Proteins identified by Peptide Mass Fingerprint (PMF).

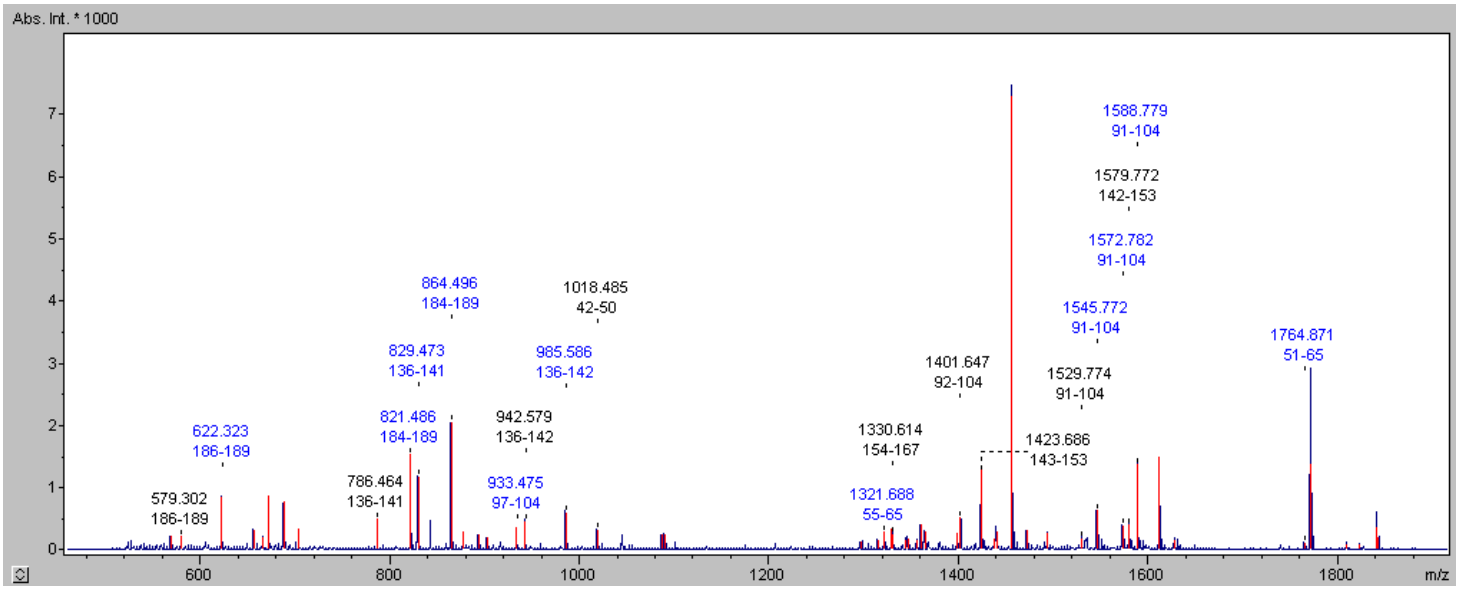
Since not all sequences of the tested proteins were available on public data, the experimental Peptide Mass Fingerprints of the recombinant autoantigens were compared to the theoretical ones either using MASCOT run on public database (NCBI nr *Homo sapiens*, release 20100616 or SwissProt *Homo sapiens* release 2010_07) or Biotools software run on single autoantigen sequence.

Each data sheet report:

- Hit number according to Supplementary Table 3.
- Matching protein, Mowse score, E-value.
- Annotated spectrum.
- Nominal mass (M_r) and calculated pI value.
- Rules for Mascot search.
- Variable modifications.
- Number of mass values searched.
- Number of mass values matched.
- Sequence Coverage.
- Matched peptides showed in Bold Red.
- Peptide assignment.
- Unmatched peptides.

LYG1, full length protein, from 20 to 194 aa

Match to: **gi|28372527** Score: **56** Expect: **0.55**
lysozyme g-like protein 1 precursor [Homo sapiens]



Nominal mass (M_r): **21417**; Calculated pI value: **8.47**

Variable modifications: Carbamyl (K),Carbamyl (N-term),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **55**
Number of mass values matched: **13**
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

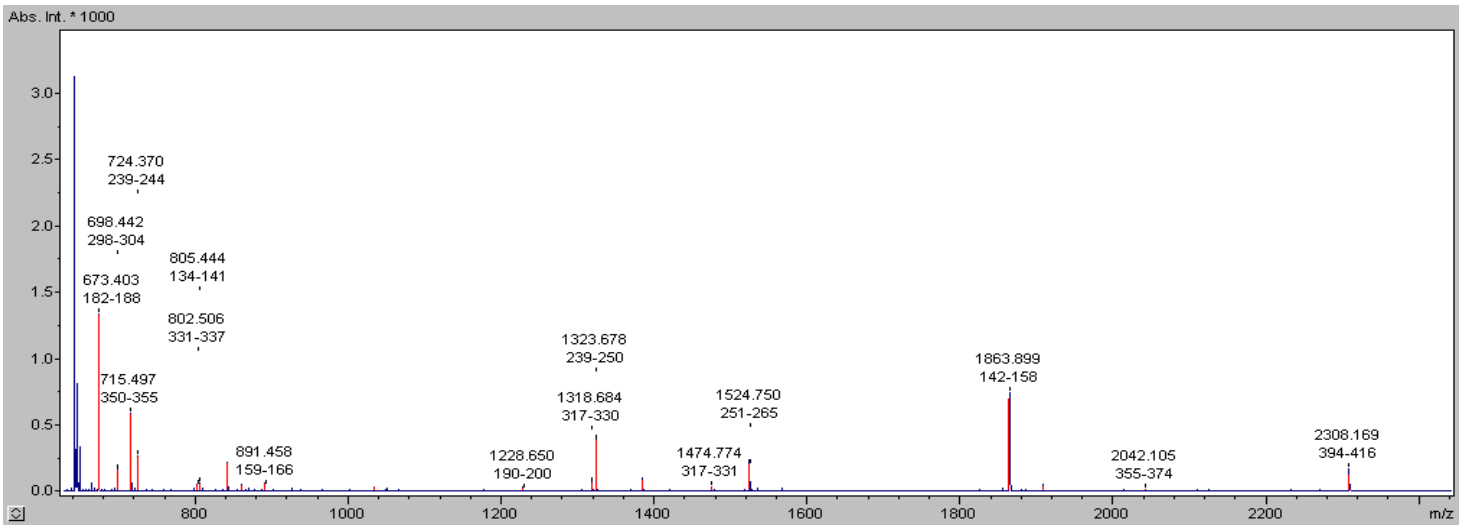
```
  1 MSALWLLLGL LALMDLSESS NWGCYGNIQS LDTPGASCGI GRRHGLNYCG
 51 VRASERLAEI DMPYLLKYQP MMQTIGQKYC MDPAVIAGVL SRKSPGDKIL
101 VNMGDRTSMV QDPGSQAPTS WISESQVSQT TEVLTTRIKE IQRRFPTWTP
151 DQYLRGGLCA YSGGAGYVRS SQDLSCDFCN DVLARAKYLK RHGF
```

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
44 - 52	1018.4848	1017.4775	1017.4814	4	0	**R.HGLNYCGVR.A**
53 - 67	1764.8707	1763.8634	1763.9127	-28	1	**R.ASERLAEIDMPYLLK.Y** Oxidation (M)
57 - 67	1321.6878	1320.6805	1320.6999	-15	0	**R.LAEIDMPYLLK.Y** Oxidation (M)
57 - 67	1364.6564	1363.6491	1363.7057	-41	0	**R.LAEIDMPYLLK.Y** Carbamyl (N-term); Oxidation (M)
94 - 106	1401.6471	1400.6398	1400.7082	-49	1	**K.SPGDKILVNMGDR.T**
99 - 106	933.4749	932.4676	932.4749	-8	0	**K.ILVNMGDR.T** Oxidation (M)
138 - 143	786.4645	785.4572	785.4759	-24	1	**R.IKEIQR.R**
138 - 143	829.4735	828.4662	828.4817	-19	1	**R.IKEIQR.R** Carbamyl (N-term)
144 - 155	1579.7720	1578.7647	1578.7943	-19	1	**R.RFPTWTPDQYLR.G**
145 - 155	1423.6856	1422.6783	1422.6932	-10	0	**R.FPTWTPDQYLR.G**
156 - 169	1330.6141	1329.6069	1329.6136	-5	0	**R.GGLCAYSGGAGYVR.S**
188 - 191	579.3020	578.2947	578.3540	-102	1	**K.YLKR.H**
188 - 191	622.3227	621.3154	621.3598	-72	1	**K.YLKR.H** Carbamyl (N-term)

No match to: 568.0690, 656.0331, 665.9808, 672.0058, 687.9805, 703.9584, 821.4856, 864.4965, 877.0337, 893.0071, 902.4594, 942.5789, 985.5859, 1086.5086, 1089.5235, 1296.6308, 1314.5945, 1328.5963, 1343.6277, 1346.5811, 1355.6033, 1359.6432, 1398.6312, 1437.6641, 1439.6714, 1455.6753, 1471.6661, 1493.6289, 1529.7744, 1545.7724, 1572.7816, 1588.7786, 1611.7654, 1627.7447, 1770.7044, 1771.6942, 1809.6458, 1822.7166, 1840.7446, 1841.7154, 2249.0089, 3399.6571

C19orf47, not full length protein, from 68 to 422 aa

Match to: **CS047_HUMAN** Score: **85** Expect: **5.8e-05**
Uncharacterized protein C19orf47 OS=Homo sapiens GN=C19orf47 PE=1 SV=1



Nominal mass (M_r): **44718**; Calculated pI value: **10.12**

Variable modifications: Carbamyl (K),Carbamyl (N-term),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **22**
Number of mass values matched: **15**
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

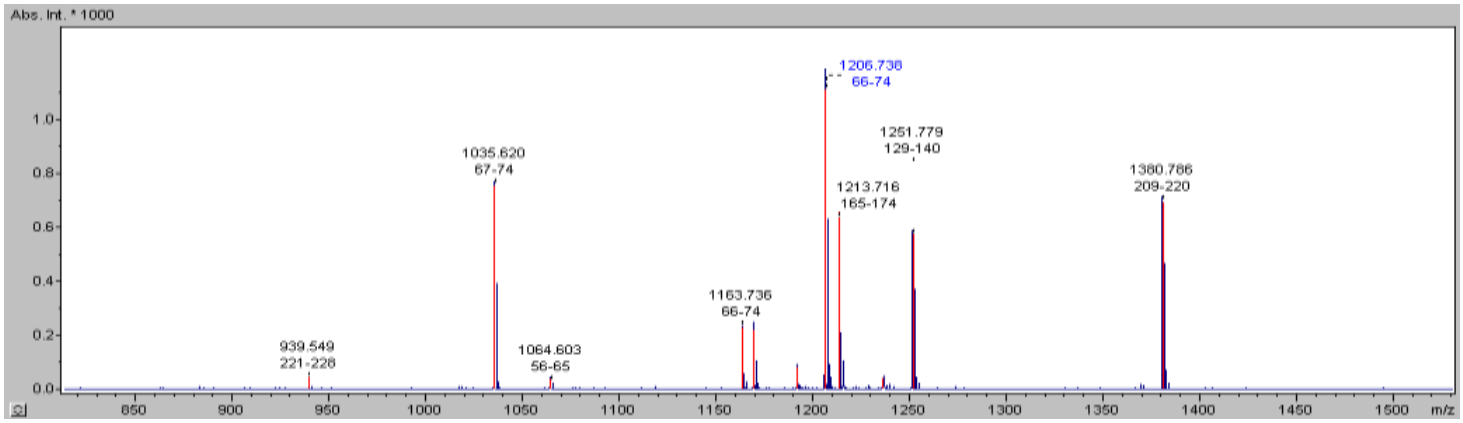
```
  1 MVMAALSLVA ACWGRAAADE SVQLPAAPGS SVRARETMVS VTMATSEWIQ
 51 FFKEAGIPPG PAVNYAVMFV DNRIQKSMLL DLNKEIMNEL GVTVVGDIIA
101 ILKHAKVVHR QDMCKAATES VPCSPSPLAG EIRRGTSAAS RMITNSLNHD
151 SPPSTPPRRP DTSTSKISVT VSNKMAAKSA KATAALARRE EESLAVPAKR
201 RRVTAEMEGK YVINMPKGTT PRTRKILEQQ QAAKGLHRTS VFDRLGAETK
251 ADTTTGSKPT GVFSRLGATP ETDEDLAWDS DNDSSSSVLQ YAGVLKKLGR
301 GPAKASPQPA LTVKAKATSS ATTAAAPTLR RLALSSRSGL ERKPESLSKV
351 SIIKRLGAAA LVPEAQDSQV TSTKSKSSAE VKVTIKRTLV GPRGSSSSEG
401 LGAQMDHAGT VSVFKRLGRR TF
```

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
134 - 141	805.4437	804.4364	804.4202	20	1	RGTSAASR.M
142 - 158	1863.8993	1862.8920	1862.8945	-1	0	MITNSLNHDSPPSTPPR.R
159 - 166	891.4576	890.4503	890.4458	5	0	RPDTSTSK.I
182 - 188	673.4025	672.3952	672.3918	5	0	ATAALAR.R
190 - 200	1228.6500	1227.6427	1227.6459	-3	1	EEESLAVPAKR.R
239 - 244	724.3702	723.3629	723.3552	11	0	TSVFDR.L
239 - 250	1323.6783	1322.6711	1322.6830	-9	1	TSVFDRLGAETK.A
251 - 265	1524.7496	1523.7424	1523.7580	-10	0	ADTTTGSKPTGVFSR.L
298 - 304	698.4425	697.4352	697.4235	17	1	LGRGPAK.A
317 - 330	1318.6842	1317.6769	1317.6888	-9	0	ATSSATTAAAPTLR.R
317 - 331	1474.7741	1473.7668	1473.7899	-16	1	ATSSATTAAAPTLRR.L
331 - 337	802.5056	801.4983	801.4821	20	1	RLALSSR.S
350 - 355	715.4973	714.4901	714.4752	21	1	VSIIKR.L
355 - 374	2042.1046	2041.0973	2041.0804	8	1	RLGAAALVPEAQDSQVTSTK.S
394 - 416	2308.1694	2307.1621	2307.0914	31	1	GSSSSEGLGAQMDHAGTVSVFKR.L

No match to: 842.5246, 861.0837, 1033.5650, 1384.7428, 1907.9667, 2737.5350, 2808.5356

METRNL, full length protein, from 45 to 311 aa

Match to: **METRL_HUMAN** Score: **59** Expect: **0.023**
Meteorin-like protein OS=Homo sapiens GN=METRNL PE=2 SV=1



Nominal mass (M_r): **34376**; Calculated pI value: **8.72**

Variable modifications: Carbamyl (K),Carbamyl (N-term),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **11**
Number of mass values matched: **8**
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
  1 MRGAARAAWG RAGQPWPRPP APGPPPPPLP LLLLLLAGLL GGAGAQYSSD
 51 RCSWKGSGLT HEAHRKEVEQ VYLRCAAGAV EWMYPTGALI VNLRPNTFSP
101 ARHLTVCIRS FTDSSGANIY LEKTGELRLL VPDGDGRPGR VQCFGLEQGG
151 LFVEATPQQD IGRRTTGFQY ELVRRHRASD LHELSAPCRP CSDTEVLLAV
201 CTSDFAVRGS IQQVTHEPER QDSAIHLRVS RLYRQKSRVF EPVPEGDGHW
251 QGRVRTLLEC GVRPGHGDFL FTGHMHFGEA RLGCAPRFKD FQRMYRDAQE
301 RGLNPCEVGT D
```

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
56 - 65	1064.6034	1063.5961	1063.5159	75	0	K.GSGLTHEAHR.K
66 - 74	1163.7360	1162.7287	1162.6346	81	1	R.KEVEQVYLR.C
66 - 74	1206.7380	1205.7307	1205.6404	75	1	R.KEVEQVYLR.C Carbamyl (N-term)
67 - 74	1035.6197	1034.6124	1034.5396	70	0	K.EVEQVYLR.C
129 - 140	1251.7787	1250.7714	1250.6731	79	0	R.LLVPDGDGRPGR.V
165 - 174	1213.7159	1212.7086	1212.6139	78	0	R.TTGFQYELVR.R
209 - 220	1380.7862	1379.7789	1379.6793	72	0	R.GSIQQVTHEPER.Q
221 - 228	939.5486	938.5413	938.4934	51	0	R.QDSAIHLR.V

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence

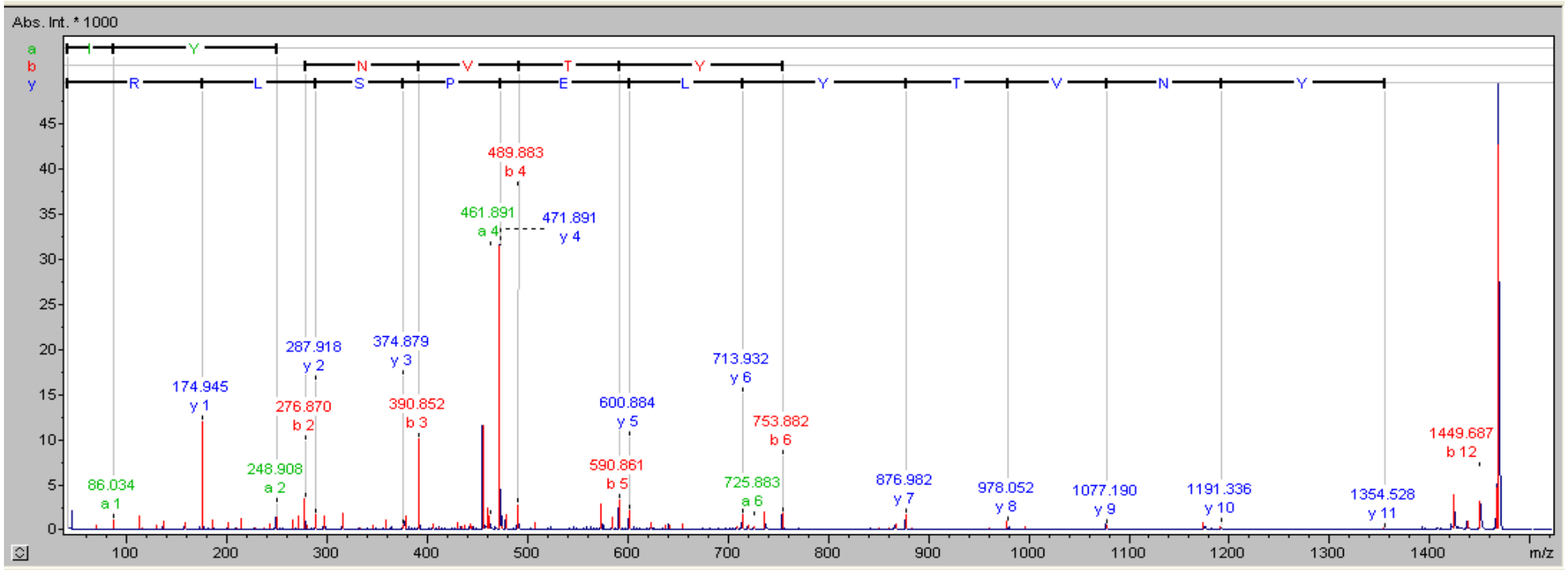
No match to: 1169.7572, 1192.0450, 1236.2238

Proteins identified from MALDI TOF/TOF

The fragmentations of selected ions were performed when the protein could not be identified from peptide mass fingerprint with a significant score. Since not all sequences of the tested proteins were available on public data, the experimental fragmentation of the recombinant autoantigens were compared to the theoretical ones either using MASCOT run on public database (NCBI nr *Homo sapiens*, release 20100616 or SwissProt *Homo sapiens* release 2010_07) or Biotools software run on single autoantigen sequence.

IL4-R, not full length protein, from 123 to 219 aa

MS/MS Fragmentation of **IYNVTYLEPSLR**



Sequence: IYNVTYLEPSLR (Mods:)

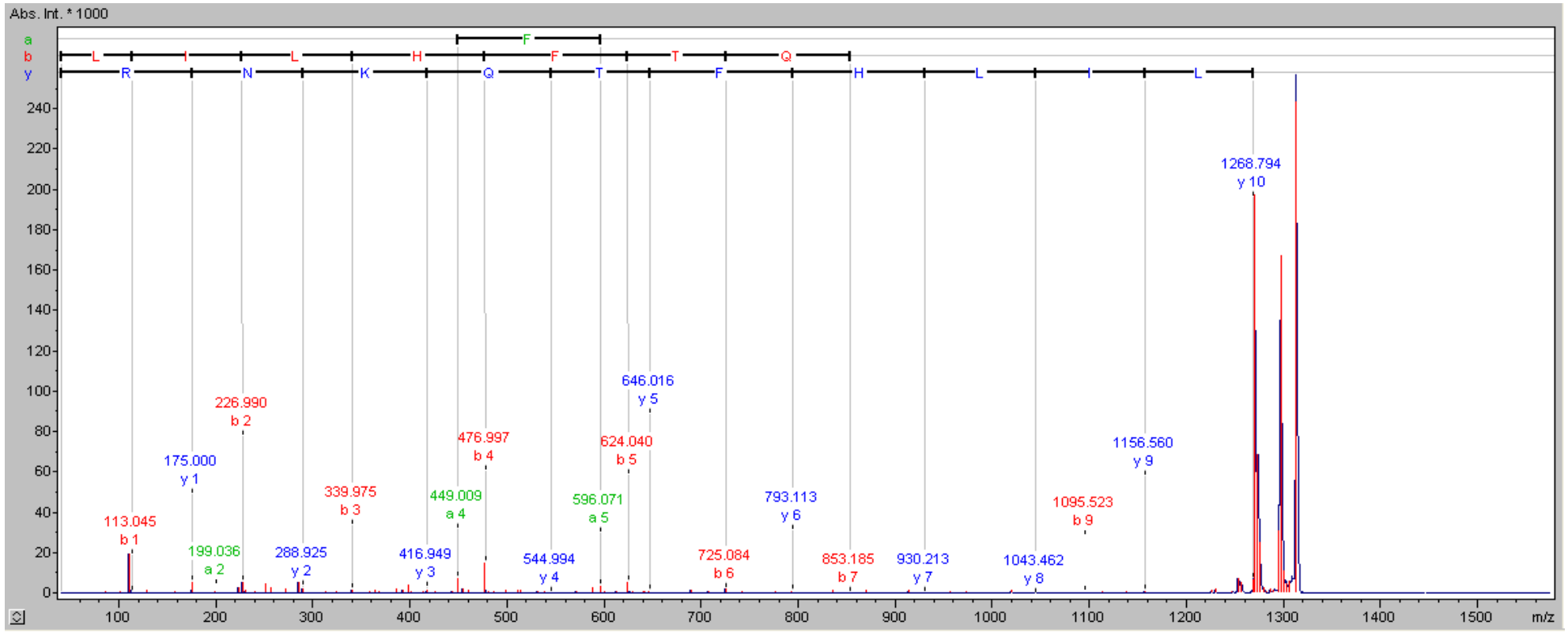
Masses: MH+(mono): 1467.784 MH+(avg): 1468.675 MS/MS Tol: 0.500 Da Peaks: 75 Above Threshold: 75 Zoom to m/z for 2+

Monoisotopic Average Calculate: Masses Threshold: 0.000 Assigned: 21 Not Assigned: 54 1+, m/z: 1467.78

	I	Y	N	V	T	Y	L	E	P	S	L	R	Ile	Tyr	Asn	Val	Thr	Tyr	Leu	Glu	Pro	Ser	Leu	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	1	2	3	4	5	6	7	8	9	10	11	12
a	I	Y	N	V	T	Y	L	E	P	S	L	R	86.096	249.160	363.203	462.271	563.319	726.382	839.466	968.509	1065.562	1152.594	1265.678	1421.779
b	I	Y	N	V	T	Y	L	E	P	S	L	R	114.091	277.155	391.198	490.266	591.314	754.377	867.461	996.504	1093.556	1180.588	1293.673	1449.774
y	I	Y	N	V	T	Y	L	E	P	S	L	R	175.119	288.203	375.235	472.288	601.330	714.414	877.478	978.525	1077.594	1191.637	1354.700	1467.784
	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Leu	Ser	Pro	Glu	Leu	Tyr	Thr	Val	Asn	Tyr	Ile

SLC22A23, not full length protein, from 123 to 219 aa

MS/MS Fragmentation of **LILHFTQKNR**



Sequence: LILHFTQKNR (Mods: N-Term: Carbamyl (N-term))

Masses: Monoisotopic Average

MH+(mono): 1268.735 MH+(avg): 1269.497 Calculate: Masses

MS/MS Tol: 1.000 Da Threshold: 0.000

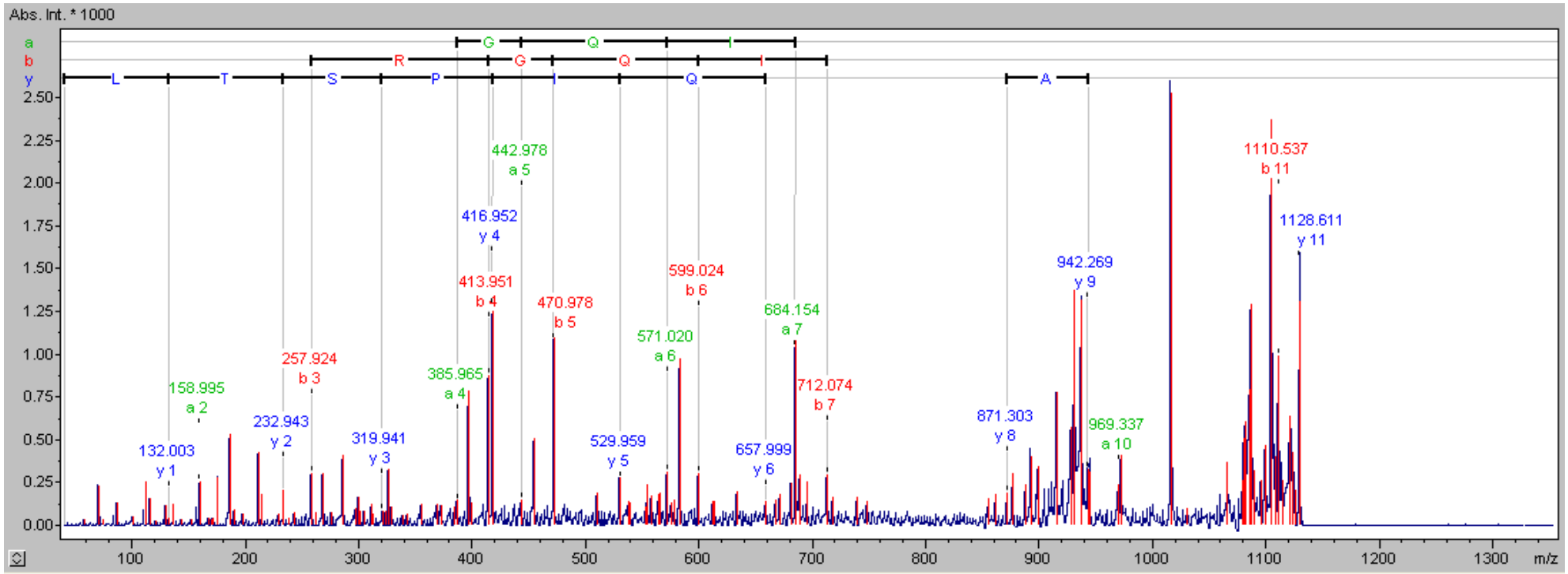
Peaks: 134 Assigned: 21 Above Threshold: 134 Not Assigned: 113

Zoom to m/z for 2+ 1+, m/z: 0.00

	L	I	L	H	F	T	Q	K	N	R	Leu	Ile	Leu	His	Phe	Thr	Gln	Lys	Asn	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
a	L	I	L	H	F	T	Q	K	N	R	85.089	198.173	311.257	448.316	595.384	696.432	824.490	952.585	1066.628	1222.729
b	L	I	L	H	F	T	Q	K	N	R	113.084	226.168	339.252	476.311	623.379	724.427	852.485	980.580	1094.623	1250.724
y	L	I	L	H	F	T	Q	K	N	R	175.119	289.162	417.257	545.315	646.363	793.432	930.490	1043.574	1156.659	1268.735
	10	9	8	7	6	5	4	3	2	1	Arg	Asn	Lys	Gln	Thr	Phe	His	Leu	Ile	Leu

UNQ5830, not full length protein, from 20 to 95 aa

MS/MS Fragmentation of **SVARGQIPSTL**



Sequence: SVARGQIPSTL (Mods:)

Masses: Monoisotopic Average

MH+(mono): 1128.637 MH+(avg): 1129.289 Calculate: Masses

MS/MS Tol: 0.500 Da Threshold: 0.000

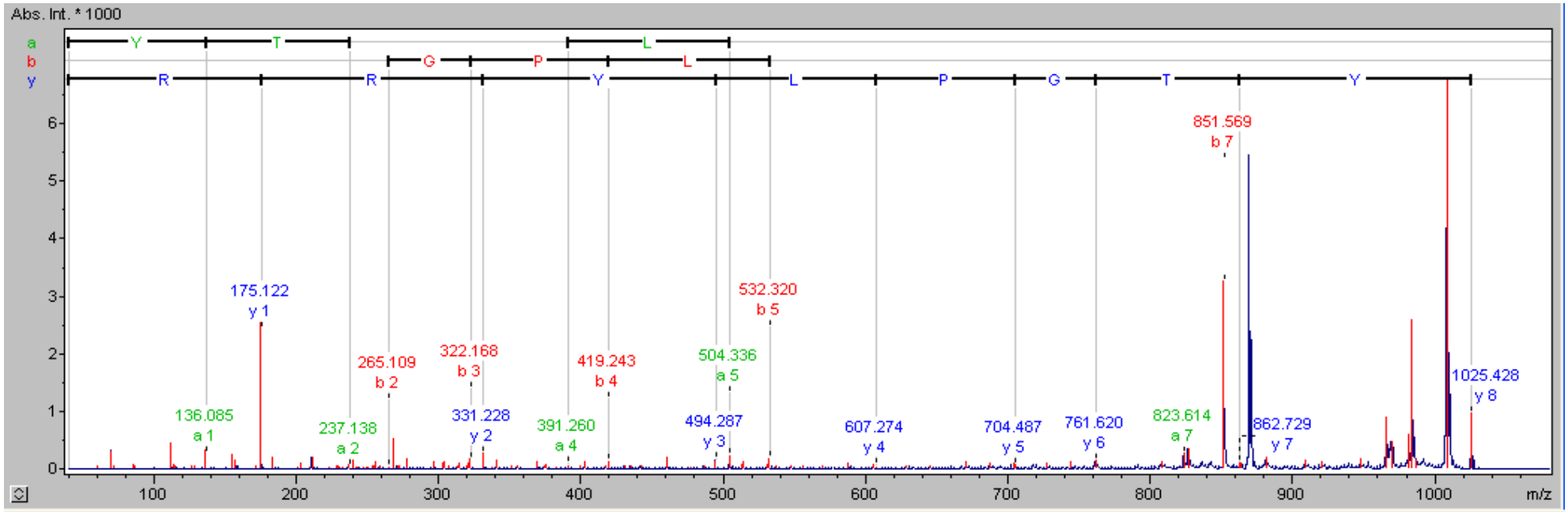
Peaks: 118 Above Threshold: 118 Assigned: 21 Not Assigned: 97

Zoom to m/z for 2+ 1+, m/z: 0.00

	S	V	A	R	G	Q	I	P	S	T	L	Ser	Val	Ala	Arg	Gly	Gln	Ile	Pro	Ser	Thr	Leu
Ion	1	2	3	4	5	6	7	8	9	10	11	1	2	3	4	5	6	7	8	9	10	11
a	S	V	A	R	G	Q	I	P	S	T	L	60.044	159.113	230.150	386.251	443.272	571.331	684.415	781.468	868.500	969.548	1082.632
b	S	V	A	R	G	Q	I	P	S	T	L	88.039	187.108	258.145	414.246	471.267	599.326	712.410	809.463	896.495	997.543	1110.627
y	S	V	A	R	G	Q	I	P	S	T	L	132.102	233.150	320.182	417.234	530.318	658.377	715.398	871.500	942.537	1041.605	1128.637
	11	10	9	8	7	6	5	4	3	2	1	Leu	Thr	Ser	Pro	Ile	Gln	Gly	Arg	Ala	Val	Ser

AL137145, not full length protein, from 83 to 183 aa

MS/MS Fragmentation of **YTGPLYRR**



Sequence: YTGPLYRR (Mods:)

Masses: Monoisotopic Average

MH+(mono): 1025.553 MH+(avg): 1026.171 Calculate: Masses

MS/MS Tol: 0.500 Da Threshold: 0.000

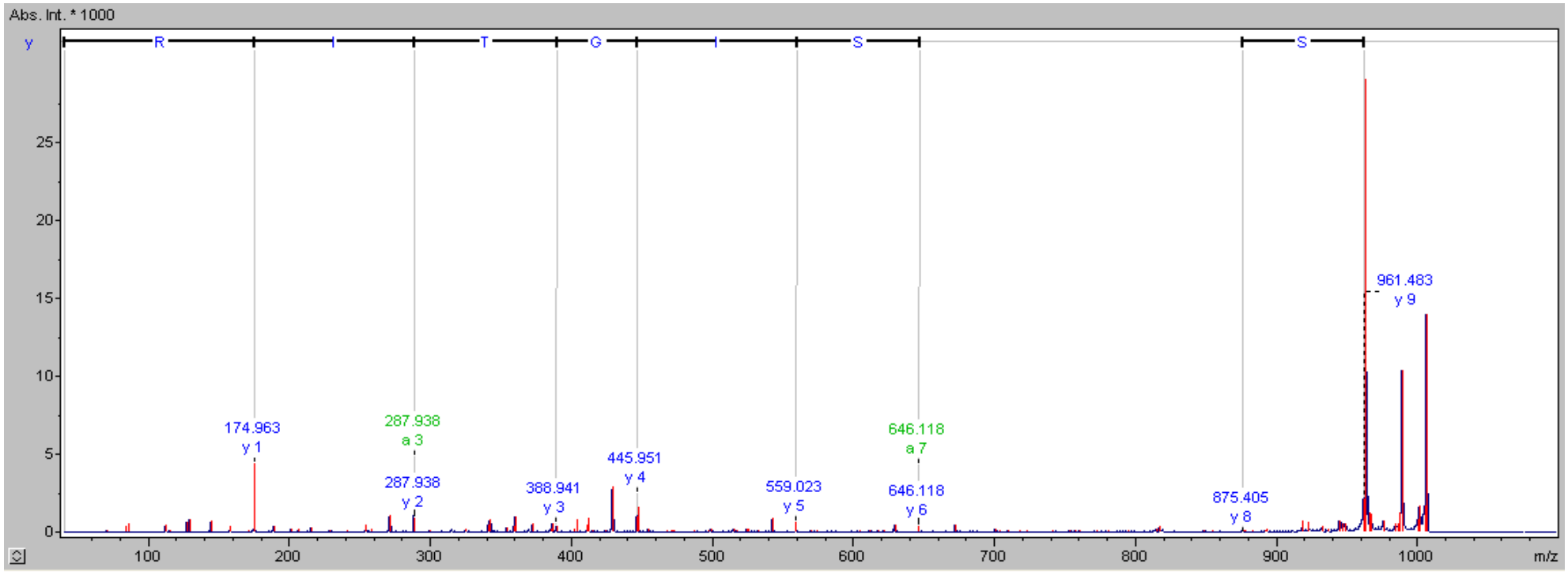
Peaks: 110 Assigned: 18 Above Threshold: 110 Not Assigned: 92

Zoom to m/z for 2+ 1+, m/z: 0.00

	Y	T	G	P	L	Y	R	R	Tyr	Thr	Gly	Pro	Leu	Tyr	Arg	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
a	Y	T	G	P	L	Y	R	R	136.076	237.123	294.145	391.198	504.282	667.345	823.446	979.547
b	Y	T	G	P	L	Y	R	R	164.071	265.118	322.140	419.193	532.277	695.340	851.441	1007.542
y	Y	T	G	P	L	Y	R	R	175.119	331.220	494.283	607.367	704.420	761.442	862.489	1025.553
	8	7	6	5	4	3	2	1	Arg	Arg	Tyr	Leu	Pro	Gly	Thr	Tyr

ZNF618, full length protein, from 16 to 107 aa

MS/MS Fragmentation of **STKSIGTIR**



Sequence: STKSIGTIR (Mods: N-Term: Carbamyl (N-term))

Masses: Monoisotopic Average

MH+(mono): 961.555 MH+(avg): 962.104 Calculate: Masses

MS/MS Tol: 0.500 Da Threshold: 0.000

Peaks: 113 Above Threshold: 113 Assigned: 10 Not Assigned: 103

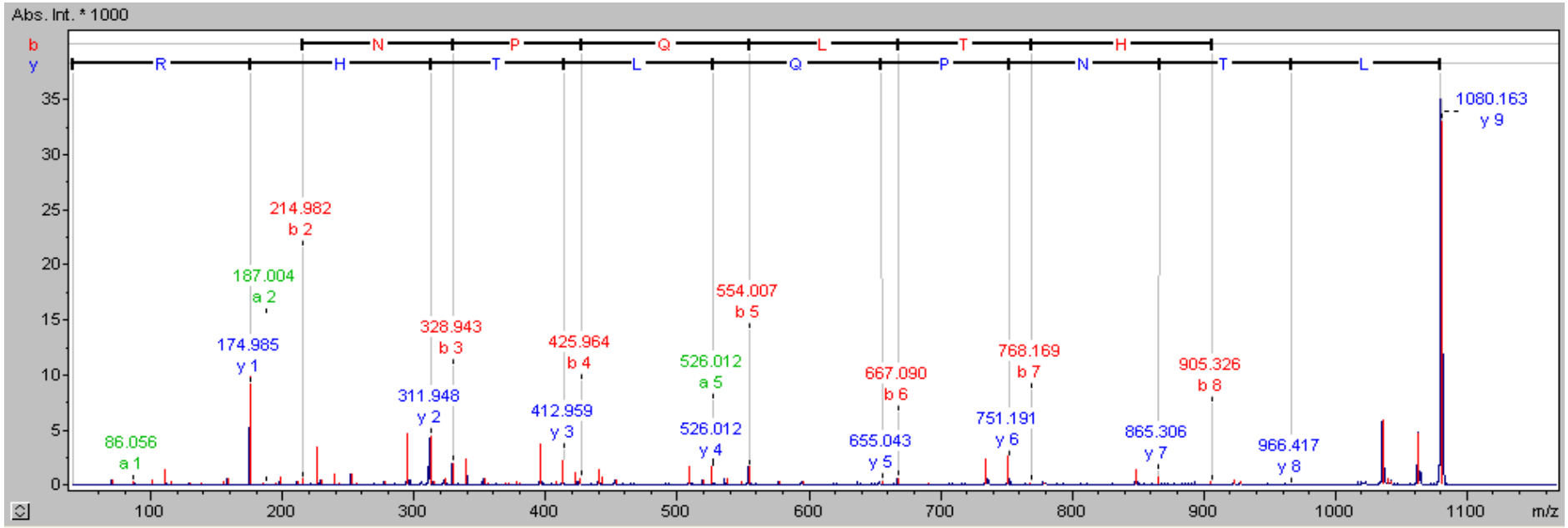
Zoom to m/z for 2+

1+, m/z: 674.36

	S	T	K	S	I	G	T	I	R	Ser	Thr	Lys	Ser	Ile	Gly	Thr	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
a	S	T	K	S	I	G	T	I	R	59.037	160.084	288.179	375.211	488.295	545.317	646.364	759.449	915.550
b	S	T	K	S	I	G	T	I	R	87.031	188.079	316.174	403.206	516.290	573.312	674.359	787.443	943.545
y	S	T	K	S	I	G	T	I	R	175.119	288.203	389.251	446.272	559.356	646.388	774.483	875.531	961.555
	9	8	7	6	5	4	3	2	1	Arg	Ile	Thr	Gly	Ile	Ser	Lys	Thr	Ser

LOC646100, full length protein, from 39 to 130 aa

Fragmentation of **LTNPQLTHR**



Sequence: LTNPQLTHR (Mods:)

Masses: Monoisotopic Average

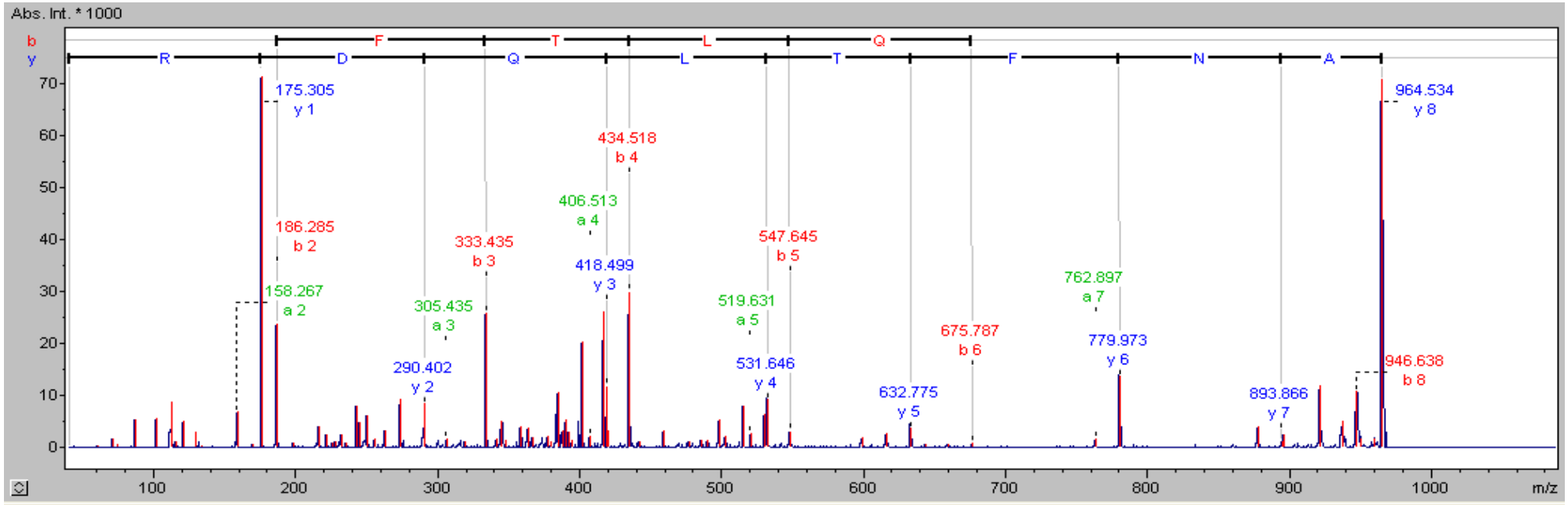
MH+(mono): 1079.596 MH+(avg): 1080.220 MS/MS Tol: 0.750 Da Peaks: 70 Above Threshold: 70 Zoom to m/z for 2+

Calculate: Masses Threshold: 0.000 Assigned: 25 Not Assigned: 45 1+, m/z: 0.00

	L	T	N	P	Q	L	T	H	R	Leu	Thr	Asn	Pro	Gln	Leu	Thr	His	Arg
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
a	L	T	N	P	Q	L	T	H	R	86.096	187.144	301.187	398.240	526.298	639.382	740.430	877.489	1033.590
b	L	T	N	P	Q	L	T	H	R	114.091	215.139	329.182	426.235	554.293	667.377	768.425	905.484	1061.585
y	L	T	N	P	Q	L	T	H	R	175.119	312.178	413.226	526.310	654.368	751.421	865.464	966.512	1079.596
i	L	T	N	P	Q	L	T	H	R	86.096	74.059	87.055	70.065	101.070	86.096	74.059	110.071	129.113
	9	8	7	6	5	4	3	2	1	Arg	His	Thr	Leu	Gln	Pro	Asn	Thr	Leu

C17orf99, full length protein, from 20 to 265 aa

MS/MS Fragmentation of ANFTLQDR



Sequence: ANFTLQDR (Mods:)

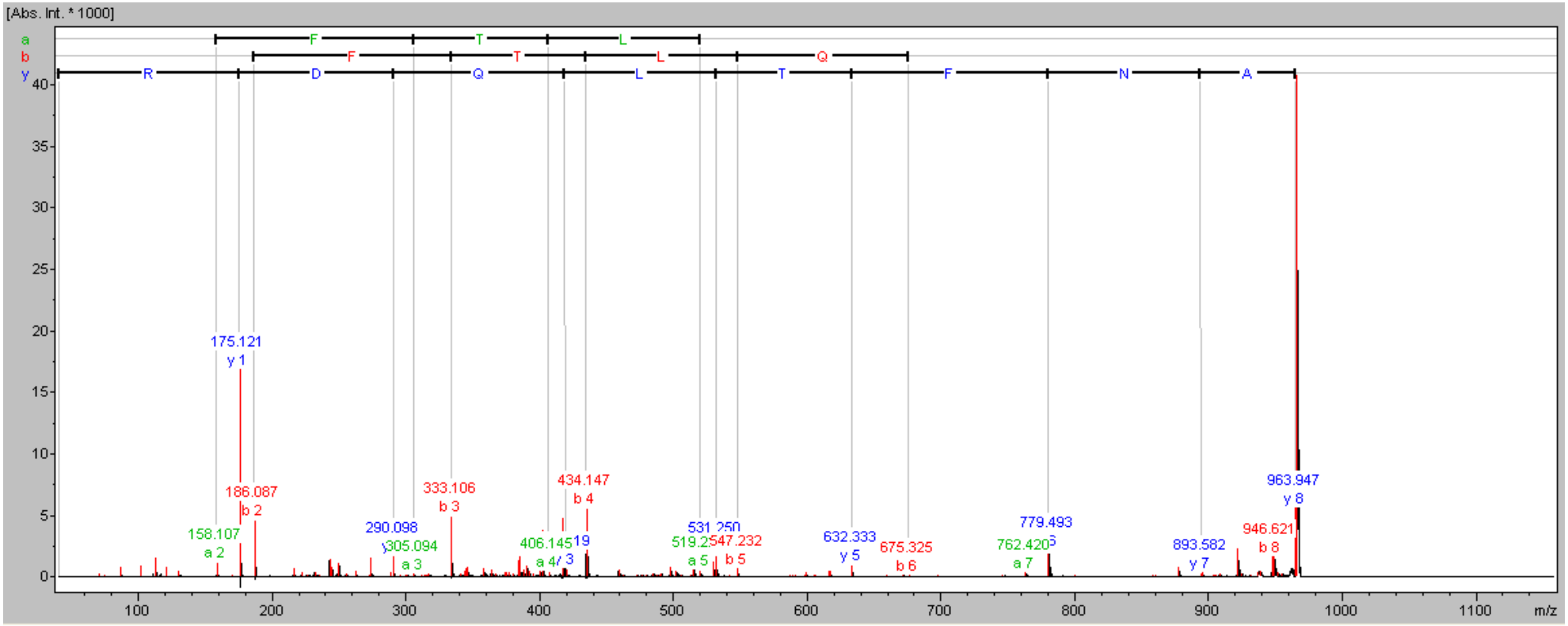
MH+(mono): 964.485 MH+(avg): 965.043 MS/MS Tol: 0.600 Da Peaks: 79 Above Threshold: 79 Zoom to m/z for 2+

Masses: Monoisotopic Average Calculate: Masses Threshold: 0.000 Assigned: 24 Not Assigned: 55 1+, m/z: 0.00

	A	N	F	T	L	Q	D	R	Ala	Asn	Phe	Thr	Leu	Gln	Asp	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
a	A	N	F	T	L	Q	D	R	44.049	158.092	305.161	406.208	519.293	647.351	762.378	918.479
b	A	N	F	T	L	Q	D	R	72.044	186.087	333.156	434.203	547.287	675.346	790.373	946.474
y	A	N	F	T	L	Q	D	R	175.119	290.146	418.204	531.289	632.336	779.405	893.448	964.485
i	A	N	F	T	L	Q	D	R	44.049	87.055	120.080	74.059	86.096	101.070	88.039	129.113
	8	7	6	5	4	3	2	1	Arg	Asp	Gln	Leu	Thr	Phe	Asn	Ala

C17orf99, not full length protein, from 57 to 180 aa

MS/MS Fragmentation of **ANFTLQDR**



Sequence: ANFTLQDR (Mods:)

Masses: Monoisotopic / Average

MH+(mono): 964.485 MH+(avg): 965.043 Calculate: Masses

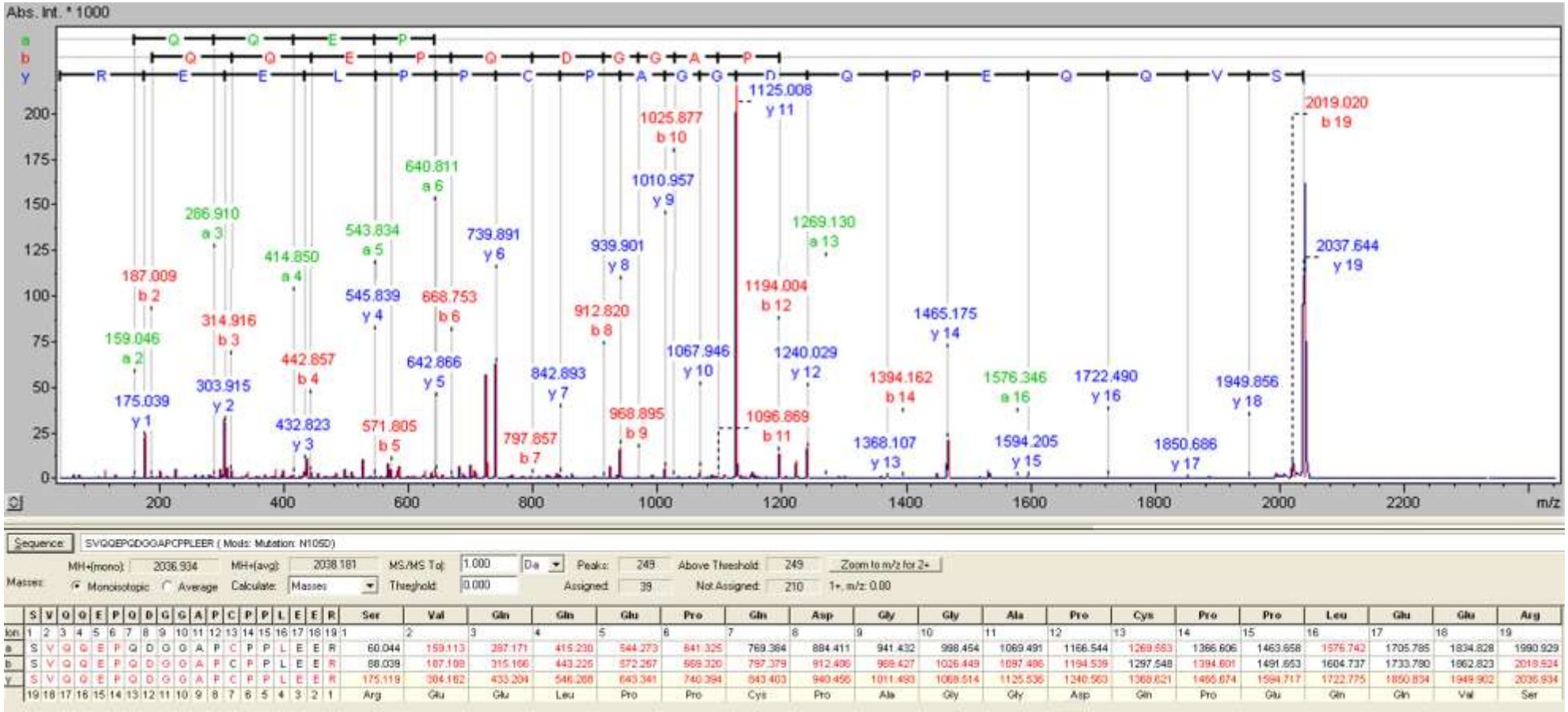
MS/MS Tol: 1.000 Threshold: 0.000

Peaks: 126 Above Threshold: 126 Assigned: 19 Not Assigned: 107

	A	N	F	T	L	Q	D	R	Ala	Asn	Phe	Thr	Leu	Gln	Asp	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
a	A	N	F	T	L	Q	D	R	44.049	158.092	305.161	406.208	519.293	647.351	762.378	918.479
b	A	N	F	T	L	Q	D	R	72.044	186.087	333.156	434.203	547.287	675.346	790.373	946.474
y	A	N	F	T	L	Q	D	R	175.119	290.146	418.204	531.289	632.336	779.405	893.448	964.485
	8	7	6	5	4	3	2	1	Arg	Asp	Gln	Leu	Thr	Phe	Asn	Ala

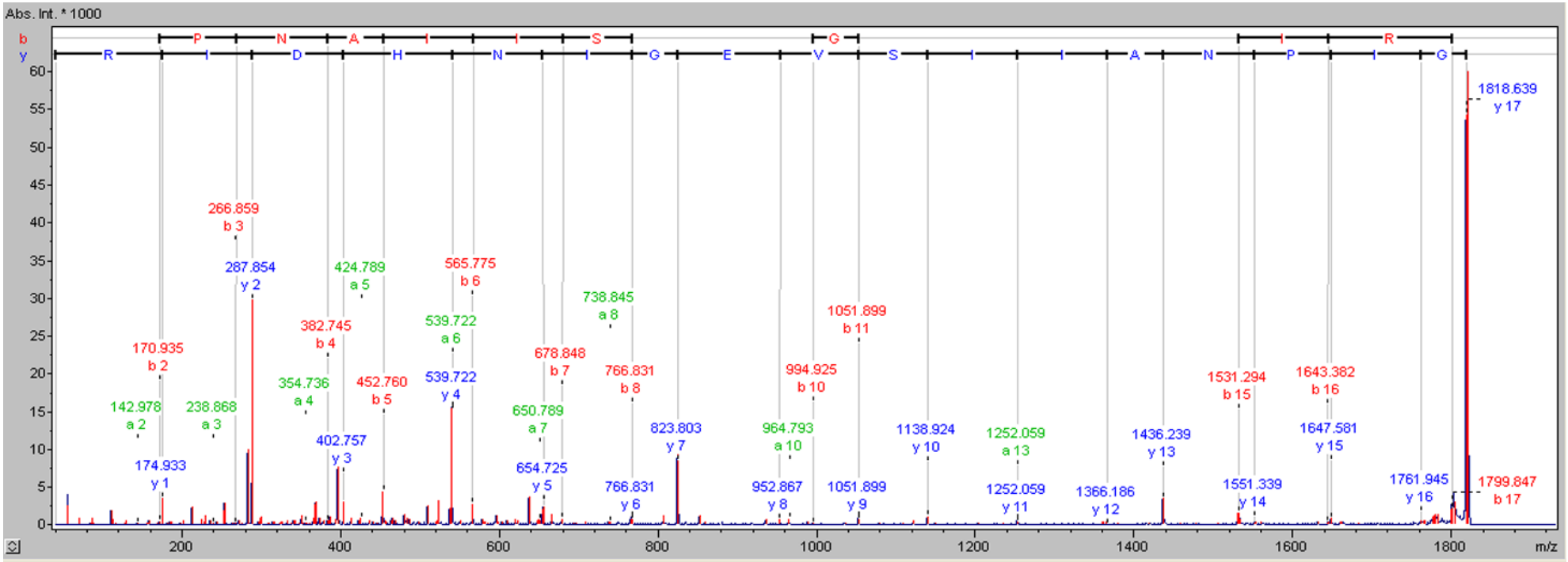
C8orf84, not full length protein, from 15 to 125 aa

MS/MS Fragmentation of **SVQQEPQDGGAPCPPLEER**



CPXM2, not full length protein, from 607 to 731 aa

MS/MS Fragmentation of **GIPNAIISVEGINHDIR**



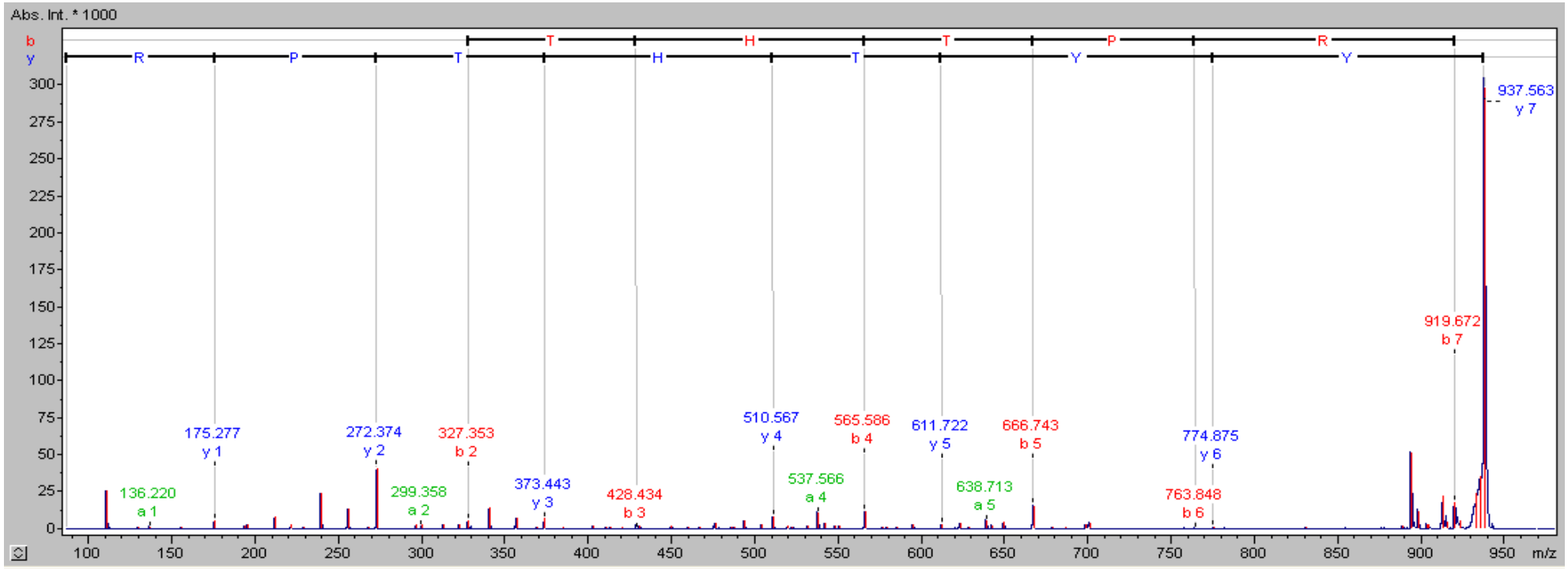
Sequence: GIPNAIISVEGINHDIR (Mods:)

Masses: Monoisotopic Average | MH+(mono): 1817.987 | MH+(avg): 1819.051 | Calculate: Masses | MS/MS Tol: 2.000 Da | Threshold: 0.000 | Peaks: 195 | Assigned: 50 | Above Threshold: 195 | Not Assigned: 145 | Zoom to m/z for 2+ | 1+, m/z: 0.00

	G	I	P	N	A	I	I	S	V	E	G	I	N	H	D	I	R	Gly	Ile	Pro	Asn	Ala	Ile	Ile	Ser	Val	Glu	Gly	Ile	Asn	His	Asp	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
a	G	I	P	N	A	I	I	S	V	E	G	I	N	H	D	I	R	30.034	143.118	240.171	354.214	425.251	538.335	651.419	738.451	837.519	966.562	1023.583	1136.667	1250.710	1387.769	1502.796	1615.880	1771.981
b	G	I	P	N	A	I	I	S	V	E	G	I	N	H	D	I	R	58.029	171.113	268.166	382.208	453.246	566.330	679.414	766.446	865.514	994.557	1051.578	1164.662	1278.705	1415.764	1530.791	1643.875	1799.976
y	G	I	P	N	A	I	I	S	V	E	G	I	N	H	D	I	R	175.119	288.203	403.230	540.289	654.332	767.416	824.437	953.480	1052.548	1139.580	1252.664	1365.748	1436.786	1550.829	1647.881	1760.965	1817.987
i	G	I	P	N	A	I	I	S	V	E	G	I	N	H	D	I	R	30.034	86.096	70.065	87.055	44.049	86.096	86.096	60.044	72.080	102.054	30.033	86.096	87.055	110.071	88.039	86.096	129.113
	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ile	Asp	His	Asn	Ile	Gly	Glu	Val	Ser	Ile	Ile	Ala	Asn	Pro	Ile	Gly

LOC648852, not full length protein, from 23 to 121 aa

MS/MS Fragmentation of **YYTHTPR**



Sequence: YYTHTPR (Mods:)

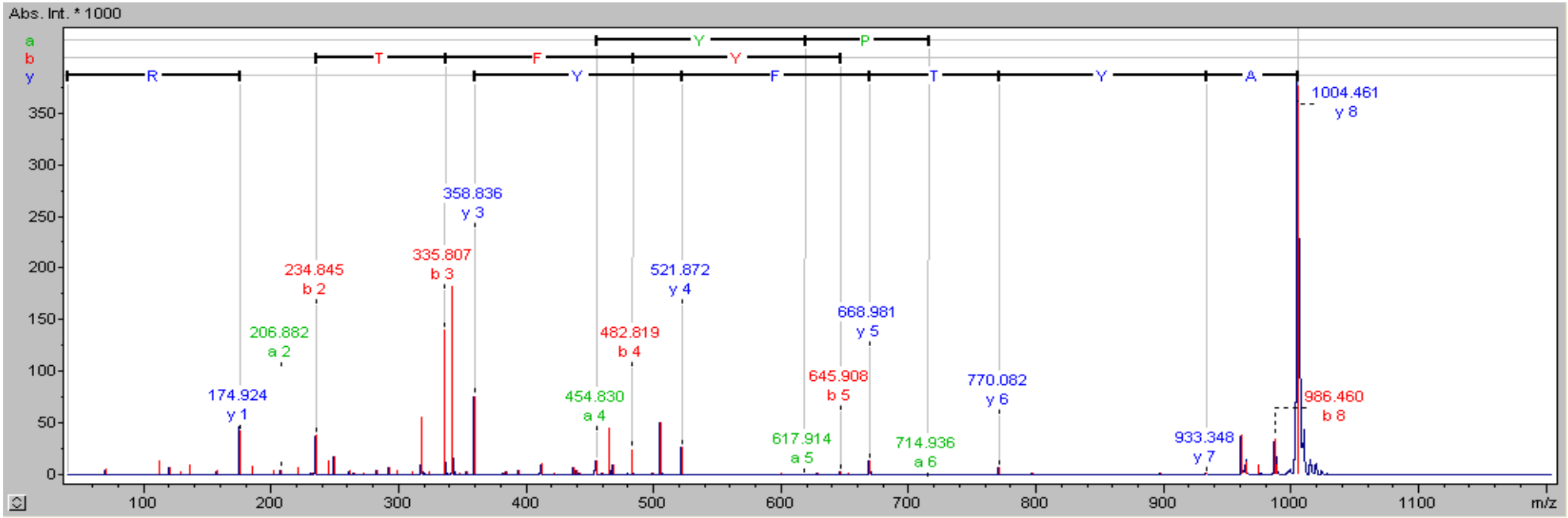
MH+(mono): 937.453 MH+(avg): 938.019 MS/MS Tol: 0.750 Da Peaks: 91 Above Threshold: 91 Zoom to m/z for 2+

Masses: Monoisotopic Average Calculate: Masses Threshold: 0.000 Assigned: 24 Not Assigned: 67 1+, m/z: 0.00

	Y	Y	T	H	T	P	R	Tyr	Tyr	Thr	His	Thr	Pro	Arg
Ion	1	2	3	4	5	6	7	1	2	3	4	5	6	7
a	Y	Y	T	H	T	P	R	136.076	299.139	400.187	537.246	638.293	735.346	891.447
b	Y	Y	T	H	T	P	R	164.071	327.134	428.182	565.241	666.288	763.341	919.442
y	Y	Y	T	H	T	P	R	175.119	272.172	373.219	510.278	611.326	774.389	937.453
i	Y	Y	T	H	T	P	R	136.076	136.075	74.059	110.071	74.059	70.065	129.113
	7	6	5	4	3	2	1	Arg	Pro	Thr	His	Thr	Tyr	Tyr

APCDD1L, not full length protein, from 24 to 135 aa

MS/MS Fragmentation of **AYTFYPSR**



Sequence: AYTFYPSR (Mods:)

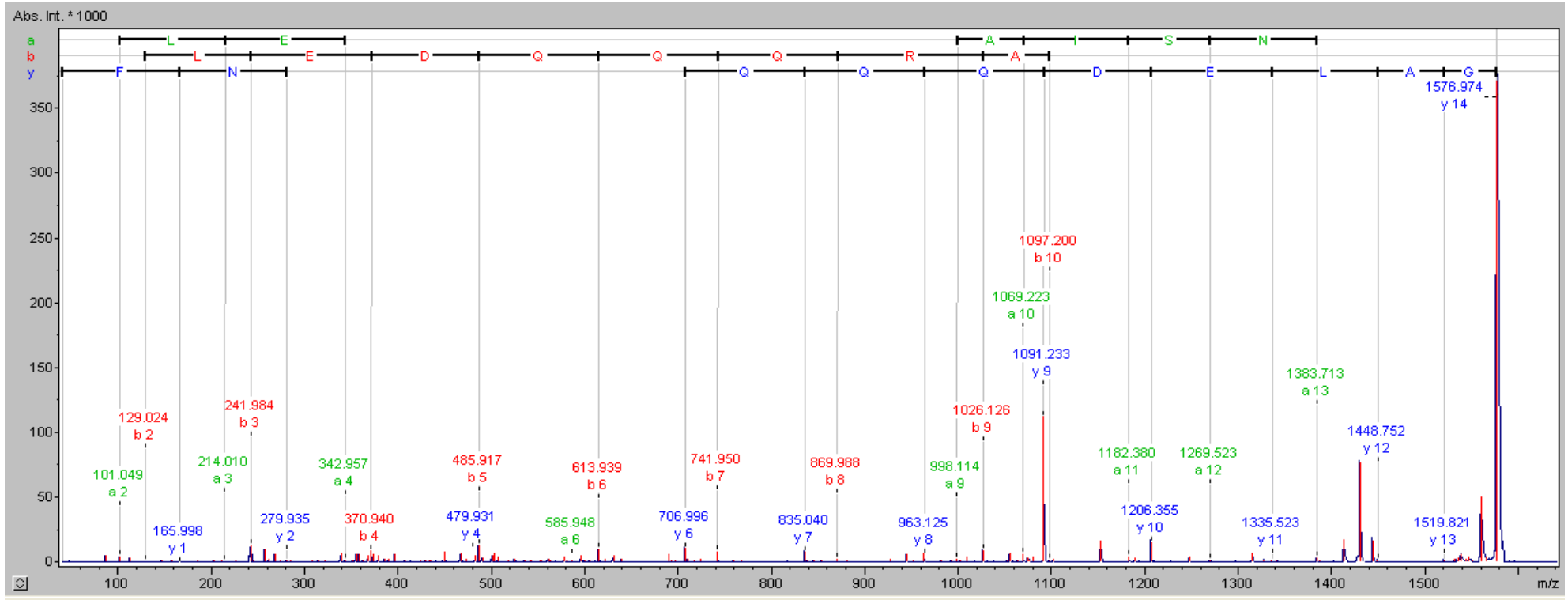
MH+(mono): 1004.484 MH+(avg): 1005.105 MS/MS Tol: 0.500 Da Peaks: 87 Above Threshold: 87 Zoom to m/z for 2+

Masses: Monoisotopic Average Calculate: Masses Threshold: 0.000 Assigned: 16 Not Assigned: 71 1+, m/z: 0.00

	A	Y	T	F	Y	P	S	R	Ala	Tyr	Thr	Phe	Tyr	Pro	Ser	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
a	A	Y	T	F	Y	P	S	R	44.049	207.113	308.160	455.229	618.292	715.345	802.377	958.478
b	A	Y	T	F	Y	P	S	R	72.044	235.108	336.155	483.224	646.287	743.340	830.372	986.473
y	A	Y	T	F	Y	P	S	R	175.119	262.151	359.204	522.267	669.335	770.383	933.446	1004.484
	8	7	6	5	4	3	2	1	Arg	Ser	Pro	Tyr	Phe	Thr	Tyr	Ala

SLC46A2, not full length protein, from 1 to 77 aa

MS/MS Fragmentation of **GALEDQQQRAISNF**



Sequence: GALEDQQQRAISNF (Mods:)

Masses: MH+(mono): 1576.771 MH+(avg): 1577.677 MS/MS Tol: 0.500 Da Peaks: 164 Above Threshold: 164 Zoom to m/z for 2+

Monoisotopic Average Calculate: Masses Threshold: 0.000 Assigned: 30 Not Assigned: 134 1+, m/z: 0.00

	G	A	L	E	D	Q	Q	Q	R	A	I	S	N	F	Gly	Ala	Leu	Glu	Asp	Gln	Gln	Gln	Arg	Ala	Ile	Ser	Asn	Phe
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
a	G	A	L	E	D	Q	Q	Q	R	A	I	S	N	F	30.034	101.071	214.155	343.198	458.225	586.283	714.342	842.400	998.501	1069.538	1182.623	1269.655	1383.698	1530.766
b	G	A	L	E	D	Q	Q	Q	R	A	I	S	N	F	58.029	129.066	242.150	371.193	486.219	614.278	742.337	870.395	1026.496	1097.533	1210.617	1297.650	1411.692	1558.761
y	G	A	L	E	D	Q	Q	Q	R	A	I	S	N	F	166.086	280.129	367.161	480.245	551.282	707.383	835.442	963.501	1091.559	1206.586	1335.629	1448.713	1519.750	1576.771
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Phe	Asn	Ser	Ile	Ala	Arg	Gln	Gln	Gln	Asp	Glu	Leu	Ala	Gly