Wang et al. "Arginylation of intact proteins in vivo involves a novel type of Arg linkage to amino acid side chains."

SUPPLEMENTAL ONLINE INFORMATION

Experimental Procedures.

Escherichia coli strains, Miscellaneous Reagents and Animal Care. BL21-CodonPlus® (DE3)-RIL and BL21(DE3) were purchased from Stratagene (USA). The recombinant mouse ATE1 isoforms and Escherichia coli Arginy-tRNA synthetase (RRS) were purified as previously described [13]. The care and treatment of mice were performed in accordance with the relevant National Institutes of Health (NIH) guidelines.

Peptides. Human angiotensin II (A9525) was purchased from Sigma; Acetylated and non-acetylated actin N-terminal peptide were synthesized by Dr. Henry Zebroski at the Rockefeller University Proteomics Resource Center; non-arginylated long actin N-terminal peptide, DN, DN-Me, and DN-All were synthesized by Genscript.

In vitro arginylation of peptides. In vitro arginylation reaction of peptides by ATE1 was modified from [13]. A typical reaction was performed in 100 µl volume, containing 50 mM Hepes, pH 7.5, 25 mM KCl, 15 mM $MgCl_2$, 0.1 mM DTT, 3 mM ATP, 1 mM Arginine, 100 µM tRNA-Arg from E.coli (Chemical Block), 6 µM RRS, 3 µM ATE1 and 100 µM peptide substrate. Reaction was mixed and incubated at 37 °C for 1 hour, followed by heating at 95^{o}C for 15 min, cooling down on ice for 20 min, and spinning at 13,000 rpm for 15 min in a tabletop microfuge. The supernatants were loaded onto C18 spin columns (The Nest Group, Inc.) prewashed with 100% acetonitrile and water, then washed with 0.1% trifluoroacetic acid (TFA) and eluted with 60% acetonitrile/0.1%TFA in water. The eluted peptide was dried with speed vacuum and re-dissolved in 0.1% TFA in water for further analysis. L-[^{13}C,^{15}N]-Arginine (Pierce) was used for arginylation of peptides for mass spectrometry and NMR, and L-Arginine (Sigma) was used for Edman sequencing. For NMR analysis, arginylated peptides were further purified by HPLC, lyophilized, and dissolved in 20 mM K_2HPO_4/KH_2PO_4 buffer, pH 6.0 and adjusted to the concentration to 1mM. To evaluate the arginylation efficiency, 12.5 µM L-[2,3,4-3H]-Arginine (PerkinElmer) instead of “cold” arginine was used in the reaction and the concentrations of $tRNA^{Arg}$ and peptides were adjusted to 50 µM. After purification with C18 spin columns, arginylated peptides were counted in a liquid scintillation counter and evaluated as counts per minute (cpm) of [3H]-Arg.

Mass spectrometry and database searches. Sample preparation and tandem MS/MS were performed as previously described [2, 14]. Protein identification was performed with Integrated Proteomics Pipeline - IP2 (Integrated Proteomics Applications, Inc., San Diego, CA. http://www.integratedproteomics.com/) using ProLuCID and DTASelect2 [14]. Spectrum raw files were extracted into ms1 and ms2 files from raw files using RawExtract 1.9.9 (http://fields.scripps.edu/downloads.php) [15], and the tandem mass spectra were searched against NCBI RefSeq protein database (http://www.ncbi.nlm.nih.gov/refseq/, downloaded on May 17, 2010). In order to accurately estimate peptide probabilities and false discovery rates, we used a decoy database containing the reversed sequences of all the proteins appended to the target database. Tandem mass spectra were matched to sequences using the ProLuCID algorithm with 50 ppm peptide mass tolerance. ProLuCID searches were done on an Intel Xeon cluster running under the Linux operating system. The search space included all fully tryptic peptide candidates that fell within the mass tolerance window with maximum 2 miscleavages. Carbamidomethylation (+57.02146 Da) of cysteine was considered as a static modification, arginylation (+156.1011 or + 166.1093) on Aspartic acid and Glutamic acid residues were considered as variable modifications.

The validity of peptide/spectrum matches (PSMs) was assessed with DTASelect2 using two SEQUEST defined parameters, the cross-correlation score (XCorr), and normalized difference in cross-correlation scores (DeltaCN). The search results were grouped by charge state (+1, +2, +3, and greater than +3) and tryptic status (fully tryptic, half-tryptic, and non-tryptic), resulting in 12 distinct sub-groups. In each one of these sub-groups, the distribution of XCorr, DeltaCN, and DeltaMass values for (a) direct and (b) decoy database PSMs was obtained, then the direct and decoy subsets were separated by discriminant analysis. Full separation of the direct and decoy PSM subsets is not generally possible; therefore, peptide match probabilities were calculated based on a nonparametric fit of the direct and decoy score distributions. A peptide confidence of 95% was set as the minimum threshold and only peptides with delta mass less than 5 ppm were accepted. The false discovery rate was calculated as the percentage of reverse decoy PSMs among all the PSMs that passed the 95% confidence threshold. After this last filtering step, we estimate that the peptide false discovery rates were below 1%. See [14] for further details on manual data validation.

Subtractive Edman degradation. For the Edman reaction, the phenylisothiocyanate (PITC) was purchased from Pierce. All other reagents were from

Sigma Aldrich. The peptide was initially dissolved in 50% aqueous pyridine and then an equal volume of 5% PITC in pyridine was added. The coupling reaction was performed by heating for 10 minutes at 50 degrees Celsius. Extractions were performed twice with 2:1 heptane/ethyl acetate solution and then lyophilized. Cleavage was performed using anhydrous TFA and the reaction was performed for 5 minutes at 37 degrees Celsius and then lyophilized. The peptide was dissolved in water and two volumes of n-butyl acetate were added. The mixture was shaken and the acetate layer was removed after separation. The peptide was lyophilized prior to mass spectrometry analysis.

NMR experiments. All NMR spectra were recorded on a Bruker Avance II 600 MHz NMR spectrometer, equipped with a Bruker TCI triple resonance cryoprobe. All NMR samples were prepared by dissolving the lyophilized compounds in a buffer with 50 mM sodium phosphate, 50 mM NaCl, and pH 6.3. The concentrations of the samples were around 0.5 mM. The spectra were recorded with Bruker Topspin standard pulse sequences at 25 °C, and the spectra were processed with Bruker Topspin software based on the manufacture suggestions.

Analysis of the sequence context around the arginylated sites. Sequence fragments of specified lengths (+/- 5, 10 or 20 positions) around the arginylated sites were extracted from the database and the overlapping fragments (resulting from closely located sites) were merged together. Frequencies of occurrence of each amino acid in the vicinity of the arginylated sites were compared to those in the full-length proteins; the significance of the deviation for each amino acid was estimated using the binomial approximation with Bonferroni correction (binomial p-values were multiplied by a factor of 20 to account for comparison of 20 amino acids). To avoid bias, titin, the longest protein in the mouse genome, was excluded from the analysis.

Statistical analysis. Calculation of standard deviation (SD) and standard error of mean (S.E.M.) was based on Student's t-distribution.

Supplemental Figure and Table Legends.

Figure S1 (related to Figure 2). Normalized side chain incorporation of Arg into a standard peptide in the presence and absence of tRNA. Error bar represents SEM, n=3

Figure S2 (related to Figures 2 and 3). MALDI TOF spectrograms showing the standard enzymatically arginylated peptide (R)-DDIAALVVDNGSGMCK before (left) and after (right) the first Edman degradation cycle. The peptide mass has reduced by one Arg, confirming its N-terminal linkage to the peptide.

Figure S3 (related to Figure 3). Colorimetric assay with Aminopeptidase B in the absence (red) and presence (green) of the inhibitor Bestatin.

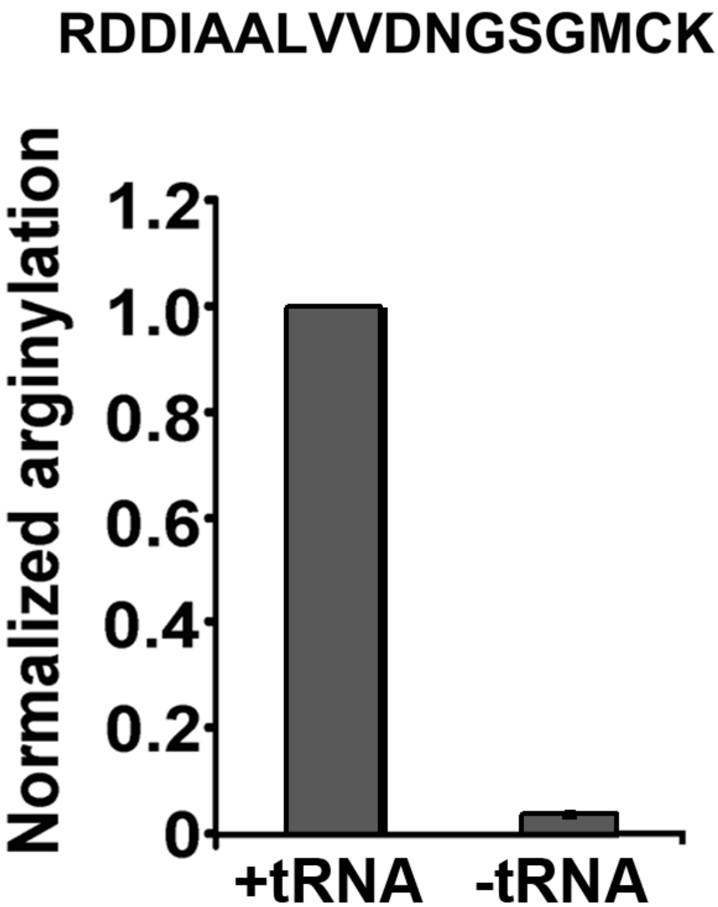
Supplemental Table 1 (related to Figure 1 and Table 1). Protein sites arginylated in vivo on the side chains of Asp and Glu showing the homology of these sites to other isoforms of the identified proteins.

Supplemental Table 2 (related to Figure 1 and Table 1). Parameters of the identified peptides.

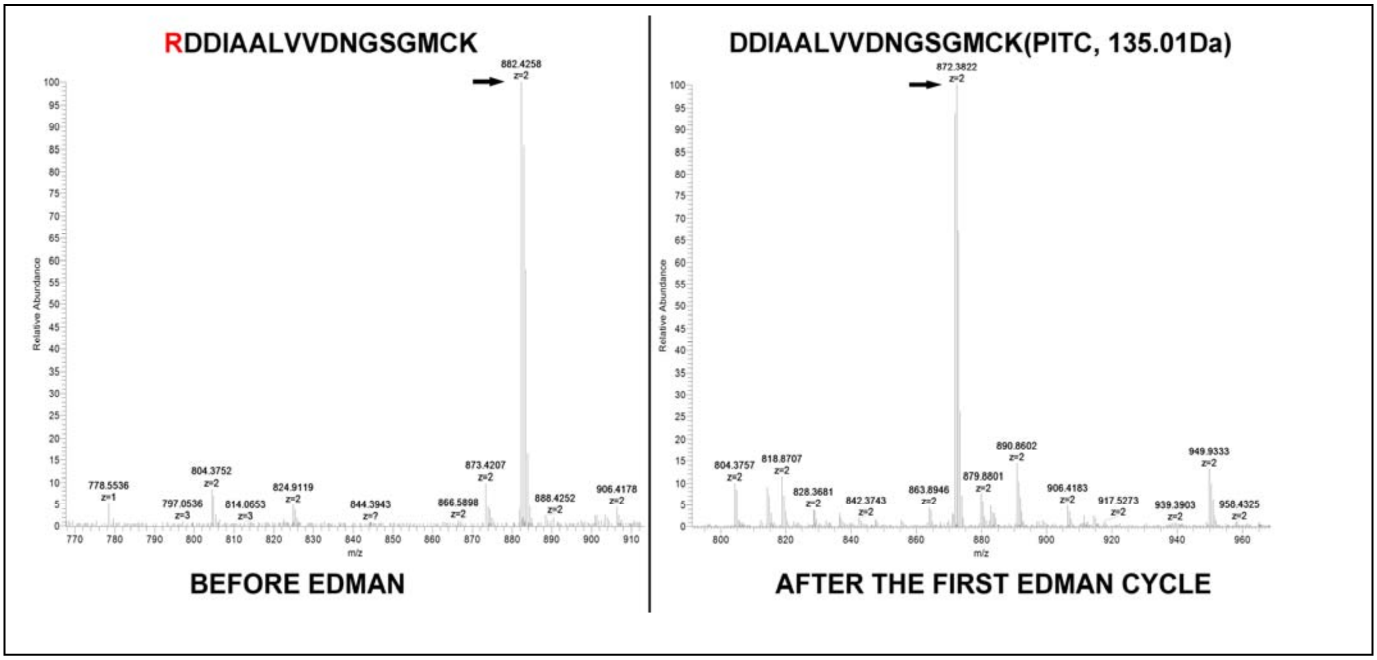
Supplemental Table 3 (related to Figure 1 and Table 1). Frequencies of amino acid occurrence within 5, 10, and 20 flanking residues to the arginylation sites.

Supplemental Dataset (related to Figure 1 and Table 1). Mass spectra of the identified side chain arginylated peptides.

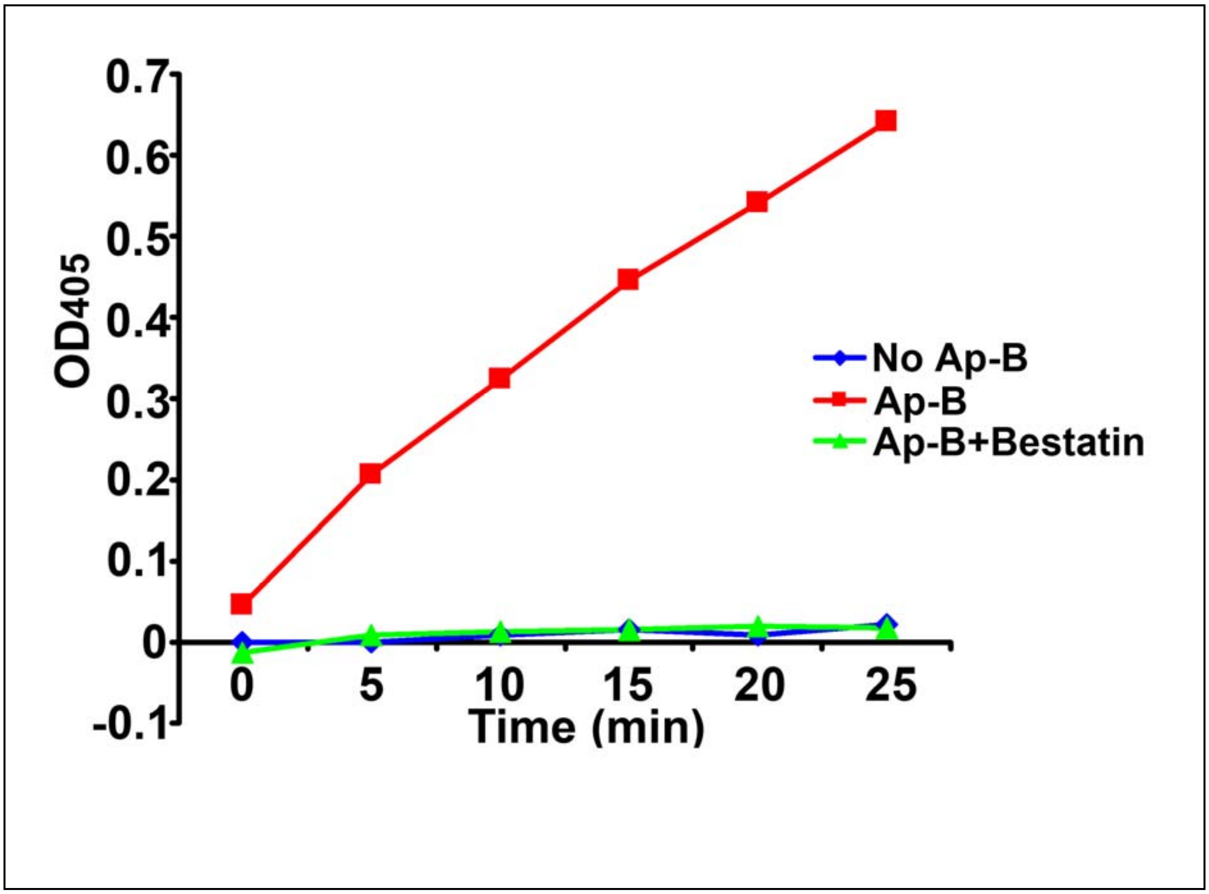
Wang_et_al_Supplemental Figure 1



Wang_et_al_Supplemental Figure 2



Wang_et_al_Supplemental_Figure_3



SUPPLEMENTAL DATASET

Mass spectra of the side chain arginylated peptides identified in vivo.

TTGIVLDSGDGVTHNVPIYEGYALPHAIMR, MH+ 3352.7107, m/z 1118.2417

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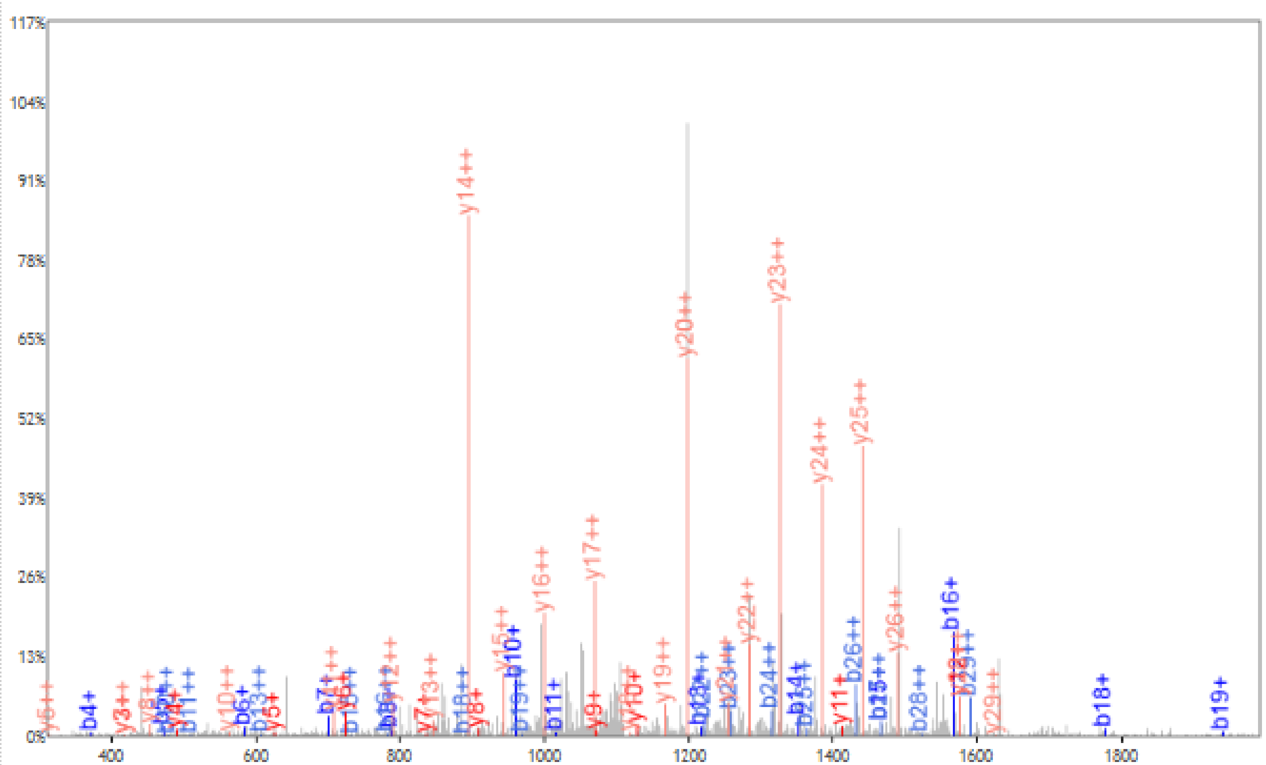

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260.1241	130.5657	3	G	28	3150.6153	1575.8113
373.2082	187.1077	4	I	27	3093.5938	1547.3006
472.2766	236.6419	5	V	26	2980.5098	1490.7585
585.3606	293.1840	6	L	25	2881.4414	1441.2243
700.3876	350.6974	7	D	24	2768.3573	1384.6823
787.4196	394.2134	8	S	23	2653.3304	1327.1688
844.4411	422.7242	9	G	22	2566.2983	1283.6528
959.4680	480.2376	10	D	21	2509.2769	1255.1421
1016.4895	508.7484	11	G	20	2394.2499	1197.6286
1115.5579	558.2826	12	V	19	2337.2285	1169.1179
1216.6056	608.8064	13	T	18	2238.1600	1119.5837
1353.6645	677.3359	14	H	17	2137.1124	1069.0598
1467.7074	734.3573	15	N	16	2000.0535	1000.5304
1566.7758	783.8916	16	V	15	1886.0105	943.5089
1663.8286	832.4179	17	P	14	1786.9421	893.9747
1776.9127	888.9600	18	I	13	1689.8893	845.4483
1939.9760	970.4916	19	Y	12	1576.8053	788.9063
2225.1197	1113.0635	20	E	11	1413.7420	707.3746
2282.1411	1141.5742	21	G	10	1128.5983	564.8028
2445.2045	1223.1059	22	Y	9	1071.5768	536.2920
2516.2416	1258.6244	23	A	8	908.5135	454.7604
2629.3256	1315.1665	24	L	7	837.4764	419.2418
2726.3784	1363.6928	25	P	6	724.3923	362.6998
2863.4373	1432.2223	26	H	5	627.3395	314.1734
2934.4744	1467.7409	27	A	4	490.2806	245.6439
3047.5585	1524.2829	28	I	3	419.2435	210.1254
3178.5990	1589.8031	29	M	2	306.1594	153.5834
		30	R	1	175.1190	88.0631

VAPEEHPTLLTEAPLNPK, MH+ 2112.1448, m/z 704.7198

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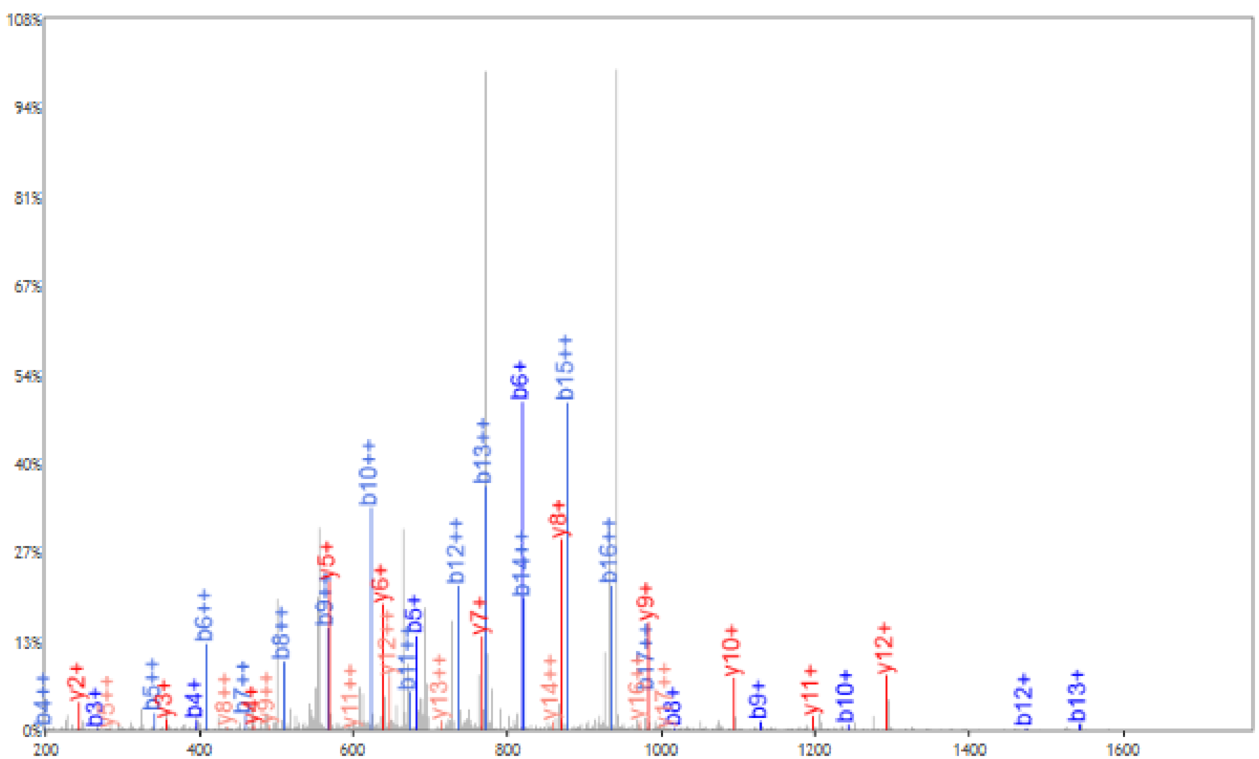

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397.2082	199.1077	4	E	15	1844.9865	922.9969
682.3519	341.6796	5	E	14	1715.9439	858.4756
819.4108	410.2090	6	H	13	1430.8002	715.9037
916.4635	458.7354	7	P	12	1293.7413	647.3743
1017.5112	509.2592	8	T	11	1196.6885	598.8479
1130.5953	565.8013	9	L	10	1095.6408	548.3241
1243.6793	622.3433	10	L	9	982.5568	491.7820
1344.7270	672.8671	11	T	8	869.4727	435.2400
1473.7696	737.3884	12	E	7	768.4250	384.7162
1544.8067	772.9070	13	A	6	639.3824	320.1949
1641.8595	821.4334	14	P	5	568.3453	284.6763
1754.9435	877.9754	15	L	4	471.2926	236.1499
1868.9865	934.9969	16	N	3	358.2085	179.6079
1966.0392	983.5233	17	P	2	244.1656	122.5864
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C: 57.02146

Variable Modifications:

E: 156.1011

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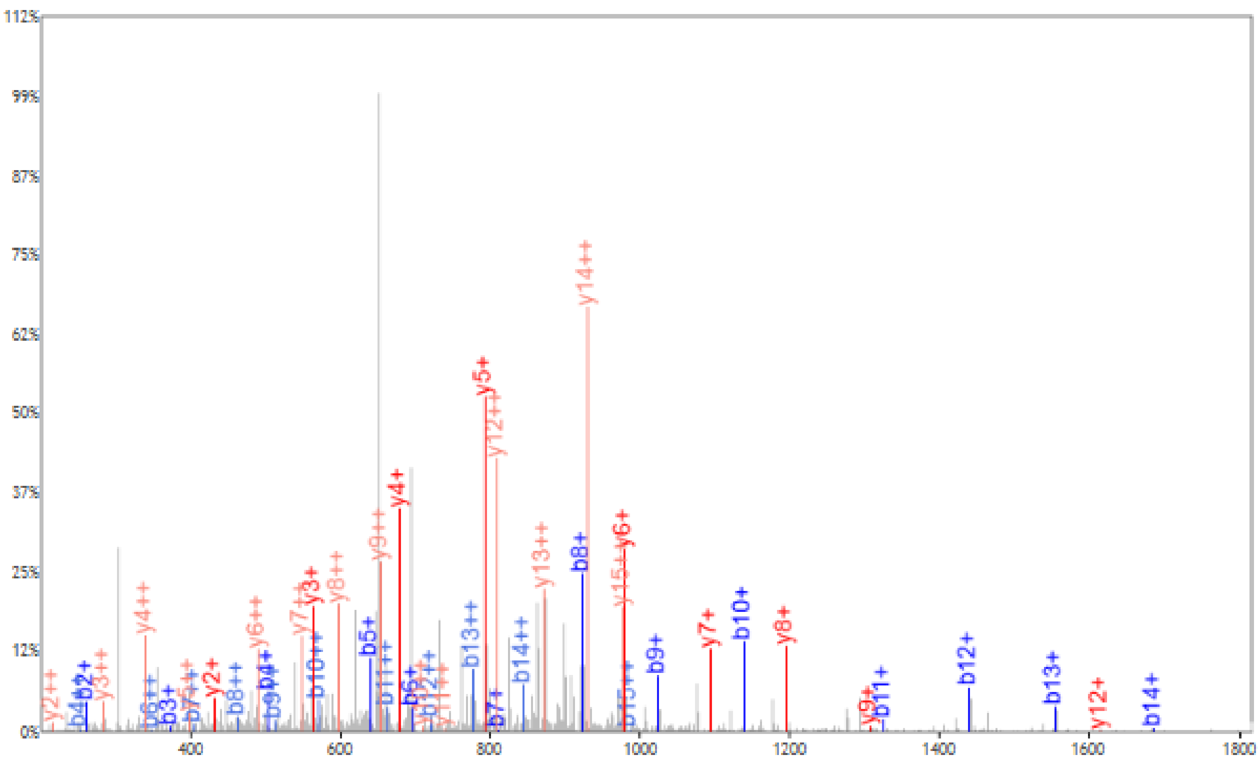

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503.2500	252.1287	4	E	13	1743.8119	872.4096
640.3089	320.6581	5	H	12	1614.7693	807.8883
697.3304	349.1688	6	G	11	1477.7104	739.3588
810.4145	405.7109	7	I	10	1420.6889	710.8481
923.4985	462.2529	8	I	9	1307.6049	654.3061
1024.5462	512.7767	9	T	8	1194.5208	597.7640
1138.5891	569.7982	10	N	7	1093.4731	547.2402
1324.6684	662.8379	11	W	6	979.4302	490.2187
1439.6954	720.3513	12	D	5	793.3509	397.1791
1554.7223	777.8648	13	D	4	678.3239	339.6656
1685.7628	843.3850	14	M	3	563.2970	282.1521
1970.9065	985.9569	15	E	2	432.2565	216.6319
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Variable Modifications:
E: 156.1011

TTGIVMDSGDGVTHTVPIYEGYALPHAILR, MH+ 3339.7154, m/z 1113.9100

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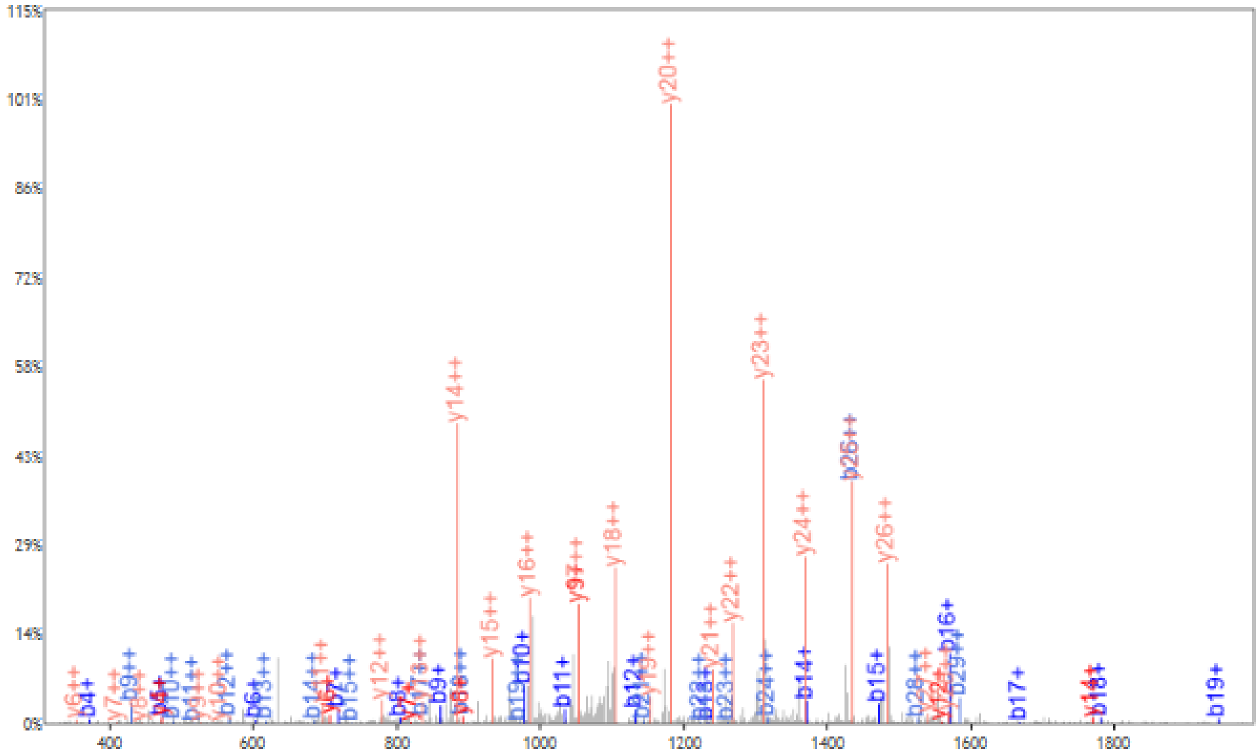

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373.2082	187.1077	4	I	27	3080.5986	1540.8029
472.2766	236.6419	5	V	26	2967.5145	1484.2609
603.3171	302.1622	6	M	25	2868.4461	1434.7267
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805.3760	403.1917	8	S	23	2622.3787	1311.6930
862.3975	431.7024	9	G	22	2535.3467	1268.1770
977.4244	489.2159	10	D	21	2478.3252	1239.6662
1034.4459	517.7266	11	G	20	2363.2982	1182.1528
1133.5143	567.2608	12	V	19	2306.2768	1153.6420
1234.5620	617.7846	13	T	18	2207.2084	1104.1078
1371.6209	686.3141	14	H	17	2106.1607	1053.5840
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2287.1023	1144.0548	21	G	10	1110.6418	555.8246
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2731.3396	1366.1734	25	P	6	706.4359	353.7216
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2939.4356	1470.2214	27	A	4	472.3242	236.6657
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		30	R	1	175.1190	88.0631

LLETIDQLHLEFAK, MH+ 1826.0170, m/z 609.3439

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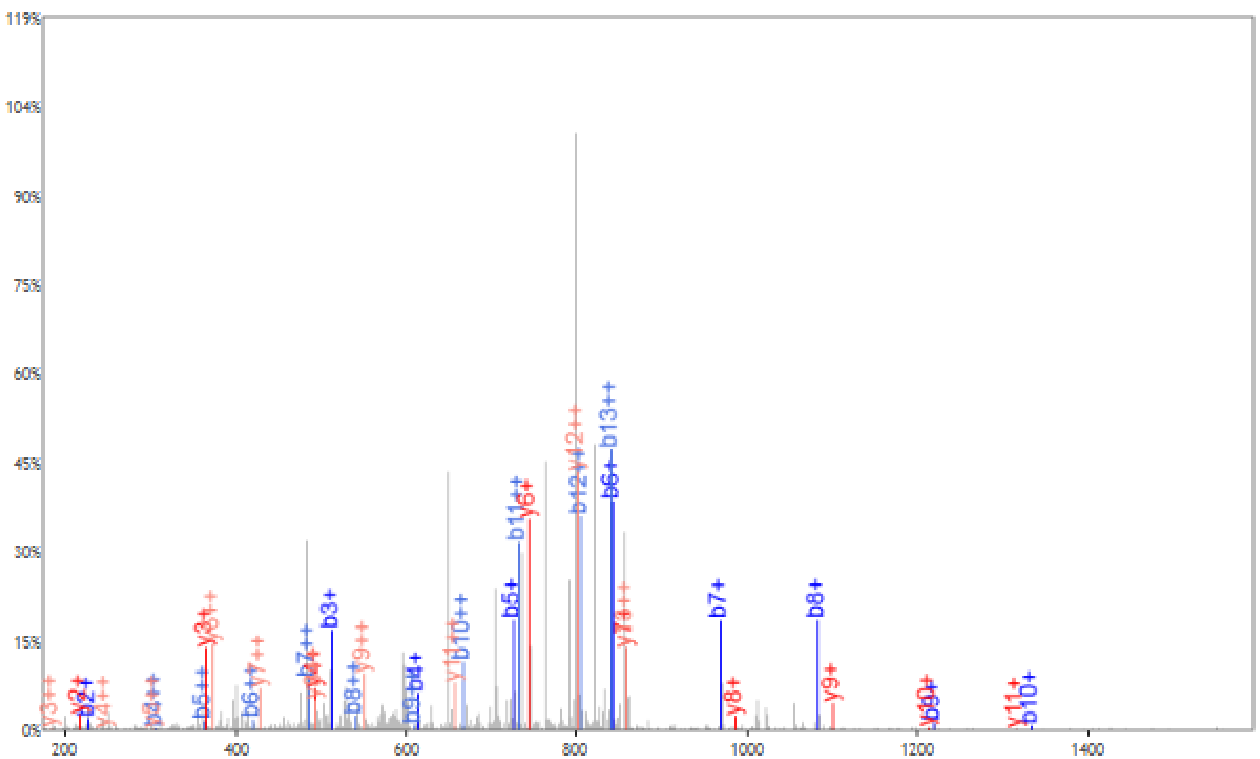

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726.4508	363.7291	5	I	10	1213.6575	607.3324
841.4778	421.2425	6	D	9	1100.5735	550.7904
969.5364	485.2718	7	Q	8	985.5465	493.2769
1082.6204	541.8139	8	L	7	857.4880	429.2476
1219.6793	610.3433	9	H	6	744.4039	372.7056
1332.7634	666.8853	10	L	5	607.3450	304.1761
1461.8060	731.4066	11	E	4	494.2609	247.6341
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1679.9115	840.4594	13	A	2	218.1499	109.5786
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Variable Modifications:
E: 156.1011

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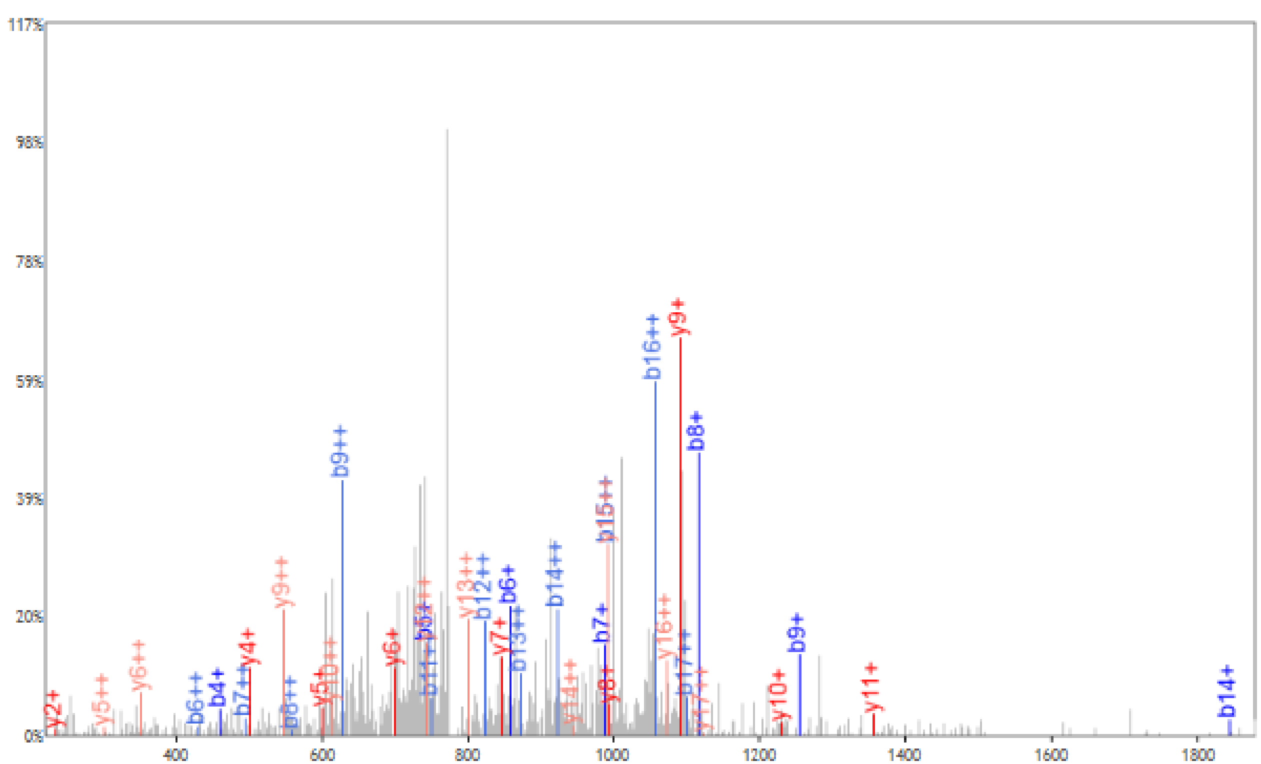

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857.4516	429.2294	6	L	13	1600.7941	800.9007
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1253.6095	627.3084	9	H	10	1228.6109	614.8091
1350.6623	675.8348	10	P	9	1091.5520	546.2796
1497.7307	749.3690	11	F	8	994.4993	497.7533
1644.7991	822.9032	12	F	7	847.4308	424.2191
1745.8468	873.4270	13	T	6	700.3624	350.6849
1844.9152	922.9613	14	V	5	599.3148	300.1610
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C: 57.02146

Variable Modifications:
E: 156.1011

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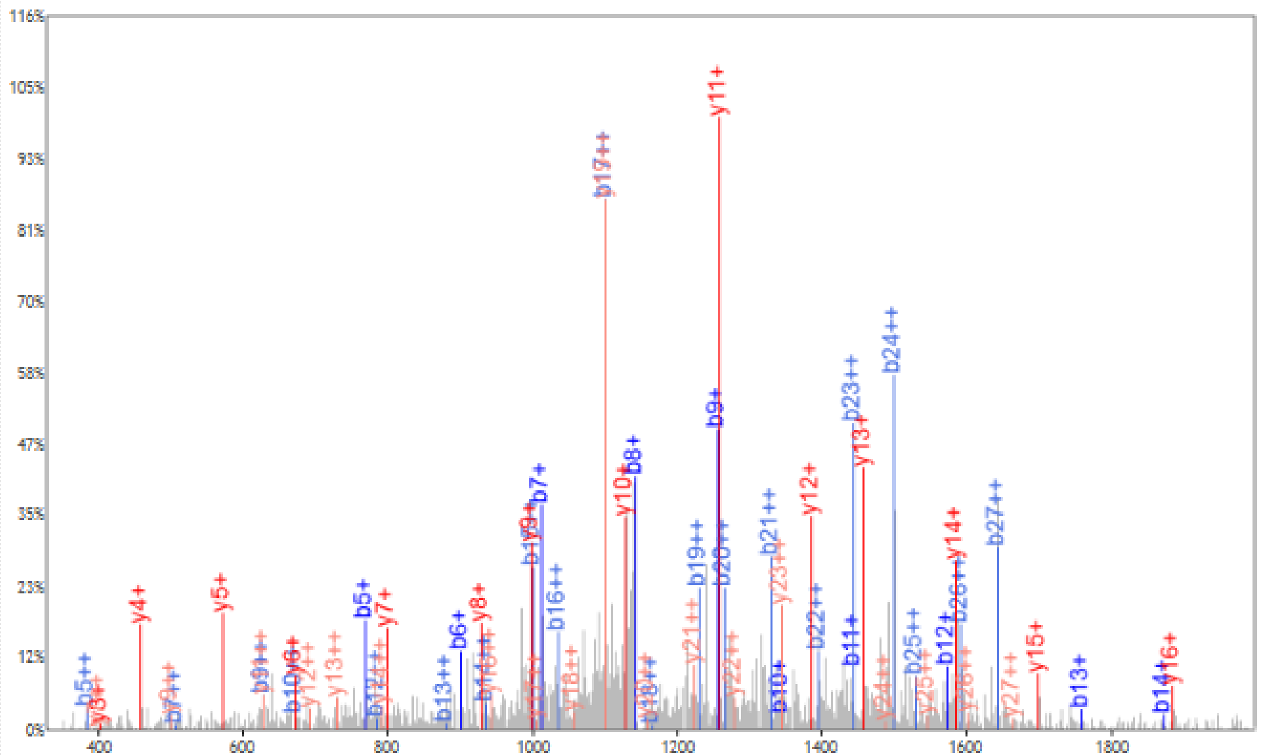

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1256.6416	628.8244	9	D	20	2316.1466	1158.5770
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1444.7213	722.8643	11	T	18	2114.0877	1057.5475
1572.7799	786.8936	12	Q	17	2013.0400	1007.0236
1758.8592	879.9332	13	W	16	1884.9814	942.9943
1871.9432	936.4753	14	L	15	1698.9021	849.9547
2000.9858	1000.9966	15	E	14	1585.8180	793.4127
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2529.2402	1265.1237	20	A	9	999.5582	500.2827
2658.2828	1329.6450	21	E	8	928.5211	464.7642
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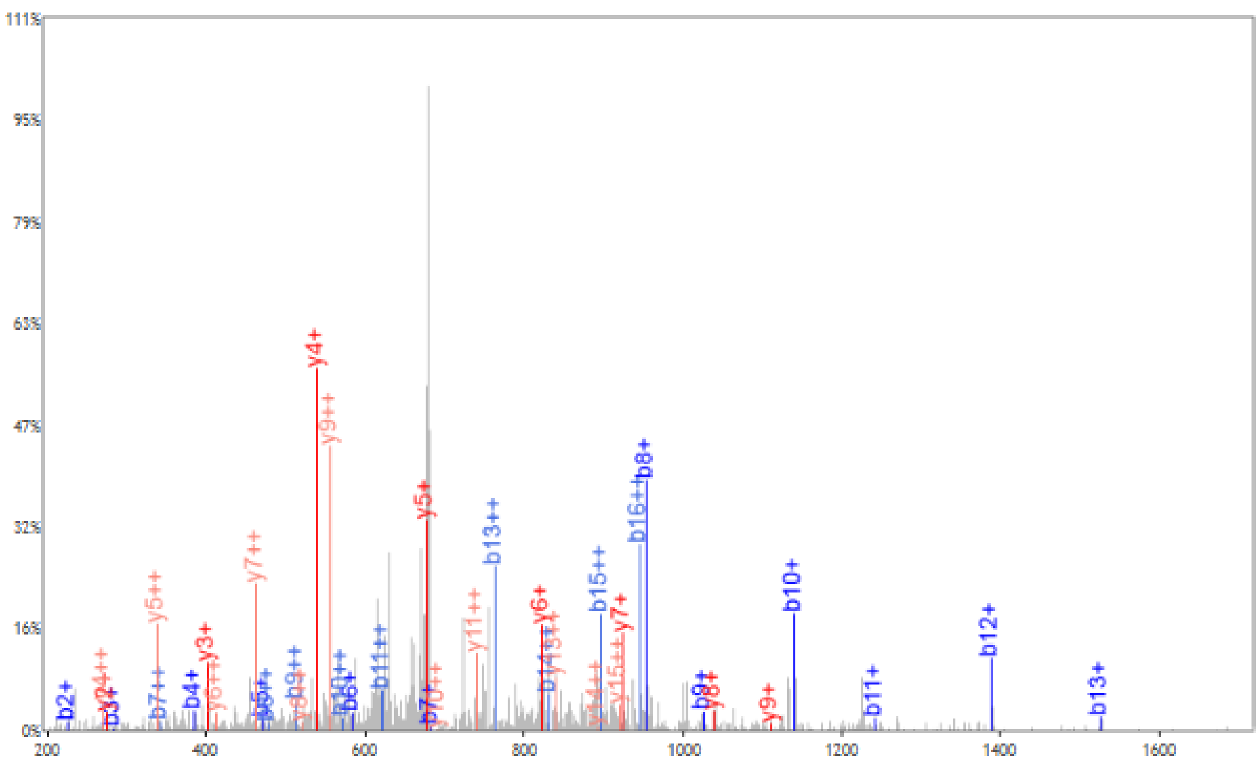
2885.4098	1443.2085	23	V	6	671.4199	336.2136
2998.4939	1499.7506	24	I	5	572.3515	286.6794
3055.5153	1528.2613	25	G	4	459.2674	230.1373
3183.5739	1592.2906	26	Q	3	402.2459	201.6266
3282.6423	1641.8248	27	V	2	274.1874	137.5973
		28	R	1	175.1190	88.0631

QPGTSLVDADTFHHQVR, MH+ 2064.0369, m/z 688.6838

File: platelet-11, Scan: 2217, Precursor m/z: 689.3545, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	17		
226.1186	113.5629	2	P	16	1935.9784	968.4928
283.1401	142.0737	3	G	15	1838.9256	919.9664
384.1878	192.5975	4	T	14	1781.9041	891.4557
471.2198	236.1135	5	S	13	1680.8565	840.9319
584.3039	292.6556	6	L	12	1593.8244	797.4159
683.3723	342.1898	7	V	11	1480.7404	740.8738
954.5003	477.7538	8	D	10	1381.6720	691.3396
1025.5374	513.2723	9	A	9	1110.5439	555.7756
1140.5644	570.7858	10	D	8	1039.5068	520.2570
1241.6120	621.3097	11	T	7	924.4799	462.7436
1388.6805	694.8439	12	F	6	823.4322	412.2197
1525.7394	763.3733	13	H	5	676.3638	338.6855
1662.7983	831.9028	14	H	4	539.3049	270.1561
1790.8569	895.9321	15	Q	3	402.2459	201.6266
1889.9253	945.4663	16	V	2	274.1874	137.5973
		17	R	1	175.1190	88.0631

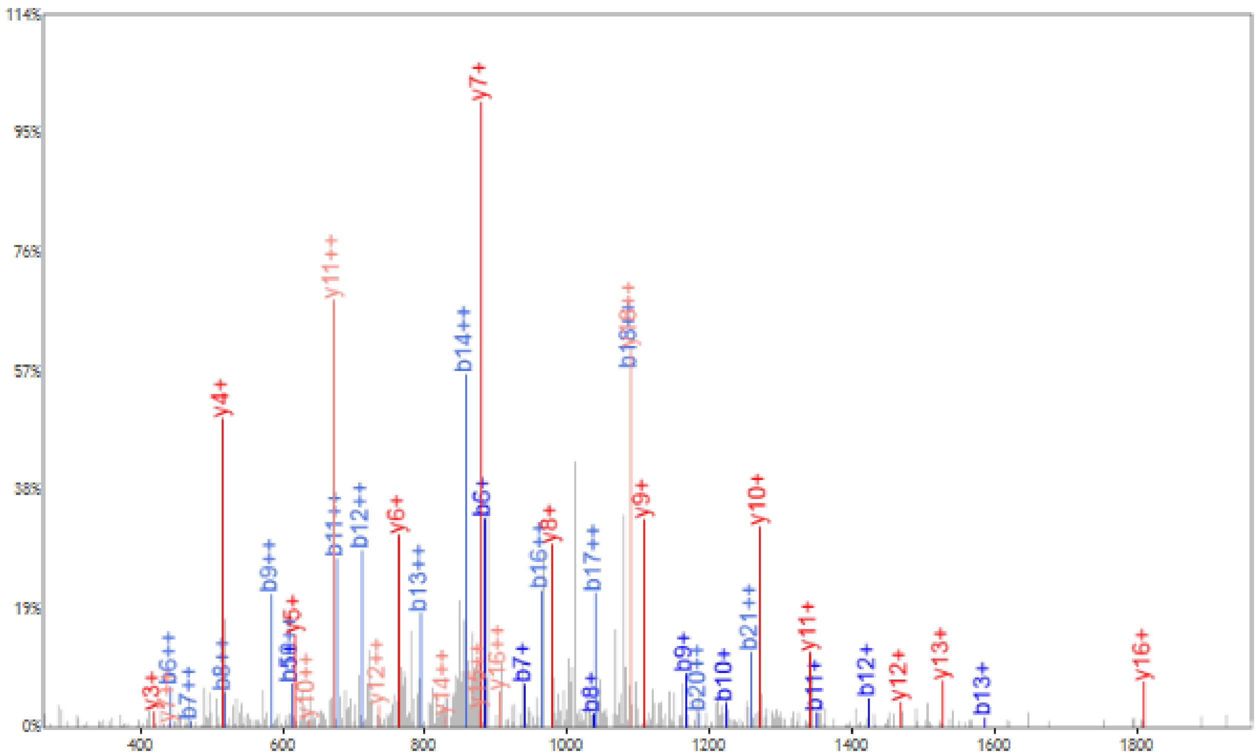
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
D: 156.1011

ITYHPDGPEGQAYEVDFTPPFR, MH+ 2692.2790, m/z 898.0979

File: platelet-8, Scan: 5406, Precursor m/z: 898.1028, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	22		
215.1390	108.0731	2	T	21	2579.1950	1290.1011
378.2023	189.6048	3	Y	20	2478.1473	1239.5773
515.2613	258.1343	4	H	19	2315.0840	1158.0456
612.3140	306.6606	5	P	18	2178.0250	1089.5162
883.4421	442.2247	6	D	17	2080.9723	1040.9898
940.4635	470.7354	7	G	16	1809.8442	905.4258
1037.5163	519.2618	8	P	15	1752.8228	876.9150
1166.5589	583.7831	9	E	14	1655.7700	828.3886
1223.5804	612.2938	10	G	13	1526.7274	763.8673
1351.6389	676.3231	11	Q	12	1469.7060	735.3566
1422.6760	711.8417	12	A	11	1341.6474	671.3273
1585.7394	793.3733	13	Y	10	1270.6103	635.8088
1714.7820	857.8946	14	E	9	1107.5469	554.2771
1813.8504	907.4288	15	V	8	978.5043	489.7558
1928.8773	964.9423	16	D	7	879.4359	440.2216
2075.9457	1038.4765	17	F	6	764.4090	382.7081
2176.9934	1089.0003	18	T	5	617.3406	309.1739
2274.0462	1137.5267	19	P	4	516.2929	258.6501
2371.0989	1186.0531	20	P	3	419.2401	210.1237
2518.1674	1259.5873	21	F	2	322.1874	161.5973
		22	R	1	175.1190	88.0631

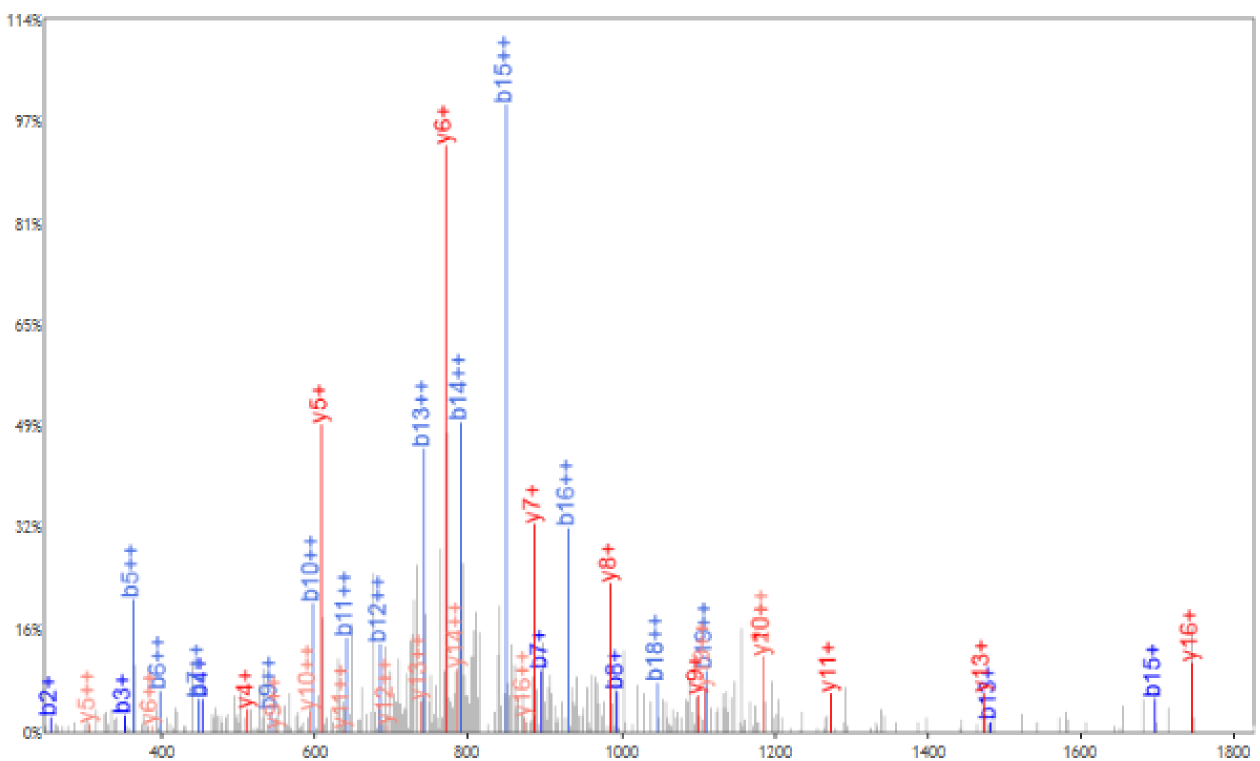
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
D: 156.1011

PRPTDATVSLSSLVDYPHQAR, MH+ 2466.2848, m/z 822.7664

File: platelet-14, Scan: 5267, Precursor m/z: 823.10284, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
98.0600	49.5337	1	P	21		
254.1612	127.5842	2	R	20	2369.2320	1185.1196
351.2139	176.1106	3	P	19	2213.1309	1107.0691
452.2616	226.6344	4	T	18	2116.0781	1058.5427
723.3896	362.1985	5	D	17	2015.0305	1008.0189
794.4268	397.7170	6	A	16	1743.9024	872.4549
895.4744	448.2409	7	T	15	1672.8653	836.9363
994.5428	497.7751	8	V	14	1571.8176	786.4125
1081.5749	541.2911	9	S	13	1472.7492	736.8782
1194.6589	597.8331	10	L	12	1385.7172	693.3622
1281.6910	641.3491	11	S	11	1272.6331	636.8202
1368.7230	684.8651	12	S	10	1185.6011	593.3042
1481.8071	741.4072	13	L	9	1098.5691	549.7882
1580.8755	790.9414	14	V	8	985.4850	493.2461
1695.9024	848.4548	15	D	7	886.4166	443.7119
1858.9657	929.9865	16	Y	6	771.3896	386.1985
1956.0185	978.5129	17	P	5	608.3263	304.6668
2093.0774	1047.0423	18	H	4	511.2736	256.1404
2221.1360	1111.0716	19	Q	3	374.2146	187.6110
2292.1731	1146.5902	20	A	2	246.1561	123.5817
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:

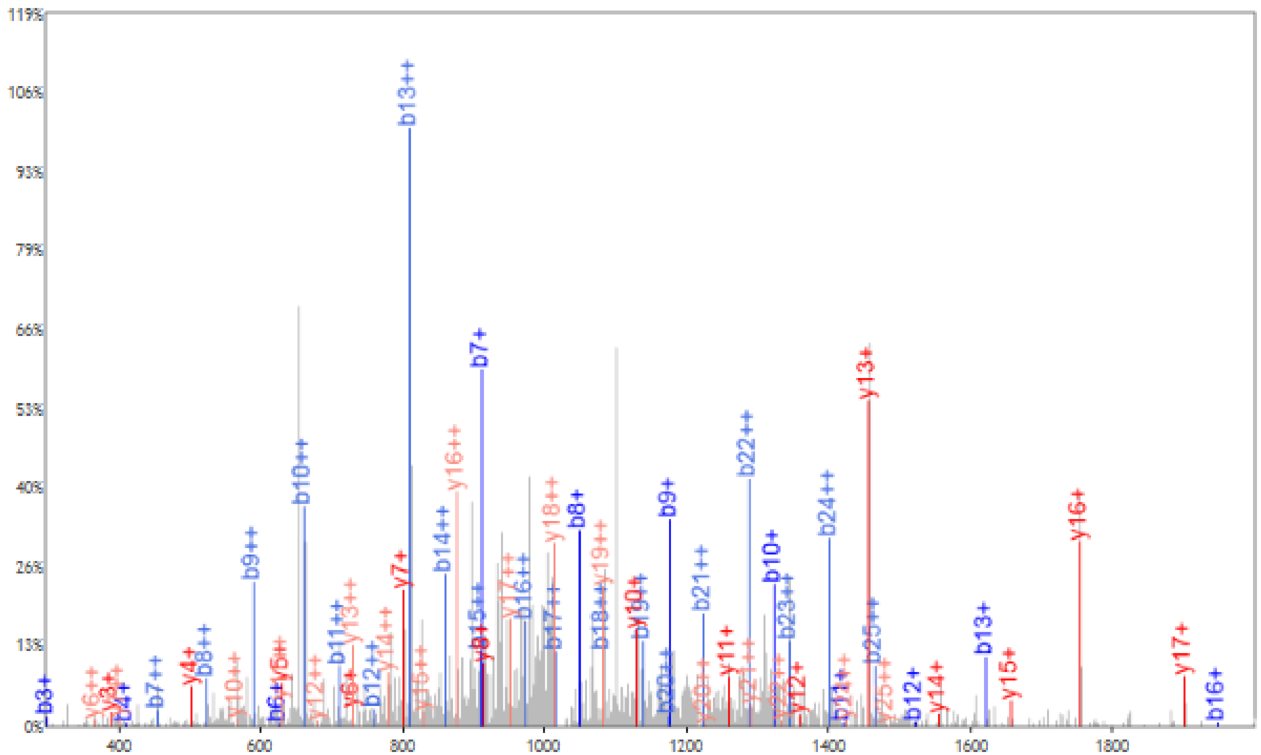
C: 57.02146

Variable Modifications:

D: 156.1011

LLALSQEHKFPTVPTKSELAVEILEK, MH+ 3076.7405, m/z 1026.2517

File: myofibril-14, Scan: 7192, Precursor m/z: 1026.9213, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	26		
227.1754	114.0913	2	L	25	2963.6564	1482.3318
298.2125	149.6099	3	A	24	2850.5724	1425.7898
411.2966	206.1519	4	L	23	2779.5352	1390.2713
498.3286	249.6679	5	S	22	2666.4512	1333.7292
626.3872	313.6972	6	Q	21	2579.4192	1290.2132
911.5309	456.2691	7	E	20	2451.3606	1226.1839
1048.5898	524.7985	8	H	19	2166.2169	1083.6121
1176.6848	588.8460	9	K	18	2029.1580	1015.0826
1323.7532	662.3802	10	F	17	1901.0630	951.0351
1420.8059	710.9066	11	P	16	1753.9946	877.5009
1521.8536	761.4304	12	T	15	1656.9418	828.9746
1620.9220	810.9647	13	V	14	1555.8942	778.4507
1717.9748	859.4910	14	P	13	1456.8257	728.9165
1819.0225	910.0149	15	T	12	1359.7730	680.3901
1947.1174	974.0624	16	K	11	1258.7253	629.8663
2034.1495	1017.5784	17	S	10	1130.6303	565.8188
2163.1921	1082.0997	18	E	9	1043.5983	522.3028
2276.2761	1138.6417	19	L	8	914.5557	457.7815
2347.3132	1174.1603	20	A	7	801.4716	401.2395
2446.3816	1223.6945	21	V	6	730.4345	365.7209
2575.4242	1288.2158	22	E	5	631.3661	316.1867
2688.5083	1344.7578	23	I	4	502.3235	251.6654
2801.5924	1401.2998	24	L	3	389.2395	195.1234
2930.6350	1465.8211	25	E	2	276.1554	138.5813
		26	K	1	147.1128	74.0600

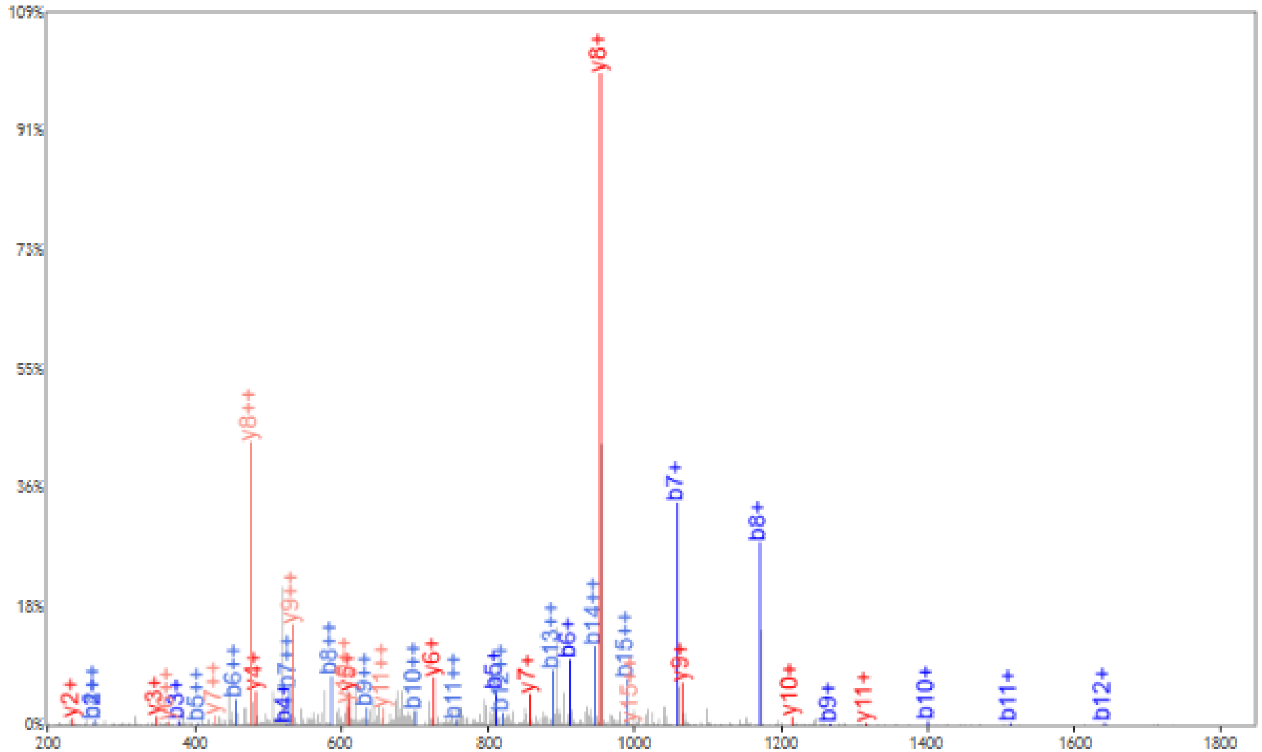
[click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011

MMDFETFLPMLQHISK, MH+ 2124.0439, m/z 708.6861

File: myofibril-10, Scan: 10494, Precursor m/z: 709.3559, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
132.0478	66.5275	1	M	16		
263.0882	132.0478	2	M	15	1993.0034	997.0053
378.1152	189.5612	3	D	14	1861.9629	931.4851
525.1836	263.0954	4	F	13	1746.9360	873.9716
810.3273	405.6673	5	E	12	1599.8675	800.4374
911.3750	456.1911	6	T	11	1314.7239	657.8656
1058.4434	529.7253	7	F	10	1213.6762	607.3417
1171.5275	586.2674	8	L	9	1066.6078	533.8075
1268.5802	634.7937	9	P	8	953.5237	477.2655
1399.6207	700.3140	10	M	7	856.4709	428.7391
1512.7048	756.8560	11	L	6	725.4304	363.2189
1640.7633	820.8853	12	Q	5	612.3464	306.6768
1777.8223	889.4148	13	H	4	484.2878	242.6475
1890.9063	945.9568	14	I	3	347.2289	174.1181
1977.9383	989.4728	15	S	2	234.1448	117.5761
		16	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:

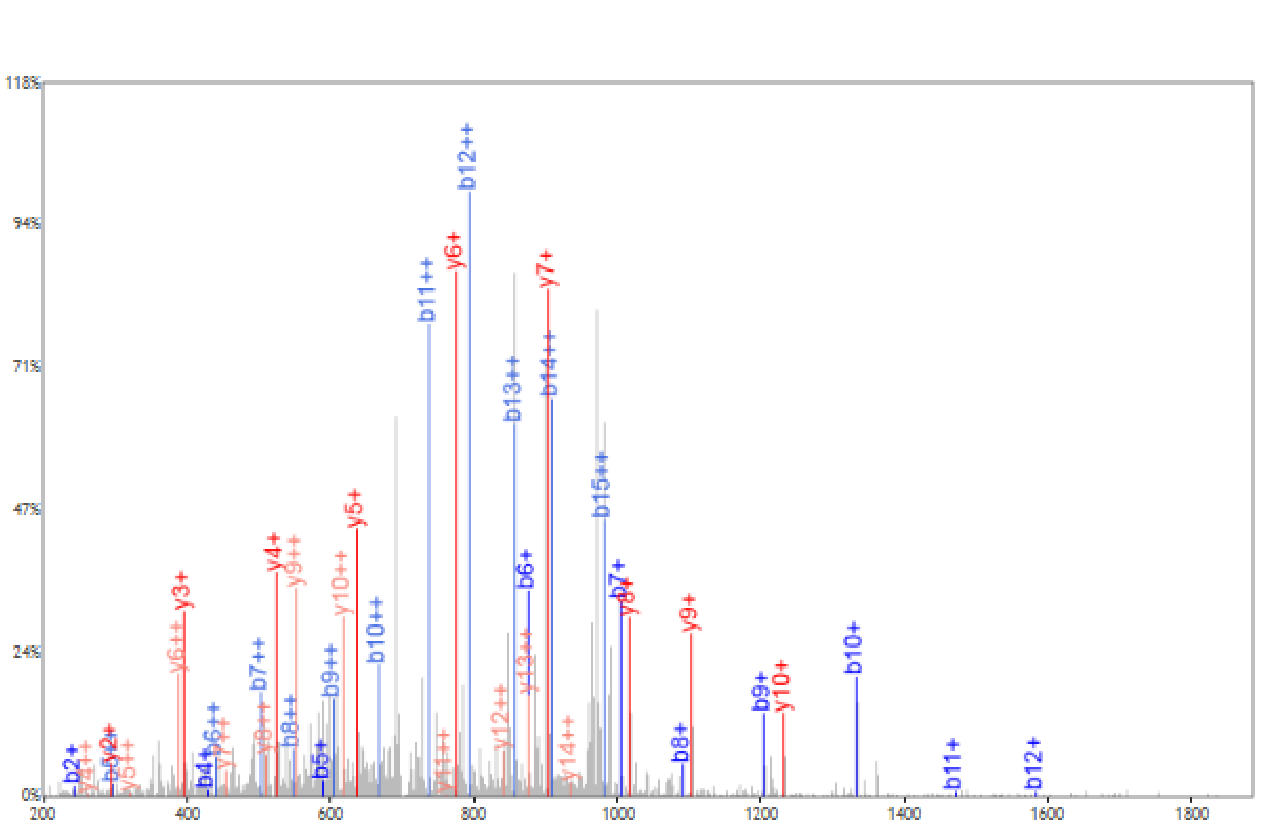
C: 57.02146

Variable Modifications:

E: 156.1011

LKNAYEESLEHLETFK, MH+ 2107.0818, m/z 703.0321

File: myofibril-9, Scan: 6230, Precursor m/z: 703.36774, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
242.1863	121.5968	2	K	15	1993.9978	997.5025
356.2292	178.6183	3	N	14	1865.9028	933.4550
427.2663	214.1368	4	A	13	1751.8599	876.4336
590.3297	295.6685	5	Y	12	1680.8228	840.9150
875.4734	438.2403	6	E	11	1517.7594	759.3834
1004.5160	502.7616	7	E	10	1232.6157	616.8115
1091.5480	546.2776	8	S	9	1103.5732	552.2902
1204.6321	602.8197	9	L	8	1016.5411	508.7742
1333.6746	667.3410	10	E	7	903.4571	452.2322
1470.7336	735.8704	11	H	6	774.4145	387.7109
1583.8176	792.4124	12	L	5	637.3556	319.1814
1712.8602	856.9337	13	E	4	524.2715	262.6394
1813.9079	907.4576	14	T	3	395.2289	198.1181
1960.9763	980.9918	15	F	2	294.1812	147.5942
		16	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:

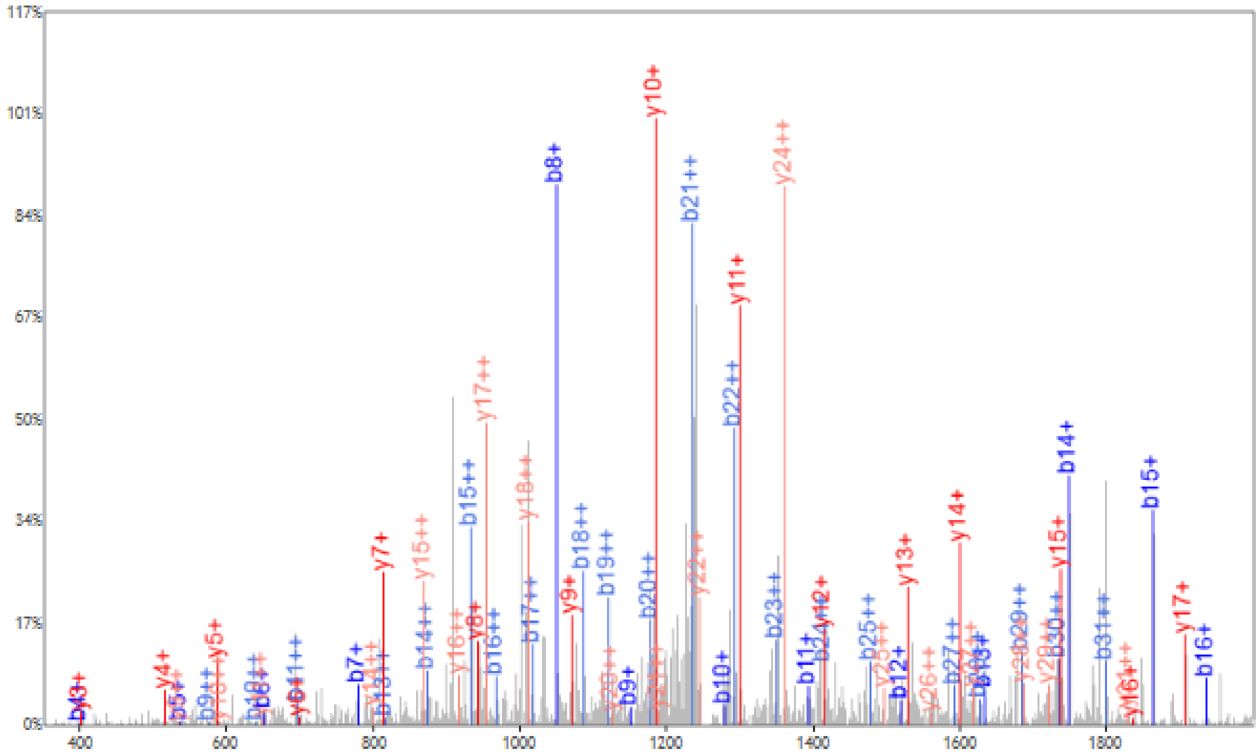
C: 57.02146

Variable Modifications:

E: 156.1011

NSQAHLKDTQLQLDDAVHANDDLKENIAIVER, MH+ 3769.9216, m/z 1257.3120

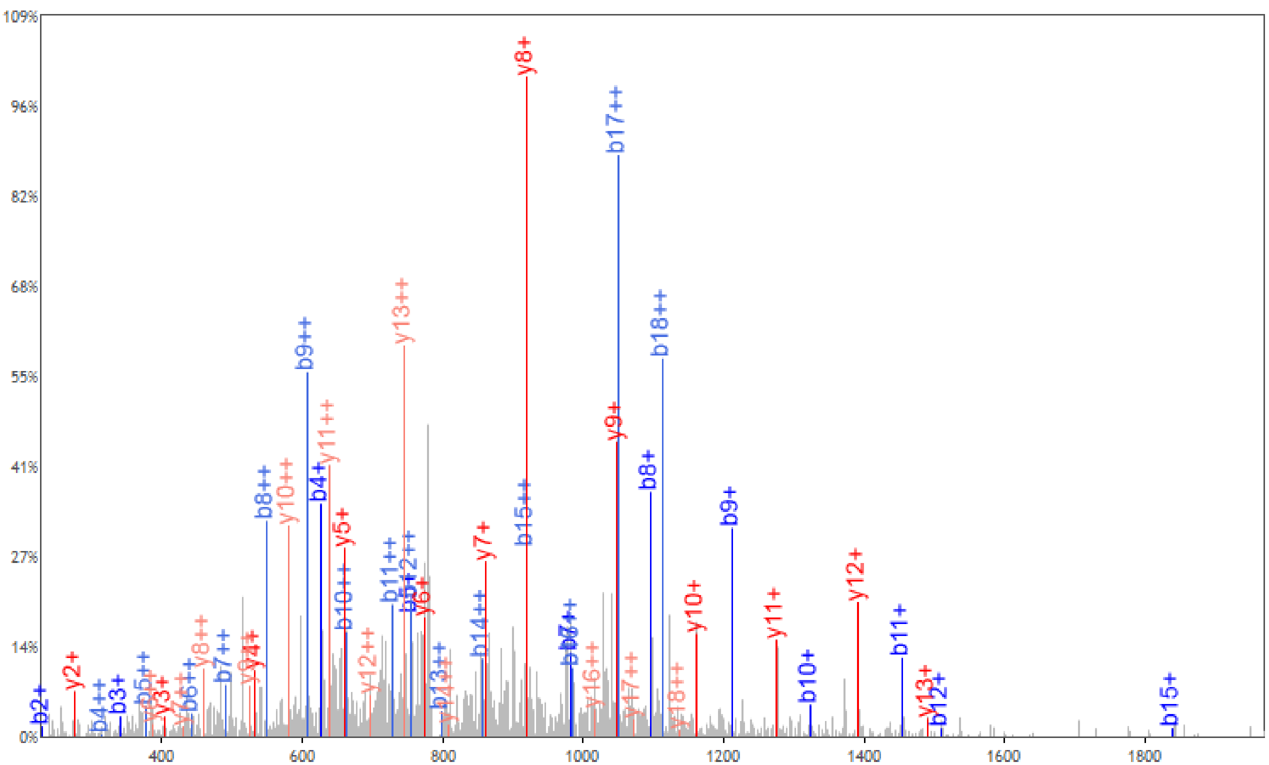
File: myofibril-10, Scan: 5634, Precursor m/z: 1257.6482, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	32		
202.0822	101.5448	2	S	31	3655.8787	1828.4430
330.1408	165.5740	3	Q	30	3568.8466	1784.9270
401.1779	201.0926	4	A	29	3440.7881	1720.8977
538.2368	269.6221	5	H	28	3369.7509	1685.3791
651.3209	326.1641	6	L	27	3232.6920	1616.8497
779.4159	390.2116	7	K	26	3119.6080	1560.3076
1050.5439	525.7756	8	D	25	2991.5130	1496.2601
1151.5916	576.2994	9	T	24	2720.3850	1360.6961
1279.6502	640.3287	10	Q	23	2619.3373	1310.1723
1392.7342	696.8708	11	L	22	2491.2787	1246.1430
1520.7928	760.9000	12	Q	21	2378.1946	1189.6010
1633.8769	817.4421	13	L	20	2250.1361	1125.5717
1748.9038	874.9555	14	D	19	2137.0520	1069.0296
1863.9308	932.4690	15	D	18	2022.0251	1011.5162
1934.9679	967.9876	16	A	17	1906.9981	954.0027
2034.0363	1017.5218	17	V	16	1835.9610	918.4841
2171.0952	1086.0512	18	H	15	1736.8926	868.9499
2242.1323	1121.5698	19	A	14	1599.8337	800.4205
2356.1752	1178.5913	20	N	13	1528.7966	764.9019
2471.2022	1236.1047	21	D	12	1414.7536	707.8805
2586.2291	1293.6182	22	D	11	1299.7267	650.3670
2699.3132	1350.1602	23	L	10	1184.6997	592.8535
2827.4081	1414.2077	24	K	9	1071.6157	536.3115
2956.4507	1478.7290	25	E	8	943.5207	472.2640
3070.4937	1535.7505	26	N	7	814.4781	407.7427
3183.5777	1592.2925	27	I	6	700.4352	350.7212
3254.6148	1627.8111	28	A	5	587.3511	294.1792
3367.6989	1684.3531	29	I	4	516.3140	258.6606
3466.7673	1733.8873	30	V	3	403.2300	202.1186
3595.8099	1798.4086	31	E	2	304.1615	152.5844
		32	R	1	175.1190	88.0631

VKLEQQVDDLEGSLEQEKK, MH+ 2371.2463, m/z 791.0870

File: myofibril-trypsin-6, Scan: 5405, Precursor m/z: 791.42413, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	19		
228.1707	114.5890	2	K	18	2272.1779	1136.5926
341.2547	171.1310	3	L	17	2144.0830	1072.5451
626.3984	313.7028	4	E	16	2030.9989	1016.0031
754.4570	377.7321	5	Q	15	1745.8552	873.4312
882.5156	441.7614	6	Q	14	1617.7966	809.4019
981.5840	491.2956	7	V	13	1489.7380	745.3727
1096.6109	548.8091	8	D	12	1390.6696	695.8385
1211.6379	606.3226	9	D	11	1275.6427	638.3250
1324.7219	662.8646	10	L	10	1160.6157	580.8115
1453.7645	727.3859	11	E	9	1047.5317	524.2695
1510.7860	755.8966	12	G	8	918.4891	459.7482
1597.8180	799.4126	13	S	7	861.4676	431.2374
1710.9021	855.9547	14	L	6	774.4356	387.7214
1839.9447	920.4760	15	E	5	661.3515	331.1794
1968.0032	984.5053	16	Q	4	532.3089	266.6581
2097.0458	1049.0266	17	E	3	404.2504	202.6288
2225.1408	1113.0740	18	K	2	275.2078	138.1075
		19	K	1	147.1128	74.0600

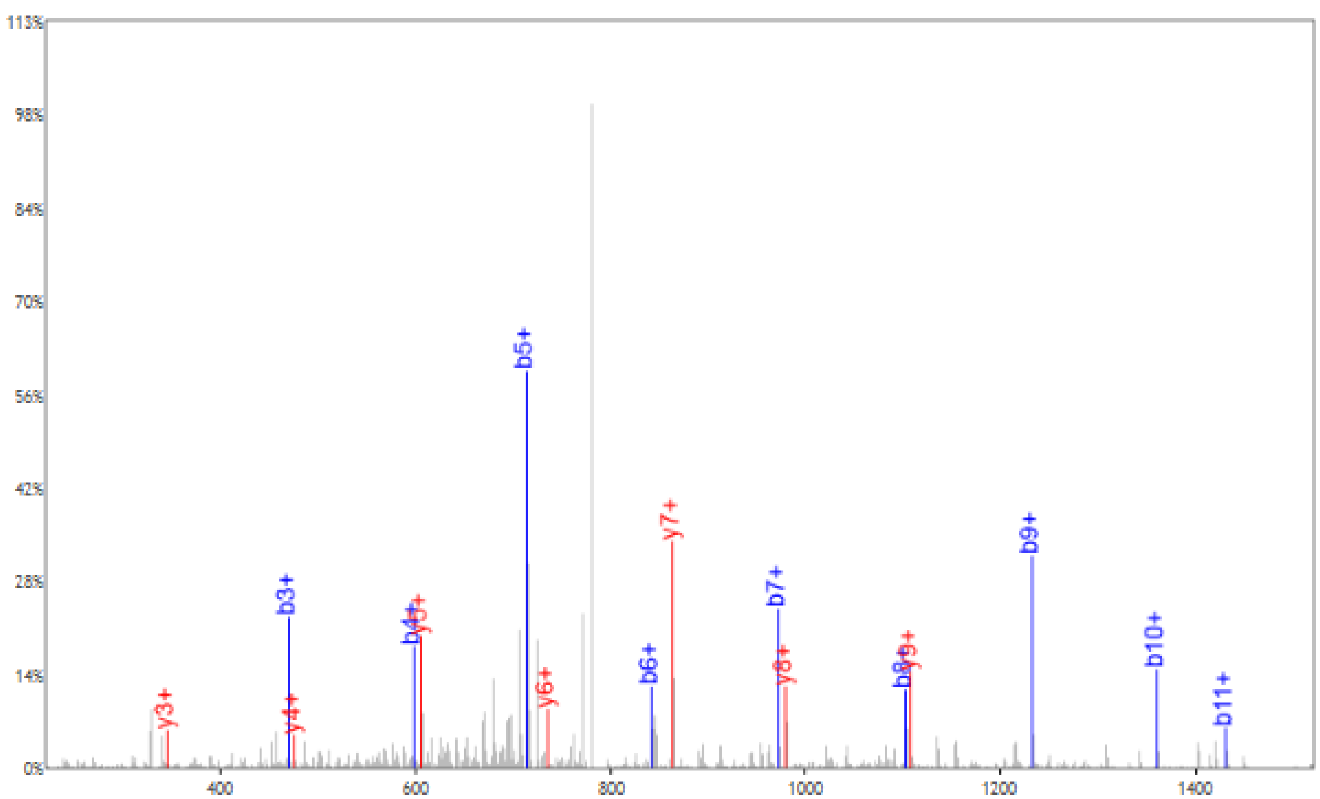
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011

LA E KDEEMEQAK, MH+ 1576.7635, m/z 788.8854

File: myofibril-trypsin-4, Scan: 3028, Precursor m/z: 789.8891, Charge: 2



b+	#	Seq	#	y+
114.0913	1	L	12	
185.1285	2	A	11	1463.6795
470.2721	3	E	10	1392.6424
598.3671	4	K	9	1107.4987
713.3941	5	D	8	979.4037
842.4366	6	E	7	864.3768
971.4792	7	E	6	735.3342
1102.5197	8	M	5	606.2916
1231.5623	9	E	4	475.2511
1359.6209	10	Q	3	346.2085
1430.6580	11	A	2	218.1499
	12	K	1	147.1128

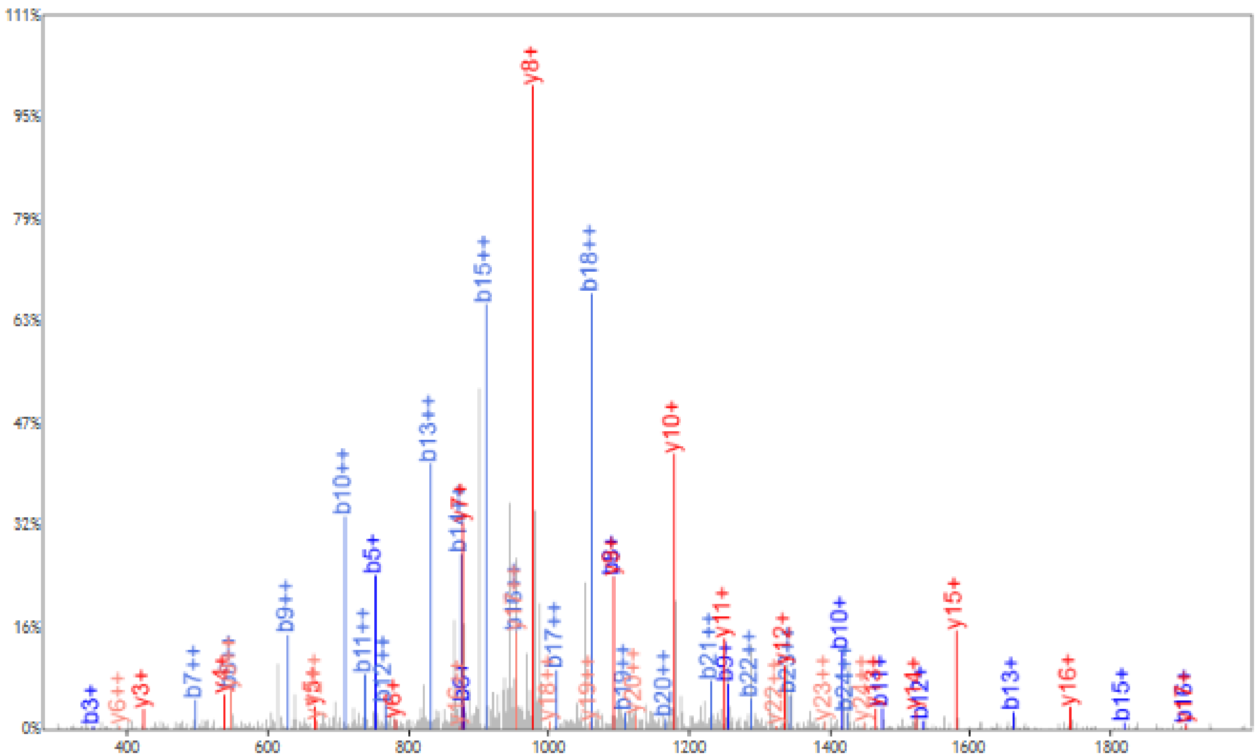
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011

VLHMDQNPYYGGESASITPLEDLYK, MH+ 2996.4458, m/z 999.4868

File: platelet-6, Scan: 6825, Precursor m/z: 999.8227, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	25		
213.1598	107.0835	2	L	24	2897.3774	1449.1923
350.2187	175.6130	3	H	23	2784.2934	1392.6503
481.2592	241.1332	4	M	22	2647.2344	1324.1209
752.3872	376.6972	5	D	21	2516.1940	1258.6006
880.4458	440.7265	6	Q	20	2245.0659	1123.0366
994.4887	497.7480	7	N	19	2117.0073	1059.0073
1091.5415	546.2744	8	P	18	2002.9644	1001.9858
1254.6048	627.8060	9	Y	17	1905.9117	953.4595
1417.6681	709.3377	10	Y	16	1742.8483	871.9278
1474.6896	737.8484	11	G	15	1579.7850	790.3961
1531.7110	766.3592	12	G	14	1522.7635	761.8854
1660.7536	830.8805	13	E	13	1465.7421	733.3747
1747.7857	874.3965	14	S	12	1336.6995	668.8534
1818.8228	909.9150	15	A	11	1249.6674	625.3374
1905.8548	953.4310	16	S	10	1178.6303	589.8188
2018.9389	1009.9731	17	I	9	1091.5983	546.3028
2119.9866	1060.4969	18	T	8	978.5142	489.7608
2217.0393	1109.0233	19	P	7	877.4666	439.2369
2330.1234	1165.5653	20	L	6	780.4138	390.7105
2459.1660	1230.0866	21	E	5	667.3297	334.1685
2574.1929	1287.6001	22	D	4	538.2871	269.6472
2687.2770	1344.1421	23	L	3	423.2602	212.1337
2850.3403	1425.6738	24	Y	2	310.1761	155.5917
		25	K	1	147.1128	74.0600

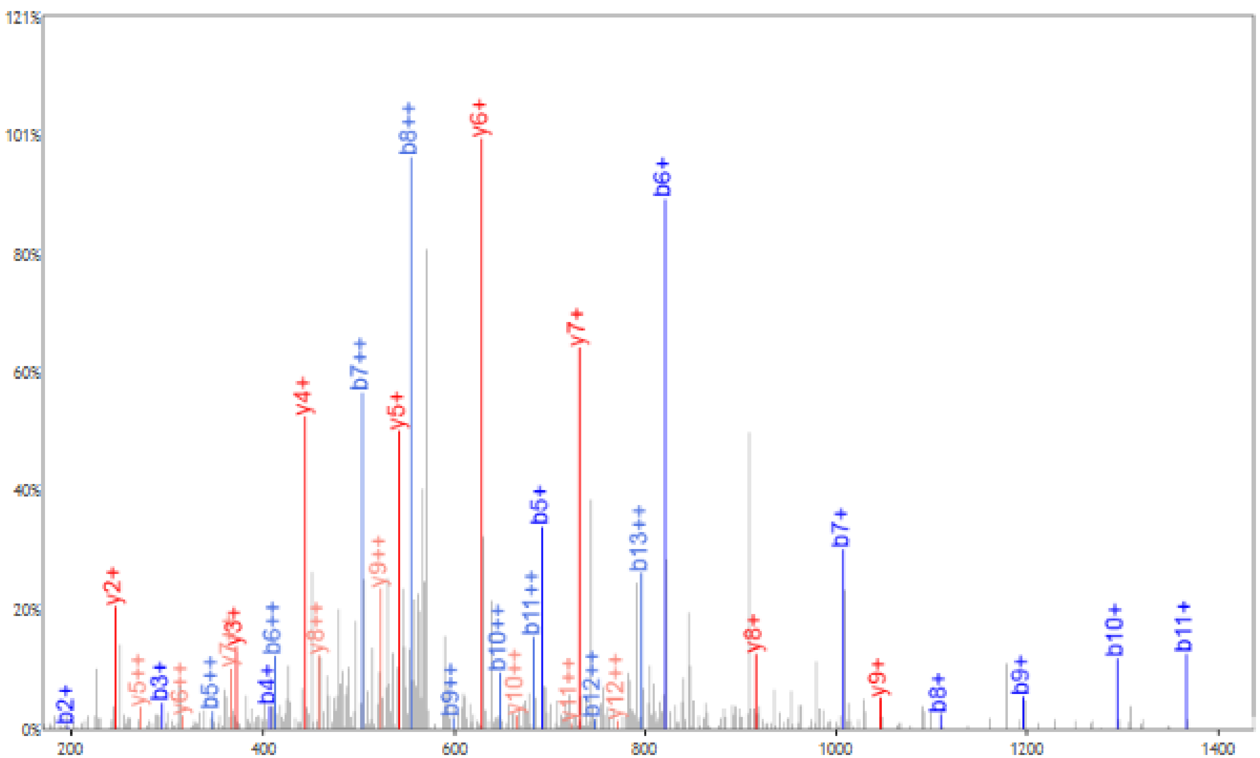
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
D: 156.1011

PPVLEEWTSVAKPK, MH+ 1736.9694, m/z 579.6613

File: platelet-10, Scan: 4534, Precursor m/z: 579.99713, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
98.0600	49.5337	1	P	14		
195.1128	98.0600	2	P	13	1639.9166	820.4619
294.1812	147.5942	3	V	12	1542.8638	771.9356
407.2653	204.1363	4	L	11	1443.7954	722.4014
692.4090	346.7081	5	E	10	1330.7114	665.8593
821.4516	411.2294	6	E	9	1045.5677	523.2875
1007.5309	504.2691	7	W	8	916.5251	458.7662
1108.5786	554.7929	8	T	7	730.4458	365.7265
1195.6106	598.3089	9	S	6	629.3981	315.2027
1294.6790	647.8431	10	V	5	542.3661	271.6867
1365.7161	683.3617	11	A	4	443.2976	222.1525
1493.8111	747.4092	12	K	3	372.2605	186.6339
1590.8638	795.9356	13	P	2	244.1656	122.5864
		14	K	1	147.1128	74.0600

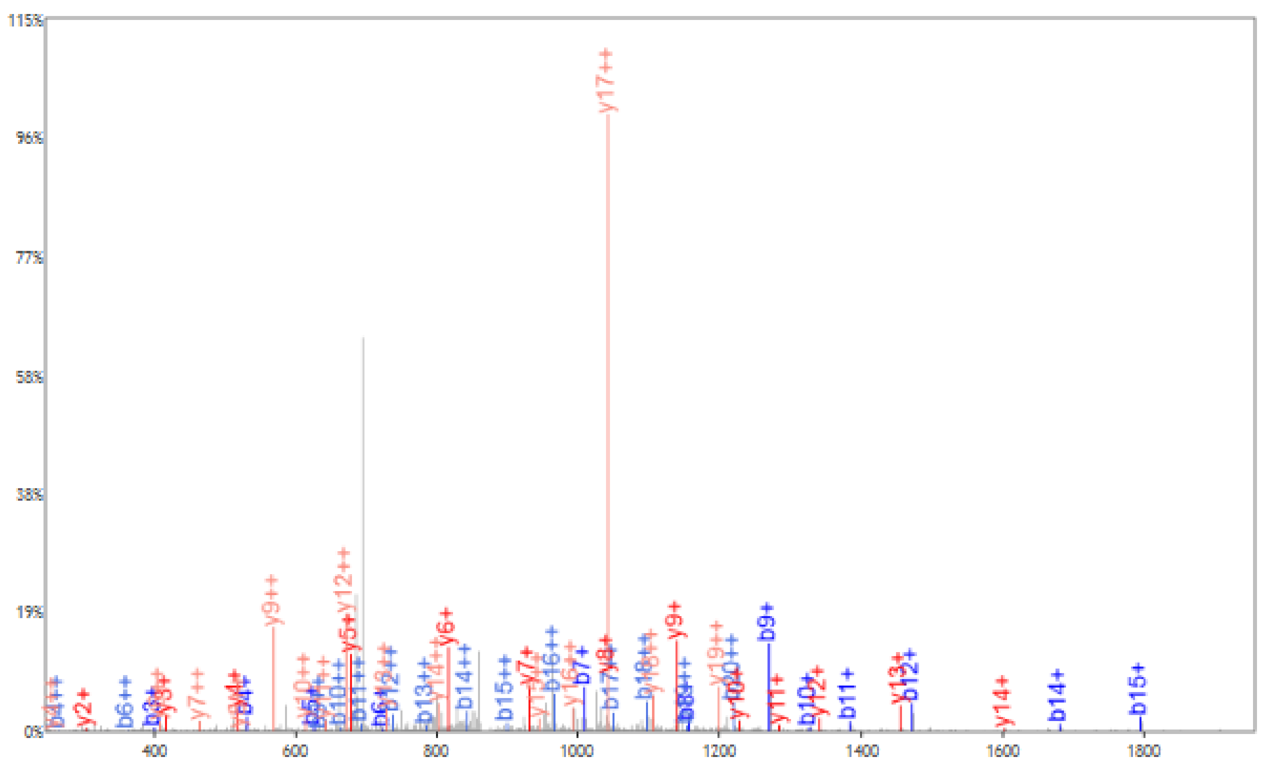
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011

LTWEPPEFDGGSPILHYVLER, MH+ 2611.3303, m/z 871.1150

File: myofibril-9, Scan: 10119, Precursor m/z: 871.4515, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	21		
215.1390	108.0731	2	T	20	2498.2463	1249.6268
401.2183	201.1128	3	W	19	2397.1986	1199.1029
530.2609	265.6341	4	E	18	2211.1193	1106.0633
627.3137	314.1605	5	P	17	2082.0767	1041.5420
724.3665	362.6869	6	P	16	1985.0239	993.0156
1009.5101	505.2587	7	E	15	1887.9712	944.4892
1156.5786	578.7929	8	F	14	1602.8275	801.9174
1271.6055	636.3064	9	D	13	1455.7591	728.3832
1328.6270	664.8171	10	G	12	1340.7321	670.8697
1385.6484	693.3279	11	G	11	1283.7106	642.3590
1472.6805	736.8439	12	S	10	1226.6892	613.8482
1569.7332	785.3702	13	P	9	1139.6572	570.3322
1682.8173	841.9123	14	I	8	1042.6044	521.8058
1795.9014	898.4543	15	L	7	929.5203	465.2638
1932.9603	966.9838	16	H	6	816.4363	408.7218
2096.0236	1048.5154	17	Y	5	679.3774	340.1923
2195.0920	1098.0496	18	V	4	516.3140	258.6606
2308.1761	1154.5917	19	L	3	417.2456	209.1264
2437.2187	1219.1130	20	E	2	304.1615	152.5844
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:

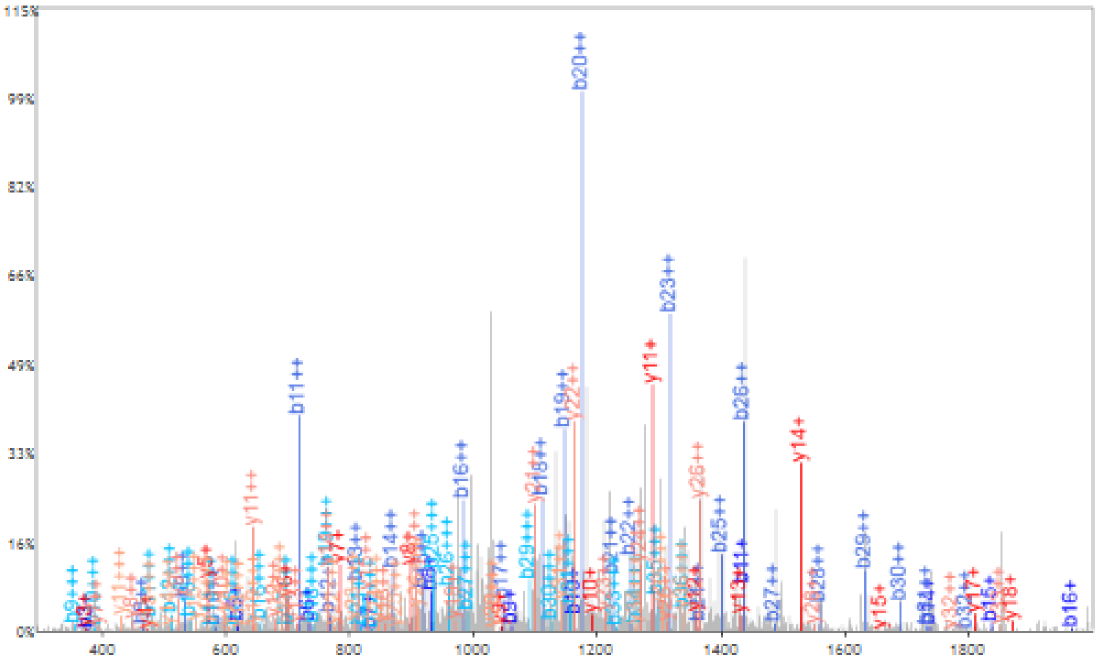
C: 57.02146

Variable Modifications:

E: 156.1011

FVESRDVVMTDTSITEEQAGPGEPAAPFFISKPVVQK, MH+ 4163.1118, m/z 1041.5334

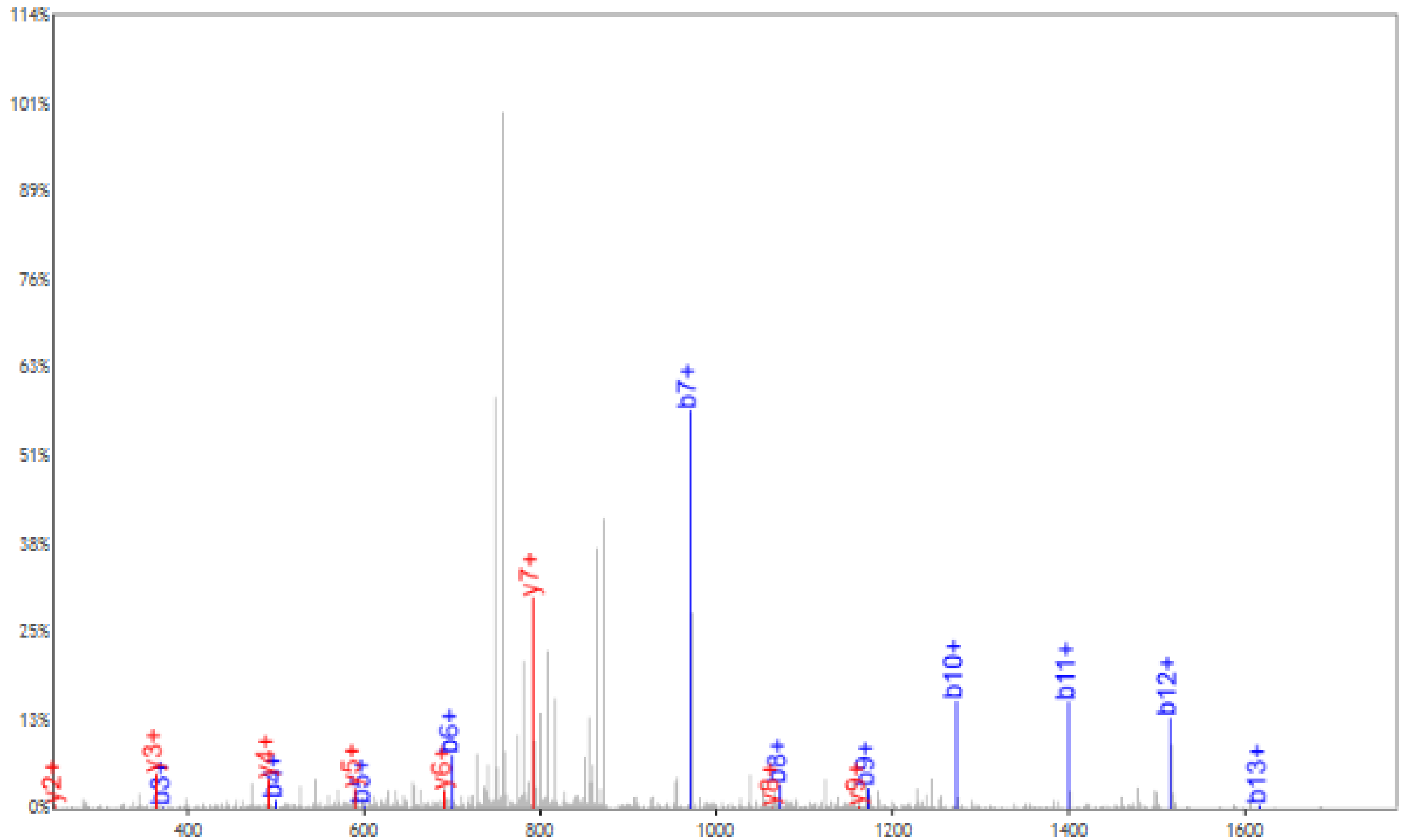
File: myofibril-9, Scan: 7049, Precursor m/z: 1041.7876, Charge: 4



b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
148.0757	74.5415	50.0301	1	F	37			
247.1441	124.0757	83.0529	2	V	36	4016.0433	2008.5253	1339.3526
376.1867	188.5970	126.0671	3	E	35	3916.9749	1958.9911	1306.3298
463.2187	232.1130	155.0778	4	S	34	3787.9323	1894.4698	1263.3156
619.3198	310.1636	207.1115	5	R	33	3700.9003	1850.9538	1234.3050
734.3468	367.6770	245.4538	6	D	32	3544.7992	1772.9032	1182.2713
833.4152	417.2112	278.4766	7	V	31	3429.7723	1715.3898	1143.9289
932.4836	466.7454	311.4994	8	V	30	3330.7038	1665.8556	1110.9061
1063.5241	532.2657	355.1795	9	M	29	3231.6354	1616.3214	1077.8833
1164.5718	582.7895	388.8621	10	T	28	3100.5949	1550.8011	1034.2032
1435.6998	718.3535	479.2381	11	D	27	2999.5473	1500.2773	1000.5206
1536.7475	768.8774	512.9207	12	T	26	2728.4192	1364.7132	910.1446
1623.7795	812.3934	541.9314	13	S	25	2627.3715	1314.1894	876.4620
1736.8636	868.9354	579.6260	14	I	24	2540.3395	1270.6734	847.4514
1837.9113	919.4593	613.3086	15	T	23	2427.2555	1214.1314	809.7567
1966.9539	983.9806	656.3228	16	E	22	2326.2078	1163.6075	776.0741
2095.9964	1048.5019	699.3370	17	E	21	2197.1652	1099.0862	733.0599
2224.0550	1112.5312	742.0232	18	Q	20	2068.1226	1034.5649	690.0457
2295.0921	1148.0497	765.7022	19	A	19	1940.0640	970.5356	647.3595
2352.1136	1176.5604	784.7094	20	G	18	1869.0269	935.0171	623.6805
2449.1664	1225.0868	817.0603	21	P	17	1812.0054	906.5064	604.6733
2506.1878	1253.5976	836.0675	22	G	16	1714.9527	857.9800	572.3224
2635.2304	1318.1189	879.0817	23	E	15	1657.9312	829.4692	553.3153
2732.2832	1366.6452	911.4326	24	P	14	1528.8886	764.9479	510.3011
2803.3203	1402.1638	935.1116	25	A	13	1431.8358	716.4216	477.9501
2874.3574	1437.6823	958.7907	26	A	12	1360.7987	680.9030	454.2711
2971.4102	1486.2087	991.1416	27	P	11	1289.7616	645.3844	430.5921
3118.4786	1559.7429	1040.1644	28	F	10	1192.7089	596.8581	398.2411
3265.5470	1633.2771	1089.1872	29	F	9	1045.6404	523.3239	349.2183
3378.6311	1689.8192	1126.8819	30	I	8	898.5720	449.7897	300.1955
3465.6631	1733.3352	1155.8926	31	S	7	785.4880	393.2476	262.5008
3593.7581	1797.3827	1198.5909	32	K	6	698.4559	349.7316	233.4902
3690.8108	1845.9091	1230.9418	33	P	5	570.3610	285.6841	190.7918
3789.8792	1895.4433	1263.9646	34	V	4	473.3082	237.1577	158.4409
3888.9477	1944.9775	1296.9874	35	V	3	374.2398	187.6235	125.4181
4017.0062	2009.0068	1339.6736	36	Q	2	275.1714	138.0893	92.3953
			37	K	1	147.1128	74.0600	49.7091

KGWQTVDTTVKDTK, MH+ 1762.9446, m/z 881.9759

File: myofibril-trypsin-10, Scan: 2971, Precursor m/z: 882.4793, Charge: 2



b+	#	Seq	#	y+
129.1022	1	K	14	
186.1237	2	G	13	1634.8496
372.2030	3	W	12	1577.8282
500.2616	4	Q	11	1391.7489
601.3093	5	T	10	1263.6903
700.3777	6	V	9	1162.6426
971.5057	7	D	8	1063.5742
1072.5534	8	T	7	792.4462
1173.6011	9	T	6	691.3985
1272.6695	10	V	5	590.3508
1400.7645	11	K	4	491.2824
1515.7914	12	D	3	363.1874
1616.8391	13	T	2	248.1605
	14	K	1	147.1128

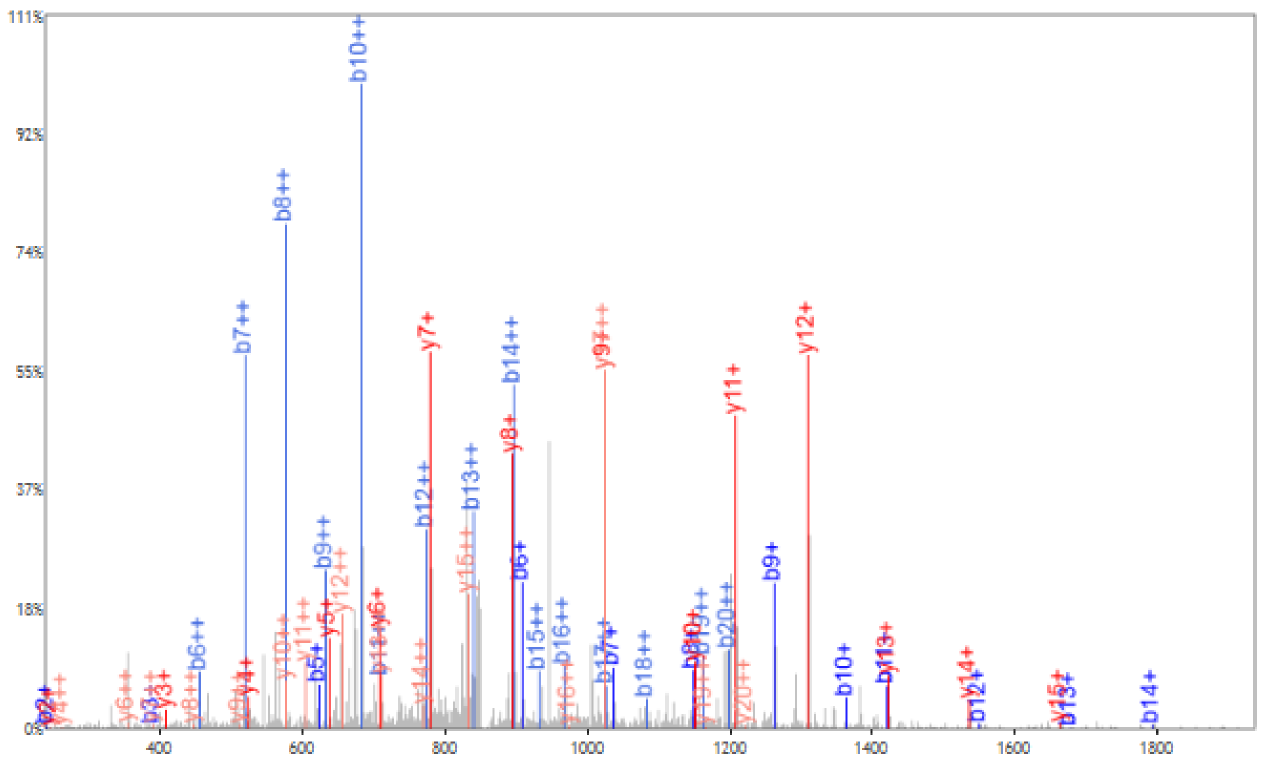
[click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
D: 156.1011

QLFHPEQLITGKEDAANNYAR, MH+ 2571.3062, m/z 857.7736

File: platelet-11, Scan: 3417, Precursor m/z: 858.111, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	21		
242.1499	121.5786	2	L	20	2443.2477	1222.1275
389.2183	195.1128	3	F	19	2330.1636	1165.5854
526.2772	263.6423	4	H	18	2183.0952	1092.0512
623.3300	312.1686	5	P	17	2046.0363	1023.5218
908.4737	454.7405	6	E	16	1948.9835	974.9954
1036.5323	518.7698	7	Q	15	1663.8398	832.4235
1149.6163	575.3118	8	L	14	1535.7812	768.3943
1262.7004	631.8538	9	I	13	1422.6972	711.8522
1363.7481	682.3777	10	T	12	1309.6131	655.3102
1420.7695	710.8884	11	G	11	1208.5654	604.7864
1548.8645	774.9359	12	K	10	1151.5440	576.2756
1677.9071	839.4572	13	E	9	1023.4490	512.2281
1792.9340	896.9707	14	D	8	894.4064	447.7068
1863.9712	932.4892	15	A	7	779.3795	390.1934
1935.0083	968.0078	16	A	6	708.3424	354.6748
2049.0512	1025.0292	17	N	5	637.3052	319.1563
2163.0941	1082.0507	18	N	4	523.2623	262.1348
2326.1575	1163.5824	19	Y	3	409.2194	205.1133
2397.1946	1199.1009	20	A	2	246.1561	123.5817
		21	R	1	175.1190	88.0631

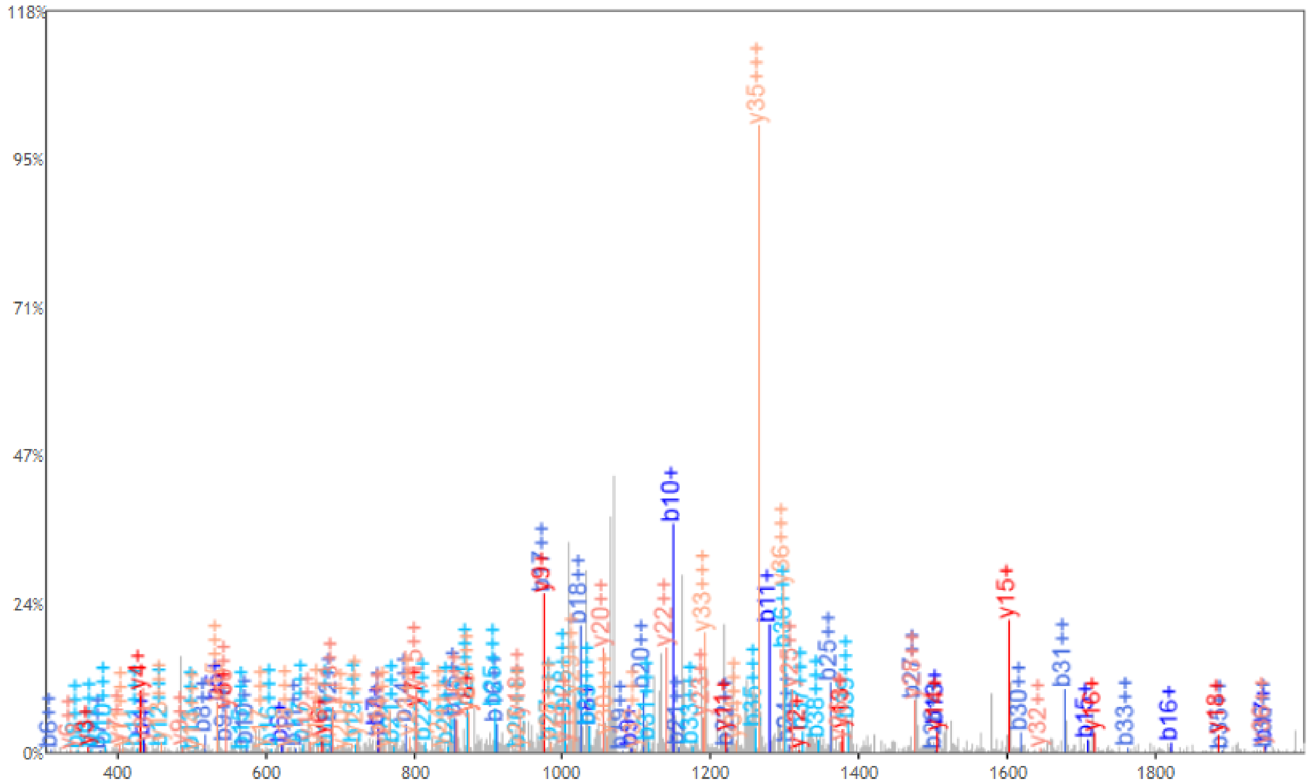
[Click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011

AQVHVSEEGGEPEAMLQVLGPKPALPEGTEDTAKEDAANR, MH+ 4327.1259, m/z 1082.5369

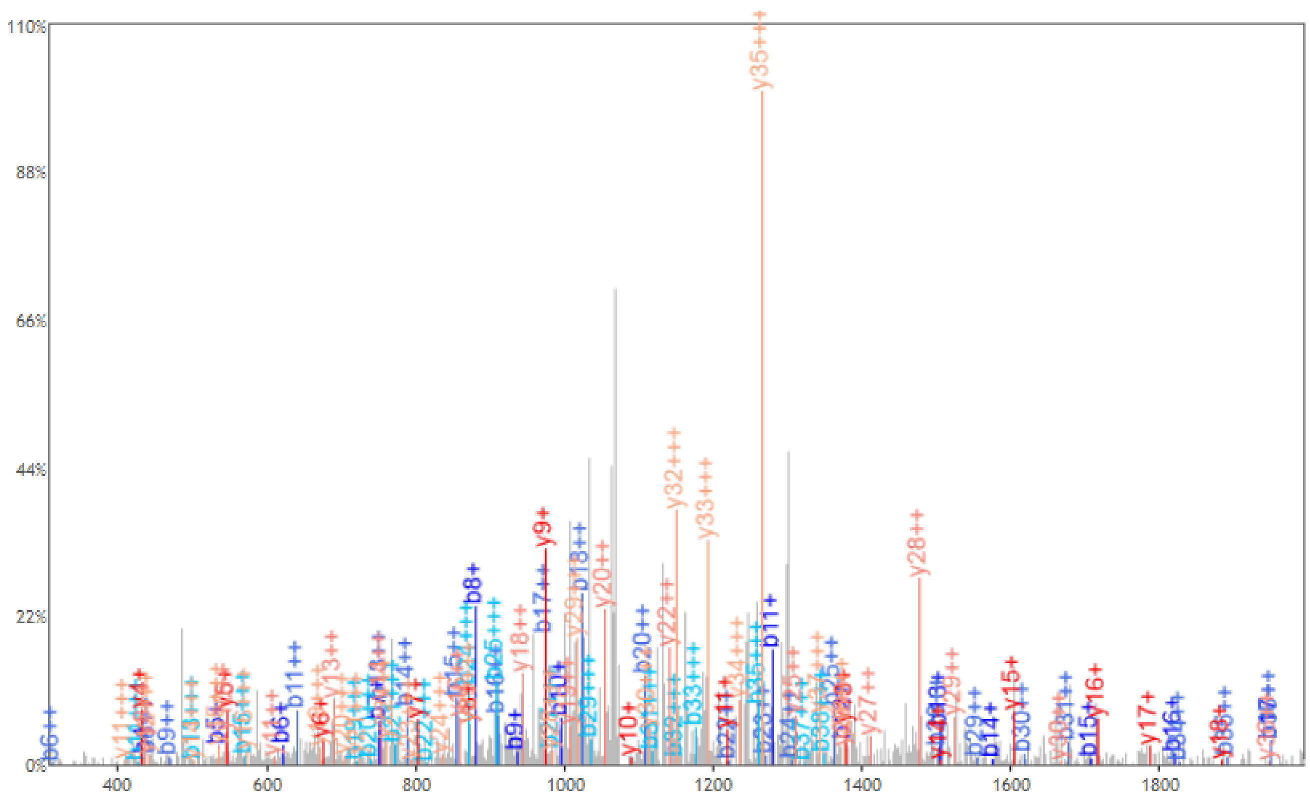
File: 080910WTPMA-11, Scan: 6387, Precursor m/z: 1082.7855, Charge: 4



b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
72.0444	36.5258	24.6863	1	A	40			
200.1030	100.5551	67.3725	2	Q	39	4256.0888	2128.5480	1419.3678
299.1714	150.0893	100.3953	3	V	38	4128.0302	2064.5187	1376.6816
436.2303	218.6188	146.0816	4	H	37	4028.9618	2014.9845	1343.6588
535.2987	268.1530	179.1044	5	V	36	3891.9029	1946.4551	1297.9725
622.3307	311.6690	208.1151	6	S	35	3792.8345	1896.9209	1264.9497
751.3733	376.1903	251.1293	7	E	34	3705.8024	1853.4049	1235.9390
1036.5170	518.7621	346.1772	8	E	33	3576.7599	1788.8836	1192.9248
1093.5385	547.2729	365.1843	9	G	32	3291.6162	1646.3117	1097.8769
1150.5599	575.7836	384.1915	10	G	31	3234.5947	1617.8010	1078.8698
1279.6025	640.3049	427.2057	11	E	30	3177.5733	1589.2903	1059.8626
1376.6553	688.8313	459.5566	12	P	29	3048.5306	1524.7690	1016.8484
1505.6979	753.3526	502.5708	13	E	28	2951.4779	1476.2426	984.4975
1576.7350	788.8711	526.2499	14	A	27	2822.4353	1411.7213	941.4833
1707.7755	854.3914	569.9300	15	M	26	2751.3982	1376.2027	917.8042
1820.8596	910.9334	607.6247	16	L	25	2620.3577	1310.6825	874.1241
1948.9181	974.9627	650.3109	17	Q	24	2507.2736	1254.1404	836.4294
2047.9866	1024.4969	683.3337	18	V	23	2379.2150	1190.1112	793.7432
2161.0706	1081.0389	721.0284	19	L	22	2280.1466	1140.5770	760.7204
2218.0921	1109.5497	740.0355	20	G	21	2167.0626	1084.0349	723.0257
2315.1448	1158.0761	772.3865	21	P	20	2110.0411	1055.5242	704.0186
2443.2398	1222.1235	815.0848	22	K	19	2012.9883	1006.9978	671.6676
2540.2926	1270.6499	847.4357	23	P	18	1884.8934	942.9503	628.9693
2611.3297	1306.1685	871.1147	24	A	17	1787.8406	894.4239	596.6184
2724.4137	1362.7105	908.8094	25	L	16	1716.8035	858.9054	572.9393
2821.4665	1411.2369	941.1604	26	P	15	1603.7194	802.3634	535.2447
2950.5091	1475.7582	984.1746	27	E	14	1506.6667	753.8370	502.8937
3007.5306	1504.2689	1003.1817	28	G	13	1377.6241	689.3157	459.8795
3108.5782	1554.7928	1036.8643	29	T	12	1320.6026	660.8049	440.8724
3237.6208	1619.3141	1079.8785	30	E	11	1219.5549	610.2811	407.1898
3352.6478	1676.8275	1118.2208	31	D	10	1090.5123	545.7598	364.1756
3453.6955	1727.3514	1151.9033	32	T	9	975.4854	488.2463	325.8333
3524.7326	1762.8699	1175.5824	33	A	8	874.4377	437.7225	292.1508
3652.8275	1826.9174	1218.2807	34	K	7	803.4006	402.2039	268.4717
3781.8701	1891.4387	1261.2949	35	E	6	675.3056	338.1565	225.7734
3896.8971	1948.9522	1299.6372	36	D	5	546.2630	273.6352	182.7592
3967.9342	1984.4707	1323.3162	37	A	4	431.2361	216.1217	144.4169
4038.9713	2019.9893	1346.9953	38	A	3	360.1990	180.6031	120.7378
4153.0142	2077.0108	1385.0096	39	N	2	289.1619	145.0846	97.0588
			40	R	1	175.1190	88.0631	59.0445

AQVHVSEEGGEPEAMLQVLGPKPALPEGTEDTAKEDAANR, MH+ 4327.1259, m/z 1082.5369

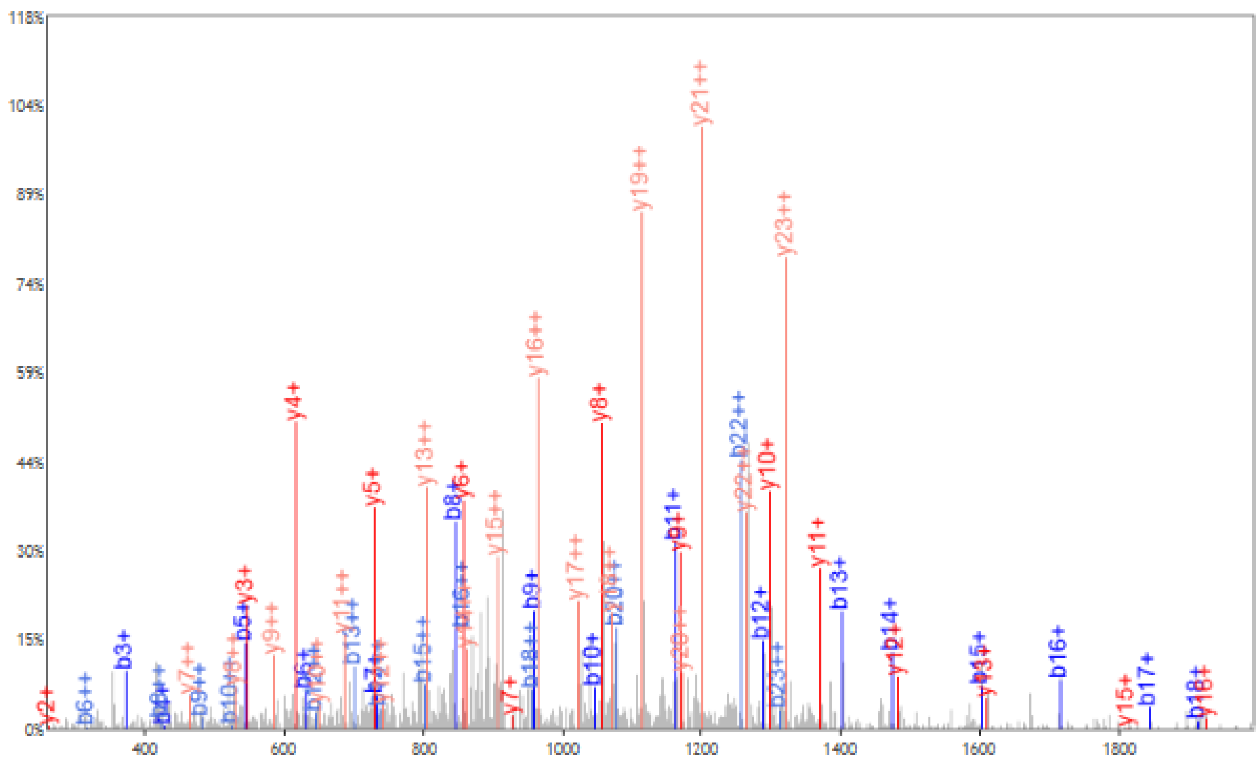
File: 080910WTPMA-11, Scan: 6354, Precursor m/z: 1083.0355, Charge: 4



b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
72.0444	36.5258	24.6863	1	A	40			
200.1030	100.5551	67.3735	2	Q	39	4256.0888	2128.5480	1419.3678
299.1714	150.0893	100.3953	3	V	38	4128.0302	2064.5187	1376.6816
436.2303	218.6188	146.0816	4	H	37	4028.9618	2014.9845	1343.6588
535.2987	268.1530	179.1044	5	V	36	3891.9029	1946.4551	1297.9725
622.3307	311.6690	208.1151	6	S	35	3792.8345	1896.9209	1264.9497
751.3733	376.1903	251.1293	7	E	34	3705.8024	1853.4049	1235.9390
880.4159	440.7116	294.1435	8	E	33	3576.7599	1788.8836	1192.9248
937.4374	469.2223	313.1506	9	G	32	3447.7173	1724.3623	1149.9106
994.4588	497.7331	332.1578	10	G	31	3390.6958	1695.8515	1130.9035
1279.6035	640.3049	427.2057	11	E	30	3333.6743	1667.3408	1111.8963
1376.6553	688.8313	459.5566	12	P	29	3048.5306	1524.7690	1016.8484
1505.6979	753.3526	502.5708	13	E	28	2951.4779	1476.2426	984.4975
1576.7350	788.8711	526.2499	14	A	27	2822.4353	1411.7213	941.4833
1707.7755	854.3914	569.9300	15	M	26	2751.3982	1376.2027	917.8042
1820.8596	910.9334	607.6247	16	L	25	2620.3577	1310.6825	874.1241
1948.9181	974.9627	650.3109	17	Q	24	2507.2736	1254.1404	836.4294
2047.9866	1024.4969	683.3337	18	V	23	2379.2150	1190.1112	793.7433
2161.0706	1081.0389	721.0284	19	L	22	2280.1466	1140.5770	760.7204
2218.0921	1109.5497	740.0355	20	G	21	2167.0626	1084.0349	723.0257
2315.1448	1158.0761	772.3865	21	P	20	2110.0411	1055.5242	704.0186
2443.2398	1222.1235	815.0848	22	K	19	2013.9883	1006.9978	671.6676
2540.2926	1270.6499	847.4357	23	P	18	1884.8934	942.9503	628.9693
2611.3297	1306.1685	871.1147	24	A	17	1787.8406	894.4239	596.6184
2724.4137	1362.7105	908.8094	25	L	16	1716.8035	858.9054	572.9393
2821.4665	1411.2369	941.1604	26	P	15	1603.7194	802.3634	535.2447
2950.5091	1475.7582	984.1746	27	E	14	1506.6667	753.8370	502.8937
3007.5306	1504.2689	1003.1817	28	G	13	1377.6241	689.3157	459.8795
3108.5782	1554.7928	1036.8643	29	T	12	1320.6026	660.8049	440.8724
3237.6208	1619.3141	1079.8785	30	E	11	1219.5549	610.2811	407.1898
3352.6478	1676.8275	1118.2208	31	D	10	1090.5123	545.7598	364.1756
3453.6955	1727.3514	1151.9033	32	T	9	975.4854	488.2463	325.8333
3524.7326	1762.8699	1175.5824	33	A	8	874.4377	437.7225	292.1508
3652.8275	1826.9174	1218.2807	34	K	7	803.4006	402.2039	268.4717
3781.8701	1891.4387	1261.2949	35	E	6	675.3056	338.1565	225.7734
3896.8971	1948.9522	1299.6372	36	D	5	546.2630	273.6352	182.7592
3967.9342	1984.4707	1323.3162	37	A	4	431.2361	216.1217	144.4169
4038.9713	2019.9893	1346.9953	38	A	3	360.1990	180.6031	120.7378
4153.0142	2077.0108	1385.0096	39	N	2	289.1619	145.0846	97.0588
			40	R	1	175.1190	88.0631	59.0445

KLEGDSTDLSDQIAELQAQIAELK, MH+ 2771.4421, m/z 924.4856

File: 080910WTPMA-11, Scan: 9804, Precursor m/z: 924.82, Charge: 3



b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	24		
242.1863	121.5968	2	L	23	2643.3472	1322.1772
371.2289	186.1181	3	E	22	2530.2631	1265.6352
428.2504	214.6288	4	G	21	2401.2205	1201.1139
543.2773	272.1423	5	D	20	2344.1990	1172.6032
630.3093	315.6583	6	S	19	2229.1721	1115.0897
731.3570	366.1821	7	T	18	2142.1401	1071.5737
846.3840	423.6956	8	D	17	2041.0924	1021.0498
959.4680	480.2376	9	L	16	1926.0655	963.5364
1046.5000	523.7537	10	S	15	1812.9814	906.9943
1161.5270	581.2671	11	D	14	1725.9494	863.4783
1289.5856	645.2964	12	Q	13	1610.9224	805.9648
1402.6696	701.8385	13	I	12	1482.8638	741.9356
1473.7067	737.3570	14	A	11	1369.7798	685.3935
1602.7493	801.8783	15	E	10	1298.7427	649.8750
1715.8334	858.4203	16	L	9	1169.7001	585.3537
1843.8920	922.4496	17	Q	8	1056.6160	528.8116
1914.9291	957.9682	18	A	7	928.5574	464.7824
2042.9877	1021.9975	19	Q	6	857.5203	429.2638
2156.0717	1078.5395	20	I	5	729.4617	365.2345
2227.1088	1114.0581	21	A	4	616.3777	308.6925
2512.2525	1256.6299	22	E	3	545.3406	273.1739
2625.3366	1313.1719	23	L	2	260.1969	130.6021
		24	K	1	147.1128	74.0600

[click] to move table

Static Modifications:
C: 57.02146

Variable Modifications:
E: 156.1011