT4]	1771.0002	291.2149



### Q72UU9

IT4 | EITGLDSEIHGEK(IT4)

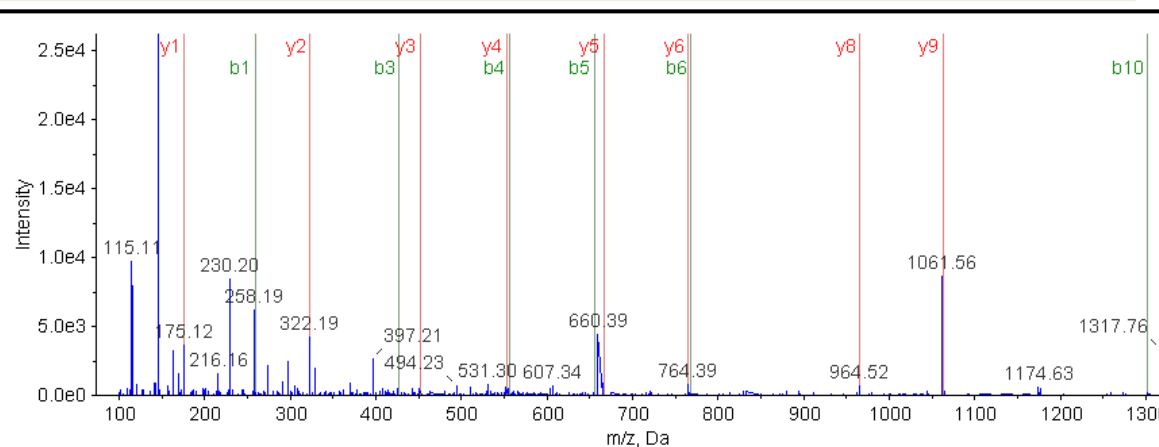
Residue	b	y
E	274.1519	1715.9054
I	387.2360	1442.7607
T	488.2837	1329.6767
G	545.3051	1228.6290
L	658.3892	1171.6075
D	773.4161	1058.5235
S	860.4482	943.4965
E	989.4908	856.4645
I	1102.5748	727.4219
H	1239.6337	614.3378
G	1296.6552	477.2789
E	1425.6978	420.2575
K(IT4)	1697.8948	291.2149



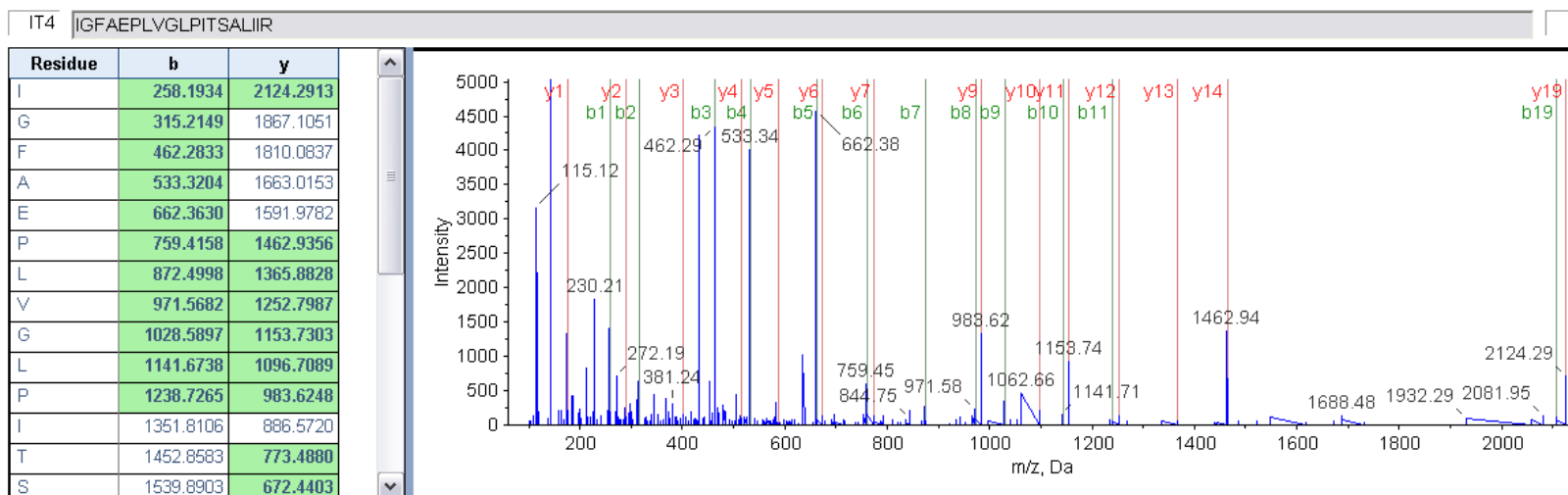
### Q72UU2

IT4 | IPAEVLTEFR

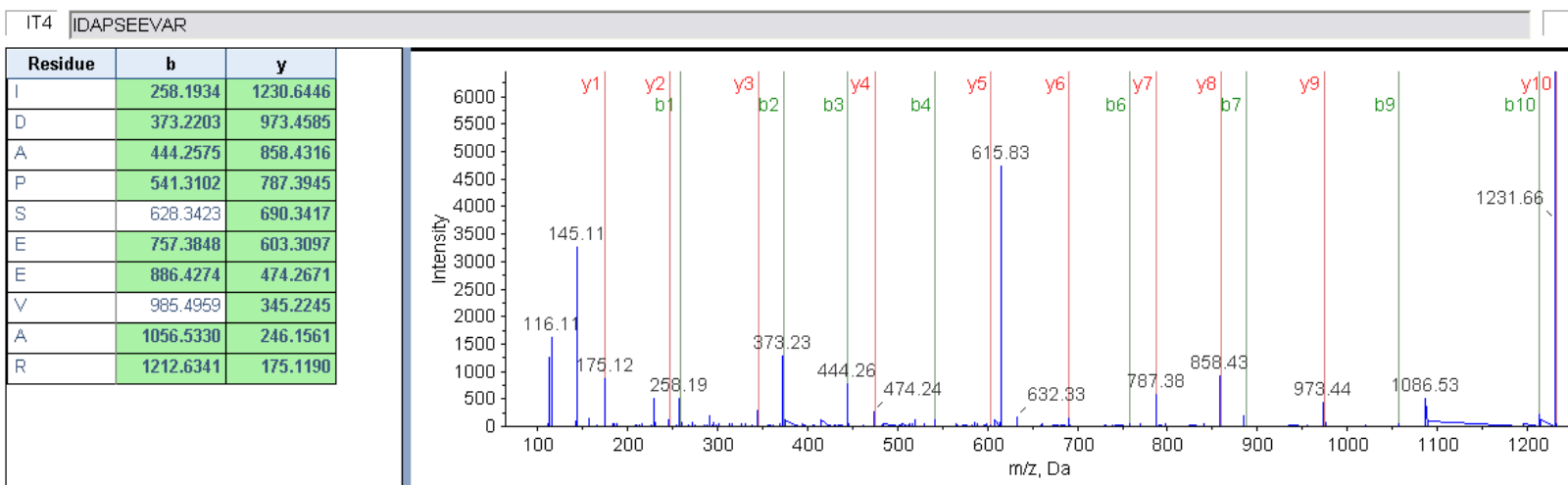
Residue	b	y
I	258.1934	1318.7487
P	355.2462	1061.5626
A	426.2833	964.5098
E	555.3259	893.4727
V	654.3943	764.4301
L	767.4784	665.3617
T	868.5260	552.2776
E	997.5686	451.2300
F	1144.6370	322.1874
R	1300.7381	175.1190



### Q72UH7



### Q72TJ7

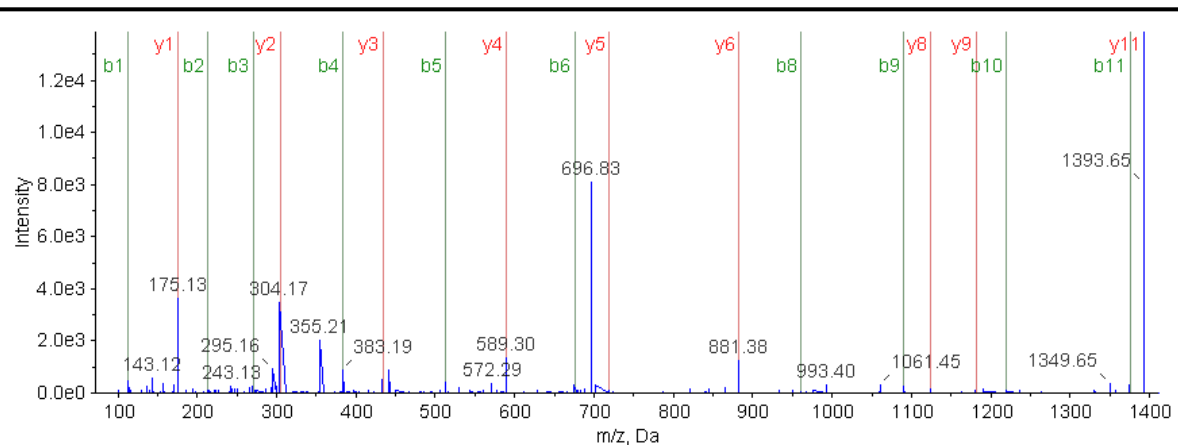




### Q72SZ8

PGQ QTGLELYEREER

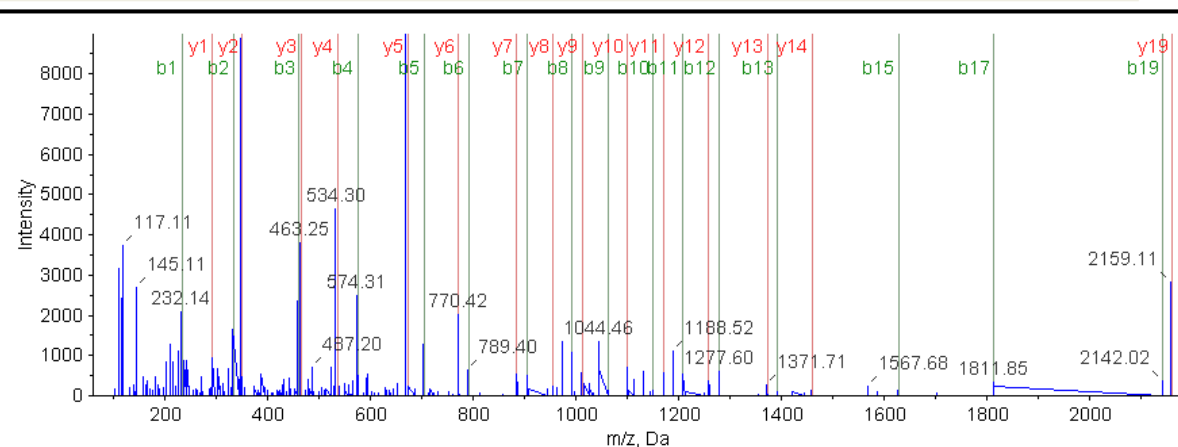
Residue	b	y
Q	112.0393	1392.6390
T	213.0870	1281.6070
G	270.1084	1180.5593
L	383.1925	1123.5378
E	512.2351	1010.4538
Y	675.2984	881.4112
E	804.3410	718.3478
R	960.4421	589.3052
E	1089.4847	433.2041
E	1218.5273	304.1615
R	1374.6284	175.1190



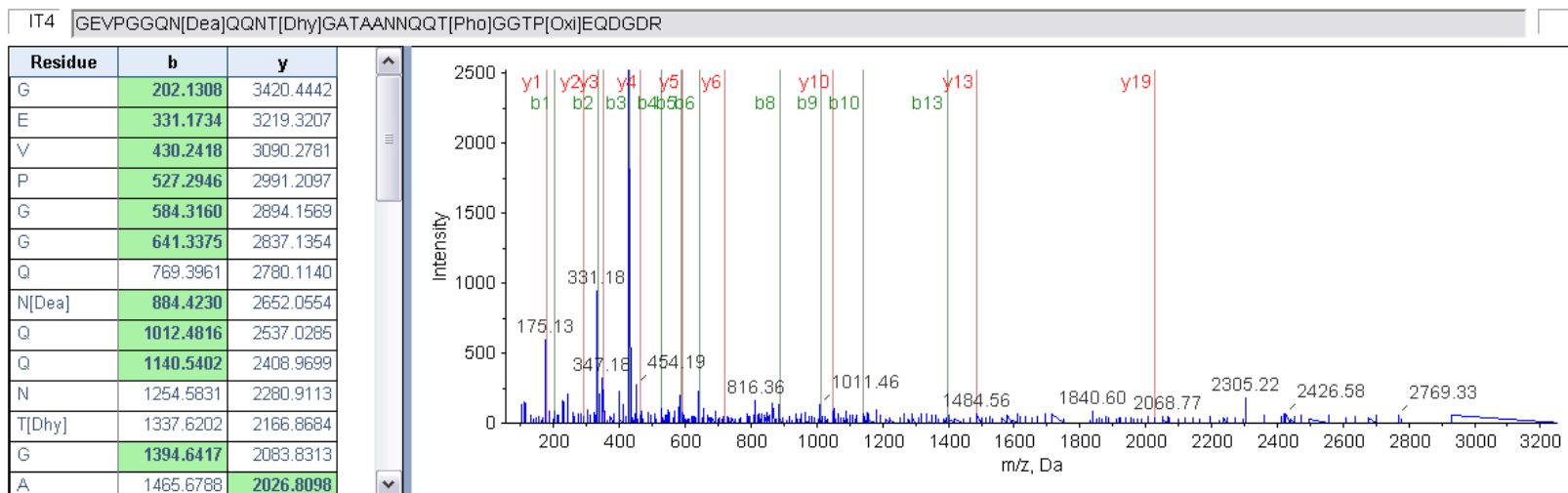
### Q72SU9

IT4 SVQDQSDSASGALVHADGK[IT4]

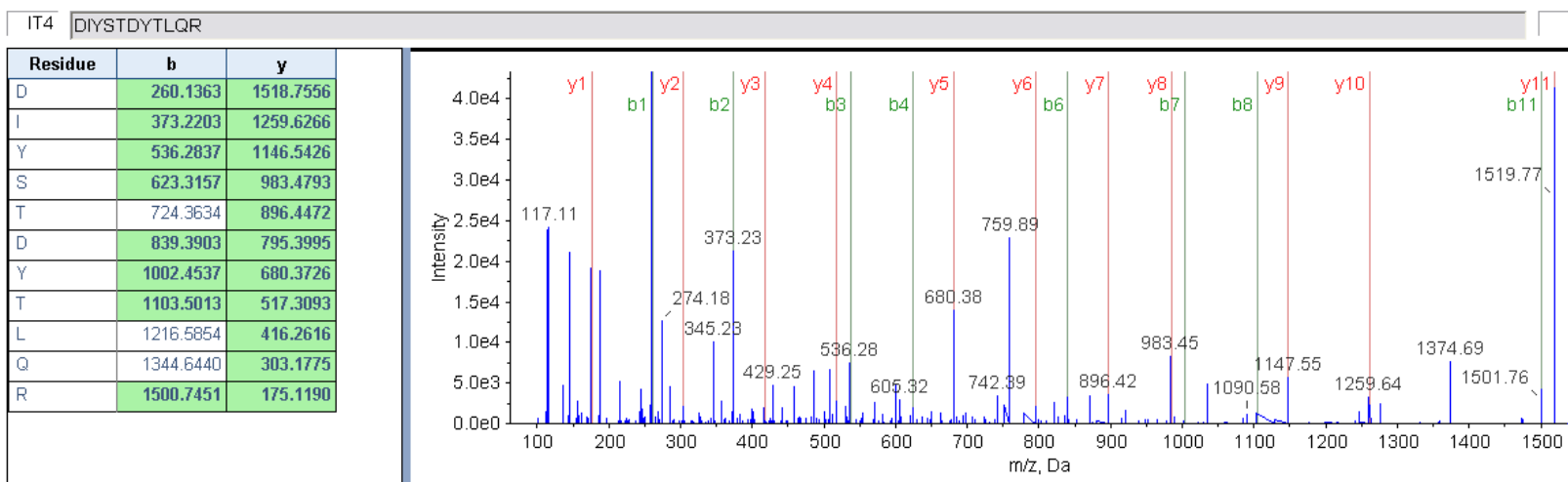
Residue	b	y
S	232.1414	2160.0771
V	331.2098	1928.9430
Q	459.2684	1829.8746
D	574.2953	1701.8160
Q	702.3539	1586.7891
S	789.3859	1458.7305
D	904.4129	1371.6985
S	991.4449	1256.6715
A	1062.4820	1169.6395
S	1149.5140	1098.6024
G	1206.5355	1011.5704
A	1277.5726	954.5489
L	1390.6567	883.5118
V	1489.7251	770.4277



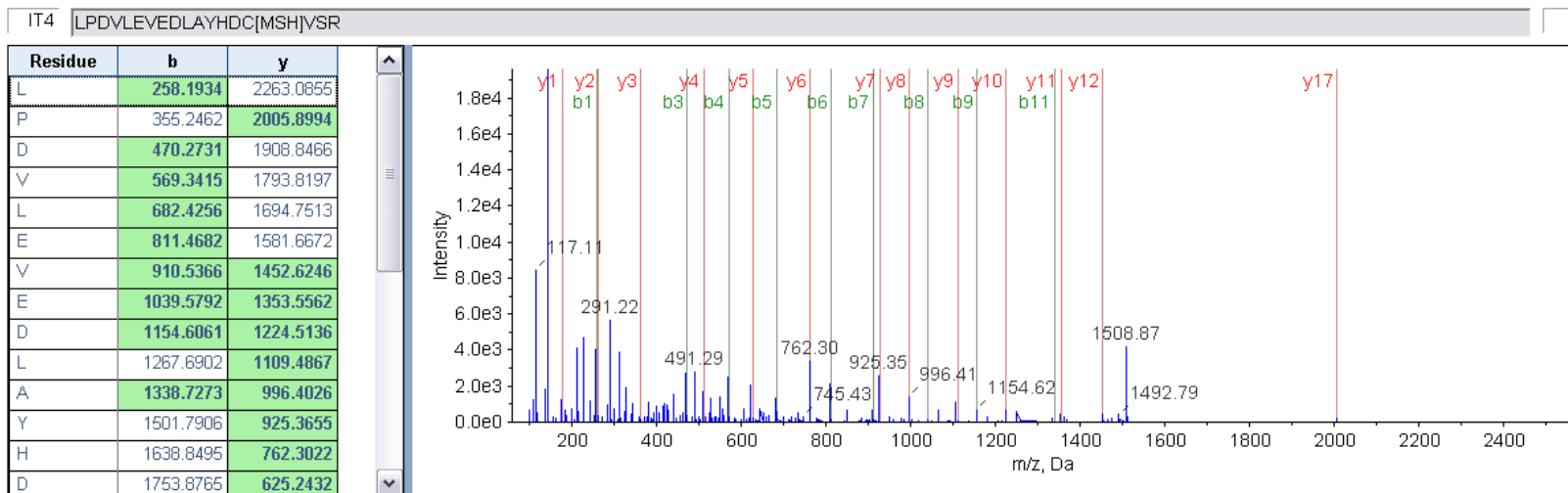
### Q72SP3



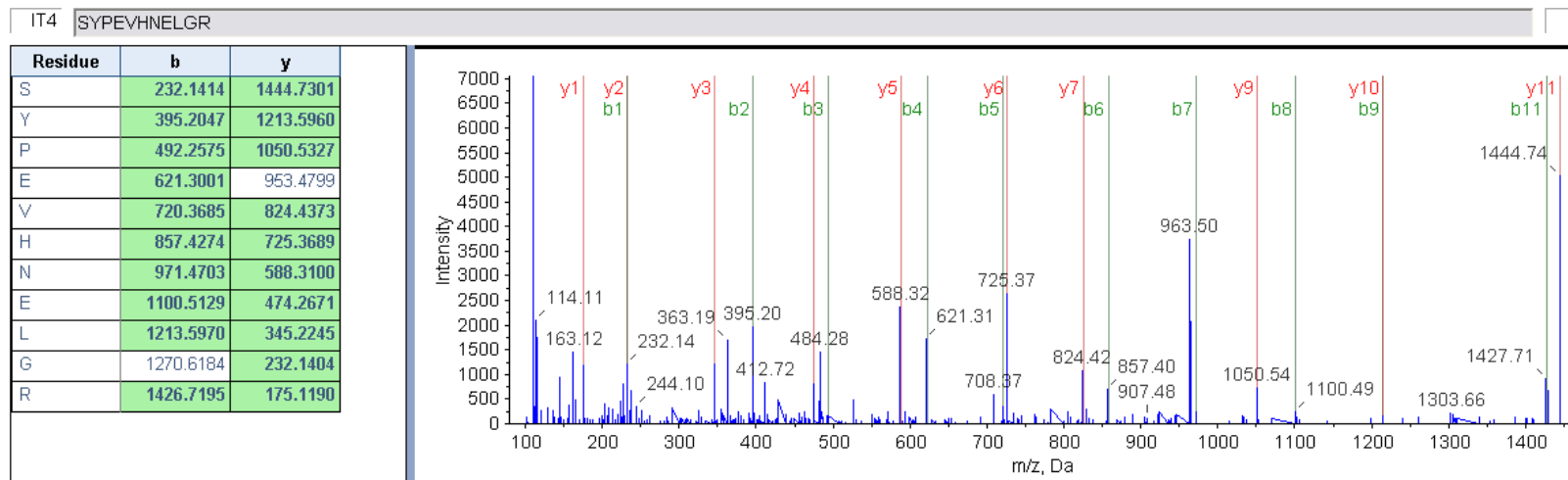
### Q72SH2



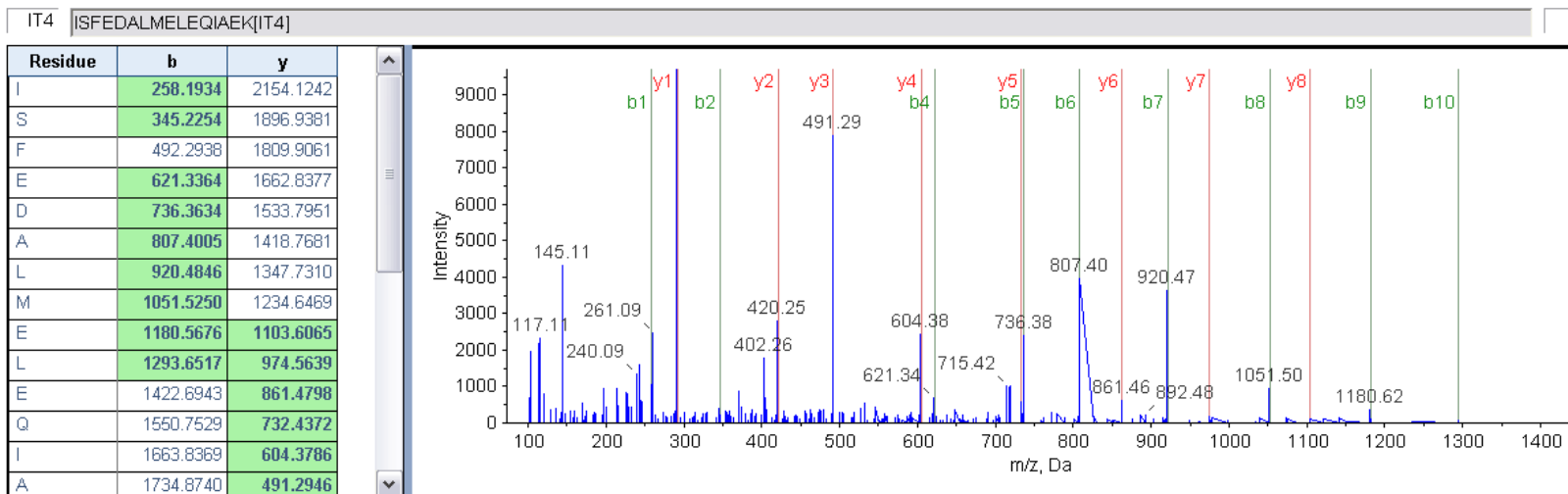
### Q72S33



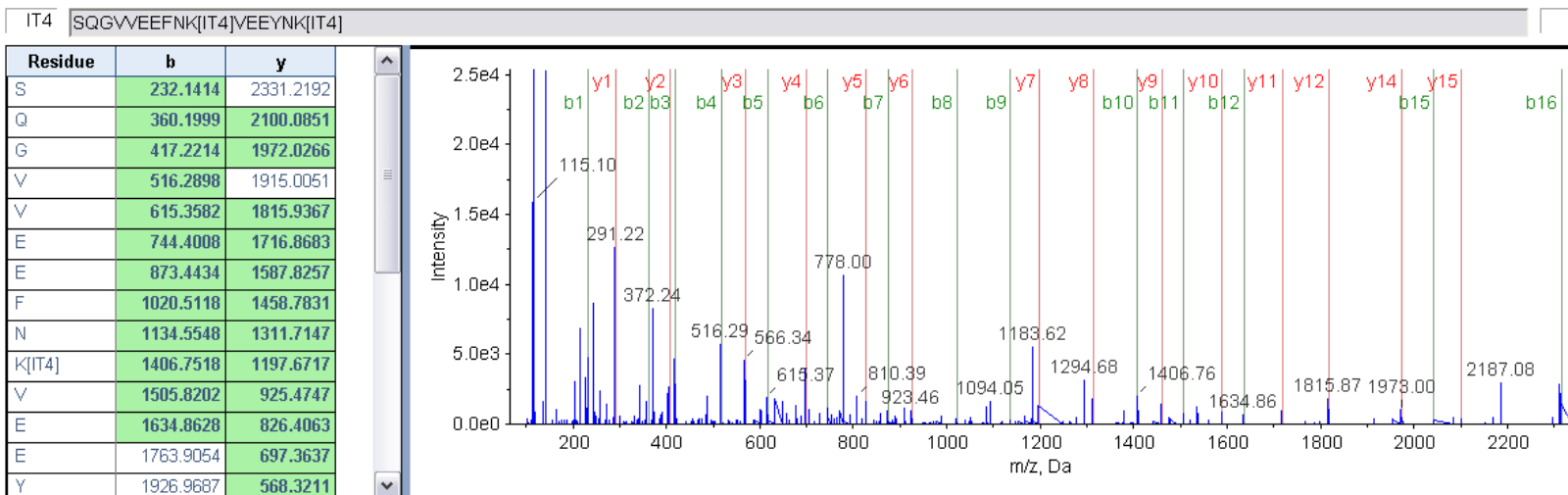
### Q72RZ8



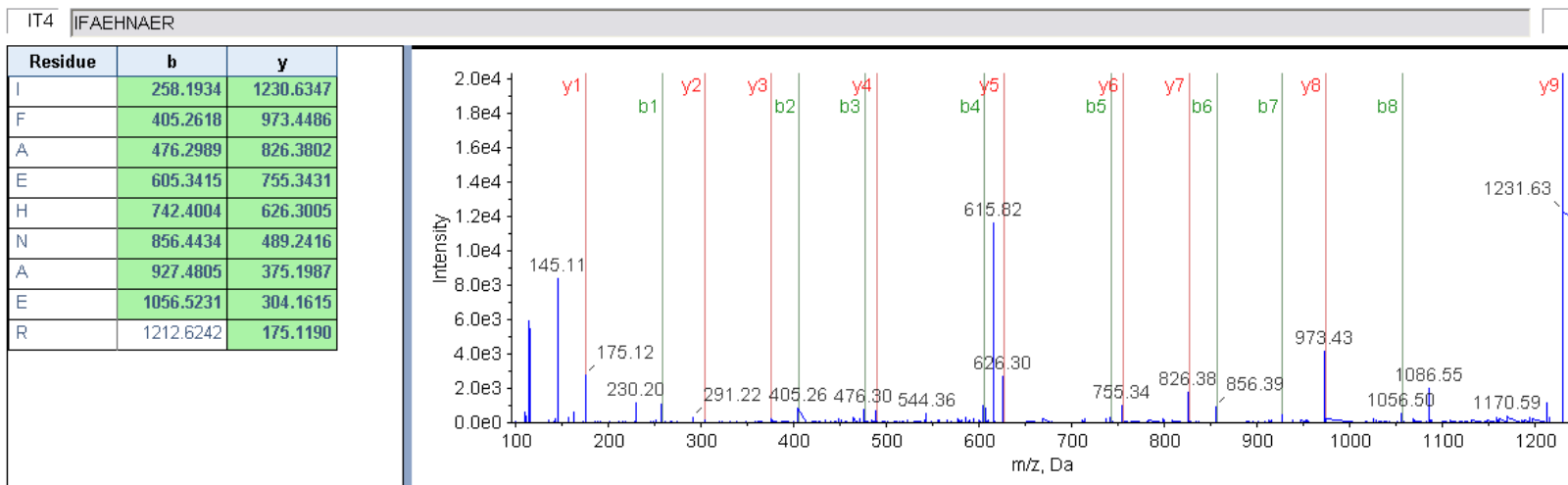
### Q72RW3



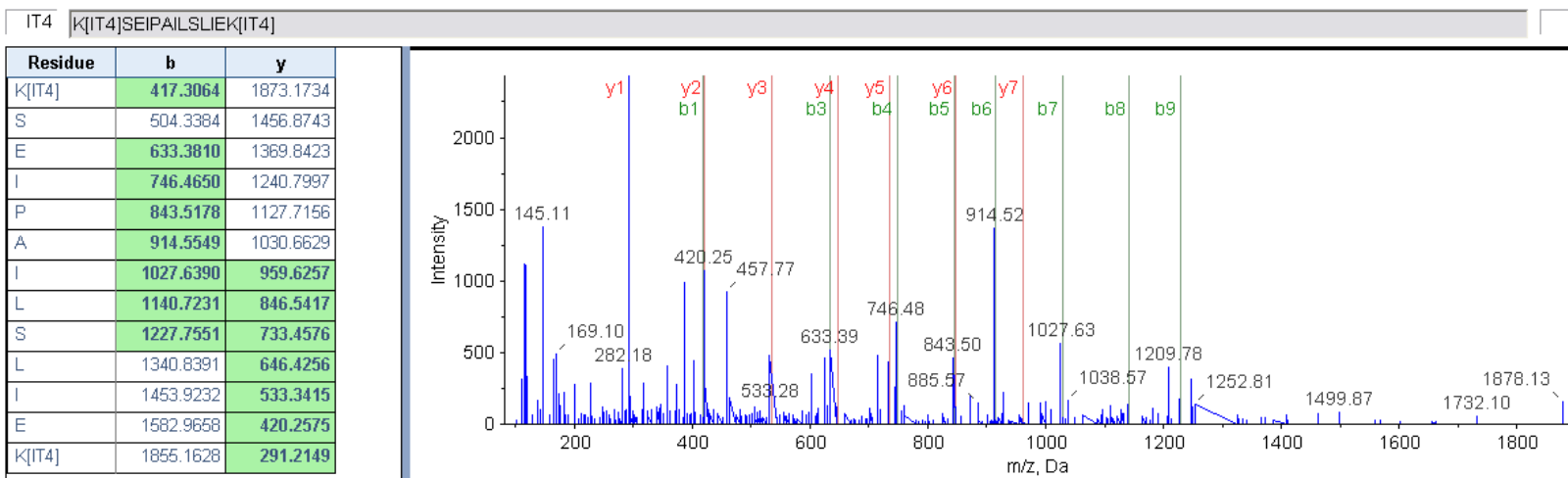
### Q72RS0



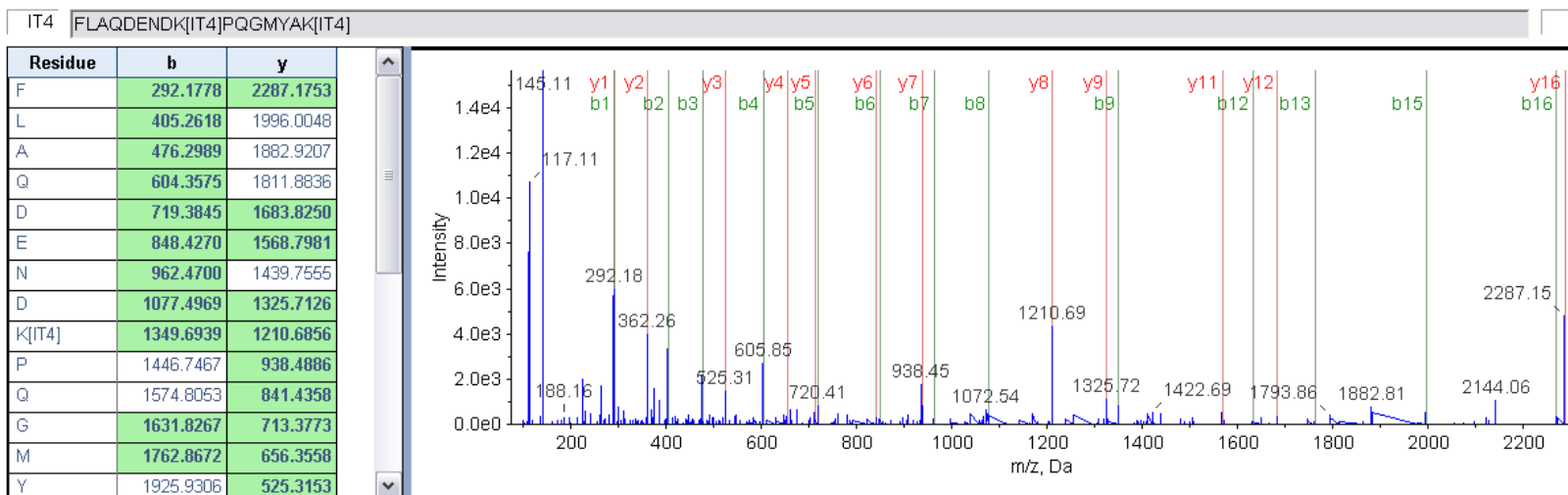
### Q72QM9



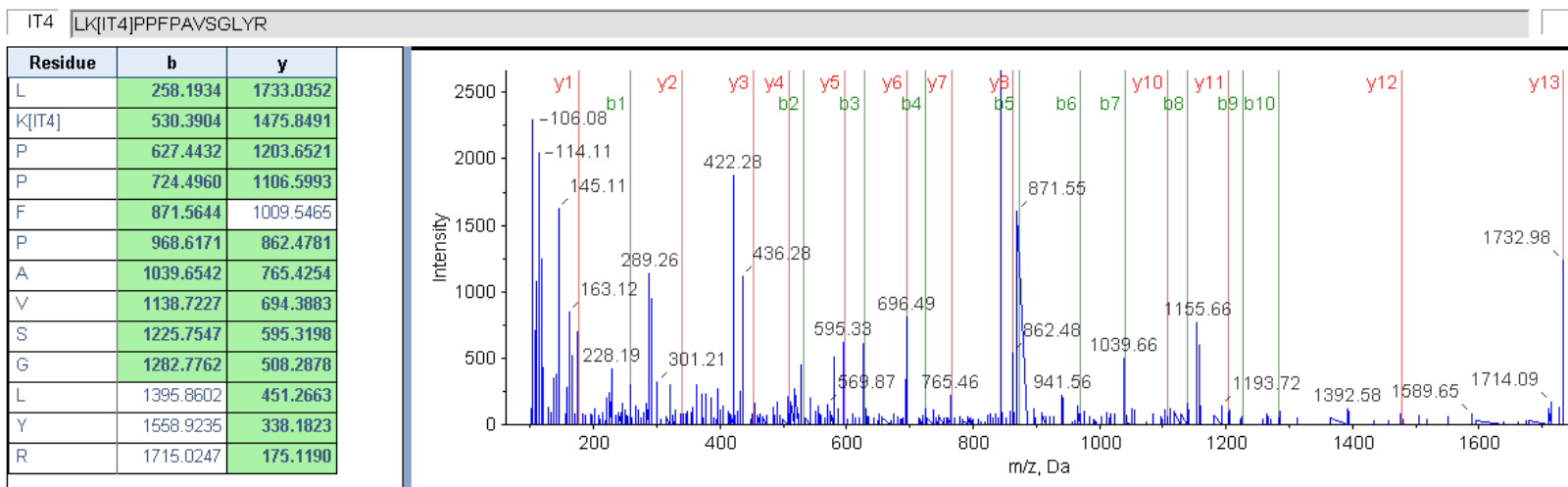
### Q72PU6



### Q72NT3



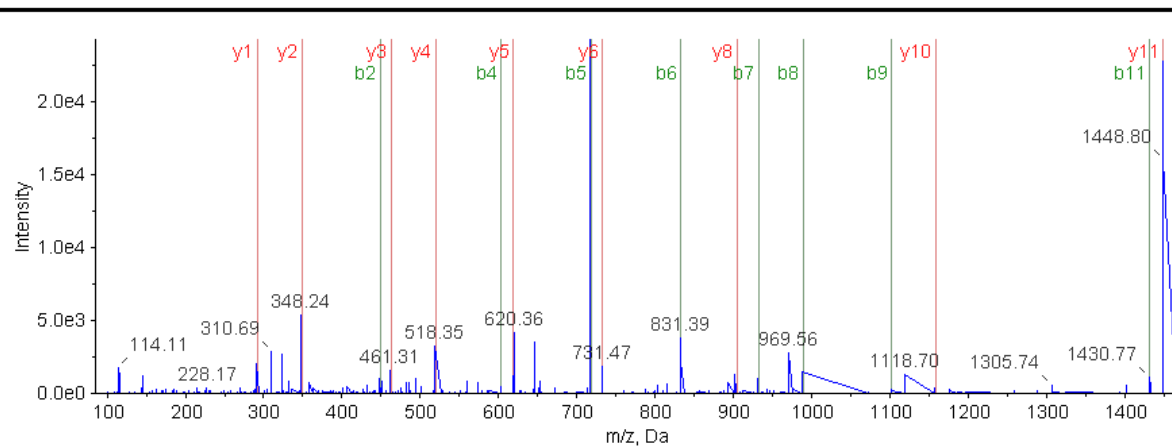
### Q72NQ6



### Q72MG4

IT4 FRPGN[Dea]NVGLGK[IT4]

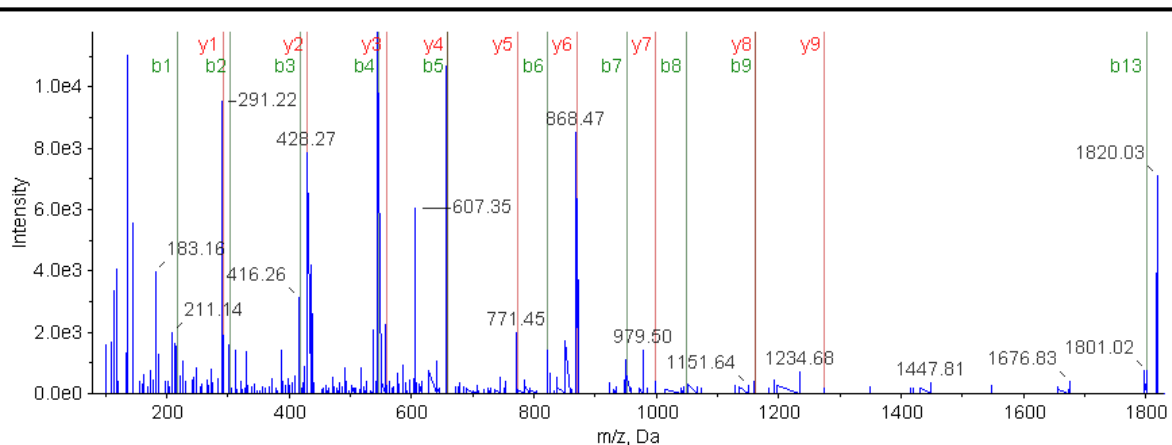
Residue	b	y
F	292.1778	1447.8260
R	448.2789	1156.6555
P	545.3316	1000.5544
G	602.3531	903.5016
N[Dea]	717.3800	846.4801
N	831.4230	731.4532
V	930.4914	617.4103
G	987.5128	518.3419
L	1100.5969	461.3204
G	1157.6184	348.2363
K[IT4]	1429.8154	291.2149



### Q72M59

IT4 ASIIEYPLTEHK[IT4]

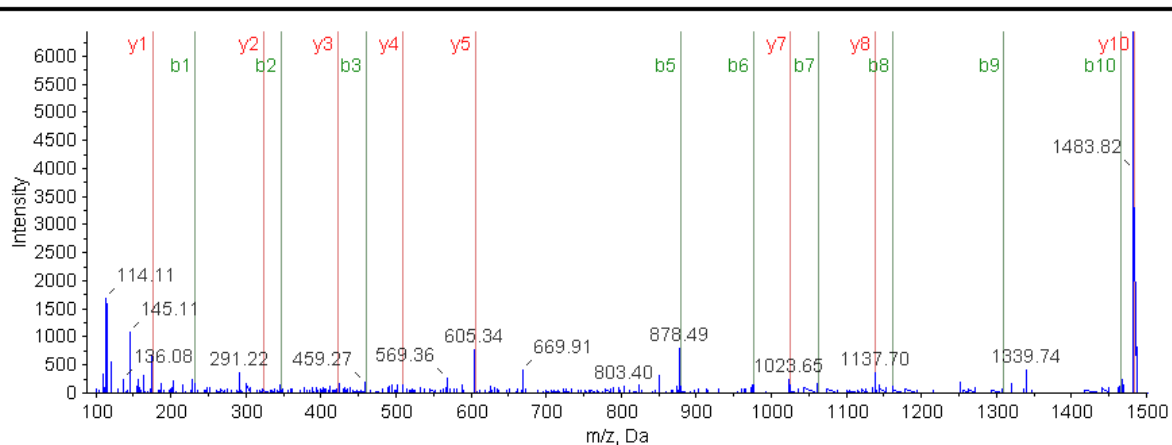
Residue	b	y
A	216.1465	1817.9887
S	303.1785	1602.8495
I	416.2625	1515.8175
E	545.3051	1402.7335
I	658.3892	1273.6909
Y	821.4525	1160.6068
E	950.4951	997.5435
P	1047.5479	868.5009
L	1160.6320	771.4481
T	1261.6796	658.3641
E	1390.7222	557.3164
H	1527.7811	428.2738
K[IT4]	1799.9782	291.2149



Q72LZ8

IT4 | SNLFLK[IT4]PSVFR

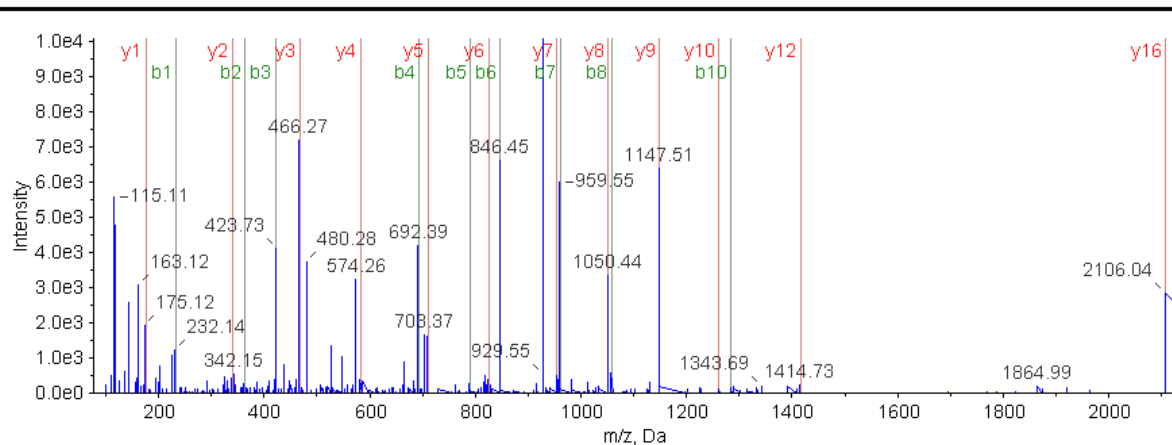
Residue	b	y
S	232.1414	1482.8671
N	346.1843	1251.7330
L	459.2684	1137.6901
F	606.3368	1024.6060
K[IT4]	878.5338	877.5376
P	975.5866	605.3406
S	1062.6186	508.2878
V	1161.6870	421.2558
F	1308.7554	322.1874
R	1464.8565	175.1190



Q72LY3

IT4 | SMGK[IT4]PGLPPEDQDQYR

Residue	b	y
S	232.1414	2106.0528
M	363.1819	1874.9187
G	420.2033	1743.8782
K[IT4]	692.4003	1686.8568
P	789.4531	1414.6597
G	846.4746	1317.6070
L	959.5586	1260.5855
P	1056.6114	1147.5014
P	1153.6642	1050.4487
E	1282.7068	953.3959
D	1397.7337	824.3533
Q	1525.7923	709.3264
D	1640.8192	581.2678
Q	1768.8778	466.2409





**Figure S1** Annotated MS/MS spectra for single peptide represented proteins. Modifications for individual amino acids are displayed in square brackets. The modification names follow the HUPO-PSI Modification Nomenclature for Mass Spectrometry standard (<http://www.unimod.org>).