Supplementary Information for

Global analysis of lysine ubiquitination by ubiquitin remnant immunoaffinity profiling

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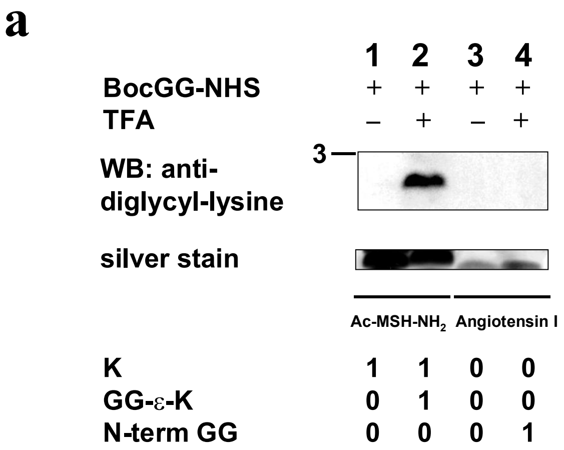
Supplementary Information includes:

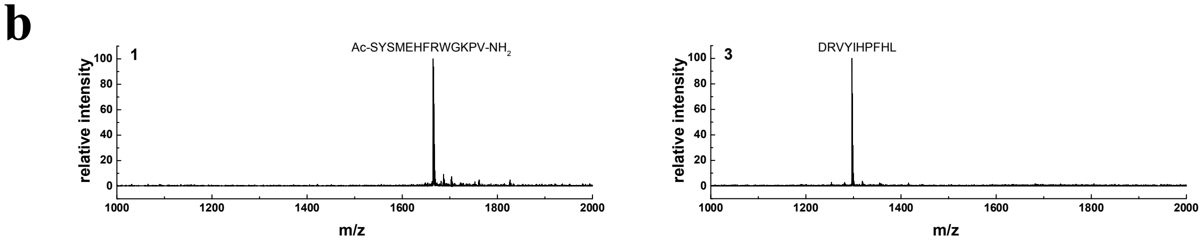
1. Supplementary Figs. 1-18.

2. Supplementary Tables 1-2.

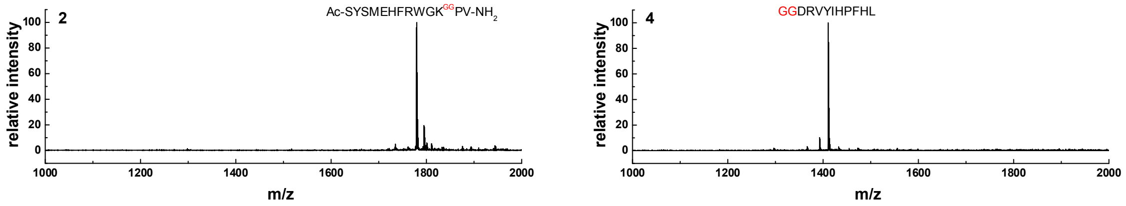
3. Supplementary references.

Supplementary Fig. 1





Ac-MSH-NH$_2$ Angiotensin I



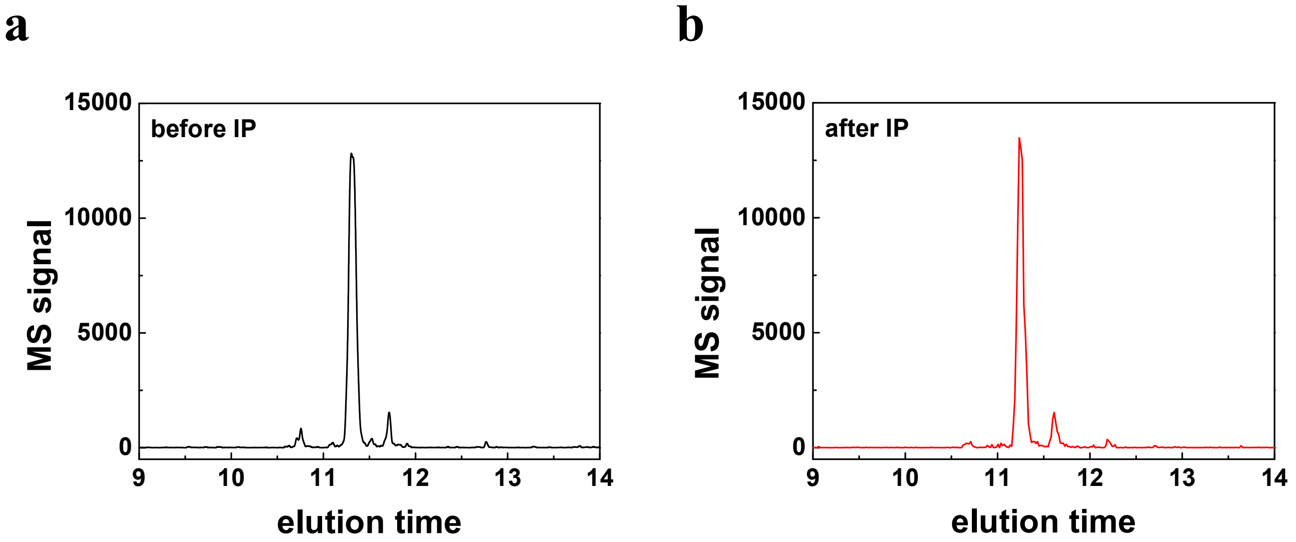
GG-modified Ac-MSH-NH$_2$ GG-modified Angiotensin I

Supplementary Fig. 1 The anti-diglycyl-lysine antibody specifically interacts with diglycine-modifications on the ε-amine of lysine and does not recognize a peptide with an N-terminal Gly-Gly sequence.

(**a**) In our tests of the specificity of the anti-diglycyl-lysine antibody, we considered the fact that 0.4% of tryptic peptides in the human proteome are predicted to contain two glycine residues as the first two N-terminal amino acids. Therefore, we tested the ability of the anti-diglycyl-lysine antibody to recognize peptides that contain this N-terminal sequence. Western blot analysis using the anti-diglycyl-lysine antibody of the following samples: (**1**) unmodified Ac-MSH-NH$_2$ peptide, which contains one internal lysine; (**2**) diglycine (GG)-modified Ac-MSH-NH$_2$ peptide, which contains a GG-modified lysine; (**3**) angiotensin I, which contains no lysines; (**4**) angiotensin I modified to contain a GlyGly sequence at the N-terminus. The numbers of lysines, GG-modified lysines (GG-ε-K), and N-terminal GG sequences are indicated in the chart at the bottom of the blot. A silver stained gel is shown to document peptide loading. The Western blotting experiment demonstrated that the antibody only interacts with the peptide containing GG-ε-K but not the peptide containing an N-terminal GlyGly sequence.

(**b**) MALDI-TOF-MS of the peptides used in the Western blot experiment above to confirm the complete modification of the lysine and the N-terminal amine in sample **2** and **4**, respectively.

Supplementary Fig. 2

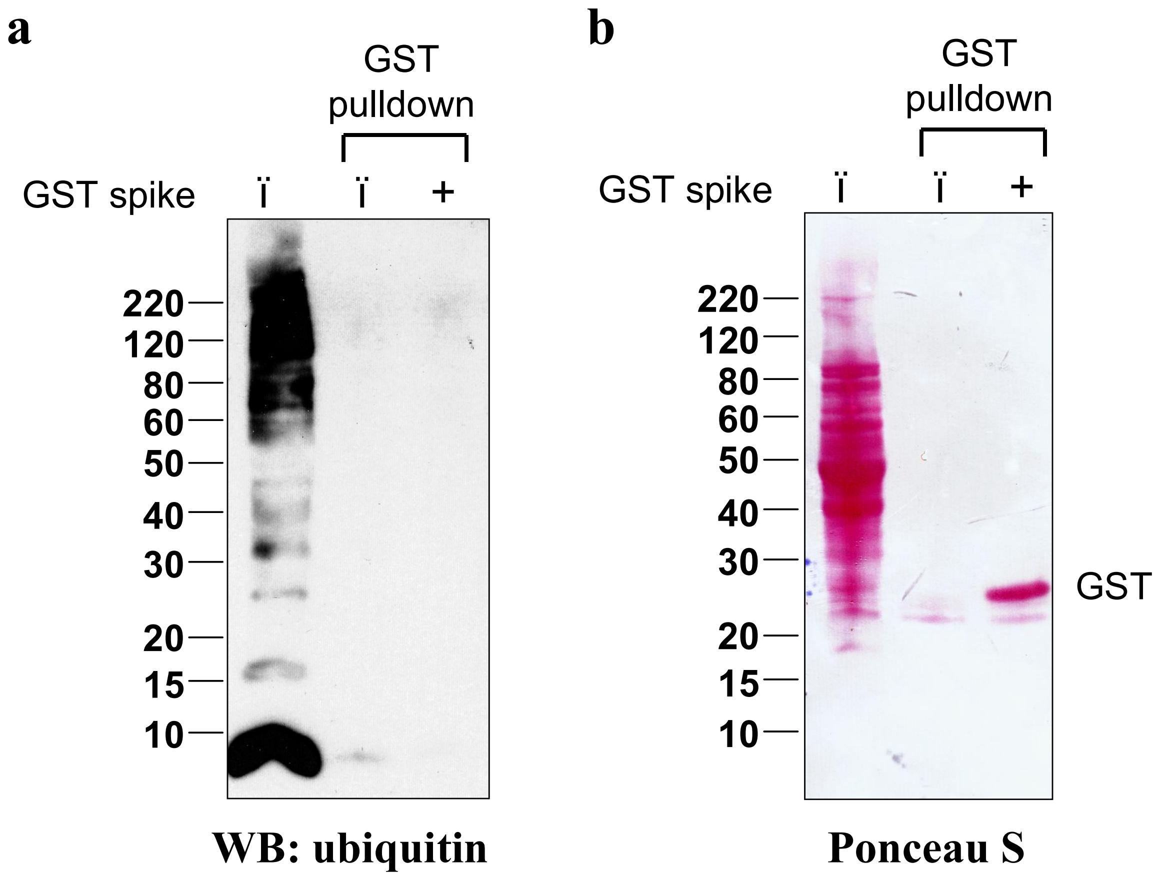


Supplementary Fig. 2 The anti-diglycyl-lysine antibody can quantitatively immunoprecipitate peptides containing diglycine-modified lysines.

(**a**) Extracted Ion Chromatography (EIC) of a sample containing a peptide with a diglycine-modified lysine before immunoprecipitation. (**b**) EIC of the anti-diglycyl-lysine antibody immunoprecipitate. The yield of the immunoprecipitation is calculated based on the areas of the peptide peaks before and after immunoprecipitation. The yield measured from the average of three independent runs is 1.1±0.2.

A GlyGly-modified Ac-MSH-NH_2 peptide, Ac-SYSMEHFRWGK*PV-NH_2 (K* representing Gly-Gly-modified lysine), was dissolved in a buffer containing 50 mM Tris-HCl (pH 7.4) and 150 mM NaCl at a concentration of 0.3 nmol/mL. 100 μL of the peptide solution was incubated with 20 μL beads coupled with the anti-diglycyl-lysine antibody, washed and eluted five times with 20 μL elution buffer (10 mM citric acid, pH 3). The samples before and after immunopurification were acidified and 1 μL of each sample was injected to LC-Q-TOF MS for the analysis in MS mode. The EIC of GlyGly-modified Ac-MSH-NH_2 peptide was integrated to calculate the yield. The result indicated that the peptide containing GlyGly-modified lysine was completely immunoprecipitated within the experimental error.

Supplementary Fig. 3

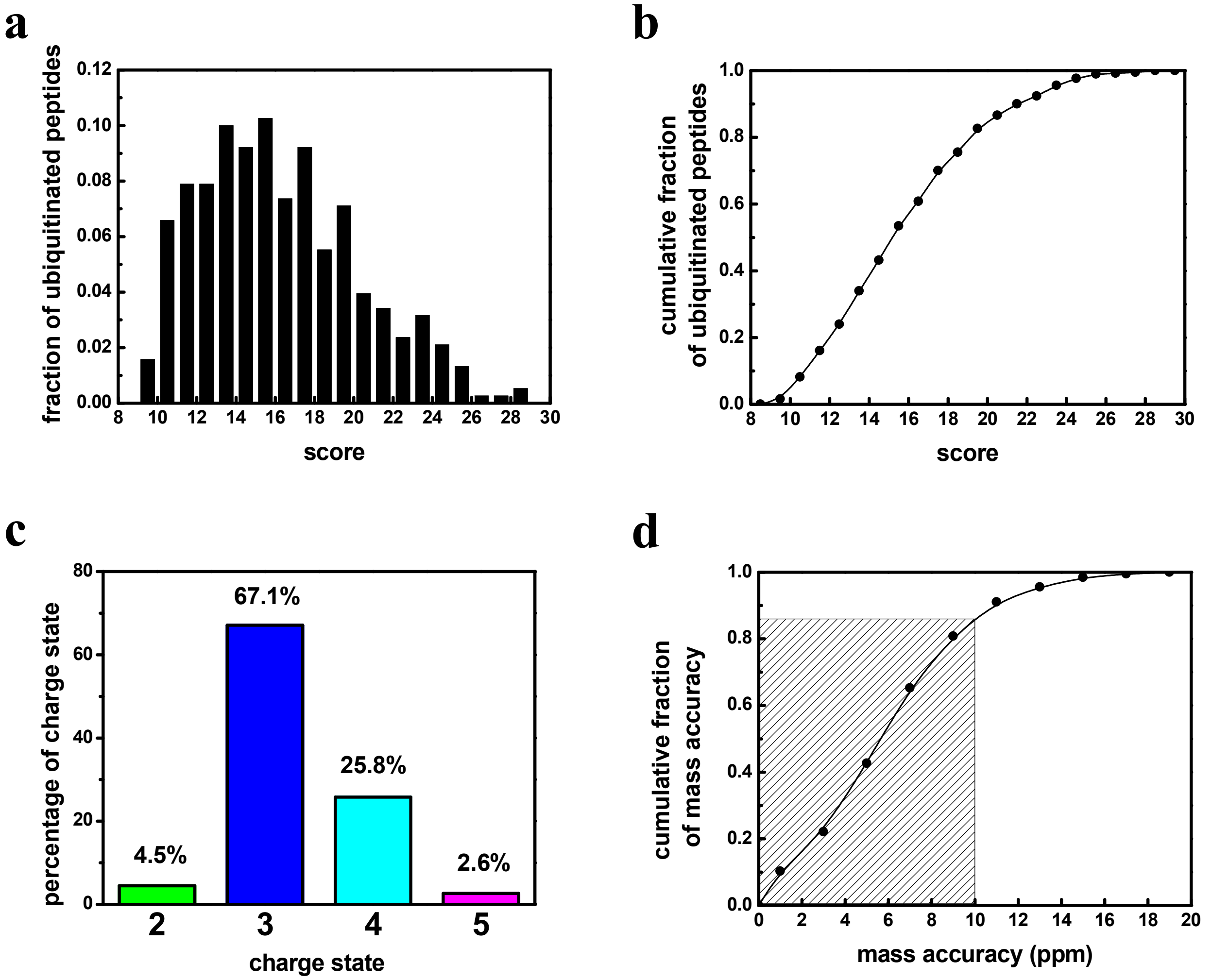


Supplementary Fig. 3 Ubiquitination does not occur to a detectable level during sample preparation.

(**a**) An anti-ubiquitin Western blot to detect the ubiquitination of GST spiked in during sample preparation. To detect whether ubiquitination could happen during the sample preparation, we spiked ~10 µg of bacterially expressed and purified ubiquitin-free glutathione S-transferase (GST), a protein that has surface lysine residues[1] and can be ubiquitinated in cells[2], to a lysate containing ~100 µg of protein at the beginning of the experiment. Then, glutathione agarose beads were added to the lysate to pull down GST for Western blot analysis. It has been shown that ubiquitinated GST can be pulled down by glutathione agarose beads[2]. In order to assay the non-specific binding, same amount of glutathione agarose beads were added to a lysate without spiking GST. Western blot analysis using an anti-ubiquitin antibody indicated numerous ubiquitinated proteins in the lysate, but absolutely no GST-dependent ubiquitination signal was detected. This indicates that the degree of *ex vivo* ubiquitination is exceedingly low under our experimental conditions. This result confirmed that the ubiquitination occurs in the cells but does not occur, at least not to a detectable level, during the sample preparation.

(**b**) Ponceau S stain to measure protein loading in the Western blot experiment in (**a**). The Ponceau S stain of the membrane confirms that GST was pulled down during the experiment.

Supplementary Fig. 4



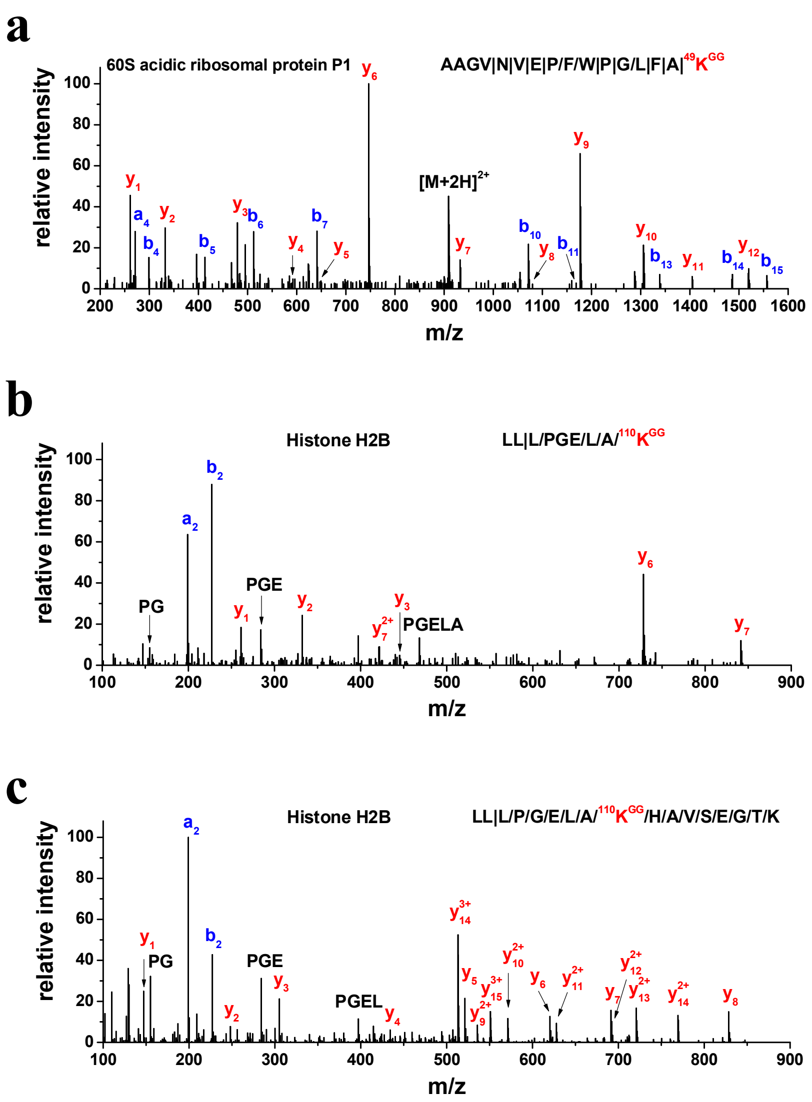
Supplementary Fig. 4 Distribution of Spectrum Mill score, charge state and mass accuracy of the ubiquitinated peptides identified in our experiments.

(**a**) Fraction and (**b**) Cumulative fraction of scores of ubiquitinated peptides identified by Spectrum Mill. The scores range from 9 to 29. About 80% of the ubiquitinated peptides have a score larger than 12.

(**c**) Charge state distribution of Spectrum Mill-identified ubiquitinated peptides. The majority (91.4%) of the ubiquitinated peptides have +3 or +4 charges. Ubiquitin remnant peptides have an additional charge since the diglycine moiety on the lysines have an amine.

(**d**) Cumulative distribution of mass accuracy (ppm) of ubiquitinated peptides identified by Spectrum Mill. More than 80% of ubiquitinated peptides have a mass accuracy of less than 10 ppm, which corresponds to a 0.01 Da mass deviation for a peptide with 1000 Da molecular weight.

Supplementary Fig. 5



Supplementary Fig. 5 Ubiquitinated peptides with C-terminal GlyGly-modified lysines are detected.

MS/MS spectra of ubiquitinated peptides from 60S acidic ribosomal protein P1 (**a**) and Histone H2B (**b**), which have a diglycine-modified lysine at the C-terminus (Lys49 and Lys110, respectively). We also detected the same ubiquitinated H2B lysine in a peptide that contained the diglycine-modified Lys at 110 but was not cleaved after this modified lysine (**c**).

The presence of the diglycine-modified lysines at C-terminus of some peptides, such as the one from Histone H2B above, indicates that the C-terminal peptide bond of the diglycine-modified lysine can also be cleaved during the sample preparation by trypsin. Overall, this cleavage is less efficient than that after unmodified lysines or arginines, presumably because the presence of a positive charge on the amino group of GlyGly allows this modified residue to interact with trypsin in a manner similar to the ε-amine of lysine. This result is consistent with a previous study[3]. In total, our experiments identified 14 (~3%) unique peptides with a C-terminal diglycine-modified lysine.

Supplementary Fig. 6

(Please see next 380 pages.)

Supplementary Fig. 6 Annotated MS/MS spectra of ubiquitinated peptides identified in HEK293 cells.

In the **Result Summary**, a list of rank, score, the percentage of the scored peak intensity (SPI%), backbone cleavage score (BCS), variable modification, peptide sequence, precursor ion mass (MH^+), precursor ion mass error (MH^+ error), protein molecular weight (MW), Swiss-Prot accession number, and protein name, is shown for the peptides, including up to five highest scored peptides, if they exist, as identified by Spectrum Mill.

In the **Detailed Result**, the peptide rank, modification site, score, SPI%, BCS, sequence map, precursor ion mass (MH^+), precursor ion mass error (MH^+ error), protein molecular weight (MW), Swiss-Prot accession number, and protein name are listed for the highest scored peptide. The symbols, \, / and |, represent *b*-ions, *y*-ions, and both *b*-ions and *y*-ions, respectively.

The table shows the m/z of experimental MS/MS fragment ions and the matched ion-types as well as the peak intensity, score of each matched ions, and delta mass (ppm) measuring the difference between the theoretical and experimental peptide precursor masses.

In the annotated spectra, matched ions are shown in red vertical segments and labeled as *b* or *y*-ions, while the unmatched ions are shown in black vertical segments. Some red vertical segments are not labeled automatically by Spectrum Mill because of the lack of space in the spectra. The detailed information about these peaks is listed in the table of fragment ions.

In total, 380 ubiquitinated peptides were detected and their annotated MS/MS spectra were provided. The number at the left upper corner of each spectrum corresponds to the number in Supplementary Table 1.

Note that some ubiquitination sites in the ubiquitinated peptides containing two diglycine-modified lysines are also identified in the ubiquitinated peptides containing a single diglycine-modified lysine. Therefore, this list has six more ubiquitinated peptides than ubiquitination sites.

1

Result Summary

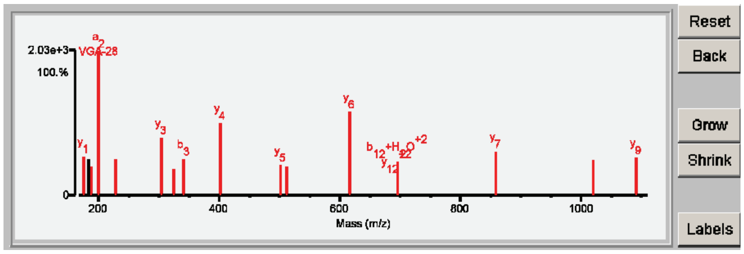
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.31	80.4	10	4/25	K51k	(R)NLLSVAYkNVVGAR(R)	1503.8642	114.0478	3.0	28082.5/4.76	HUMAN	P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3
1	19.31	80.4	10	4/25	K50k	(R)NLLSVAYkNVVGAR(R)	1503.8642	114.0478	3.0	28218.9/4.76	HUMAN	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4
1	19.31	80.4	10	4/25	K50k	(R)NLLSVAYkNVVGAR(R)	1503.8642	114.0478	3.0	28302.7/4.80	HUMAN	P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2
1	19.31	80.4	10	4/25	K49k	(R)NLLSVAYkNVVGAR(R)	1503.8642	114.0478	3.0	27745.3/4.73	HUMAN	P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1
2	16.55	78.3	8	5/25	None	(R)NLLSVAYKNVVGGQR(A)	1617.9071	0.0048	3.0	27774.2/4.68	HUMAN	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.31	80.4	10	4/25	K51k	(R) N L|L\S V/A/Y/k/N/V/V/G A/R (R)	1503.8642	114.0478	3.0	28082.5/4.76	HUMAN	P31946	283	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3
1	19.31	80.4	10	4/25	K50k	(R) N L|L\S V/A/Y/k/N/V/V/G A/R (R)	1503.8642	114.0478	3.0	28218.9/4.76	HUMAN	Q04917	329	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4
1	19.31	80.4	10	4/25	K50k	(R) N L|L\S V/A/Y/k/N/V/V/G A/R (R)	1503.8642	114.0478	3.0	28302.7/4.80	HUMAN	P61981	341	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2
1	19.31	80.4	10	4/25	K49k	(R) N L|L\S V/A/Y/k/N/V/V/G A/R (R)	1503.8642	114.0478	3.0	27745.3/4.73	HUMAN	P63104	387	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1

Fragment-ion (m/z)	70.064	72.080	84.080	86.095	87.053	136.074	141.100	155.118	159.111	175.115	183.111
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.04 0.20 PR -14.6	0.17 1.16 0.50 V -10.8	10.02 69.87 -0.70	0.58 4.03 0.22 LI -13.1	2.66 18.57 0.50 a_1 -38.9 0.50 NR -26.3	0.11 0.75 1.00 Y -15.4	2.80 19.50 -0.19	3.09 21.53 -0.22	4.04 28.20 0.50 SV-28 -20.1	3.85 26.84 1.50 y_1 -22.0	3.66 25.52 -0.26

Fragment-ion (m/z)	187.105	200.138	228.135	303.176	324.181	341.216	402.247	501.316	510.777^{+2}	615.359	695.885^{+2}	857.494	1020.573	1091.593
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.84 19.78 0.75 SV -22.0	14.34 100.00 0.50 a_2 -11.7 VGA-28 -11.7	3.62 25.28 0.75 b_2 -0.7 VGA -0.7	5.67 39.55 1.50 y_3 -3.4	2.69 18.77 0.25 b_3-NH_3 -37.3	3.60 25.11 0.50 b_3 -10.9	7.12 49.69 1.50 y_4 2.1	2.95 20.55 1.50 y_5 2.9	2.91 20.29 1.50 y_8^{+2} -11.9	8.29 57.79 1.50 y_6 2.6	3.36 23.40 1.50 $b_{12}+H_2O^{+2}$ -5.7 y_{12}^{+2} -12.9	4.37 30.46 1.50 y_7 -1.4	3.54 24.67 1.50 y_8 14.0	3.73 26.02 1.50 y_9 -2.3



2

Result Summary

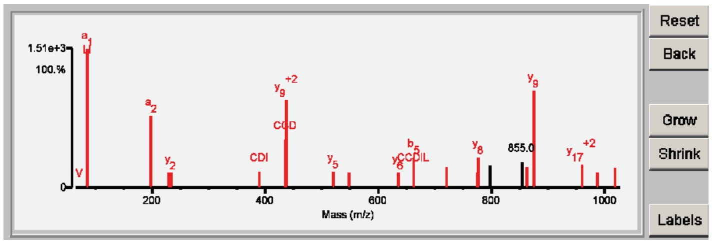
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.38	89.2	10	4/25	K106k	(K)LICCDILDVLDkHLIPAANTGESK(V)	2695.3793	114.0592	5.8	29174.1/4.63	HUMAN	P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1
2	11.42	68.1	6	9/25	K118k	(K)LICCDILDVLDKHLIPAANTGESk(V)	2695.3793	114.0592	5.8	29174.1/4.63	HUMAN	P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.38	89.2	10	4/25	K106k	(K) L I/C C D\I|L/D V L D k H L/I/P/A A/N/T G E/S K (V)	2695.3793	114.0592	5.8	29174.1/4.63	HUMAN	P62258	317	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Fragment-ion (m/z)	72.078	84.079	86.095	199.180	229.116	234.138	389.155	436.096	437.716^{+2}	521.251	549.170	635.301
Frac. Inten.(% of TIC)	0.11	0.06	17.41	9.06	1.86	1.86	1.97	5.97	10.94	2.04	1.88	1.91
Rel. Inten.(% of BP)	0.62	0.33	100.00	52.01	10.70	10.71	11.34	34.26	62.85	11.69	10.77	10.97
Score	0.50	0.50	0.50 0.50	0.50	0.75	1.50	0.75	0.75	1.50	1.50	0.75	1.50
Ion-type	V	KQ	a_1 LI	a_2	LD	y_2	CDI	CCD	y_9^{+2}	y_5	CCDI	y_6
Delta ppm	-35.7	-22.3	-27.0 -14.2	-8.5	-13.9	-27.9	13.5	-1.9	-2.0	-9.7	-20.0	2.2

Fragment-ion (m/z)	662.254	721.400	775.342	776.370^{+2}	777.366	797.947^{+2}	854.974^{+2}	861.752^{+3}	874.427	961.517^{+2}	987.521	1018.039^{+2}	1048.570
Frac. Inten.(% of TIC)	3.85	2.56	1.82	1.85	3.83	2.80	3.18	2.65	12.07	2.93	1.92	2.45	3.01
Rel. Inten.(% of BP)	22.11	14.70	10.46	10.61	21.98	16.08	18.28	15.22	69.31	16.82	11.05	14.09	17.31
Score	0.75	0.75	0.50	-0.11	1.50	-0.16	-0.18	1.50	1.50	1.50	1.50	1.50	-0.17
Ion-type	b_5 CCDIL	DkHLI	b_6		y_8			y_{22}^{+3}	y_9	y_{17}^{+2}	y_{10}	y_{18}^{+2}	
Delta ppm	-15.9 -15.9	-0.6	-9.4		-9.7			-5.0	0.4	15.5	10.4	-5.7	



3

Result Summary

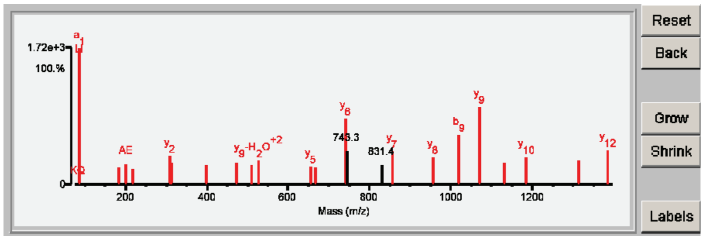
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.12	93.4	14	2/25	K196k	(R)LAkAAFDDAIAELDTLSEESYK(D)	2400.1817	114.0568	5.5	29174.1/4.63	HUMAN	P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.12	93.4	14	2/25	K196k	(R) L A\k A A F D D\A\I|A/E|L/D/T/L/S/E/E/S/Y K (D)	2400.1817	114.0568	5.5	29174.1/4.63	HUMAN	P62258	317	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Fragment-ion (m/z)	84.081	86.096	185.130	201.082	217.082	310.177	314.168	397.209	473.733^{+2}	509.263^{+2}	526.251	527.243^{+2}	655.301
Frac. Inten.(% of TIC)	0.09	17.28	2.09	2.60	1.93	3.65	2.79	2.41	2.71	2.48	2.10	2.97	2.25
Rel. Inten.(% of BP)	0.52	100.00	12.12	15.05	11.16	21.15	16.16	13.95	15.67	14.33	12.13	17.18	13.00
Score	0.50	0.50 0.50	0.75	0.75	0.75	1.50	0.75	1.50	0.50	0.50	1.50	0.50	1.50
Ion-type	KQ	a_1 LI	b_2 IA	AE	ES	y_2	AEL	y_3	b_8^{+2}	b_9^{+2}	y_4	y_9-H_2O^{+2}	y_5
Delta ppm	6.2	-21.2 -8.4	1.9 1.9	-30.7	-3.2	1.8	-11.9	1.9	-5.1	17.7	0.3	4.8	11.1

Fragment-ion (m/z)	665.827^{+2}	742.330	743.331^{+2}	831.418^{+2}	855.417	956.463	1017.504	1071.474	1130.564	1184.587	1313.588	1384.636
Frac. Inten.(% of TIC)	2.19	8.28	4.23	2.40	4.17	3.48	6.31	9.89	2.77	3.44	3.08	4.40
Rel. Inten.(% of BP)	12.69	47.92	24.49	13.88	24.10	20.12	36.53	57.25	16.05	19.89	17.85	25.47
Score	0.50	1.50	-0.24	-0.14	1.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	b_{12}^{+2}	y_6			y_7	y_8	b_9	y_9	b_{10}	y_{10}	y_{11}	y_{12}
Delta ppm	-14.4	6.0			8.6	6.5	2.8	-9.6	-19.1	15.7	-17.7	-8.5



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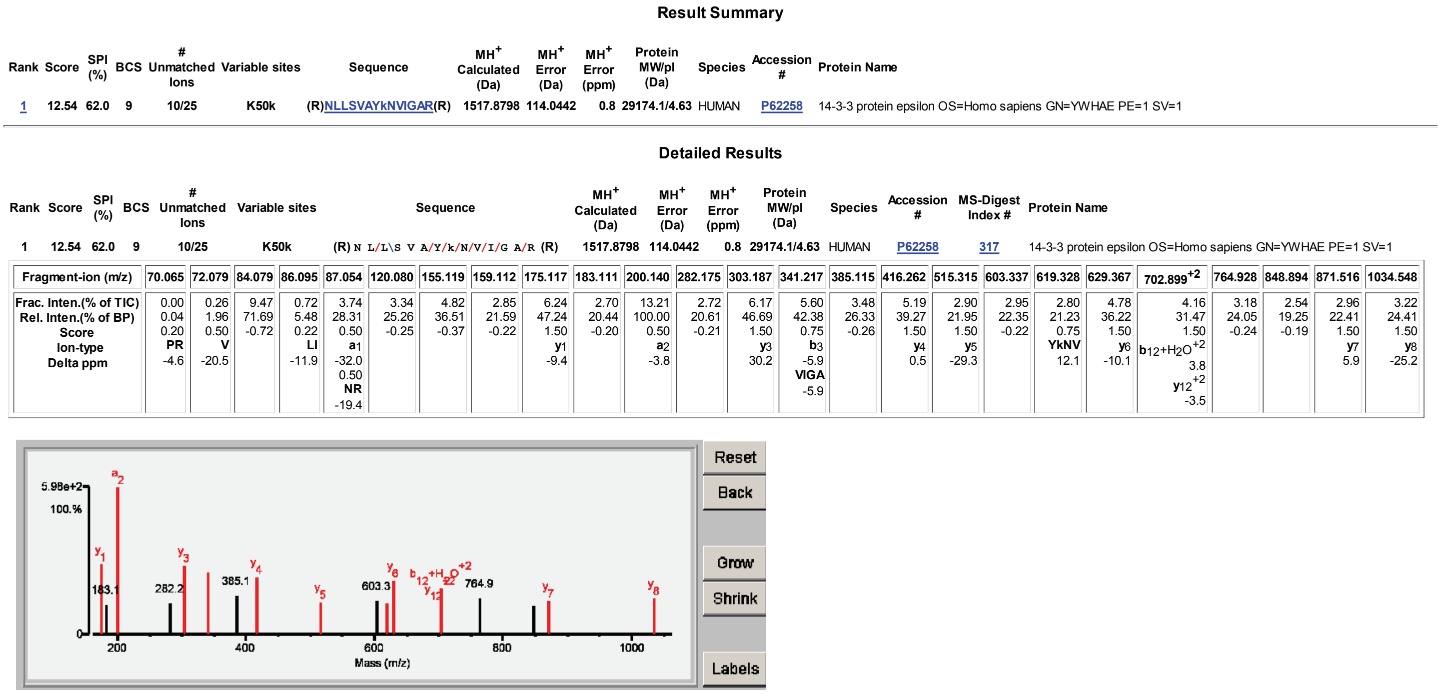

Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.54	62.0	9	10/25	K50k	(R)NLLSVAYkNVIGAR(R)	1517.8798	114.0442	0.8	29174.1/4.63	HUMAN	P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.54	62.0	9	10/25	K50k	(R) N L/L\S V A/Y/k/N/V/I/G A/R (R)	1517.8798	114.0442	0.8	29174.1/4.63	HUMAN	P62258	317	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Fragment-ion (m/z)	70.065	72.079	84.079	86.095	87.054	120.080	155.119	159.112	175.117	183.111	200.140	282.175
Frac. Inten.(% of TIC)	0.00	0.26	9.47	0.72	3.74	3.34	4.82	2.85	6.24	2.70	13.21	2.72
Rel. Inten.(% of BP)	0.04	1.96	71.69	5.48	28.31	25.26	36.51	21.59	47.24	20.44	100.00	20.61
Score	0.20	0.50	-0.72	0.22	0.50	-0.25	-0.37	-0.22	1.50	-0.20	0.50	-0.21
Ion-type	PR	V		LI	a_1				y_1		a_2	
Delta ppm	-4.6	-20.5		-11.9	-32.0				-9.4		-3.8	
					0.50							
					NR							
					-19.4							

Fragment-ion (m/z)	303.187	341.217	385.115	416.262	515.315	603.337	619.328	629.367	702.899^{+2}	764.928	848.894	871.516	1034.548
Frac. Inten.(% of TIC)	6.17	5.60	3.48	5.19	2.90	2.95	2.80	4.78	4.16	3.18	2.54	2.96	3.22
Rel. Inten.(% of BP)	46.69	42.38	26.33	39.27	21.95	22.35	21.23	36.22	31.47	24.05	19.25	22.41	24.41
Score	1.50	0.75	-0.26	1.50	1.50	-0.22	0.75	1.50	1.50	-0.24	-0.19	1.50	1.50
Ion-type	y_3	b_3		y_4	y_5		YkNV	y_6	$b_{12}+H_2O^{+2}$			y_7	y_8
Delta ppm	30.2	-5.9		0.5	-29.3		12.1	-10.1	3.8			5.9	-25.2
		VIGA							y_{12}^{+2}				
		-5.9							-3.5				

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Result Summary

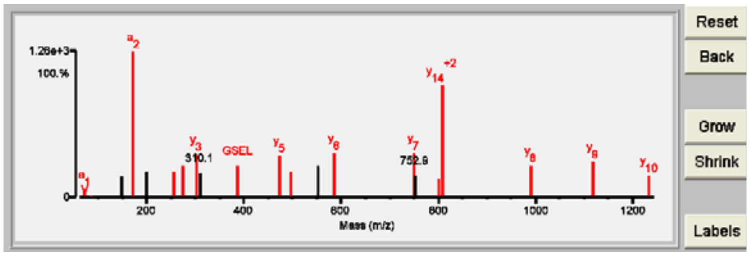
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.93	88.4	8	5/24	K258k	(R)VVGSELIQkYLGDGPK(L)	1702.9374	114.0569	7.7	49184.8/5.87	HUMAN	P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1
2	11.24	71.8	4	9/24	K265k	(R)VVGSELIQKYLGDGPk(L)	1702.9374	114.0569	7.7	49184.8/5.87	HUMAN	P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.93	88.4	8	5/24	K258k	(R) V V|G S E L/I/Q/k/Y/L/G D/G P K (L)	1702.9374	114.0569	7.7	49184.8/5.87	HUMAN	P62191	520859	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.081	84.079	86.095	147.104	171.149	199.143	200.145	256.087	274.102	301.186	310.150
Frac. Inten.(% of TIC)	0.00	0.93	0.23	0.18	2.48	18.04	2.80	3.12	3.15	4.00	5.26	2.95
Rel. Inten.(% of BP)	0.03	5.15	1.29	1.02	13.77	100.00	15.54	17.28	17.44	22.18	29.16	16.34
Score	0.20	0.50	0.50	0.22	-0.08	0.50	0.50	-0.10	0.50	0.75	1.50	-0.10
Ion-type	PR	a_1	KQ	LI		a_2	b_2		GSE-H$_2$O	GSE	y_3	
Delta ppm	-18.9	-17.7	-21.1	-17.7		-4.6	-12.1		-28.9	-7.9	-4.8	
		0.50										
		V										
		-2.4										

Fragment-ion (m/z)	387.190	473.246	496.264^{+2}	551.805	586.319	749.392	752.897^{+2}	800.931^{+2}	809.937^{+2}	991.525	1119.582	1232.659
Frac. Inten.(% of TIC)	3.88	5.20	3.10	3.94	5.52	5.51	2.66	2.21	13.79	4.00	4.36	2.70
Rel. Inten.(% of BP)	21.50	28.81	17.21	21.81	30.60	30.52	14.73	12.23	76.44	22.16	24.19	14.96
Score	0.75	1.50	1.50	-0.13	1.50	1.50	-0.09	0.50	1.50	1.50	1.50	1.50
Ion-type	GSEL	y_5	y_8^{+2}		y_6	y_7		y_{14}-H$_2$O^{+2}	y_{14}^{+2}	y_8	y_9	y_{10}
Delta ppm	3.0	23.2	0.2		-0.5	12.4		13.6	14.1	3.9	2.7	-3.6



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Result Summary

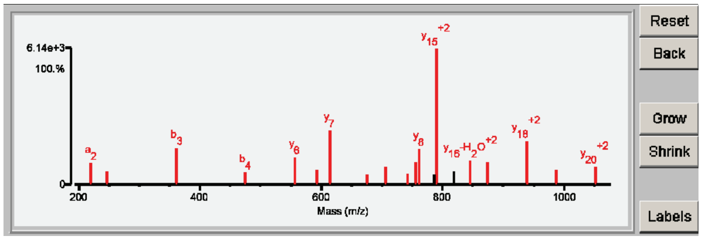
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.06	96.0	10	2/25	K210k	(R)FVNLGIEPPkGVLLFGPPGTGK(T)	2237.2693	114.0422	-0.3	48634.1/5.71	HUMAN	P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3
2	10.39	62.3	5	10/25	K222k	(R)FVNLGIEPPKGVLLFGPPGTGk(T)	2237.2693	114.0422	-0.3	48634.1/5.71	HUMAN	P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.06	96.0	10	2/25	K210k	(R) F V|N\L|G I E/P/P k G V/L/L/F/G/P P G T G K (T)	2237.2693	114.0422	-0.3	48634.1/5.71	HUMAN	P35998	520925	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Fragment-ion (m/z)	72.082	84.082	86.097	120.079	219.149	247.147	361.191	474.272	556.311	593.336	613.331	674.359^{+2}
Frac. Inten.(% of TIC)	0.07	0.07	0.24	0.09	3.87	2.32	6.36	2.21	4.69	2.57	9.58	1.79
Rel. Inten.(% of BP)	0.30	0.30	1.01	0.38	16.21	9.73	26.65	9.28	19.68	10.79	40.15	7.51
Score	0.50	0.50	0.22	1.00	0.50	0.50	0.50	0.50	1.50	0.75	1.50	0.25
Ion-type	V	KQ	LI	a_1	a_2	b_2	b_3	b_4	y_6	PPkGV	y_7	b_{12}-H_2O^{+2}
Delta ppm	11.4	8.6	9.0	-25.6 1.00 F -16.5	-5.0	8.1	8.2	0.2	3.5	-9.0	0.3	-23.8

Fragment-ion (m/z)	706.424	741.429	756.394	760.400	786.944^{+2}	789.953^{+2}	819.504	845.468^{+2}	873.481	939.519^{+2}	986.567	987.556^{+2}	1053.078^{+2}
Frac. Inten.(% of TIC)	3.15	1.88	3.91	6.18	1.69	23.85	2.30	4.24	3.89	7.61	1.81	2.56	3.06
Rel. Inten.(% of BP)	13.22	7.88	16.38	25.89	7.06	100.00	9.64	17.78	16.32	31.92	7.59	10.75	12.83
Score	0.75	1.50	0.25	1.50	-0.07	1.50	-0.10	0.50	1.50	1.50	1.50	0.50	1.50
Ion-type	PPkGVL	y^{++}_{14}	b_7-NH_3	y_8		y_{15}^{+2}		y_{16}-H_2O^{+2}	y_9	y_{18}^{+2}	y_{10}	y_{19}-NH_3^{+2}	y_{20}^{+2}
Delta ppm	-1.7	2.2	0.2	1.0		-1.0		-1.7	-2.2	-9.4	0.5	-1.1	-12.8



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Result Summary

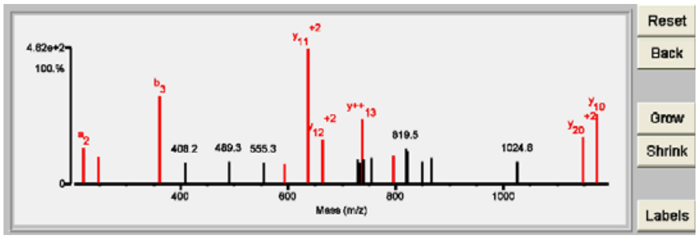
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.94	65.2	8	12/25	K210k K222k	(R)FVNLGIEPPkGVLLFGPPGTGkTLCAR(A)	2838.5699	228.0947	2.9	48634.1/5.71	HUMAN	P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.94	65.2	8	12/25	K210k K222k	(R) F V\N\L G I E/P P k G V L/L/F/G/P/P G T G k T L C A R (A)	2838.5699	228.0947	2.9	48634.1/5.71	HUMAN	P35998	520925	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Fragment-ion (m/z)	70.066	86.093	120.079	219.145	247.147	361.183	408.225	489.271	555.272^{+2}	593.335	636.320^{+2}	664.856^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.06 0.20 PR 8.2	0.31 1.99 0.22 LI -35.1	0.16 1.01 1.00 a_1 -27.3 1.00 F -18.1	4.22 27.10 0.50 a_2 -23.2	3.12 20.01 0.50 b_2 6.1	10.14 65.03 0.50 b_3 -15.0	2.47 15.82 -0.16	2.54 16.30 -0.16	2.51 16.08 -0.16	2.37 15.20 0.75 PPkGV -11.4	15.59 100.00 1.50 y_{11}^{+2} -15.7	5.15 33.04 1.50 y_{12}^{+2} 22.7

Fragment-ion (m/z)	729.866	732.420	738.390	738.850	754.410^{+2}	794.913^{+2}	819.514	820.878^{+2}	849.765	865.482^{+3}	1024.591	1147.648^{+2}	1174.571
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.88 18.47 -0.18	2.43 15.56 -0.16	7.39 47.43 1.50 y^{++}_{13} 20.6	2.81 18.04 -0.18	3.04 19.49 -0.19	3.29 21.09 1.50 y_{14}^{+2} -5.5	4.09 26.25 -0.26	3.87 24.82 -0.25	2.56 16.41 -0.16	2.98 19.12 -0.19	2.65 17.00 -0.17	5.42 34.75 1.50 y_{20}^{+2} 19.5	8.04 51.57 1.50 y_{10} -24.9



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Result Summary

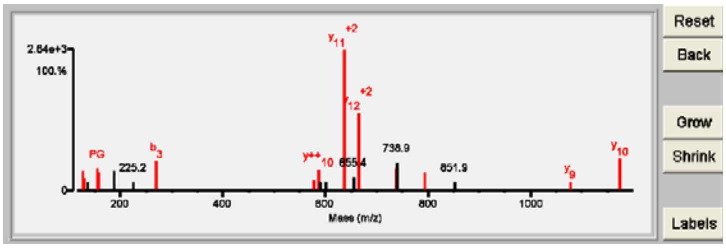
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.24	76.9	7	10/25	K222k	(K)GVLLFGPPGTGkTLCAR(A)	1743.9574	114.0577	8.0	48634.1/5.71	HUMAN	P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.24	76.9	7	10/25	K222k	(K) G V\L|L/F/G/P/P/G T G k T L C A R (A)	1743.9574	114.0577	8.0	48634.1/5.71	HUMAN	P35998	520925	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Fragment-ion (m/z)	70.064	84.079	86.095	87.099	127.085	129.100	136.073	155.079	157.094	187.142	225.155	270.183
Frac. Inten.(% of TIC)	0.01	1.61	0.47	2.36	3.46	2.17	1.64	3.85	3.27	3.57	1.69	5.23
Rel. Inten.(% of BP)	0.02	6.49	1.88	9.52	13.97	8.74	6.63	15.52	13.18	14.38	6.83	21.10
Score	0.20	-0.06	0.22	-0.10	0.50	0.50 0.50	-0.07	0.75	0.50	-0.14	-0.07	0.50
Ion-type	**PR**		**LI**		**PG**-28	a_2 **RKQ**		**PG**	b_2			b_3
Delta ppm	-8.9		-14.2		-20.4	-22.7 -14.2		-23.2	-29.6			1.4

Fragment-ion (m/z)	578.803^{+2}	587.804	588.308	601.315	636.329^{+2}	655.356	664.843^{+2}	738.369	738.889	794.922^{+2}	851.936^{+2}	1077.548	1174.585
Frac. Inten.(% of TIC)	1.88	3.72	1.61	1.67	24.79	2.37	13.60	3.87	4.88	3.39	1.65	1.56	5.69
Rel. Inten.(% of BP)	7.58	15.01	6.48	6.72	100.00	9.55	54.83	15.60	19.70	13.68	6.67	6.29	22.95
Score	0.50	1.50	-0.06	-0.07	1.50	-0.10	1.50	1.50	-0.20	1.50	-0.07	1.50	1.50
Ion-type	y_{10}-H_2O^{+2}	y^{++}_{10}			y_{11}^{+2}		y_{12}^{+2}	y^{++}_{13}		y_{14}^{+2}		y_9	y_{10}
Delta ppm	8.6	0.2			-1.2		3.0	-8.6		6.9		1.0	-12.9



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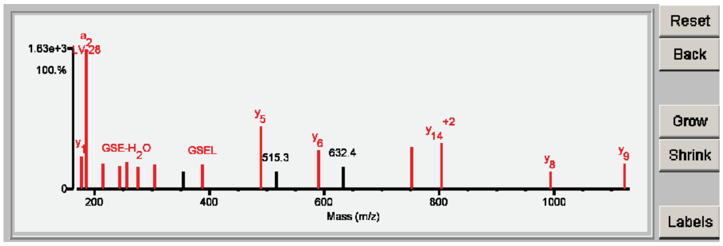
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.56	85.3	8	6/25	K248k	(R)VIGSELVQkYVGEGAR(M)	1704.9279	114.0731	16.6	48634.1/5.71	HUMAN	P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3
2	5.86	53.5	1	11/25	None	(K)EIVTNIQRGFIESGKK(D)	1819.0072	-0.0062	-3.4	94048.1/7.97	HUMAN	Q5TYW2	Ankyrin repeat domain-containing protein 20A1 OS=Homo sapiens GN=ANKRD20A1 PE=2 SV=1
2	5.86	53.5	1	11/25	None	(K)EIVTNIQRGFIESGKK(D)	1819.0072	-0.0062	-3.4	94087.1/8.12	HUMAN	Q5SQ80	Ankyrin repeat domain-containing protein 20A2 OS=Homo sapiens GN=ANKRD20A2 PE=2 SV=1
2	5.86	53.5	1	11/25	None	(K)EIVTNIQRGFIESGKK(D)	1819.0072	-0.0062	-3.4	94108.1/8.12	HUMAN	Q5VUR7	Ankyrin repeat domain-containing protein 20A3 OS=Homo sapiens GN=ANKRD20A3 PE=4 SV=1
2	5.86	53.5	1	11/25	None	(K)EIVTNIQRGFIESGKK(D)	1819.0072	-0.0062	-3.4	94149.2/8.11	HUMAN	Q4UJ75	Ankyrin repeat domain-containing protein 20A4 OS=Homo sapiens GN=ANKRD20A4 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.56	85.3	8	6/25	K248k	(R) V I|G S E L V/Q/k/Y/V/G E/G A/R (M)	1704.9279	114.0731	16.6	48634.1/5.71	HUMAN	P35998	520925	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3

Fragment-ion (m/z)	70.064	72.081	84.080	86.096	87.096	120.080	136.079	141.101	175.119	185.166	213.159	243.142	256.094	274.106	303.174	354.170	387.195	489.249	515.266	588.312	632.370	751.377	803.920^{+2}	993.514	1121.583
Frac. Inten.(% of TIC)	0.00	0.61	0.36	0.97	2.53	3.44	0.15	3.30	4.73	20.37	3.66	3.31	3.84	3.27	3.58	2.60	3.64	9.13	2.48	5.63	3.21	6.24	6.63	2.60	3.72
Rel. Inten.(% of BP)	0.02	3.00	1.75	4.75	12.41	16.87	0.74	16.20	23.24	100.00	17.98	16.25	18.84	16.05	17.59	12.74	17.86	44.80	12.17	27.61	15.78	30.64	32.55	12.74	18.24
Score	0.20	0.50 0.50	0.50	0.22	-0.12	-0.17	1.00	-0.16	1.50	0.50	0.75	0.75	0.50	0.75	1.50	-0.13	0.75	1.50	-0.12	1.50	-0.16	1.50	1.50	1.50	1.50
Ion-type	PR	a_1 V	KQ	LI			Y		y_1	a_2 LV-28	b_2 LV	EL	GSE-H_2O	GSE	y_3		GSEL	y_5		y_6		y_7	y_{14}^{+2}	y_8	y_9
Delta ppm	-18.9	-17.7 -2.4	-4.5	-6.1			23.6		-0.9	-1.3 -1.3	-7.7 -7.7	28.3	-0.8	4.2	-12.3		17.2	14.7		3.2		5.2	9.6	2.5	12.1



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Result Summary

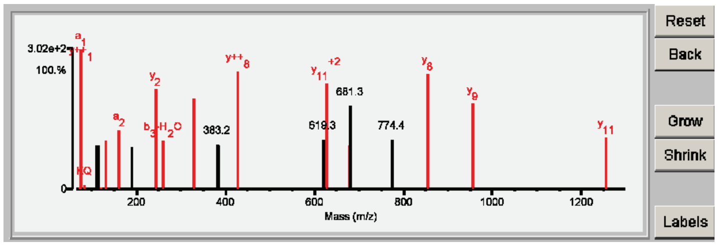
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.49	69.4	6	9/25	K310k	(K)TSSAFVGkTPEASPEPK(D)	1732.8752	114.0432	0.2	105836.9/5.25	HUMAN	Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.49	69.4	6	9/25	K310k	(K) T S S A F/V/G k/T/P E A S P E/P/K (D)	1732.8752	114.0432	0.2	105836.9/5.25	HUMAN	Q99460	265435	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2

Fragment-ion (m/z)	60.041	70.065	72.079	74.060	84.081	110.068	116.071	120.077	130.083	161.094	191.114	244.167	258.105
Frac. Inten.(% of TIC)	3.29	0.00	0.09	9.53	0.31	2.94	3.01	0.15	3.28	4.05	2.90	6.85	3.30
Rel. Inten.(% of BP)	34.53	0.04	0.92	100.00	3.26	30.88	31.54	1.60	34.43	42.49	30.41	71.84	34.59
Score	-0.35	0.20	0.50	1.50	0.50	-0.31	-0.32	1.00	0.50	0.50	-0.30	1.50	0.25
Ion-type		PR	V	a_1 y^{++}_1	KQ			F	y_1-NH_3	a_2		y_2	b_3-H_2O
Delta ppm		-6.1	-23.2	-12.7 2.2	5.0			-29.8	-21.2	7.0		5.9	-19.2

Fragment-ion (m/z)	329.142	383.194	385.155	427.720	619.307	627.816^{+2}	677.364^{+2}	681.277	774.373	854.407	955.484	1254.609
Frac. Inten.(% of TIC)	6.19	3.10	2.94	8.07	3.42	7.23	2.98	5.69	3.36	7.91	5.84	3.58
Rel. Inten.(% of BP)	64.88	32.47	30.85	84.64	35.82	75.82	31.21	59.67	35.26	82.95	61.23	37.51
Score	0.25	-0.32	-0.31	1.50	-0.36	1.50	1.50	-0.60	-0.35	1.50	1.50	1.50
Ion-type	b_4-H_2O			y^{++}_8		y_{11}^{+2}	y_{12}^{+2}			y_8	y_9	y_{11}
Delta ppm	-14.5			9.0		-5.7	15.3			-21.7	11.0	-18.9



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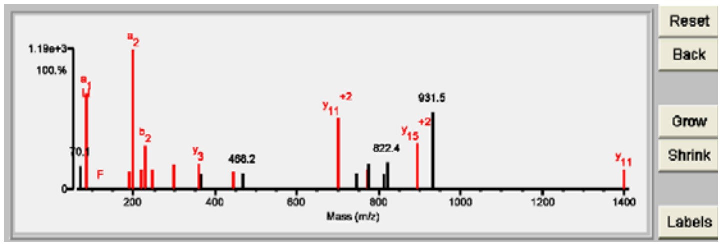
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.10	73.2	7	9/25	K122k	(R)IIAFVGSPVEDNEkDLVK(L)	1973.0590	114.0560	6.2	40736.9/4.68	HUMAN	P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1
2	11.77	67.9	5	11/25	K126k	(R)IIAFVGSPVEDNEKDLVk(L)	1973.0590	114.0560	6.2	40736.9/4.68	HUMAN	P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1
3	3.24	56.0	3	17/25	M409m K401k	(K)LLAQkAAEAEQEmQRIK(A)	1957.0535	130.0614	11.3	69690.6/6.11	HUMAN	P35240	Merlin OS=Homo sapiens GN=NF2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.10	73.2	7	9/25	K122k	(R) I I|A|F|V/G S/P V E D N E k D/L/V K (L)	1973.0590	114.0560	6.2	40736.9/4.68	HUMAN	P55036	530917	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1

Fragment-ion (m/z)	70.062	84.075	86.094	120.079	191.116	199.180	219.108	227.171	246.182	298.210	359.269	364.199	445.273	468.249	700.356^{+2}	744.378	772.375^{+2}	773.389^{+2}	813.411	821.923	822.405	895.456^{+2}	930.980	931.461	1399.689
Frac. Inten.(% of TIC)	2.66	1.76	11.19	0.05	2.02	16.22	2.30	5.08	2.22	2.80	3.04	1.80	1.98	1.88	8.19	1.89	2.25	2.94	1.76	3.06	3.18	5.33	5.16	8.96	2.27
Rel. Inten.(% of BP)	16.41	10.84	68.96	0.33	12.44	100.00	14.17	31.32	13.71	17.23	18.73	11.08	12.23	11.62	50.49	11.65	13.84	18.15	10.86	18.87	19.60	32.84	31.78	55.20	14.01
Score	-0.16	-0.11	0.50 0.50	1.00	0.50	0.50	0.75	0.50	1.50	0.50	1.50	-0.11	0.50	-0.12	1.50	-0.12	1.50	-0.18	-0.11	1.50	-0.20	1.50	1.50	-0.55	1.50
Ion-type			a_1 LI	F	AF-28	a_2	AF	b_2	y_2	b_3	y_3		b_4		y_{11}^{+2}		y_{13}^{+2}			y^{++}_{14}		y_{15}^{+2}	y^{++}_{16}		y_{11}
Delta ppm			-31.7 -31.7	-17.3	-9.4	-0.5	-22.8	-19.8	2.8	-8.1	11.7		-18.7		-0.7		-11.5			6.4		4.7	10.3		-12.8



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Result Summary

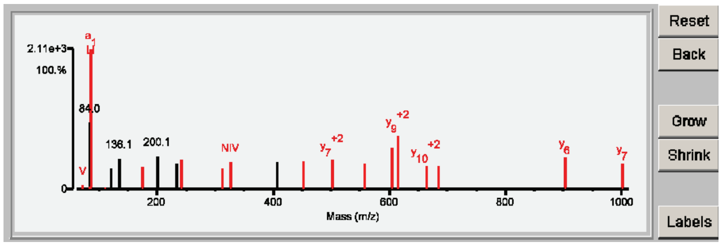
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.20	72.3	10	6/25	K40k	(R)LQAQQDAVNIVCHSkTR(S)	1968.0080	114.0582	7.3	40736.9/4.68	HUMAN	P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.20	72.3	10	6/25	K40k	(R) L Q\A\Q Q D\A/V/N/I/V/C H/S k T/R (S)	1968.0080	114.0582	7.3	40736.9/4.68	HUMAN	P55036	530917	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.081	84.044	84.080	86.096	110.070	120.078	129.101	136.076	175.120	200.136	233.126	242.147
Frac. Inten.(% of TIC)	0.01	0.51	9.03	0.41	19.11	0.18	2.88	0.10	4.09	3.00	4.48	3.49	4.08
Rel. Inten.(% of BP)	0.04	2.67	47.24	2.13	100.00	0.95	15.08	0.52	21.38	15.68	23.44	18.27	21.35
Score	0.20	0.50	-0.47	0.50	0.50	1.00	-0.15	0.20	-0.21	1.50	-0.23	-0.18	0.50
Ion-type	PR	V		KQ	a_1	H		RKQ		y_1			b_2
Delta ppm	-0.4	-2.4		-6.8	-22.3	-13.4		-11.1		4.8			-14.9
					0.50								
					LI								
					-9.6								

Fragment-ion (m/z)	313.179	327.204	406.199	451.722^{+2}	501.257^{+2}	557.794	605.340	614.817^{+2}	664.352^{+2}	684.343	902.420	1001.497
Frac. Inten.(% of TIC)	2.86	3.71	3.73	3.87	3.94	3.48	5.58	7.34	3.23	3.13	4.32	3.44
Rel. Inten.(% of BP)	14.97	19.42	19.50	20.26	20.62	18.20	29.22	38.42	16.90	16.40	22.62	17.99
Score	0.50	0.75	-0.19	1.50	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	b_3	NIV		y_6^{+2}	y_7^{+2}	$y{+}{+}_8$	y_4	y_9^{+2}	y_{10}^{+2}	b_6	y_6	y_7
Delta ppm	-29.1	-0.5		11.3	12.8	2.8	5.5	3.9	5.0	15.2	-6.7	2.6



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Result Summary

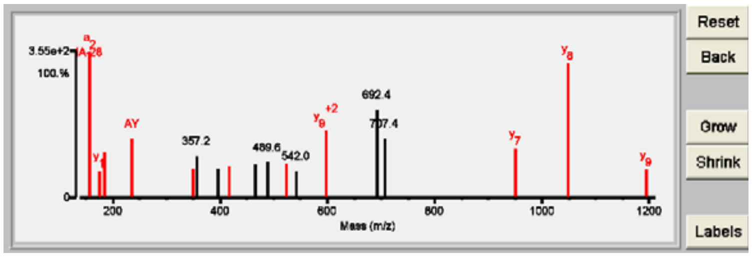
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.70	60.5	6	10/25	K119k	(R)AIAYLFPSGLFEkR(A)	1611.8893	114.0598	9.8	45835.1/9.54	HUMAN	P82933	28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.70	60.5	6	10/25	K119k	(R) A I\A Y L/F/P/S G L F E/k/R (A)	1611.8893	114.0598	9.8	45835.1/9.54	HUMAN	P82933	696951	28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2

Fragment-ion (m/z)	62.009	70.065	84.082	86.095	87.100	120.077	136.077	157.131	175.120	185.130	235.110	348.204
Frac. Inten.(% of TIC)	2.78	0.01	3.44	0.59	4.65	0.16	0.29	13.28	2.41	4.19	5.43	2.71
Rel. Inten.(% of BP)	20.92	0.05	25.94	4.46	35.02	1.19	2.18	100.00	18.18	31.58	40.88	20.41
Score	-0.21	0.20	-0.26	0.22	-0.35	1.00	1.00	0.50	1.50	0.75	0.75	0.75
Ion-type		PR		LI		F	Y	a_2 IA-28	y_1	b_2 IA	AY	AYL
Delta ppm		-6.1		-20.0		-28.1	8.2	-20.6 -20.6	4.8	3.0 3.0	4.6	30.8

Fragment-ion (m/z)	357.225	396.227	417.243	466.206	489.601	524.283^{+2}	541.952	597.818^{+2}	692.402	707.357	950.515	1047.543	1194.603
Frac. Inten.(% of TIC)	3.83	2.70	2.86	3.00	3.27	3.17	2.43	6.11	8.02	5.37	4.48	12.21	2.60
Rel. Inten.(% of BP)	28.81	20.36	21.51	22.61	24.64	23.88	18.33	46.01	60.36	40.46	33.75	91.91	19.59
Score	-0.29	-0.20	1.50	-0.23	-0.25	1.50	-0.18	1.50	-0.60	-0.40	1.50	1.50	1.50
Ion-type			y_2			y_8^{+2}		y_9^{+2}			y_7	y_8	y_9
Delta ppm			-32.5			0.5		2.3			10.0	-14.1	-20.2



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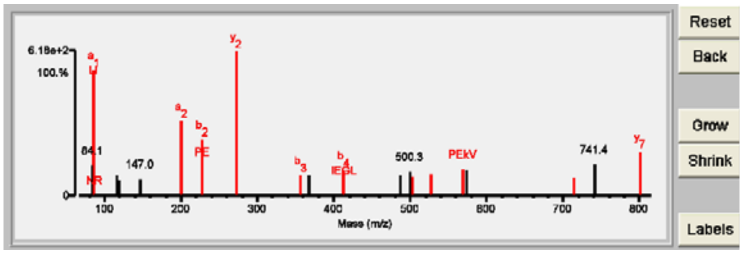
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.75	73.2	8	10/25	K135k	(K)LIEGLPEkVLSLVDDPR(N)	1893.0692	114.0529	5.0	48117.7/8.83	HUMAN	Q9BZE1	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2
2	5.92	55.5	1	13/25	M87m	(K)ALLEGLHmLLTQKDRPR(R)	1991.1219	16.0002	2.6	55134.5/8.83	HUMAN	Q5VWM6	PRAME family member 13 OS=Homo sapiens GN=PRAMEF13 PE=3 SV=1
2	5.92	55.5	1	13/25	M87m	(K)ALLEGLHmLLTQKDRPR(R)	1991.1219	16.0002	2.6	49433.8/8.70	HUMAN	Q5SWL7	PRAME family member 14 OS=Homo sapiens GN=PRAMEF14 PE=2 SV=1
2	5.92	55.5	1	13/25	M87m	(K)ALLEGLHmLLTQKDRPR(R)	1991.1219	16.0002	2.6	55162.5/8.93	HUMAN	O95521	PRAME family member 1 OS=Homo sapiens GN=PRAMEF1 PE=2 SV=2
2	5.92	55.5	1	13/25	M87m	(K)ALLEGLHmLLTQKDRPR(R)	1991.1219	16.0002	2.6	54872.0/8.12	HUMAN	O60811	PRAME family member 2 OS=Homo sapiens GN=PRAMEF2 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.75	73.2	8	10/25	K135k	(K) L I\E\G\L\P E k V L/S/L V/D D/P R (N)	1893.0692	114.0529	5.0	48117.7/8.83	HUMAN	Q9BZE1	636953	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2

Fragment-ion (m/z)	70.066	84.046	84.080	86.096	87.053	116.080	120.079	147.047	199.177	227.095	227.172	272.171	356.217	368.271	413.228	486.273	500.284	502.238	526.326	568.314	573.021^{+3}	714.377	741.433^{+2}	801.410	881.540
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.03 0.20 PR 11.1	0.06 0.33 1.00 E 15.6	3.67 21.02 -0.21	15.11 86.64 0.50 a_1 -17.7 0.50 LI -4.9	0.06 0.34 0.33 NR -28.6	2.52 14.46 -0.14	1.92 11.03 -0.11	2.07 11.87 -0.12	9.04 51.81 0.50 a_2 -23.0	3.45 19.77 0.75 PE -37.6	6.78 38.84 0.50 b_2 -21.6	17.44 100.00 1.50 y_2 -1.9	2.49 14.26 0.50 b_3 -7.0	2.45 14.02 -0.14	3.13 17.94 0.75 b_4 -29.4 IEGL -29.4	2.47 14.18 -0.14	2.93 16.81 -0.17	2.38 13.62 1.50 y_4 25.7	2.54 14.57 0.50 b_5 2.2	3.28 18.81 0.75 PEkV 6.4	3.00 17.21 -0.17	2.09 12.00 1.50 y_6 -1.0	3.77 21.62 -0.22	5.34 30.63 1.50 y_7 0.2	2.00 11.46 -0.11



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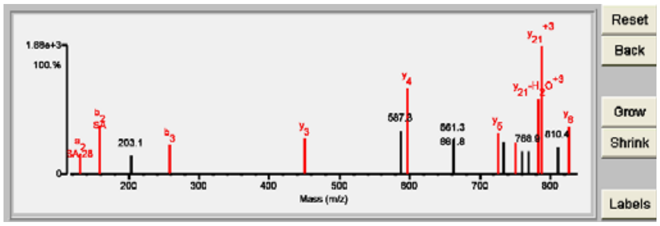
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.31	61.8	6	12/25	K138k K139k	(R)SAVPPGADkkAEAGAGSATEFQFR(G)	2392.1892	228.0826	-1.2	18897.9/10.15	HUMAN	P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1
2	5.57	55.1	3	12/25	None	(K)QIKDDNQEIASMERQLTDTKEK(I)	2620.2883	-0.0165	-6.3	69239.7/5.73	HUMAN	Q96LB3	Intraflagellar transport protein 74 homolog OS=Homo sapiens GN=IFT74 PE=2 SV=1
3	5.28	56.0	2	12/25	K78k	(K)VSASGTPGTPQSSQRVCSPCTTIk(A)	2506.2024	114.0693	10.1	37899.5/5.98	HUMAN	A6NCF6	Putative MAGE domain-containing protein MAGEA13P OS=Homo sapiens GN=MAGEA13P PE=5 SV=1
4	5.09	52.0	3	13/25	None	(K)EKTDTLQREMSAIEQNDDKIQK(L)	2620.2883	-0.0165	-6.3	69239.7/5.74	HUMAN	RQ96LB3	REVERSE Intraflagellar transport protein 74 homolog OS=Homo sapiens GN=IFT74 PE=2 SV=1
5	3.90	51.8	3	12/25	None	(K)TVAPPTHISESAMFESFSQLLAEK(K)	2620.2963	-0.0246	-9.4	191100.8/5.74	HUMAN	RQ9P1Z9	REVERSE Uncharacterized protein KIAA1529 OS=Homo sapiens GN=KIAA1529 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.31	61.8	6	12/25	K138k K139k	(R) S A\V|P P G A D k k A E A G A G S A/T/E/F/Q F R (G)	2392.1892	228.0826	-1.2	18897.9/10.15	HUMAN	P46783	663631	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1

Fragment-ion (m/z)	70.066	72.082	86.095	102.053	131.081	159.076	203.108	258.143	450.242	587.044^{+2}	587.278^{+2}	597.314	661.329	661.824	726.350	733.352^{+2}	750.046^{+3}	760.366	768.886	782.374^{+3}	788.372^{+3}	810.395^{+2}	827.394	874.899^{+2}	883.900^{+2}
Frac. Inten.(% of TIC)	0.00	0.30	2.07	0.12	2.35	5.55	2.06	3.27	4.06	4.52	4.89	9.72	3.77	2.11	4.63	3.66	3.54	2.50	2.54	8.45	14.46	3.00	5.35	3.26	3.81
Rel. Inten.(% of BP)	0.02	2.09	14.33	0.81	16.23	38.34	14.25	22.58	28.10	31.23	33.84	67.21	26.04	14.60	31.99	25.30	24.49	17.30	17.57	58.43	100.00	20.76	36.99	22.53	26.35
Score	0.20	0.50	-0.14	1.00	0.50	0.75	-0.14	0.50	1.50	-0.31	-0.34	1.50	-0.26	-0.15	1.50	-0.25	0.50	-0.17	-0.18	0.50	1.50	-0.21	1.50	-0.23	-0.26
Ion-type	PR	V		E	a_2 SA-28	b_2 SA		b_3	y_3			y_4			y_5		$y_{20}-H_2O^{+3}$			$y_{21}-H_2O^{+3}$	y_{21}^{+3}		y_6		
Delta ppm	12.5	12.8		-16.2	-1.6 -1.6	-2.6 -2.6		-8.3	-8.5			-0.1			-9.6		21.8			-8.5	-15.4		-12.2		



Nature Biotechnology: doi: 10.1038/nbt.1654

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Result Summary

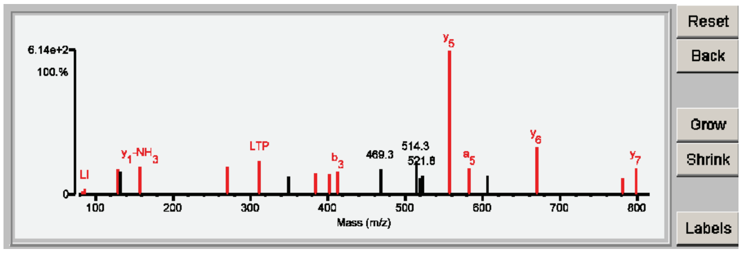
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.75	69.7	5	8/25	K43k	(K)kGLTPSQIGVILR(D)	1381.8526	114.0431	0.1	17222.4/10.53	HUMAN	P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.75	69.7	5	8/25	K43k	(K) k G L\T P S/Q/I/G V/I L R (D)	1381.8526	114.0431	0.1	17222.4/10.53	HUMAN	P62277	668175	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2

Fragment-ion (m/z)	70.065	72.076	84.079	86.096	101.067	129.104	132.076	157.095	158.093	270.175	312.203	349.198	384.250
Frac. Inten.(% of TIC)	0.01	7.17	0.42	0.75	0.16	3.77	3.35	2.75	4.16	4.16	5.08	2.72	3.21
Rel. Inten.(% of BP)	0.05	33.56	1.97	3.53	0.74	17.66	15.69	12.85	19.47	19.47	23.76	12.73	15.03
Score	0.20	-0.34	0.50	0.22		0.50	-0.16	0.75	0.50	0.75	0.75	-0.13	0.50
Ion-type	PR		KQ	LI	KQ	RKQ GV-28		GV	y_1-NH$_3$	GVI	LTP		y_3-NH$_3$
Delta ppm	-1.8		-19.9	-10.8		15.2 6.7		-20.1	3.1	-28.2	31.8		-27.9

Fragment-ion (m/z)	401.295	413.255	469.305	514.295^{+2}	519.303^{+2}	521.761^{+2}	557.371	583.337	605.785^{+2}	670.468	781.485	798.516
Frac. Inten.(% of TIC)	2.98	3.38	3.84	5.04	2.52	2.79	21.37	3.89	2.86	7.13	2.53	3.94
Rel. Inten.(% of BP)	13.96	15.83	17.95	23.58	11.79	13.06	100.00	18.18	13.37	33.36	11.84	18.46
Score	1.50	0.50	-0.18	-0.24	-0.12	-0.13	1.50	0.50	-0.13	1.50	0.50	1.50
Ion-type	y_3	b_3					y_5	a_5		y_6	y_7-NH$_3$	y_7
Delta ppm	19.2	6.8					-9.8	-35.7		10.6	-10.0	-3.9



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Result Summary

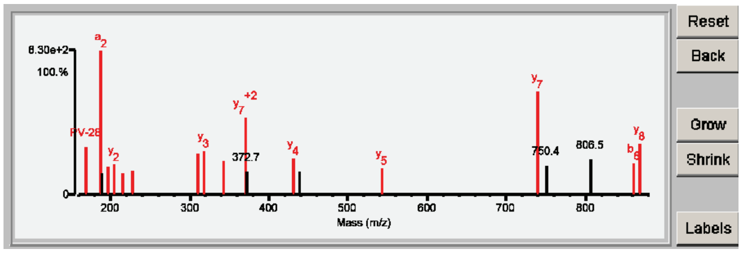
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.88	74.3	9	6/25	K50k	(R)TLQYkLLEPVLLLGK(E)	1728.0670	114.0515	4.6	16445.4/10.21	HUMAN	P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.88	74.3	9	6/25	K50k	(R) T L\Q\Y k L\L/E/P V/L/L/L/G K (E)	1728.0670	114.0515	4.6	16445.4/10.21	HUMAN	P62249	672877	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2

Fragment-ion (m/z)	70.063	72.078	84.077	86.096	101.073	169.128	187.143	188.142	197.127	204.141	215.136	227.183
Frac. Inten.(% of TIC)	0.00	0.07	12.59	0.47	0.08	4.78	14.33	2.13	2.71	3.05	2.18	2.40
Rel. Inten.(% of BP)	0.03	0.49	87.82	3.29	0.59	33.33	100.00	14.88	18.91	21.28	15.22	16.74
Score	0.20	0.50	-0.88	0.22	0.50	0.50	0.50	-0.15	0.75	1.50	0.50	0.75
Ion-type	PR	V		LI	QK	PV-28	a_2		b_2-H_2O PV	y_2	b_2	LL
Delta ppm	-26.1	-37.1		-8.4	16.4	-41.6	-9.6		-13.5 -13.5	34.9	-17.3	26.8

Fragment-ion (m/z)	310.206	317.222	343.199	370.254^{+2}	372.717^{+2}	430.304	439.231	543.387	739.510	750.382^{+2}	806.464^{+2}	861.462	868.558
Frac. Inten.(% of TIC)	4.13	4.39	3.38	7.63	2.30	3.59	2.26	2.64	10.19	2.93	3.48	3.17	5.08
Rel. Inten.(% of BP)	28.82	30.65	23.59	53.26	16.05	25.07	15.80	18.45	71.07	20.45	24.25	22.13	35.44
Score	0.75	1.50	0.50	1.50	-0.16	1.50	-0.16	1.50	1.50	-0.20	-0.24	0.50	1.50
Ion-type	PVL	y_3	b_3	y_7^{+2}		y_4		y_5	y_7			b_6	y_8
Delta ppm	-23.6	10.9	2.1	-8.3		3.3		1.0	3.5			-24.9	9.1



Result Summary

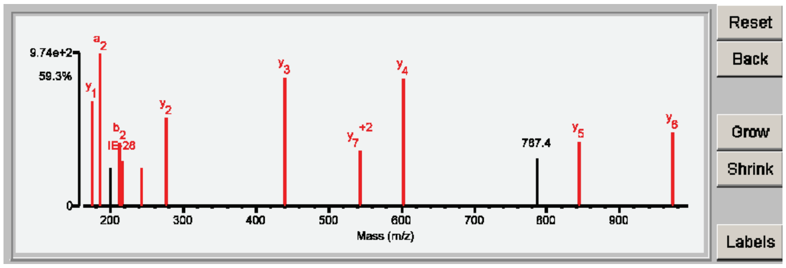
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.04	73.0	7	6/24	K19k	(R)VIIEkYYTR(L)	1184.6674	114.0518	6.8	15550.2/9.85	HUMAN	P08708	40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2
2	4.42	51.2	1	11/24	None	(R)VGGTGGAVSELVPR(S)	1298.7063	0.0129	9.9	102048.7/5.28	HUMAN	Q9Y5H7	Protocadherin alpha-5 OS=Homo sapiens GN=PCDHA5 PE=1 SV=1
2	4.42	51.2	1	11/24	None	(R)VGGTGGAVSELVPR(S)	1298.7063	0.0129	9.9	102716.2/4.93	HUMAN	Q9UN73	Protocadherin alpha-6 OS=Homo sapiens GN=PCDHA6 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.04	73.0	7	6/24	K19k	(R) V I|I/E/k/Y/Y/T/R (L)	1184.6674	114.0518	6.8	15550.2/9.85	HUMAN	P08708	337184	40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2

Fragment-ion (m/z)	70.065	72.081	84.080	86.096	87.053	87.099	110.070	112.086	129.102	136.075	141.102	175.121
Frac. Inten.(% of TIC)	0.00	0.65	17.76	1.25	0.08	3.45	2.30	0.06	0.11	0.18	3.27	7.27
Rel. Inten.(% of BP)	0.02	3.68	100.00	7.04	0.48	19.43	12.94	0.34	0.60	0.99	18.42	40.93
Score	0.20	0.50	-0.81	0.22	0.33	-0.16	-0.11	0.33	0.20	1.00	-0.15	1.50
Ion-type	PR	a_1		LI	NR			R	RKQ	Y		y_1
Delta ppm	2.5	-16.3		-0.3	-21.7			-6.5	-1.1	-7.3		11.7
		0.50										
		V										
		-1.0										

Fragment-ion (m/z)	185.166	199.179	213.160	215.138	243.142	276.165	439.233	543.787^{+2}	602.293	787.407	844.434	973.475
Frac. Inten.(% of TIC)	10.52	2.63	4.36	3.10	2.62	6.12	8.84	3.79	8.75	3.30	4.49	5.10
Rel. Inten.(% of BP)	59.28	14.81	24.56	17.46	14.77	34.47	49.79	21.32	49.26	18.56	25.31	28.73
Score	0.50	-0.12	0.50	0.50	0.75	1.50	1.50	1.50	1.50	-0.15	1.50	1.50
Ion-type	a_2		b_2	IE-28	IE	y_2	y_3	y_7^{+2}	y_4		y_5	y_6
Delta ppm	-1.8		-4.0	-11.7	26.6	-6.6	7.6	7.8	-0.8		2.9	1.5



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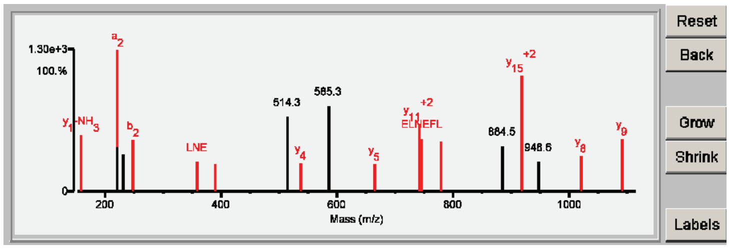
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.47	64.0	8	8/25	K18k	(K)FVADGIFkAELNEFLTR(E)	1970.0382	114.0681	12.1	26688.5/9.68	HUMAN	P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.47	64.0	8	8/25	K18k	(K) F V|A D G I/F k/A/E L/N/E/F/L T R (E)	1970.0382	114.0681	12.1	26688.5/9.68	HUMAN	P23396	683973	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Fragment-ion (m/z)	70.063	72.080	84.079	86.095	120.079	141.068	158.089	219.149	220.151	230.147	247.145	357.184	389.248	514.311	536.317	585.348	665.360	741.394^{+2}	746.385	779.413	884.490^{+2}	919.468^{+2}	948.559^{+2}	1021.540	1092.582
Frac. Inten.(% of TIC)	0.00	0.09	6.28	0.25	0.32	2.46	4.87	12.19	3.81	3.15	4.47	2.51	2.32	6.43	2.41	7.36	2.39	5.75	4.58	4.32	3.96	9.90	2.57	3.03	4.57
Rel. Inten.(% of BP)	0.04	0.75	51.54	2.06	2.64	20.22	39.98	100.00	31.23	25.88	36.65	20.60	19.04	52.79	19.77	60.43	19.64	47.14	37.56	35.48	32.47	81.26	21.06	24.85	37.54
Score	0.20	0.50	-0.52	0.22	1.00 1.00	-0.20	0.50	0.50	-0.31	-0.26	0.50	0.75	1.50	-0.53	1.50	-0.60	1.50	1.50	0.75	1.50	-0.32	1.50	-0.21	1.50	1.50
Ion-type	PR	V		LI	a_1 F		y_1-NH_3	a_2			b_2	LNE	y_3		y_4		y_5	y_{11}^{+2}	ELNEFL	y_6		y_{15}^{+2}		y_8	y_9
Delta ppm	-26.1	-16.3		-16.6	-25.6 -16.5		-20.3	-5.9			-1.6	16.9	-6.9		-4.3		-2.1	4.6	15.5	11.1		-8.1		8.6	12.4



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Result Summary

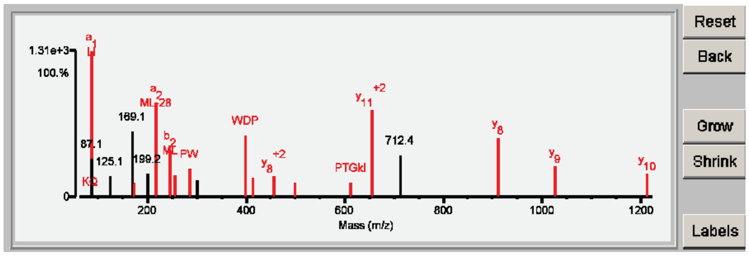
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.79	77.5	6	6/25	K197k	(K)IMLPWDPTGkIGPK(K)	1552.8556	114.0526	5.8	26688.5/9.68	HUMAN	P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2
2	15.31	73.8	6	8/25	K201k	(K)IMLPWDPTGKIGPk(K)	1552.8556	114.0526	5.8	26688.5/9.68	HUMAN	P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.79	77.5	6	6/25	K197k	(K) I M|L/P/W/D/P T G k/I G P K (K)	1552.8556	114.0526	5.8	26688.5/9.68	HUMAN	P23396	683973	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Fragment-ion (m/z)	70.065	84.079	86.097	87.096	125.074	159.088	169.135	171.107	199.177	217.135	245.131	256.149	284.149
Frac. Inten.(% of TIC)	0.01	0.11	15.94	4.21	2.26	0.06	7.15	1.60	2.58	10.33	5.08	2.39	3.06
Rel. Inten.(% of BP)	0.04	0.71	100.00	26.43	14.17	0.36	44.87	10.02	16.16	64.80	31.88	14.98	19.16
Score	0.20	0.50	0.50	-0.26	-0.14	2.00	-0.45	0.75	-0.16	0.50	0.75	0.50	0.75
Ion-type	PR	KQ	a_1			W		IG		a_2	b_2	PW-28	PW
Delta ppm	-1.8	-25.9	-2.6			-22.5		-37.4		-15.7	-7.4	14.3	29.0
			0.50							ML-28	ML		
			LI							-15.7	-7.4		
			10.2										

Fragment-ion (m/z)	300.185	399.159	414.275	456.264^{+2}	500.214	611.340	655.346^{+2}	711.882	712.396	911.523	1026.554	1212.631
Frac. Inten.(% of TIC)	1.78	6.73	2.09	2.21	1.63	1.55	9.43	3.01	4.53	6.42	3.35	2.48
Rel. Inten.(% of BP)	11.15	42.19	13.13	13.87	10.24	9.75	59.15	18.86	28.38	40.27	21.04	15.56
Score	-0.11	0.75	1.50	1.50	0.75	0.75	1.50	1.50	-0.28	1.50	1.50	1.50
Ion-type		WDP	y_4	y_8^{+2}	WDPT	PTGkI	y_{11}^{+2}	$y{++}_{12}$		y_8	y_9	y_{10}
Delta ppm		-21.8	9.2	-10.5	-1.7	-20.3	-4.7	-11.8		-9.1	-3.6	-5.1



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Result Summary

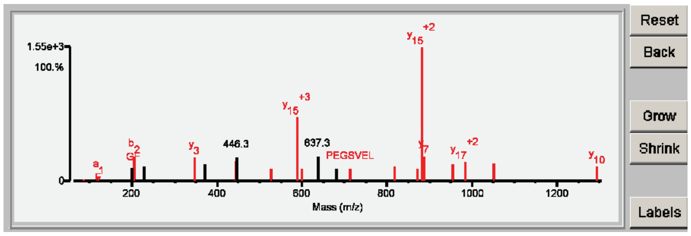
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.40	80.5	8	6/25	K90k	(R)FGFPEGSVELYAEkVATR(G)	2000.0124	114.0588	7.5	26688.5/9.68	HUMAN	P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2
2	4.24	51.3	2	16/25	M1m	(-)mSVVGIDLGFLNCYIAVAR(S)	2098.0824	15.9888	-2.9	94487.0/5.63	HUMAN	O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=2
3	3.24	51.3	0	15/25	K424k	(K)EFGWPLEKAYNYVkQK(R)	2000.0276	114.0435	0.3	115511.7/5.87	HUMAN	Q8WYL5	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2
3	3.24	51.3	0	15/25	K418k	(K)EFGWPLEkAYNYVKQK(R)	2000.0276	114.0435	0.3	115511.7/5.87	HUMAN	Q8WYL5	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2
3	3.24	51.3	0	15/25	K426k	(K)EFGWPLEKAYNYVKQk(R)	2000.0276	114.0435	0.3	115511.7/5.87	HUMAN	Q8WYL5	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.40	80.5	8	6/25	K90k	(R) F/G|F/P E G S V/E L/Y/A/E k V/A T R (G)	2000.0124	114.0588	7.5	26688.5/9.68	HUMAN	P23396	341987	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Fragment-ion (m/z)	70.066	86.098	120.079	136.075	199.177	205.094	227.168	347.204	371.178	444.759^{+2}	446.264^{+2}	526.299
Frac. Inten.(% of TIC)	0.00	0.24	0.71	0.13	2.44	4.71	2.78	4.34	3.11	3.75	4.35	2.31
Rel. Inten.(% of BP)	0.02	0.95	2.81	0.53	9.66	18.68	11.02	17.20	12.31	14.88	17.24	9.15
Score	0.20	0.22	1.00 1.00	1.00	-0.10	0.75	-0.11	1.50	-0.12	1.50	-0.17	1.50
Ion-type	PR	LI	a_1 F	Y		b_2 GF		y_3		y_7^{+2}		y++$_8$
Delta ppm	12.5	13.6	-23.1 -14.0	-5.8		-19.3 -19.3		-0.7		23.4		36.7

Fragment-ion (m/z)	588.313^{+3}	599.278	637.334	679.209	712.354	817.458	872.928^{+2}	881.946^{+2}	888.486	955.519^{+2}	984.002^{+2}	1051.552	1293.697
Frac. Inten.(% of TIC)	12.07	2.35	4.62	2.21	2.32	2.70	2.18	25.23	4.68	3.13	3.49	3.40	2.74
Rel. Inten.(% of BP)	47.85	9.33	18.30	8.77	9.20	10.68	8.62	100.00	18.56	12.41	13.84	13.46	10.87
Score	1.50	0.75	-0.18	-0.09	0.75	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_{15}^{+3}	PEGSVE			PEGSVEL	y_6	y_{15}-H_2O^{+2}	y_{15}^{+2}	y_7	y_{16}^{+2}	y_{17}^{+2}	y_8	y_{10}
Delta ppm	15.4	16.1			2.7	7.0	-21.7	-6.9	-4.8	34.3	5.2	-0.7	13.3



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Result Summary

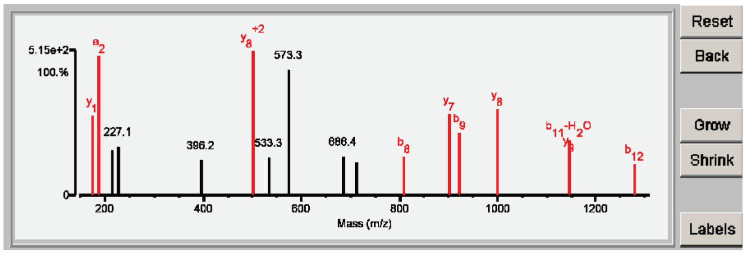
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.37	60.6	7	10/25	K142k	(R)TLTAVHDAILEDLVFPSEIVGkR(I)	2523.3817	114.0229	-7.6	22127.0/10.09	HUMAN	P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.37	60.6	7	10/25	K142k	(R) T L T A V H D A\I\L E D\L V/F/P/S E I V G k/R (I)	2523.3817	114.0229	-7.6	22127.0/10.09	HUMAN	P62081	690005	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.081	84.042	84.078	86.095	86.133	101.070	110.070	120.077	175.116	187.142	215.129	227.066
Frac. Inten.(% of TIC)	0.01	0.15	0.12	3.21	0.61	3.28	2.94	0.17	0.20	6.61	11.43	3.70	4.07
Rel. Inten.(% of BP)	0.04	1.24	1.01	26.89	5.13	27.46	24.66	1.41	1.66	55.42	95.84	31.01	34.14
Score	0.20	0.50	1.00 1.00	-0.27	0.22	-0.27	-0.25	1.00	1.00	1.50	0.50	-0.31	-0.34
Ion-type	PR	V	b_1-H_2O E		LI			H	F	y_1	a_2		
Delta ppm	-23.2	-3.8	-42.7 -29.6		-17.7			-15.2	-28.9	-19.1	-19.2		

Fragment-ion (m/z)	396.197	500.278^{+2}	533.263	573.336^{+2}	686.425^{+2}	711.930	809.443	902.495	922.490	999.548	1146.619	1279.652
Frac. Inten.(% of TIC)	2.87	11.93	3.16	10.33	3.20	2.68	3.21	6.69	5.20	7.09	4.53	2.63
Rel. Inten.(% of BP)	24.04	100.00	26.49	86.63	26.80	22.44	26.89	56.08	43.59	59.42	37.95	22.04
Score	-0.24	1.50	-0.26	-0.87	-0.27	-0.22	0.50	1.50	0.50	1.50	1.50	0.50
Ion-type		y_8^{+2}					b_8	y_7	b_9	y_8	b_{11}-H_2O y_9	b_{12}
Delta ppm		-10.3					32.8	-11.6	-11.1	-9.8	2.1 -6.8	-1.5



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Result Summary

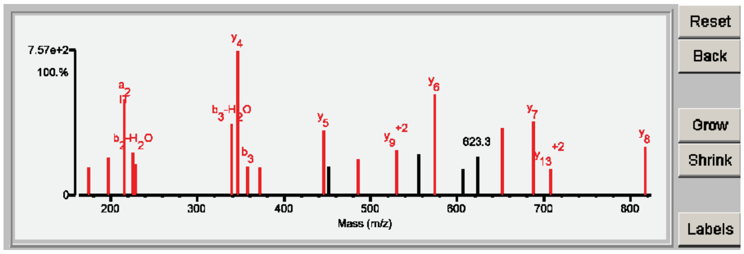
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.64	76.5	9	6/25	K49k	(R)ELNITAAkEIEVGGGR(K)	1656.8915	114.0555	7.1	22127.0/10.09	HUMAN	P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.64	76.5	9	6/25	K49k	(R) E L N|I/T A A/k/E/I/E/V/G G G/R (K)	1656.8915	114.0555	7.1	22127.0/10.09	HUMAN	P62081	690005	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1

Fragment-ion (m/z)	72.078	84.081	86.096	136.073	175.114	197.131	215.139	225.122	228.130	339.166	346.185	357.172	372.172
Frac. Inten.(% of TIC)	0.07	9.16	0.41	3.69	2.15	2.97	7.49	3.34	2.45	5.55	11.29	2.26	2.19
Rel. Inten.(% of BP)	0.65	81.10	3.66	32.66	19.06	26.33	66.32	29.58	21.67	49.14	100.00	19.99	19.40
Score	0.50	-0.81	0.22	-0.33	1.50	0.50	0.75	0.25	0.75	0.25	1.50	0.50	0.75
Ion-type	V		LI		y_1	IT-H_2O	a_2 IT	b_2-H_2O	NI	b_3-H_2O	y_4	b_3	EIE
Delta ppm	-37.1		-9.6		-26.6	6.3	-6.6 -6.6	-12.3	-24.8	-4.7	4.2	-15.6	-15.6

Fragment-ion (m/z)	445.252	451.255	485.262	529.786^{+2}	555.285	574.301	606.310	623.320	651.352^{+2}	687.378	707.877^{+2}	816.429
Frac. Inten.(% of TIC)	5.09	2.30	2.86	3.49	3.21	7.92	2.09	3.03	5.27	5.80	2.09	3.84
Rel. Inten.(% of BP)	45.07	20.35	25.30	30.86	28.39	70.10	18.54	26.79	46.68	51.32	18.47	33.96
Score	1.50	-0.20	0.75	1.50	-0.28	1.50	-0.19	-0.27	1.50	1.50	1.50	1.50
Ion-type	y_5		kEI	y_9^{+2}		y_6			y_{12}^{+2}	y_7	y_{13}^{+2}	y_8
Delta ppm	0.5		-21.5	6.3		10.9			12.5	-0.7	-12.4	10.3



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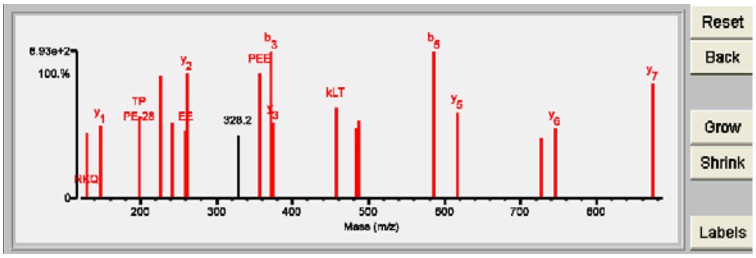
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.77	93.2	10	2/25	K128k	(K)GAkLTPEEEEILNK(K)	1570.8323	114.0580	8.9	24205.3/10.32	HUMAN	P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2
2	6.77	63.2	1	8/25	K81k	(K)NLIEEEEPTLkAGK(K)	1570.8323	114.0580	8.9	24205.3/10.32	HUMAN	RP62241	REVERSE 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.77	93.2	10	2/25	K128k	(K) G A k\L\T\P E/E/E/E/I/L/N/K (K)	1570.8323	114.0580	8.9	24205.3/10.32	HUMAN	P62241	691655	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2

Fragment-ion (m/z)	70.066	84.080	86.097	101.067	102.056	129.101	130.085	147.111	199.110	227.105	241.085	259.094	261.155	328.231	356.143	371.202	374.244	457.271	484.285	487.334	585.342	616.368	727.338	745.413	874.444
Frac. Inten.(% of TIC)	0.01	0.86	0.50	3.37	0.21	0.22	3.57	3.90	4.49	6.69	4.11	3.68	6.85	3.44	6.80	8.00	4.13	4.99	3.78	4.24	8.01	4.71	3.34	3.83	6.26
Rel. Inten.(% of BP)	0.18	10.74	6.27	42.10	2.66	2.72	44.58	48.75	56.03	83.50	51.31	45.98	85.48	42.98	84.88	99.94	51.57	62.33	47.16	52.95	100.00	58.77	41.76	47.82	78.13
Score	0.20	0.50	0.22	-0.42	1.00	0.20	0.50	1.50	0.75	0.75	0.50	0.75	1.50	-0.43	0.75	0.50	1.50	0.75	0.50	1.50	0.50	1.50	0.75	1.50	1.50
Ion-type	PR	KQ	LI		E	RKQ	y_1-NH_3	y_1	TP	PE	EE-H_2O	EE	y_2		PEE	b_3	y_3	kLT	b_4	y_4	b_5	y_5	PEEEEI	y_6	y_7
Delta ppm	8.2	-12.8	0.9		6.3	-8.1	-8.9	-12.9	5.4	3.4	8.7	2.9	-1.7		-8.8	-7.4	10.4	-16.2	-8.9	20.8	9.3	2.7	31.5	5.6	-8.4
									PE-28																
									5.4																



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Result Summary

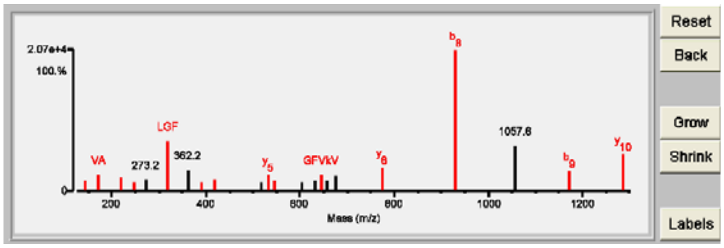
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.43	71.9	3	10/25	K344k K347k	(R)VLGFVkVAkEQGAK(V)	1473.8788	228.0951	5.5	53802.2/5.69	HUMAN	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3
2	9.18	65.1	2	12/25	K344k K352k	(R)VLGFVkVAKEQGAk(V)	1473.8788	228.0951	5.5	53802.2/5.69	HUMAN	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.43	71.9	3	10/25	K344k K347k	(R) V L G F | V k V A | k | E Q G A K (V)	1473.8788	228.0951	5.5	53802.2/5.69	HUMAN	P49189	18407	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3

Fragment-ion (m/z)	120.084	143.122	171.117	219.158	247.152	273.167	318.192	362.184	389.268	417.263	518.281	532.293
Frac. Inten.(% of TIC)	0.19	1.94	2.97	2.49	1.59	2.23	9.36	4.01	1.77	2.24	1.62	3.03
Rel. Inten.(% of BP)	0.71	7.37	11.26	9.45	6.02	8.44	35.48	15.18	6.69	8.49	6.15	11.48
Score	1.00	0.50	0.75	0.50	0.75	-0.08	0.75	-0.15	0.50	0.75	-0.06	1.50
Ion-type	**F**	**VA**-28	**VA**	**FV**-28	**FV**		**LGF**		a_4 **LGFV**-28	b_4 **LGFV**		y_5
Delta ppm	25.2	17.6	20.4	32.9	26.7		31.1		31.6 31.6	29.9 29.9		39.0

Fragment-ion (m/z)	546.315	604.323	631.364	645.380	658.355^{+2}	675.359	774.427	928.542	1057.584	1170.681	1285.702	1315.685	1384.766
Frac. Inten.(% of TIC)	1.88	1.62	2.02	3.03	2.02	2.81	4.45	26.38	8.35	3.73	6.81	1.67	1.78
Rel. Inten.(% of BP)	7.14	6.15	7.67	11.49	7.64	10.65	16.88	100.00	31.65	14.16	25.82	6.34	6.75
Score	0.75	-0.06	-0.08	0.75	-0.08	-0.11	1.50	0.50	-0.32	0.50	1.50	-0.06	-0.07
Ion-type	**GFVk**			**GFVkV**			y_6	b_8		b_9	y_{10}		
Delta ppm	18.8			11.0			20.9	-22.0		-16.9	-15.8		



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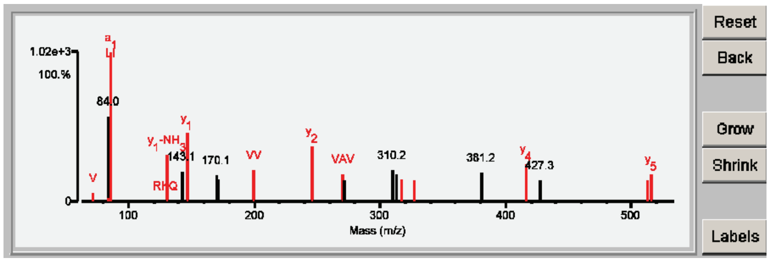
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.47	61.2	6	10/25	K292k	(R)LkVGLQVVAVK(A)	1153.7667	114.0419	-0.8	61055.0/5.70	HUMAN	P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.47	61.2	6	10/25	K292k	(R) L k V G\L Q/V/V/A/V/K (A)	1153.7667	114.0419	-0.8	61055.0/5.70	HUMAN	P10809	96413	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2

Fragment-ion (m/z)	72.081	84.045	84.080	86.097	101.069	129.099	130.085	143.117	147.111	170.058	171.136	199.146	246.179	270.178	271.159	310.165	313.204	317.213	327.194	381.209	416.284	427.284	512.315	515.355	624.416
Frac. Inten.(% of TIC)	0.92	9.89	0.58	17.40	0.15	0.12	5.41	3.55	8.03	3.00	2.53	3.65	6.52	3.19	2.50	3.71	3.19	2.67	2.47	3.35	4.43	2.44	2.44	3.26	4.59
Rel. Inten.(% of BP)	5.31	56.86	3.34	100.00	0.84	0.69	31.09	20.41	46.13	17.24	14.57	21.00	37.49	18.32	14.35	21.34	18.33	15.36	14.20	19.24	25.46	14.04	14.03	18.77	26.40
Score	0.50	-0.57	0.50	0.50		0.20	0.50	-0.20	1.50	-0.17	-0.15	0.75	1.50	0.75	-0.14	-0.21	-0.18	1.50	0.75	-0.19	1.50	-0.14	0.75	1.50	-0.26
Ion-type	V		KQ	a_1	KQ	RKQ	y_1-NH_3		y_1			VV	y_2	VAV				y_3	QVV		y_4		b_4	y_5	
Delta ppm	-2.4		-4.5	-8.4		-22.0	-10.4		-9.5			2.5	-7.0	-15.2				-15.9	-30.5		-5.6		-9.4	-0.9	
				0.50																			kVGL		
				LI																			-9.4		
				4.3																					



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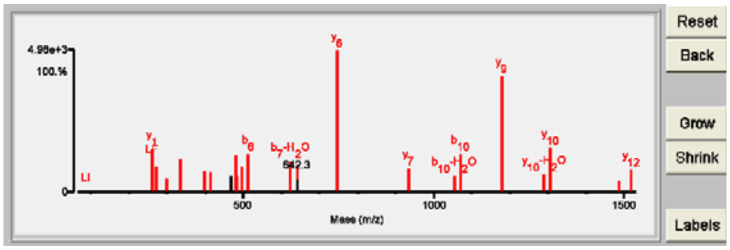
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.01	96.3	9	2/25	K49k	(K)AAGVNVEPFWPGLFAk(A)	1702.8952	114.0490	3.3	11514.0/4.26	HUMAN	P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1
2	6.21	59.9	3	13/25	K3470k	(R)IETLSPNNALFEKVk(V)	1702.9374	114.0067	-19.9	514666.7/5.95	HUMAN	RQ96JB1	REVERSE Dynein heavy chain 8, axonemal OS=Homo sapiens GN=DNAH8 PE=1 SV=2
3	5.46	59.9	2	13/25	K3468k	(R)IETLSPNNALFEkVK(V)	1702.9374	114.0067	-19.9	514666.7/5.95	HUMAN	RQ96JB1	REVERSE Dynein heavy chain 8, axonemal OS=Homo sapiens GN=DNAH8 PE=1 SV=2

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>18.01</td><td>96.3</td><td>9</td><td>2/25</td><td>K49k</td><td>(K) A A G V|N\V|E|P F/W|P G L/F|A/k (A)</td><td>1702.8952</td><td>114.0490</td><td>3.3</td><td>11514.0/4.26</td><td>HUMAN</td><td>P05386</td><td>632593</td><td>60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1</td></tr>
</table>

Fragment-ion (m/z)	72.082	86.095	261.158	271.175	299.173	332.193	396.197	413.218	467.269	479.261	484.288	495.253	512.284	623.316	641.327	642.323^{+2}	746.419	932.498	1053.519	1071.520	1176.621	1287.651	1305.659	1485.737	1518.761
Frac. Inten.(% of TIC)	0.04	0.06	5.44	3.34	1.82	4.23	2.63	2.51	2.09	4.70	2.07	3.33	4.81	3.87	3.36	1.63	17.82	2.91	2.05	4.76	14.58	2.18	5.51	1.39	2.87
Rel. Inten.(% of BP)	0.23	0.35	30.53	18.74	10.20	23.75	14.74	14.10	11.70	26.35	11.64	18.67	26.96	21.69	18.83	9.15	100.00	16.34	11.50	26.70	81.79	12.24	30.91	7.80	16.12
Score	0.50	0.22	1.50	0.50	0.50	1.50	0.25	0.50	-0.12	1.50	0.50	0.25	0.50	0.25	0.50	-0.09	1.50	1.50	0.25	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	V	LI	y_1	a_4	b_4	y_2	b_5-NH$_3$	b_5		y_3	a_6	b_6-NH$_3$	b_6	b_7-H$_2$O	b_7		y_6	y_7	b_{10}-H$_2$O	b_{10}	y_9	y_{10}-H$_2$O	y_{10}	b_{14}	y_{12}
Delta ppm	11.4	-20.0	7.2	-8.7	3.4	2.0	20.0	5.6		-0.1	-1.9	-9.4	-0.4	0.1	1.2		-1.3	-0.9	2.7	-6.9	0.7	-1.1	-2.5	-10.9	-8.3
			LF			LFA																			
			-12.5			-13.4																			



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Result Summary

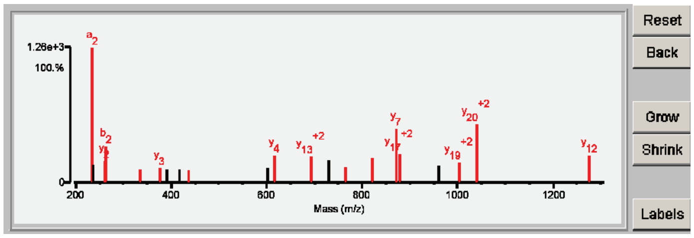
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.91	82.6	11	7/25	K21k	(R)YVASYLLAALGGNSSPSAkDIK(K)	2225.1812	114.0417	-0.5	11665.0/4.42	HUMAN	P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1
2	17.65	77.0	9	9/25	K24k	(R)YVASYLLAALGGNSSPSAKDIk(K)	2225.1812	114.0417	-0.5	11665.0/4.42	HUMAN	P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.91	82.6	11	7/25	K21k	(R) Y V|A|S Y/L/L/A A/L/G G N S S/P S A/k/D/I K (K)	2225.1812	114.0417	-0.5	11665.0/4.42	HUMAN	P05387	632663	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Fragment-ion (m/z)	84.080	86.095	136.073	137.071	235.144	236.148	260.196	263.140	334.180	375.216	390.212	417.218
Frac. Inten.(% of TIC)	0.11	0.15	0.58	1.98	21.52	2.79	3.35	5.82	2.05	2.25	2.15	2.04
Rel. Inten.(% of BP)	0.50	0.71	2.70	9.19	100.00	12.98	15.55	27.06	9.55	10.46	10.01	9.47
Score	0.50	0.22	1.00	-0.09	0.50	-0.13	1.50	0.50	0.50	1.50	-0.10	-0.09
Ion-type	KQ	LI	a_1		a_2		y_2	b_2	b_3	y_3		
Delta ppm	-5.7	-21.2	-24.9 1.00 Y -16.8		-5.5		-4.9	0.3	8.6	-20.8		

Fragment-ion (m/z)	436.739^{+2}	601.319^{+2}	617.360	694.368^{+2}	729.323^{+2}	765.379^{+2}	821.937^{+2}	872.484	878.486^{+2}	960.498	1003.524^{+2}	1039.050^{+2}	1274.617
Frac. Inten.(% of TIC)	1.96	2.28	4.24	4.21	3.55	2.58	4.01	8.52	4.44	2.59	3.23	9.29	4.31
Rel. Inten.(% of BP)	9.10	10.61	19.69	19.55	16.50	11.97	18.63	39.61	20.62	12.06	15.02	43.20	20.05
Score	1.50	-0.11	1.50	1.50	-0.17	1.50	1.50	1.50	1.50	-0.12	1.50	1.50	1.50
Ion-type	y_7^{+2}		y_4	y_{13}^{+2}		y_{15}^{+2}	y_{16}^{+2}	y_7	y_{17}^{+2}		y_{19}^{+2}	y_{20}^{+2}	y_{12}
Delta ppm	-14.3		-3.1	7.6		-27.4	-5.4	-0.1	2.2		-7.4	0.3	-13.4



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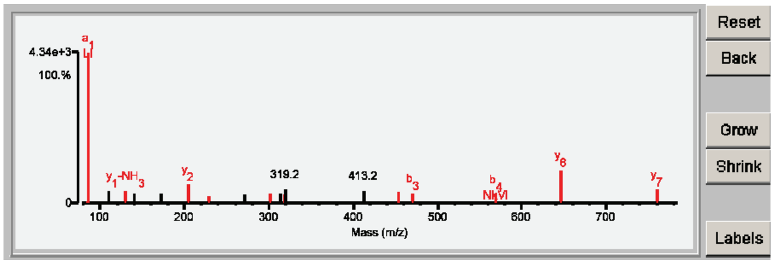
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	**10.66**	**75.3**	**6**	**10/25**	**K41k**	**(R)LNkVISELNGK(N)**	**1214.7103**	**114.0421**	**-0.6**	**11665.0/4.42**	HUMAN	**P05387**	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	**10.66**	**75.3**	**6**	**10/25**	**K41k**	**(R)** L N\k\V|I/S E L/N/G K **(N)**	**1214.7103**	**114.0421**	**-0.6**	**11665.0/4.42**	HUMAN	**P05387**	**632663**	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Fragment-ion (m/z)	**69.071**	**70.065**	**72.081**	**84.081**	**85.086**	**86.097**	**87.056**	**110.072**	**129.103**	**130.088**	**141.102**	**173.124**	**204.134**	**228.135**	**271.173**	**301.149**	**314.211**	**318.176**	**319.186^{+2}**	**413.246**	**453.254**	**470.267**	**569.346**	**647.335**	**760.425**
Frac. Inten.(% of TIC) **Rel. Inten.(% of BP)** **Score** **Ion-type** **Delta ppm**	2.94 7.44 -0.07	0.11 0.27 -0.00	0.20 0.51 0.50 **V** -3.8	0.67 1.69 0.50 **KQ** 7.4	2.03 5.12 -0.05	39.59 100.00 0.50 **a$_1$** -1.4 0.50 **LI** 11.3	0.09 0.22 0.33 **NR** 11.6	3.14 7.92 -0.08	0.10 0.25 0.20 **RKQ** 4.3	3.22 8.12 0.50 y$_1$-NH$_3$ 14.2	2.46 6.21 -0.06	2.67 6.73 -0.07	4.81 12.16 1.50 **y$_2$** -3.3	2.00 5.05 0.75 **b$_2$** 0.2 **LN** 0.2	2.11 5.33 -0.05	2.67 6.73 0.50 y$_3$-NH$_3$ -4.5	2.53 6.38 -0.06	2.22 5.62 1.50 **y$_3$** -5.3	3.41 8.61 -0.09	3.32 8.39 -0.08	2.77 7.00 0.25 b$_3$-NH$_3$ 16.5	2.56 6.47 0.50 **b$_3$** -13.5	2.30 5.82 0.75 **b$_4$** 7.3 **NkVI** 7.3	8.60 21.72 1.50 **y$_6$** -1.5	3.51 8.86 1.50 **y$_7$** 6.8



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Result Summary

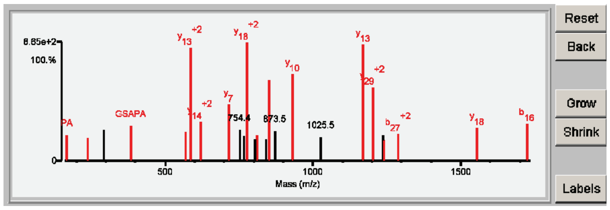
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.22	81.7	9	8/25	K61k	(K)NIEDVIAQGIGkLASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK(K)	4012.0986	114.0404	-0.6	11665.0/4.42	HUMAN	P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.22	81.7	9	8/25	K61k	(K) NIEDV\IAQGIGkLAS\V|PAGGAVAVSA/A|PGSA/A/PAA/GSA/PAAAEEK (K)	4012.0986	114.0404	-0.6	11665.0/4.42	HUMAN	P05387	632663	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

Fragment-ion (m/z)	169.095	240.134	295.136	384.183	571.260	585.290^{+2}	620.821^{+2}	715.357	754.418	767.864	776.879^{+2}	803.936
Frac. Inten.(% of TIC)	2.25	2.01	2.72	3.03	2.50	9.81	3.39	4.93	2.69	2.11	10.29	1.92
Rel. Inten.(% of BP)	21.87	19.53	26.39	29.42	24.31	95.27	32.97	47.84	26.11	20.54	100.00	18.67
Score	0.75	0.75	-0.26	0.75	0.50	1.50	1.50	1.50	-0.26	-0.21	1.50	-0.19
Ion-type	PA	PAA		GSAPA	b_5	y_{13}^{+2}	y_{14}^{+2}	y_7			y_{18}^{+2}	
Delta ppm	-18.0	-5.3		-14.5	-23.8	-6.6	13.8	-7.4			-6.7	

Fragment-ion (m/z)	812.425	843.405	852.972^{+2}	873.450^{+2}	930.448	1025.472	1169.573	1202.607^{+2}	1235.639^{+2}	1240.603	1287.653^{+2}	1552.752	1722.938
Frac. Inten.(% of TIC)	2.29	1.92	6.96	2.63	7.54	2.03	10.08	6.40	2.26	1.79	2.33	2.90	3.22
Rel. Inten.(% of BP)	22.22	18.65	67.59	25.53	73.29	19.76	97.91	62.15	21.97	17.35	22.64	28.14	31.31
Score	1.50	-0.19	0.25	-0.26	1.50	-0.20	1.50	1.50	-0.22	1.50	0.50	1.50	0.50
Ion-type	$b{++}_{15}$ $y{++}_{19}$		b_{16}-H_2O^{+2}		y_{10}		y_{13}	y_{29}^{+2}		y_{14}	b_{27}^{+2}	y_{18}	b_{16}
Delta ppm	-17.7 27.7		4.8		-4.8		-6.1	-1.6		-10.8	-35.4	-5.0	-1.1



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Result Summary

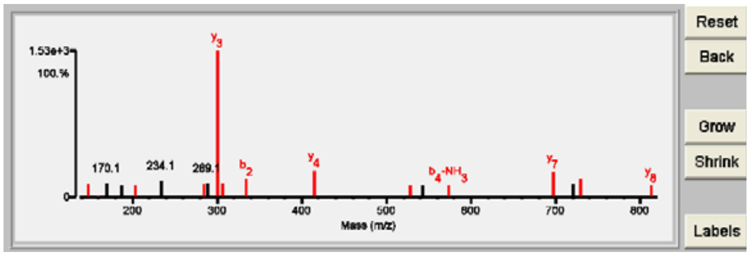
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.61	73.4	8	8/25	K169k	(R)WFQQkYDGIILPGK(-)	1692.9108	114.0524	5.3	20252.5/9.64	HUMAN	P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.61	73.4	8	8/25	K169k	(R) W F\Q Q k Y/D/G I/I/L/P/G/K (-)	1692.9108	114.0524	5.3	20252.5/9.64	HUMAN	P62913	585835	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2

Fragment-ion (m/z)	84.044	84.080	86.096	129.099	130.071	136.076	147.110	159.090	170.059	187.140	204.132	234.123
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.73 11.34 -0.11	0.20 0.62 0.50 KQ -8.0	0.30 0.90 0.22 LI -7.3	0.09 0.28 0.20 RKQ -25.9	4.31 13.08 -0.13	0.12 0.36 1.00 Y -0.7	2.87 8.70 1.50 y_1 -20.4	0.30 0.91 2.00 a_1 -14.9 2.00 W -8.0	3.14 9.54 -0.10	2.72 8.27 -0.08	2.68 8.14 1.50 y_2 -10.1	3.75 11.40 -0.11

Fragment-ion (m/z)	284.202	289.133	301.185	306.158	334.155	414.266	527.347	543.307	573.232	697.457	719.928^{+2}	728.398^{+2}	812.494
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.82 8.56 0.75 GII 14.2	3.34 10.14 -0.10	32.92 100.00 1.50 y_3 -6.1	3.15 9.56 0.50 a_2 -11.1	4.00 12.14 0.50 b_2 -4.2	5.97 18.14 1.50 y_4 -11.8	2.65 8.04 1.50 y_5 -15.9	2.58 7.84 -0.08	2.77 8.40 0.25 b_4-NH_3 -25.8	5.85 17.77 1.50 y_7 -5.1	3.03 9.21 -0.09	3.97 12.05 0.50 y_{12}-H_2O^{+2} -5.0	2.75 8.35 1.50 y_8 7.3



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Result Summary

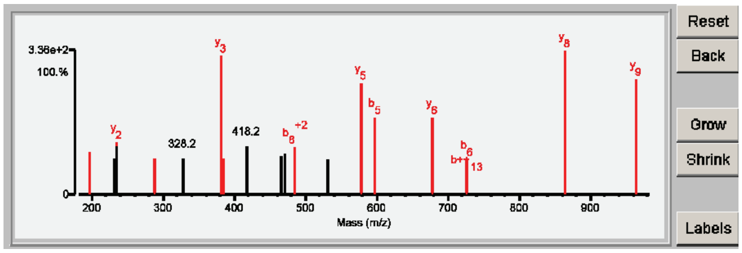
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.91	73.8	9	8/25	K38k	(R)AAkVLEQLTGQTPVFSK(A)	1817.0167	114.0478	2.5	20252.5/9.64	HUMAN	P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.91	73.8	9	8/25	K38k	(R) A A k\V L\E\Q L|T/G Q/T/P\V/F/S K (A)	1817.0167	114.0478	2.5	20252.5/9.64	HUMAN	P62913	585835	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2

Fragment-ion (m/z)	84.079	86.097	101.068	129.064	129.101	131.084	197.128	230.617	234.146	235.138	289.171	328.191
Frac. Inten.(% of TIC)	0.18	0.27	0.20	0.15	0.12	3.23	3.37	2.94	4.24	3.88	2.88	2.91
Rel. Inten.(% of BP)	1.57	2.37	1.74	1.26	1.08	28.00	29.16	25.50	36.73	33.60	24.96	25.20
Score		0.22	0.50	0.20		-0.28	0.75	-0.25	1.50	-0.34	1.50	-0.25
Ion-type	QK	LI	QK	QKR	QKR		PV		y_2		y^{++}_5	
Delta ppm		4.3	-26.1	-15.9			-9.4		5.0		1.2	

Fragment-ion (m/z)	381.208	385.220	418.234	465.733	470.259^{+2}	484.277^{+2}	531.287^{+2}	577.337	597.357	678.373	726.408	863.461	964.496
Frac. Inten.(% of TIC)	11.10	2.89	3.94	3.12	3.31	3.76	2.82	8.89	6.13	6.15	2.78	11.54	9.20
Rel. Inten.(% of BP)	96.16	25.02	34.14	27.05	28.72	32.59	24.46	77.06	53.11	53.32	24.10	100.00	79.71
Score	1.50	0.50	-0.34	-0.27	-0.29	0.50	-0.24	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y_3	b_3				b_8^{+2}		y_5	b_5	y_6	b_6 b^{++}_{13}	y_8	y_9
Delta ppm	-14.8	-1.5				-10.8		5.2	-27.1	-12.8	-10.8 15.0	-1.3	-13.8



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Result Summary

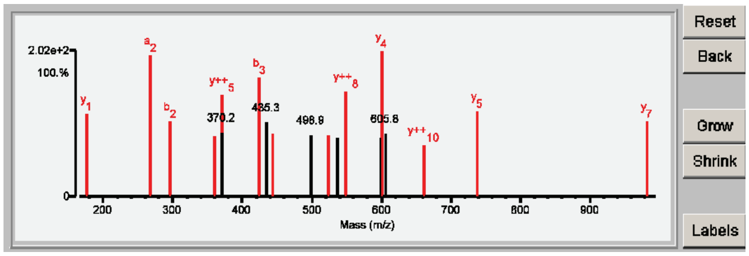
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.00	70.7	11	8/25	K140k	(K)FFEVILIDPFHkAIR(R)	1845.0422	114.0520	4.6	24146.2/11.62	HUMAN	P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.00	70.7	11	8/25	K140k	(K) F F\E\V\I/L I/D/P/F/H/k/A I/R (R)	1845.0422	114.0520	4.6	24146.2/11.62	HUMAN	P61313	590423	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2

Fragment-ion (m/z)	70.064	86.096	110.074	120.078	121.081	175.121	267.141	295.144	359.237	369.708	370.225	424.187
Frac. Inten.(% of TIC)	0.01	1.30	0.18	0.68	3.25	4.84	8.28	4.42	3.56	5.96	3.75	6.98
Rel. Inten.(% of BP)	0.11	15.14	2.09	7.94	37.96	56.49	96.68	51.59	41.63	69.57	43.81	81.47
Score	0.20	0.22	1.00	1.00	-0.38	1.50	0.50	0.50	1.50	1.50	-0.44	0.50
Ion-type	PR	LI	H	a_1		y_1	a_2	b_2	y_3	y^{++}_{5}		b_3
Delta ppm	-13.2	-6.1	20.2	-29.8 1.00 F -20.6		9.4	-33.3	-4.7	-7.9	-37.3		-3.1

Fragment-ion (m/z)	434.775^{+2}	435.271	443.244	498.945	523.245	537.267	549.290	599.302	601.380	605.831^{+3}	662.365	738.448	982.538
Frac. Inten.(% of TIC)	3.52	4.35	3.73	3.65	3.61	3.50	6.17	3.51	8.56	3.73	3.03	5.02	4.43
Rel. Inten.(% of BP)	41.13	50.84	43.61	42.62	42.17	40.83	72.10	40.98	100.00	43.61	35.33	58.57	51.68
Score	-0.41	-0.51	1.50	-0.43	0.50	-0.41	1.50	-0.41	1.50	-0.44	1.50	1.50	1.50
Ion-type			y^{++}_{6}		b_4		y^{++}_{8}		y_4		y^{++}_{10}	y_5	y_7
Delta ppm			-28.0		-20.7		-11.0		3.1		-23.0	15.4	-20.9



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Result Summary

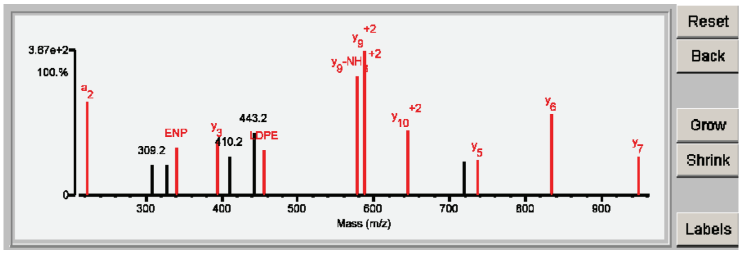
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.85	63.6	6	11/25	K13k	(R)YSLDPENPTkSCK(S)	1538.7155	114.0567	8.3	21397.2/10.18	HUMAN	P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3
2	8.97	58.8	5	12/25	K16k	(R)YSLDPENPTKSCk(S)	1538.7155	114.0567	8.3	21397.2/10.18	HUMAN	P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.85	63.6	6	11/25	K13k	(R) Y S L/D/P E/N/P/T k/S C K (S)	1538.7155	114.0567	8.3	21397.2/10.18	HUMAN	P18621	593383	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3

Fragment-ion (m/z)	70.064	72.077	86.093	87.055	136.075	137.075	148.038	185.114	189.086	201.111	223.104
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.07 0.20 **PR** -8.9	3.97 31.66 -0.32	0.32 2.56 0.22 **LI** -35.1	0.11 0.89 0.33 **NR** -9.1	0.42 3.36 1.00 a_1 -10.9 1.00 **Y** -2.9	3.59 28.66 -0.29	2.80 22.36 -0.22	3.60 28.74 -0.29	2.70 21.54 -0.22	2.68 21.41 -0.21	8.08 64.47 0.50 a_2 -19.8

Fragment-ion (m/z)	309.188	327.152	341.140	394.167	410.200	443.219	455.215	579.252^{+2}	587.779^{+2}	645.289^{+2}	719.315^{+2}	737.380	834.407	948.441
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.67 21.30 -0.21	2.67 21.30 -0.21	4.13 32.97 0.75 **ENP** -18.1	4.80 38.34 1.50 y_3 -22.0	3.40 27.11 -0.27	5.38 42.98 -0.43	3.87 30.92 0.75 **LDPE** 0.6	10.31 82.27 0.50 $y_9\text{-NH}_3^{+2}$ -24.7	12.53 100.00 1.50 y_9^{+2} -1.0	5.59 44.59 1.50 y_{10}^{+2} -7.1	2.96 23.62 -0.24	3.08 24.63 1.50 y_5 25.4	7.01 55.96 1.50 y_6 -8.5	3.32 26.53 1.50 y_7 -16.5



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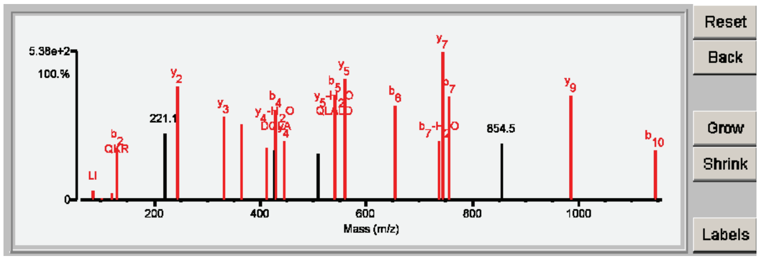
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.94	87.0	11	4/25	K119k	(R)AGGkILTFDQLALDSPK(G)	1773.9745	114.0475	2.4	21634.6/11.73	HUMAN	Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.94	87.0	11	4/25	K119k	(R) A G\G k\I\L\T\F/D Q|L A/L/D/S/P K (G)	1773.9745	114.0475	2.4	21634.6/11.73	HUMAN	Q07020	594913	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2

Fragment-ion (m/z)	70.065	84.080	86.096	101.069	120.079	129.063	221.128	244.093	244.165	331.192	364.147	413.257	425.272	428.223	446.228	508.280	541.305	559.311	654.386	737.424	743.429	755.439	854.532	986.511	1145.590
Frac. Inten.(% of TIC)	0.00	0.45	0.62	0.13	0.42	3.19	4.09	3.99	7.00	5.16	4.64	3.22	3.10	5.52	3.64	2.87	6.47	7.49	5.84	3.60	9.15	6.40	3.50	6.47	3.05
Rel. Inten.(% of BP)	0.03	4.93	6.78	1.39	4.55	34.86	44.72	43.64	76.53	56.36	50.71	35.25	33.88	60.34	39.85	31.41	70.68	81.87	63.82	39.36	100.00	69.95	38.23	70.70	33.40
Score	0.20	0.50	0.22	0.50	1.00	0.50	-0.45	0.75	1.50	1.50	0.75	0.75	-0.34	0.75	1.50	-0.31	0.75	1.50	0.50	0.25	1.50	0.50	-0.38	1.50	0.50
Ion-type	**PR**	**KQ**	**LI**	a_2	**F**	b_2		**DQ**	y_2	y_3	**TFD**	**GkI**		b_4	y_4		b_5	y_5	b_6	b_7-H_2O	y_7	b_7		y_9	b_{10}
Delta ppm	2.5	-10.4	-10.8	-32.0	-16.5	-32.9		-4.9	-3.6	-16.9	-11.0	12.8		-8.0	7.3		-10.3	4.6	-12.1	-9.6	-0.6	-3.7		-4.5	-5.5
						0.50								y_4-H_2O			y_5-H_2O								
				KQ		**QKR**								20.8			12.5								
						-24.4								**DQLA**			**QLALD**								
														18.3			10.5								



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Result Summary

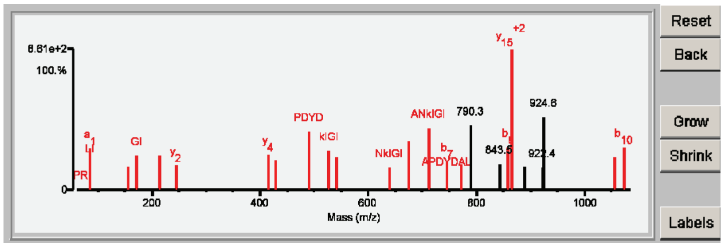
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.72	79.4	8	5/25	K152k	(R)LAPDYDALDVANkIGII(-)	1800.9742	114.0563	7.0	17695.1/10.44	HUMAN	P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.72	79.4	8	5/25	K152k	(R) L A/P D Y D\A\L|D V\A/N k/I G/I I (-)	1800.9742	114.0563	7.0	17695.1/10.44	HUMAN	P62750	603145	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1

Fragment-ion (m/z)	70.066	86.096	157.132	171.112	213.085	245.179	415.293	428.217	491.180	526.341	541.307	640.371
Frac. Inten.(% of TIC)	0.00	4.12	2.29	3.40	3.40	2.49	3.51	2.95	5.73	3.87	3.28	2.20
Rel. Inten.(% of BP)	0.02	29.58	16.46	24.44	24.43	17.88	25.20	21.22	41.14	27.81	23.56	15.84
Score	0.20	0.50	0.50	0.75	0.75	1.50	1.50	0.75	0.75	0.75	0.75	0.75
Ion-type	PR	a_1	a_2	GI	PD	y_2	y_4	ANk	PDYD	kIGI	ANkI	NkIGI
Delta ppm	12.5	-18.9	-15.5	-11.1	-14.5	-27.6	2.9	-21.3	2.9	10.0	-6.0	-12.5
		0.50										
		LI										
		-6.1										

Fragment-ion (m/z)	675.295	711.418	746.333	771.467	790.327	843.513	859.421	865.945^{+2}	889.393	922.432^{+2}	924.629	1056.599	1073.511
Frac. Inten.(% of TIC)	4.85	6.16	2.85	2.60	6.40	2.55	4.26	13.92	2.28	2.16	7.15	3.29	4.28
Rel. Inten.(% of BP)	34.88	44.28	20.46	18.68	46.03	18.35	30.61	100.00	16.39	15.54	51.41	23.66	30.73
Score	0.75	0.75	0.75	1.50	-0.46	-0.18	0.50	1.50	-0.16	-0.16	-0.51	1.50	0.50
Ion-type	b_6	ANkIGI	b_7	y_6			b_8	y_{15}^{+2}				y_9	b_{10}
Delta ppm	-7.2	2.8	-5.4	-6.5			0.2	-8.1				-5.4	-5.1
	PDYDAL		APDYDAL										
	-7.2		-5.4										



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Result Summary

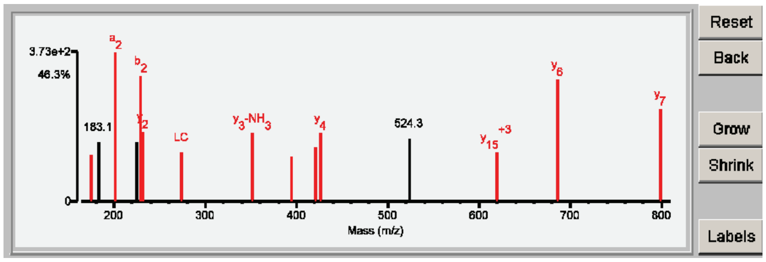
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.93	68.3	7	6/24	K12k	(K)VELCSFSGYkIYPGHGR(R)	1969.9589	114.0637	10.0	17779.1/11.26	HUMAN	P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1
2	3.39	55.5	0	11/24	None	(R)LQAAQSDLGPDREVQTVEK(T)	2084.0618	-0.0393	-18.8	231619.2/6.57	HUMAN	RQ92817	REVERSE Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.93	68.3	7	6/24	K12k	(K) V E|L C S F S/G Y k/I/Y P/G H/G/R (R)	1969.9589	114.0637	10.0	17779.1/11.26	HUMAN	P83731	605091	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	73.085	84.081	86.094	102.054	120.080	133.046	136.075	175.114	183.114
Frac. Inten.(% of TIC)	0.00	0.80	4.17	20.00	0.35	0.16	0.24	4.52	0.23	2.88	3.66
Rel. Inten.(% of BP)	0.02	4.01	20.83	100.00	1.77	0.80	1.21	22.59	1.15	14.42	18.28
Score	0.20	0.50 0.50	-0.16	-0.75	0.22	1.00	1.00	-0.17	1.00	1.50	-0.14
Ion-type	PR	a_1 V			LI	E	F		Y	y_1	
Delta ppm	-0.4	-21.8 -6.6			-22.4	-7.4	-4.0		-8.7	-30.6	

Fragment-ion (m/z)	201.123	225.118	229.117	232.138	274.116	352.174	395.132	421.213^{+3}	426.219	524.285	619.318^{+3}	686.340	799.417
Frac. Inten.(% of TIC)	9.24	3.65	7.83	4.29	3.04	4.26	2.83	3.38	4.21	3.89	3.06	7.52	5.78
Rel. Inten.(% of BP)	46.22	18.26	39.16	21.43	15.19	21.28	14.17	16.88	21.05	19.44	15.29	37.62	28.90
Score	0.50	-0.14	0.50	1.50	0.75	0.50	0.75	1.50	1.50	-0.15	1.50	1.50	1.50
Ion-type	a_2		b_2	y_2	LC	y_3-NH$_3$	CSF	y_{10}^{+3}	y_4		y_{15}^{+3}	y_6	y_7
Delta ppm	-6.3		-8.6	-11.3	-27.7	4.6	-17.6	-15.0	-3.5		25.6	4.7	-5.3



Result Summary

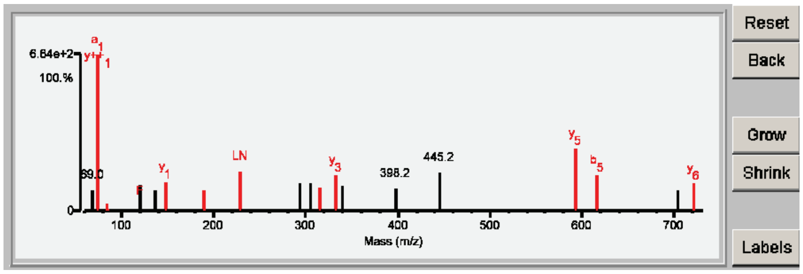
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.72	66.3	5	9/24	K27k	(R)TDGkVFQFLNAK(C)	1367.7318	114.0513	5.6	17779.1/11.26	HUMAN	P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.72	66.3	5	9/24	K27k	(R) T D G k V\F/Q/F L/N A/K (C)	1367.7318	114.0513	5.6	17779.1/11.26	HUMAN	P83731	605091	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1

Fragment-ion (m/z)	69.040	72.079	74.059	84.080	86.095	101.072	120.078	121.087	129.099	136.072	147.111	189.085
Frac. Inten.(% of TIC)	3.14	0.14	23.24	1.00	0.38	0.17	0.75	3.78	0.14	3.00	4.22	2.99
Rel. Inten.(% of BP)	13.50	0.61	100.00	4.32	1.62	0.74	3.24	16.26	0.59	12.90	18.17	12.88
Score	-0.13	0.50	1.50	0.50	0.22		1.00	-0.16	0.20	-0.13	1.50	0.50
Ion-type		V	a_1	KQ	LI	KQ	F		RKQ		y_1	a_2
Delta ppm		-17.7	-30.2	-8.0	-16.6		-19.8		-22.8		-10.2	-15.8
			y^{++}_1									
			-15.4									

Fragment-ion (m/z)	228.132	294.150	305.198	315.162	332.187	340.161	398.197	445.248	592.351	615.298	704.366	720.388
Frac. Inten.(% of TIC)	5.81	4.14	4.07	3.51	5.30	3.68	3.19	5.70	9.33	5.32	3.01	3.98
Rel. Inten.(% of BP)	25.00	17.83	17.52	15.09	22.82	15.82	13.73	24.54	40.13	22.88	12.94	17.14
Score	0.75	-0.18	-0.18	0.50	1.50	-0.16	-0.14	-0.25	1.50	0.50	-0.13	1.50
Ion-type	LN			y_3-NH_3	y_3				y_5	b_5		y_6
Delta ppm	-14.8			-13.3	-18.2				9.9	-20.9		-21.5



Result Summary

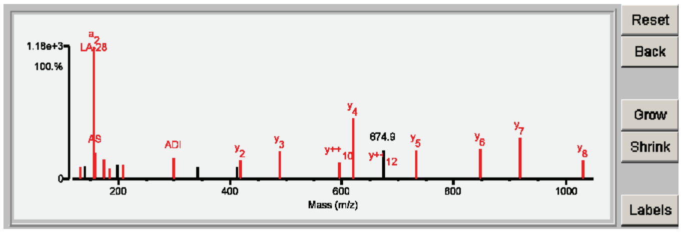
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.09	80.8	10	8/25	K93k	(R)AITGASLADIMAkR(N)	1417.7832	114.0537	7.0	17779.1/11.26	HUMAN	P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1
2	7.86	63.3	5	15/25	M36m K44k	(K)LSTmGLIALQAkR(E)	1401.8246	130.0122	-16.7	83638.4/5.65	HUMAN	RQ1L5Z9	REVERSE LON peptidase N-terminal domain and RING finger protein 2 OS=Homo sapiens GN=LONRF2 PE=2 SV=2
3	6.56	52.4	2	13/25	K315k	(R)ALAIIDAASkSMVK(T)	1417.8083	114.0285	-9.4	62184.1/6.58	HUMAN	RQ14194	REVERSE Dihydropyrimidinase-related protein 1 OS=Homo sapiens GN=CRMP1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.09	80.8	10	8/25	K93k	(R) A I|T G/A S/L/A/D/I/M/A/k/R (N)	1417.7832	114.0537	7.0	17779.1/11.26	HUMAN	P83731	605091	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1

Fragment-ion (m/z)	74.059	84.082	86.096	87.102	131.080	141.101	157.132	159.076	175.116	185.125	198.095	209.128
Frac. Inten.(% of TIC)	2.01	2.10	0.84	2.22	1.87	2.14	21.59	4.32	3.26	1.84	2.22	2.32
Rel. Inten.(% of BP)	9.32	9.73	3.89	10.27	8.64	9.90	100.00	20.01	15.09	8.53	10.29	10.74
Score	-0.09	-0.10	0.22	-0.10	0.50	-0.10	0.50	0.75	1.50	0.75	-0.10	1.50
Ion-type			LI		AS-28		a_2 LA-28	AS	y_1	b_2 LA		y++$_2$
Delta ppm			-3.8		-17.6		-13.6 -13.6	-11.4	-18.0	-25.1 -25.1		-19.9

Fragment-ion (m/z)	300.152	342.190	412.219	417.255	488.289	595.313	619.331	674.358	674.856	732.422	847.448	918.488	1031.566
Frac. Inten.(% of TIC)	3.38	1.88	1.87	3.01	4.59	2.69	9.79	1.80	4.71	4.71	4.98	6.73	3.13
Rel. Inten.(% of BP)	15.64	8.73	8.67	13.96	21.24	12.47	45.37	8.35	21.82	21.82	23.09	31.20	14.48
Score	0.75	-0.09	-0.09	1.50	1.50	1.50	1.50	1.50	-0.22	1.50	1.50	1.50	1.50
Ion-type	ADI			y_2	y_3	y++$_{10}$	y_4	y++$_{12}$		y_5	y_6	y_7	y_8
Delta ppm	-16.3			-5.4	-10.6	-14.8	-6.0	3.1		4.9	3.2	5.5	-0.3



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Result Summary

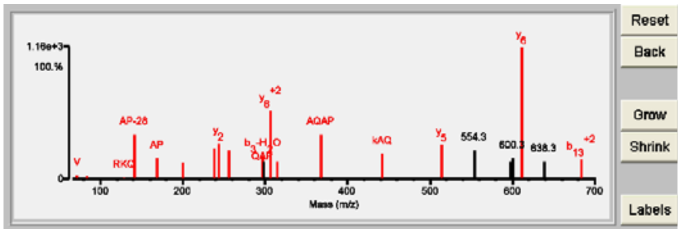
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.95	81.5	5	6/25	K134k	(K)AKDQTkAQAAAPASVPAQAPK(R)	2049.1087	114.0678	11.5	17752.2/11.67	HUMAN	P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2
2	13.01	77.7	5	7/25	K130k	(K)AkDQTKAQAAAPASVPAQAPK(R)	2049.1087	114.0678	11.5	17752.2/11.67	HUMAN	P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2
3	7.27	58.5	2	12/25	K561k	(R)AASSVPNLKKTNAQAAPkPR(K)	2049.1563	114.0202	-10.5	112212.0/6.93	HUMAN	Q66K74	Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2
4	4.55	60.6	2	12/25	K1895k K1901k	(K)KAPPVTKDPSSLkATPGIk(D)	1935.1273	228.0492	-16.9	222658.9/6.15	HUMAN	Q9UKL3	CASP8-associated protein 2 OS=Homo sapiens GN=CASP8AP2 PE=1 SV=1
5	3.31	56.2	1	13/25	None	(R)KASDERLTVTGGVPASAPPPGR(E)	2163.1517	0.0249	11.5	122676.5/6.01	HUMAN	RQ9ULE0	REVERSE Protein WWC3 OS=Homo sapiens GN=WWC3 PE=2 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.95	81.5	5	6/25	K134k	(K) A K D Q T k A Q A A A P A\S V/P/A Q/A/P K (R)	2049.1087	114.0678	11.5	17752.2/11.67	HUMAN	P47914	610387	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

Fragment-ion (m/z)	60.045	70.066	72.080	84.081	101.070	129.103	141.100	169.095	200.105	238.120	244.164	256.133	297.156
Frac. Inten.(% of TIC)	3.44	0.02	0.61	0.34	0.09	0.19	6.55	3.14	2.49	4.50	5.25	4.31	3.46
Rel. Inten.(% of BP)	17.65	0.10	3.16	1.76	0.44	0.97	33.64	16.15	12.79	23.15	26.97	22.12	17.80
Score	-0.18	0.20	0.50	0.50		0.20	0.50	0.75	0.75	0.50	1.50	0.75	0.75
Ion-type		PR	V	KQ	KQ	RKQ	AP-28	AP	QA	PAS-H_2O	y_2	PAS	b_3-H_2O QAP
Delta ppm		5.3	-10.8	2.7		6.7	-27.2	-16.9	5.2	0.8	-7.2	9.1	-4.5 -4.5

Fragment-ion (m/z)	298.156	306.182^{+2}	315.202	368.192	442.242	514.305	554.345	597.300^{+2}	600.308^{+2}	611.351	638.300	683.853^{+2}
Frac. Inten.(% of TIC)	2.62	10.12	2.65	6.60	3.80	5.10	4.22	2.53	3.15	19.46	2.51	2.85
Rel. Inten.(% of BP)	13.46	51.99	13.61	33.90	19.55	26.22	21.67	13.02	16.20	100.00	12.88	14.66
Score	-0.13	1.50	1.50	0.75	0.75	1.50	-0.22	-0.13	-0.16	1.50	-0.13	0.50
Ion-type		y_6^{+2}	y_3	AQAP	kAQ	y_5				y_6		b_{13}^{+2}
Delta ppm		8.8	-2.2	-4.7	-0.8	13.5				-0.7		-7.6



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Result Summary

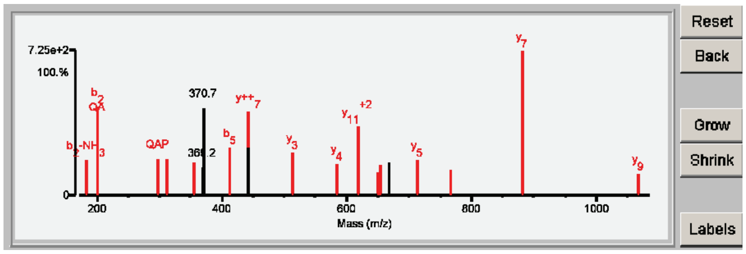
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.01	76.3	8	6/25	K149k	(K)AQAAAPASVPAQAPkR(T)	1533.8496	114.0404	-1.5	17752.2/11.67	HUMAN	P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.01	76.3	8	6/25	K149k	(K) A Q\A A/A|P A/S V|P A/Q/A/P k R (T)	1533.8496	114.0404	-1.5	17752.2/11.67	HUMAN	P47914	610387	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

Fragment-ion (m/z)	60.046	70.065	72.081	84.078	159.107	183.078	200.101	297.155	311.168	355.201	369.192	370.697^{+2}	413.213
Frac. Inten.(% of TIC)	2.07	0.00	0.09	0.07	2.68	3.40	8.54	3.56	3.51	3.20	2.72	8.47	4.67
Rel. Inten.(% of BP)	14.70	0.03	0.62	0.47	19.07	24.18	60.79	25.32	25.00	22.77	19.34	60.32	33.26
Score	-0.15	0.20	0.50	0.50	-0.19	0.25	0.75	0.75	0.75	0.75	-0.19	-0.60	0.50
Ion-type		PR	V	KQ		b_2-NH_3	b_2 QA	QAP	AAPA	SVPA			b_5
Delta ppm		2.5	3.1	-31.8		2.1	-17.3 -17.3	-5.8	-13.4	5.9			-6.1

Fragment-ion (m/z)	441.249	441.751	514.309	585.332	618.334^{+2}	650.340	653.865^{+2}	668.298	713.404	767.397	881.496	1067.567
Frac. Inten.(% of TIC)	8.06	4.61	4.19	3.08	6.64	2.28	2.97	3.18	3.42	2.47	14.05	2.08
Rel. Inten.(% of BP)	57.37	32.85	29.79	21.92	47.27	16.21	21.15	22.63	24.31	17.62	100.00	14.83
Score	1.50	-0.33	1.50	1.50	1.50	0.25	1.50	-0.23	1.50	0.50	1.50	1.50
Ion-type	$y{+}{+}_7$		y_3	y_4	y_{11}^{+2}	b_8-H_2O	y_{12}^{+2}		y_5	b_9 y_6-NH_3	y_7	y_9
Delta ppm	-5.3		-1.0	-25.5	-20.4	20.5	-0.1		-1.4	-11.4 -24.6	0.6	-27.1



Nature Biotechnology: doi: 10.1038/nbt.1654

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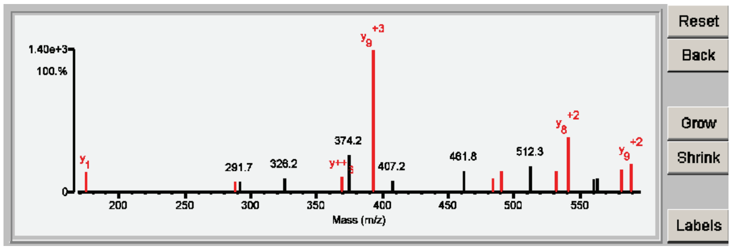
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.22	62.8	8	12/24	K131k	(K)GDVPTkRPPVLR(A)	1334.7903	114.0563	9.2	29995.8/10.61	HUMAN	P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.22	62.8	8	12/24	K131k	(K) G D V/P/T/k/R/P/P V/L/R (A)	1334.7903	114.0563	9.2	29995.8/10.61	HUMAN	P62424	629511	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2

Fragment-ion (m/z)	70.065	72.082	86.104	127.053	142.094	149.025	175.119	288.195	291.684	326.203^{+3}	369.229	374.241^{+3}	393.244^{+3}	407.233	461.823^{+2}	484.317	490.314^{+2}	512.318^{+2}	531.816^{+2}	540.836^{+2}	560.849	563.330	581.383	589.360^{+2}
Frac. Inten.(% of TIC)	0.02	0.58	1.95	3.06	1.78	4.36	3.54	1.90	1.92	2.52	2.59	6.69	25.24	2.04	3.69	2.50	3.84	4.54	3.84	9.73	2.32	2.38	3.96	5.02
Rel. Inten.(% of BP)	0.08	2.29	7.74	12.13	7.04	17.27	14.02	7.51	7.61	9.98	10.26	26.50	100.00	8.08	14.63	9.90	15.24	17.99	15.23	38.55	9.19	9.43	15.71	19.90
Score	0.20	0.50	-0.08	-0.12	-0.07	-0.17	1.50	1.50	-0.08	-0.10	1.50	-0.26	1.50	-0.08	-0.15	1.50	1.50	-0.18	0.50	1.50	-0.09	-0.09	1.50	1.50
Ion-type	PR	V					y_1	y_2			$y{+}{+}_6$		y_9^{+3}			y_4	y_7^{+2}		$y_8\text{-}H_2O^{+2}$	y_8^{+2}			y_5	y_9^{+2}
Delta ppm	-0.4	17.0					-1.4	-27.5			-36.2		0.9			-14.0	5.1		-26.3	0.8			9.7	-2.4



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Result Summary

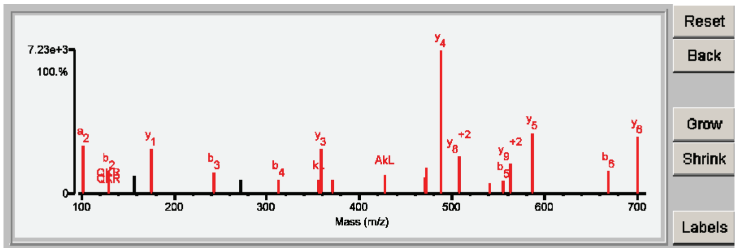
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.45	86.5	8	3/25	K217k	(K)GALAkLVEAIR(T)	1140.7099	114.0430	0.1	29995.8/10.61	HUMAN	P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2
2	8.27	60.0	4	12/25	None	(R)LRERVLELAR(G)	1254.7641	-0.0111	-8.9	76119.6/5.76	HUMAN	Q8NE01	Metal transporter CNNM3 OS=Homo sapiens GN=CNNM3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.45	86.5	8	3/25	K217k	(K) G A|L|A|k|L|V/E/A I/R (T)	1140.7099	114.0430	0.1	29995.8/10.61	HUMAN	P62424	629511	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2

Fragment-ion (m/z)	72.081	84.081	86.097	101.071	129.067	129.100	157.134	175.119	242.153	271.158	313.192	356.229	359.242
Frac. Inten.(% of TIC)	0.25	9.23	0.76	6.21	2.83	0.05	2.38	5.75	2.75	1.91	1.75	1.88	5.85
Rel. Inten.(% of BP)	1.35	49.60	4.08	33.34	15.21	0.27	12.80	30.88	14.76	10.24	9.41	10.08	31.41
Score	0.50	-0.50	0.22	0.50	0.50		-0.13	1.50	0.50	-0.10	0.50	0.75	1.50
Ion-type	V		LI	a_2	b_2	QKR		y_1	b_3		b_4	kL	y_3
Delta ppm	5.9		9.0	-7.3	-1.9			0.3	6.1		10.8	-5.1	5.8
					0.50								
					QKR								
					6.6								

Fragment-ion (m/z)	370.246^{+2}	427.265	470.272	471.796^{+2}	488.282	507.307^{+2}	540.345	555.326	563.851^{+2}	587.350	668.411	700.430
Frac. Inten.(% of TIC)	1.83	2.40	2.08	3.42	18.62	4.90	1.41	1.61	3.92	7.88	2.99	7.35
Rel. Inten.(% of BP)	9.84	12.88	11.15	18.36	100.00	26.34	7.59	8.65	21.06	42.35	16.06	39.47
Score	0.50	0.75	0.50	1.50	1.50	1.50	0.75	0.50	1.50	1.50	0.50	1.50
Ion-type	a_7^{+2}	AkL	y_4-H_2O	y_7^{+2}	y_4	y_8^{+2}	LAkL	b_5	y_9^{+2}	y_5	b_6	y_6
Delta ppm	1.5	-5.7	-1.4	12.8	-1.3	-3.2	-11.3	-0.9	0.4	-1.9	2.0	-7.3



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Result Summary

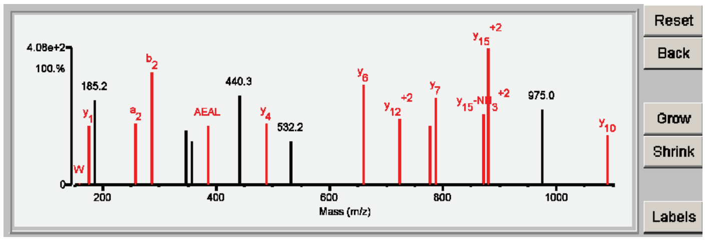
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.40	65.8	7	8/25	K302k	(R)VWTSQLkSTIQTAEALR(L)	1932.0549	114.0560	6.4	59609.5/8.49	HUMAN	Q16875	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.40	65.8	7	8/25	K302k	(R) V W|T S Q/L k/S T I/Q/T A/E A L/R (L)	1932.0549	114.0560	6.4	59609.5/8.49	HUMAN	Q16875	204273	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1

Fragment-ion (m/z)	72.079	84.041	84.079	86.095	101.068	127.085	159.086	175.116	185.166	258.162	286.148	346.160^{+2}	356.185
Frac. Inten.(% of TIC)	0.38	4.77	0.27	0.39	0.13	7.92	0.09	3.83	5.54	4.04	7.37	3.59	2.88
Rel. Inten.(% of BP)	4.19	53.26	3.03	4.40	1.42	88.47	0.97	42.81	61.92	45.12	82.34	40.14	32.11
Score	0.50 0.50	-0.38	0.50	0.22		-0.63	2.00	1.50	-0.44	0.50	0.50	-0.29	-0.23
Ion-type	a_1 V		KQ	LI	KQ		W	y_1		a_2	b_2		
Delta ppm	-45.4 -30.2		-22.3	-15.4			-36.3	-19.1		2.4	-28.7		

Fragment-ion (m/z)	385.205	440.280	488.284	532.236	660.370	722.904^{+2}	777.944^{+2}	788.429	872.485^{+2}	880.983^{+2}	975.029^{+2}	1089.582
Frac. Inten.(% of TIC)	3.88	5.89	4.02	2.84	6.58	4.34	3.84	5.67	4.65	8.95	4.92	3.22
Rel. Inten.(% of BP)	43.33	65.75	44.90	31.75	73.50	48.43	42.89	63.32	51.89	100.00	54.93	35.99
Score	0.75	-0.47	1.50	-0.23	1.50	1.50	0.50	1.50	0.50	1.50	-0.39	1.50
Ion-type	AEAL		y_4		y_6	y_{12}^{+2}	$y_{13}\text{-}H_2O^{+2}$	y_7	$y_{15}\text{-}NH_3^{+2}$	y_{15}^{+2}		y_{10}
Delta ppm	-10.3		3.4		3.2	-8.1	14.0	3.4	22.6	5.0		-7.2



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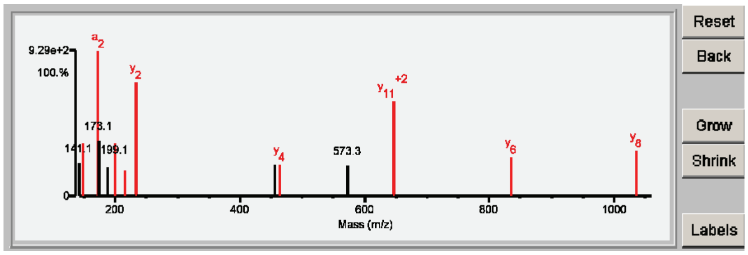
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.93	74.5	6	10/24	K59k	(K)VVGAQSLkEMVSK(L)	1375.7614	114.0662	15.6	53140.3/6.80	HUMAN	P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.93	74.5	6	10/24	K59k	(K) V V|G A Q/S L/k E/M V/S/K (L)	1375.7614	114.0662	15.6	53140.3/6.80	HUMAN	P52209	2667	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3

Fragment-ion (m/z)	70.066	72.081	84.046	84.081	86.096	101.071	120.080	129.088	136.076	141.102	147.111	171.149	173.129	187.139	199.080	199.143	216.127	234.149	455.297	464.250	573.308	646.342^{+2}	835.454	1035.559
Frac. Inten.(% of TIC)	0.09	1.40	0.12	0.68	0.40	0.59	2.50	7.87	5.60	3.22	5.25	14.40	5.48	2.88	3.19	5.28	2.58	11.29	3.18	3.20	3.02	9.39	3.90	4.47
Rel. Inten.(% of BP)	0.63	9.75	0.83	4.75	2.81	4.12	17.36	54.66	38.90	22.38	36.47	100.00	38.04	19.98	22.19	36.68	17.95	78.45	22.10	22.20	20.98	65.26	27.06	31.07
Score	-0.00	0.50 0.50	1.00	0.50	0.22		-0.05	-0.17	-0.12	-0.07	1.50	0.50	-0.12	-0.06	-0.07	0.50	0.50	1.50	-0.07	1.50	-0.06	1.50	1.50	1.50
Ion-type		a_1 V	E	KQ	LI	KQ					y_1	a_2				b_2	y_2-H_2O	y_2		y_4		y_{11}^{+2}	y_6	y_8
Delta ppm		-12.1 3.1	22.7	0.3	-6.1						-10.9	-8.7				-9.0	-33.2	16.9		-7.8		7.8	23.4	8.3



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Result Summary

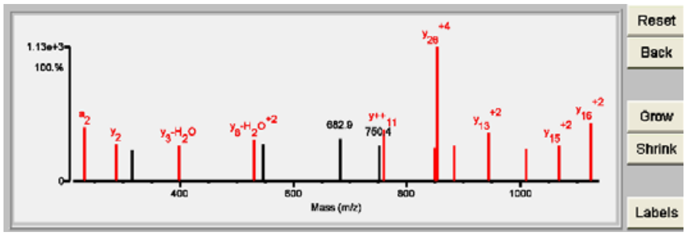
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.48	65.3	8	8/25	K86k	(K)YPIEHGIITNWDDMEkIWHHTFYNELR(V)	3457.6423	114.0651	6.2	42019.2/5.23	HUMAN	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	16.48	65.3	8	8/25	K86k	(K)YPIEHGIITNWDDMEkIWHHTFYNELR(V)	3457.6423	114.0651	6.2	42051.3/5.23	HUMAN	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.48	65.3	8	8/25	K86k	(K) Y/P I E H G I I/T N W/D/D/M/E k/I W H H T F Y N E/L R (V)	3457.6423	114.0651	6.2	42019.2/5.23	HUMAN	P68032	12371	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	16.48	65.3	8	8/25	K86k	(K) Y/P I E H G I I/T N W/D/D/M/E k/I W H H T F Y N E/L R (V)	3457.6423	114.0651	6.2	42051.3/5.23	HUMAN	P68133	12707	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.078	84.082	86.096	104.054	110.071	136.073	147.041	159.091	233.126	288.209	317.197^{+2}
Frac. Inten.(% of TIC)	0.01	3.46	6.45	0.25	4.55	0.14	0.74	4.64	0.24	5.72	4.00	3.39
Rel. Inten.(% of BP)	0.07	24.31	45.32	1.74	32.01	0.95	5.19	32.61	1.68	40.22	28.11	23.85
Score	0.20	-0.24	-0.45	0.22	-0.32	1.00	1.00	-0.33	2.00	0.50	1.50	-0.24
Ion-type	PR			LI		H	a_1		W	a_2	y_2	
Delta ppm	-14.6			-10.8		-0.7	-19.8		-2.4	-11.8	19.4	
							1.00					
							Y					
							-19.8					

Fragment-ion (m/z)	399.225	531.254^{+2}	547.288	682.935^{+5}	750.358^{+3}	758.380	848.655^{+4}	852.892^{+4}	883.723^{+3}	943.968^{+2}	1009.515^{+2}	1066.993^{+2}	1124.505^{+2}
Frac. Inten.(% of TIC)	3.80	4.45	3.90	4.51	3.84	5.49	3.64	14.23	3.81	5.12	3.52	3.84	6.28
Rel. Inten.(% of BP)	26.71	31.30	27.39	31.67	27.02	38.58	25.57	100.00	26.80	35.99	24.73	26.99	44.13
Score	0.50	0.50	-0.27	-0.32	-0.27	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_3-H_2O	y_8-H_2O^{+2}				y^{++}_{11}	y_{26}-NH_3^{+4}	y_{26}^{+4}	y_{19}^{+3}	y_{13}^{+2}	y_{14}^{+2}	y_{15}^{+2}	y_{16}^{+2}
Delta ppm	-24.4	-15.2				1.8	0.7	-21.7	-14.7	-0.4	26.4	-8.3	-9.3



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Result Summary

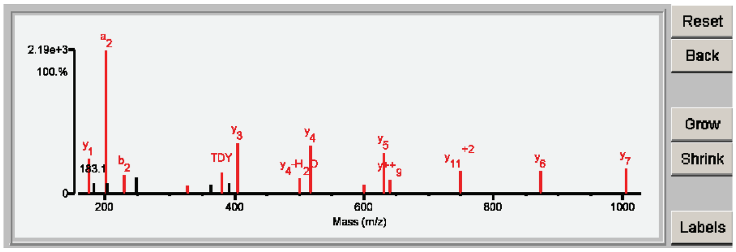
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.27	78.8	8	8/25	K193k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	42009.2/5.24	HUMAN	P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	16.27	78.8	8	8/25	K192k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	42003.4/5.39	HUMAN	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2
1	16.27	78.8	8	8/25	K191k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	41737.0/5.29	HUMAN	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	16.27	78.8	8	8/25	K193k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	42019.2/5.23	HUMAN	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	16.27	78.8	8	8/25	K191k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	41793.1/5.31	HUMAN	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	16.27	78.8	8	8/25	K192k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	41877.1/5.31	HUMAN	P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	16.27	78.8	8	8/25	K193k	(R)DLTDYLMkILTER(G)	1610.8458	114.0545	6.7	42051.3/5.23	HUMAN	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1
2	8.61	68.9	2	12/25	None	(R)LDLAVVRYESKFER(L)	1724.9330	-0.0326	-18.9	42324.7/8.65	HUMAN	RQ8IUS5	REVERSE Abhydrolase domain-containing protein 7 OS=Homo sapiens GN=ABHD7 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.27	78.8	8	8/25	K193k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	42009.2/5.24	HUMAN	P62736	12247	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	16.27	78.8	8	8/25	K192k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	42003.4/5.39	HUMAN	Q562R1	12273	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2
1	16.27	78.8	8	8/25	K191k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	41737.0/5.29	HUMAN	P60709	12305	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	16.27	78.8	8	8/25	K193k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	42019.2/5.23	HUMAN	P68032	12371	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	16.27	78.8	8	8/25	K191k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	41793.1/5.31	HUMAN	P63261	12403	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	16.27	78.8	8	8/25	K192k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	41877.1/5.31	HUMAN	P63267	12441	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	16.27	78.8	8	8/25	K193k	(R) D L|T D/Y L/M/k/I/L/T E/R (G)	1610.8458	114.0545	6.7	42051.3/5.23	HUMAN	P68133	12707	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Fragment-ion (m/z)	72.081	84.079	86.096	129.101	136.074	141.094	175.118	183.119	201.122	202.127	229.120
Frac. Inten.(% of TIC)	1.25	9.07	0.36	0.04	0.31	1.45	5.70	1.76	23.55	1.68	3.06
Rel. Inten.(% of BP)	5.30	38.52	1.53	0.16	1.31	6.17	24.20	7.47	100.00	7.12	13.00
Score	-0.05	-0.39	0.22	0.20	1.00	-0.06	1.50	-0.07	0.50	-0.07	0.50
Ion-type			LI	RKQ	Y		y_1		a_2		b_2
Delta ppm			-8.4	-10.4	-12.4		-8.3		-11.3		4.4

Fragment-ion (m/z)	249.156	328.229	363.190	380.139	391.226	405.208	500.278	518.295	600.334	631.379	640.843	748.887^{+2}	873.519	1004.573
Frac. Inten.(% of TIC)	2.73	1.40	1.47	3.61	1.80	8.31	2.50	7.93	1.51	6.69	2.25	3.77	3.71	4.10
Rel. Inten.(% of BP)	11.59	5.95	6.25	15.32	7.66	35.27	10.63	33.66	6.40	28.41	9.55	16.01	15.74	17.42
Score	-0.12	0.75	-0.06	0.75	-0.08	1.50	0.50	1.50	0.75	1.50	1.50	1.50	1.50	1.50
Ion-type		ILT		TDY		y_3	y_4-H_2O	y_4	MkIL	y_5	y^{++}_9	y_{11}^{+2}	y_6	y_7
Delta ppm		15.3		-20.6		-3.5	-8.6	3.1	-34.6	2.8	-18.7	-7.0	4.8	16.9



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Result Summary

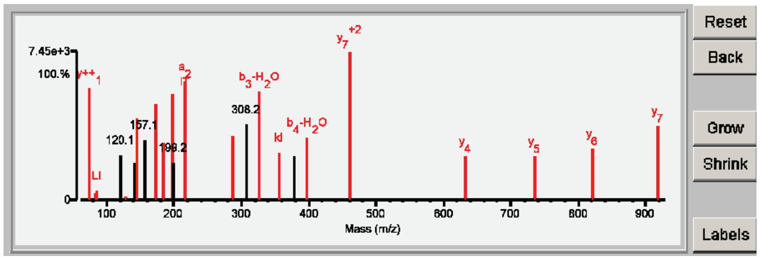
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.37	80.6	5	6/25	K328k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	42009.2/5.24	HUMAN	P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	13.37	80.6	5	6/25	K326k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	41737.0/5.29	HUMAN	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	13.37	80.6	5	6/25	K328k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	42019.2/5.23	HUMAN	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	13.37	80.6	5	6/25	K326k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	41793.1/5.31	HUMAN	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	13.37	80.6	5	6/25	K327k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	41877.1/5.31	HUMAN	P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	13.37	80.6	5	6/25	K328k	(K)EITALAPSTMkIK(I)	1402.7974	114.0493	4.2	42051.3/5.23	HUMAN	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1
2	10.04	70.1	4	8/25	K330k	(K)EITALAPSTMKIk(I)	1402.7974	114.0493	4.2	42009.2/5.24	HUMAN	P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.37	80.6	5	6/25	K328k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	42009.2/5.24	HUMAN	P62736	12247	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	13.37	80.6	5	6/25	K326k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	41737.0/5.29	HUMAN	P60709	12305	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	13.37	80.6	5	6/25	K328k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	42019.2/5.23	HUMAN	P68032	12371	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	13.37	80.6	5	6/25	K326k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	41793.1/5.31	HUMAN	P63261	12403	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	13.37	80.6	5	6/25	K327k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	41877.1/5.31	HUMAN	P63267	12441	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	13.37	80.6	5	6/25	K328k	(K) EITALA/P/S/T/MkI/K (I)	1402.7974	114.0493	4.2	42051.3/5.23	HUMAN	P68133	12707	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Fragment-ion (m/z)	70.065	74.061	84.081	86.096	120.080	129.065	141.101	145.096	157.127	173.091	185.125	197.128
Frac. Inten.(% of TIC)	0.02	7.35	0.48	0.63	2.92	0.20	2.40	5.34	3.91	6.21	3.77	6.88
Rel. Inten.(% of BP)	0.17	75.85	4.95	6.51	30.19	2.09	24.81	55.16	40.32	64.14	38.94	71.05
Score	0.20	1.50	0.50	0.22	-0.30	0.20	-0.25	0.50	-0.40	0.75	0.75	0.50
Ion-type	PR	y^{++}_1	KQ	LI		QKR		TA-28		TA	LA	IT-H_2O
Delta ppm	1.1	11.6	-2.1	-3.8		-5.8		-12.1		-10.2	-24.0	-7.9

Fragment-ion (m/z)	199.181	215.140	286.169	308.159	326.170	356.229	379.195	397.209	459.758^{+2}	633.375	734.423	821.456	918.506
Frac. Inten.(% of TIC)	2.46	7.72	4.19	4.90	7.04	3.07	2.84	4.06	9.69	2.88	2.88	3.33	4.83
Rel. Inten.(% of BP)	25.39	79.64	43.22	50.58	72.67	31.67	29.34	41.95	100.00	29.69	29.69	34.35	49.87
Score	-0.25	0.75	0.75	-0.51	0.25	0.75	-0.29	0.25	1.50	1.50	1.50	1.50	1.50
Ion-type		a_2 IT	TAL		b_3-H_2O	kI		b_4-H_2O	y_7^{+2}	y_4	y_5	y_6	y_7
Delta ppm		-1.9 -1.9	-27.7		-6.3	-2.3		-1.2	1.1	0.4	0.1	0.8	-1.8



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Result Summary

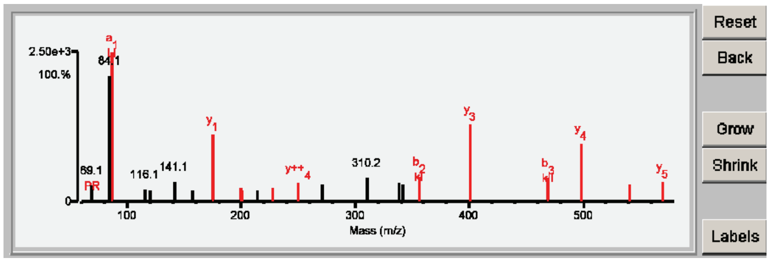
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.50	63.6	6	11/25	K330k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	42009.2/5.24	HUMAN	P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	11.50	63.6	6	11/25	K329k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	42003.4/5.39	HUMAN	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2
1	11.50	63.6	6	11/25	K328k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	41737.0/5.29	HUMAN	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	11.50	63.6	6	11/25	K330k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	42019.2/5.23	HUMAN	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	11.50	63.6	6	11/25	K328k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	41793.1/5.31	HUMAN	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	11.50	63.6	6	11/25	K329k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	41877.1/5.31	HUMAN	P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	11.50	63.6	6	11/25	K330k	(K)IkIIAPPER(K)	1036.6513	114.0526	8.4	42051.3/5.23	HUMAN	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.50	63.6	6	11/25	K330k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	42009.2/5.24	HUMAN	P62736	6124	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
1	11.50	63.6	6	11/25	K329k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	42003.4/5.39	HUMAN	Q562R1	6137	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2
1	11.50	63.6	6	11/25	K328k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	41737.0/5.29	HUMAN	P60709	6153	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	11.50	63.6	6	11/25	K330k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	42019.2/5.23	HUMAN	P68032	6186	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
1	11.50	63.6	6	11/25	K328k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	41793.1/5.31	HUMAN	P63261	6202	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
1	11.50	63.6	6	11/25	K329k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	41877.1/5.31	HUMAN	P63267	6221	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
1	11.50	63.6	6	11/25	K330k	(K) I k\I\I/A/P/P E/R (K)	1036.6513	114.0526	8.4	42051.3/5.23	HUMAN	P68133	6354	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

Fragment-ion (m/z)	69.069	70.065	84.081	86.097	116.068	120.080	129.102	141.101	157.135	175.118	199.104	201.118	214.117
Frac. Inten.(% of TIC)	2.09	0.02	16.16	19.14	1.53	1.47	0.07	2.59	1.44	8.52	1.66	1.42	1.40
Rel. Inten.(% of BP)	10.90	0.11	84.41	100.00	7.99	7.66	0.39	13.55	7.52	44.52	8.66	7.43	7.32
Score	-0.11	0.20	-0.84	0.50	-0.08	-0.08	0.20	-0.14	-0.08	1.50	0.50	1.50	-0.07
Ion-type		PR		a_1			RKQ			y_1	PE-28	y++$_3$	
Delta ppm		-1.8		-9.6			1.2			-7.1	-23.2	37.3	
				0.50									
				LI									
				3.2									

Fragment-ion (m/z)	227.099	249.638	271.138	310.219	338.221	341.192	356.224	401.216	469.315	498.270	540.358	569.316
Frac. Inten.(% of TIC)	1.76	2.42	2.17	3.02	2.34	2.23	3.24	9.92	3.02	7.47	2.28	2.61
Rel. Inten.(% of BP)	9.21	12.62	11.35	15.80	12.24	11.63	16.93	51.82	15.79	39.03	11.93	13.66
Score	0.75	1.50	-0.11	-0.16	-0.12	-0.12	0.75	1.50	0.75	1.50	0.75	1.50
Ion-type	PE	y++$_4$					b_2	y_3	b_3	y_4	kIIA	y_5
Delta ppm	-21.3	2.9					-17.2	3.0	1.7	5.3	12.8	20.6
							kI		kII			
							-17.2		1.7			



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Result Summary

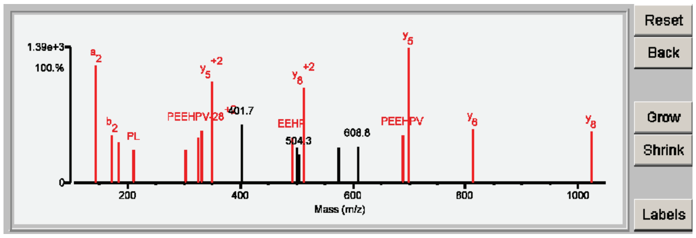
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.67	78.9	4	7/25	K113k	(R)VAPEEHPVLLTEAPLNPkANR(E)	2295.2456	114.0674	10.2	41737.0/5.29	HUMAN	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	13.67	78.9	4	7/25	K113k	(R)VAPEEHPVLLTEAPLNPkANR(E)	2295.2456	114.0674	10.2	41793.1/5.31	HUMAN	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
2	5.89	60.9	1	11/25	K351k	(K)VEDVSAVEIVGGATRIPAVkER(I)	2295.2667	114.0463	1.4	96865.5/5.28	HUMAN	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.67	78.9	4	7/25	K113k	(R) V A\P E E H P V L L T E A/P L/N/P k A N R (E)	2295.2456	114.0674	10.2	41737.0/5.29	HUMAN	P60709	12305	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	13.67	78.9	4	7/25	K113k	(R) V A\P E E H P V L L T E A/P L/N/P k A N R (E)	2295.2456	114.0674	10.2	41793.1/5.31	HUMAN	P63261	12403	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.079	84.080	86.096	102.052	143.116	171.112	183.150	211.145	302.131	325.186	331.169^{+2}
Frac. Inten.(% of TIC)	0.01	0.49	4.65	0.18	0.09	9.77	4.02	3.43	2.75	2.75	3.83	4.33
Rel. Inten.(% of BP)	0.11	4.34	41.42	1.57	0.78	87.08	35.80	30.58	24.48	24.47	34.18	38.55
Score	0.20	0.50 0.50	-0.29	0.22	1.00	0.50	0.50	0.50	0.75	0.75	0.75	0.50
Ion-type	**PR**	**a_1** **V**		**LI**	**E**	**a_2**	**b_2**	**PL**-28	**PL**	**TEA**	**LNP**	**PEEHPV**-28^{+2}
Delta ppm	-3.2	-35.7 -20.5		-10.8	-30.9	-18.8	-9.9	-3.8	-2.8	-16.4	-5.3	0.0

Fragment-ion (m/z)	350.202^{+2}	401.716^{+2}	493.214	500.272	504.274^{+2}	512.293^{+2}	573.279^{+2}	608.804^{+2}	689.340	699.390	813.436	1023.567	1216.629
Frac. Inten.(% of TIC)	8.40	4.89	3.81	2.96	2.37	7.87	2.92	3.02	3.94	11.22	4.44	4.23	3.65
Rel. Inten.(% of BP)	74.86	43.55	33.97	26.40	21.09	70.14	26.02	26.94	35.12	100.00	39.55	37.72	32.55
Score	1.50	-0.30	0.75	-0.18	-0.15	1.50	-0.18	-0.19	0.75	1.50	1.50	1.50	-0.22
Ion-type	y_5^{+2}		**EEHP**			y_8^{+2}			**PEEHPV**	y_5	y_6	y_8	
Delta ppm	10.1		18.0			9.1			19.6	0.4	4.7	-2.8	



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Result Summary

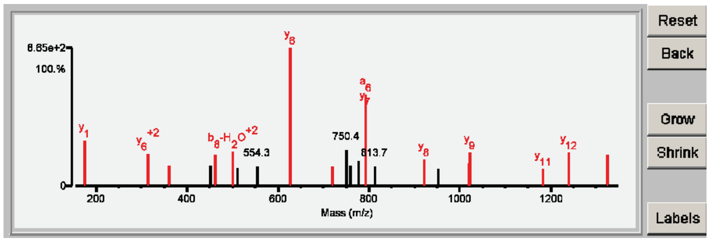
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.04	74.6	11	9/25	K291k	(R)kDLYANTVLSGGTTMYPGIADR(M)	2343.1649	114.0654	9.2	41737.0/5.29	HUMAN	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	17.04	74.6	11	9/25	K291k	(R)kDLYANTVLSGGTTMYPGIADR(M)	2343.1649	114.0654	9.2	41793.1/5.31	HUMAN	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.04	74.6	11	9/25	K291k	(R) k D L Y A N T\V|L/S/G/G T/T/M/Y/P G I/A D/R (M)	2343.1649	114.0654	9.2	41737.0/5.29	HUMAN	P60709	12305	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
1	17.04	74.6	11	9/25	K291k	(R) k D L Y A N T\V|L/S/G/G T/T/M/Y/P G I/A D/R (M)	2343.1649	114.0654	9.2	41793.1/5.31	HUMAN	P63261	12403	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1

Fragment-ion (m/z)	72.079	84.083	86.096	175.117	314.679^{+2}	361.183	452.236	460.737^{+2}	501.267^{+2}	510.894^{+3}	554.273	628.347	719.836^{+2}
Frac. Inten.(% of TIC)	0.14	2.54	0.15	5.83	4.16	2.60	2.69	3.98	4.42	2.38	2.55	17.70	2.43
Rel. Inten.(% of BP)	0.78	14.36	0.82	32.92	23.51	14.71	15.19	22.49	24.97	13.43	14.43	100.00	13.73
Score	0.50	-0.14	0.22	1.50	1.50	1.50	-0.15	0.50	0.25	-0.13	-0.14	1.50	1.50
Ion-type	V		LI	y_1	y_6^{+2}	y_3		b_7^{+2}	$b_8\text{-}H_2O^{+2}$			y_6	y_{14}^{+2}
Delta ppm	-21.9		-1.5	-14.0	13.7	-0.9		20.2	20.3			9.1	-24.3

Fragment-ion (m/z)	750.366	759.396	777.413^{+2}	791.402	813.736	922.440	952.779	1019.522	1023.500	1181.564	1238.583	1325.596
Frac. Inten.(% of TIC)	4.55	2.68	3.25	11.68	2.52	3.43	2.26	2.94	4.39	2.27	4.39	4.06
Rel. Inten.(% of BP)	25.72	15.16	18.34	65.97	14.25	19.40	12.74	16.62	24.77	12.80	24.77	22.96
Score	-0.26	-0.15	-0.18	1.50	-0.14	1.50	-0.13	0.50	1.50	1.50	1.50	1.50
Ion-type				a_6 y_7		y_8		b_8	y_9	y_{11}	y_{12}	y_{13}
Delta ppm				-5.2 -3.8		-5.8		5.0	6.6	1.9	0.0	-14.9



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Result Summary

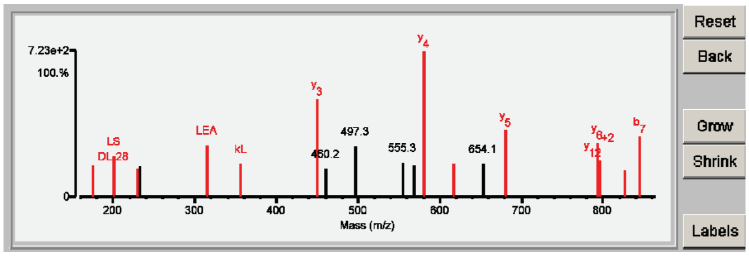
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.06	75.6	8	7/25	K196k K209k	(K)EkGSTLDLSDLEAEkLVMFQR(R)	2409.2330	228.1152	11.1	41522.9/9.07	HUMAN	O00767	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.06	75.6	8	7/25	K196k K209k	(K) E k G S T\L D\L S/D L E A E k/L/V/M/F Q/R (R)	2409.2330	228.1152	11.1	41522.9/9.07	HUMAN	O00767	8933	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2

Fragment-ion (m/z)	70.064	72.079	84.081	86.096	120.078	132.080	175.117	201.128	229.119	233.165	314.168	356.232	450.240
Frac. Inten.(% of TIC)	0.00	0.36	0.40	0.97	0.09	2.76	3.34	4.25	2.93	3.19	5.35	3.50	10.19
Rel. Inten.(% of BP)	0.02	2.37	2.65	6.40	0.58	18.16	21.97	27.97	19.27	20.98	35.21	23.02	67.04
Score	0.20	0.50	0.50	0.22	1.00	-0.18	1.50	0.75	0.75	-0.21	0.75	0.75	1.50
Ion-type	**PR**	**V**	**KQ**	**LI**	**F**		y_1	**LS**	**DL**		**LEA**	**kL**	y_3
Delta ppm	-17.5	-21.9	0.3	-4.9	-23.9		-11.1	19.6 **DL**-28 19.6	-1.7		-13.2	5.5	-13.6

Fragment-ion (m/z)	460.214	497.260	555.255^{+2}	568.198	581.277	617.282	654.134^{+2}	680.375	793.434	796.920^{+2}	827.397	845.399
Frac. Inten.(% of TIC)	2.89	5.27	3.55	3.30	15.20	3.47	3.48	6.97	5.62	3.79	2.79	6.33
Rel. Inten.(% of BP)	18.99	34.66	23.34	21.73	100.00	22.85	22.91	45.83	36.94	24.93	18.38	41.66
Score	-0.19	-0.35	-0.23	-0.22	1.50	0.50	-0.23	1.50	1.50	1.50	0.25	0.50
Ion-type					y_4	b_5		y_5	y_6	y_{12}^{+2}	b_7-H_2O	b_7
Delta ppm					-16.9	-13.3		28.9	-6.6	14.5	7.6	-2.4



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Result Summary

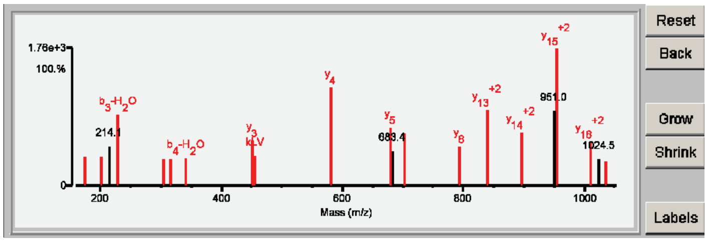
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.65	80.6	11	5/25	K209k	(K)GSTLDLSDLEAEkLVMFQR(R)	2152.0954	114.0589	7.0	41522.9/9.07	HUMAN	O00767	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.65	80.6	11	5/25	K209k	(K) G S T/L/D/L/S D L E A E/k/L/V/M/F/Q/R (R)	2152.0954	114.0589	7.0	41522.9/9.07	HUMAN	O00767	8933	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2

Fragment-ion (m/z)	72.080	74.060	86.096	175.116	201.117	214.118	228.096	229.112	303.178	316.156	341.176	450.241	455.296
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.08 0.63 0.50 V -16.3	3.69 29.88 -0.30	0.22 1.75 0.22 LI -8.4	2.58 20.95 1.50 y_1 -18.0	2.63 21.31 0.75 LS -35.1 DL-28 -35.1	3.57 28.96 -0.29	6.34 51.38 0.25 b_3-H_2O -10.9	2.66 21.58 0.75 DL -30.5	2.38 19.29 1.50 y_2 0.6	2.33 18.86 0.75 SDL 15.8	2.47 20.05 0.25 b_4-H_2O -22.1	4.03 32.63 1.50 y_3 -10.8	2.69 21.79 0.75 kLV -5.1

Fragment-ion (m/z)	581.285	680.354	683.370^{+3}	702.032^{+3}	793.434	840.444^{+2}	896.973^{+2}	950.996^{+2}	954.481^{+2}	1011.024^{+2}	1024.534	1035.575
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	8.76 71.04 1.50 y_4 -2.3	5.19 42.05 1.50 y_5 -0.8	3.07 24.88 -0.25	4.70 38.11 0.50 y_{17}-H_2O^{+3} 3.5	3.50 28.36 1.50 y_6 -6.7	6.79 55.01 1.50 y_{13}^{+2} 22.7	4.82 39.08 1.50 y_{14}^{+2} 7.5	6.66 53.97 -0.54	12.34 100.00 1.50 y_{15}^{+2} 1.0	3.94 31.93 1.50 y_{16}^{+2} 1.3	2.37 19.19 -0.19	2.21 17.93 1.50 y_7 -1.3



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Result Summary

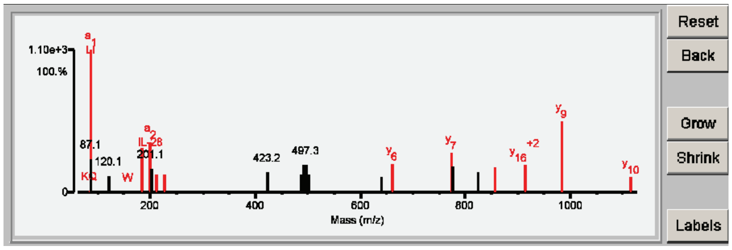
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.98	66.2	6	11/25	K12k	(R)LLLNNGAkMPILGLGTWK(S)	1939.1198	114.0535	5.1	35853.6/6.52	HUMAN	P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.98	66.2	6	11/25	K12k	(R) L L|L/N N G A k/M/P I/L/G L G T W K (S)	1939.1198	114.0535	5.1	35853.6/6.52	HUMAN	P15121	18937	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3

Fragment-ion (m/z)	70.063	84.083	86.095	87.098	120.081	159.088	183.148	199.182	201.120	211.140	227.178	423.194	488.800
Frac. Inten.(% of TIC)	0.00	0.18	19.59	4.53	2.31	0.07	6.05	6.89	3.20	2.40	2.40	2.83	2.40
Rel. Inten.(% of BP)	0.01	0.92	100.00	23.10	11.78	0.35	30.88	35.19	16.32	12.24	12.23	14.42	12.27
Score	0.20	0.50	0.50 0.50	-0.23	-0.12	2.00	0.50	0.50	-0.16	0.75	0.75	-0.14	-0.12
Ion-type	PR	KQ	a_1 LI			W	PI-28	a_2 IL-28		PI	b_2 IL		
Delta ppm	-24.6	30.0	-34.0 -21.2			-25.0	-14.7	1.1 1.1		-24.6	7.5 7.5		

Fragment-ion (m/z)	492.267^{+2}	497.287	501.896^{+3}	640.660	661.355	774.439	776.504^{+2}	824.353	857.487^{+2}	914.009^{+2}	984.588	1115.619
Frac. Inten.(% of TIC)	3.73	3.74	2.51	2.17	3.92	5.45	3.57	2.82	3.46	3.80	9.81	2.17
Rel. Inten.(% of BP)	19.02	19.09	12.82	11.07	20.03	27.84	18.22	14.37	17.68	19.41	50.05	11.08
Score	-0.19	-0.19	-0.13	-0.11	1.50	1.50	-0.18	-0.14	1.50	1.50	1.50	1.50
Ion-type					y_6	y_7			y_{15}^{+2}	y_{16}^{+2}	y_9	y_{10}
Delta ppm					-17.5	-15.7			32.5	9.3	0.2	-8.2



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Result Summary

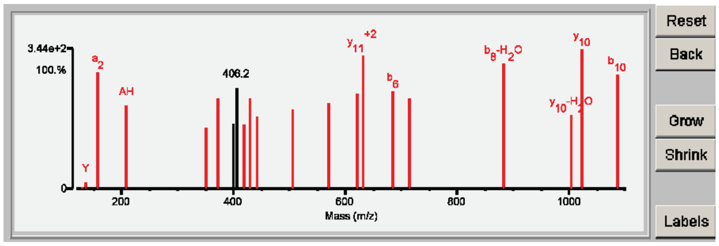
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.24	85.8	8	3/25	K153k	(K)AIAHYEQSADYYkGEESNSSANK(C)	2562.1379	114.0539	4.1	33232.9/5.23	HUMAN	P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3
1	16.24	85.8	8	3/25	K153k	(K)AIAHYEQSADYYkGEESNSSANK(C)	2562.1379	114.0539	4.1	33557.1/5.32	HUMAN	Q9H115	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=2 SV=2
2	7.07	62.6	5	8/25	K163k	(K)AIAHYEQSADYYKGEESNSSANk(C)	2562.1379	114.0539	4.1	33232.9/5.23	HUMAN	P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3
2	7.07	62.6	5	8/25	K163k	(K)AIAHYEQSADYYKGEESNSSANk(C)	2562.1379	114.0539	4.1	33557.1/5.32	HUMAN	Q9H115	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.24	85.8	8	3/25	K153k	(K) AIAHYE\QSAD\Y/Y/k/GEES/N/S/SANK (C)	2562.1379	114.0539	4.1	33232.9/5.23	HUMAN	P54920	361752	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3
1	16.24	85.8	8	3/25	K153k	(K) AIAHYE\QSAD\Y/Y/k/GEES/N/S/SANK (C)	2562.1379	114.0539	4.1	33557.1/5.32	HUMAN	Q9H115	361759	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=2 SV=2

Fragment-ion (m/z)	60.043	84.045	84.080	86.094	129.101	136.076	157.131	209.098	350.135	372.168	400.151^{+2}	406.213^{+2}
Frac. Inten.(% of TIC)	5.41	0.19	0.27	0.16	0.11	0.36	6.14	4.34	3.22	4.77	3.44	5.33
Rel. Inten.(% of BP)	73.75	2.54	3.66	2.18	1.54	4.85	83.71	59.18	43.88	65.09	46.91	72.67
Score	-0.74	1.00	0.50	0.22	0.20	1.00	0.50	0.75	0.75	0.75	-0.47	-0.73
Ion-type		E	KQ	LI	RKQ	Y	a_2	AH	ADY	AHY		
Delta ppm		6.1	-11.6	-27.0	-6.5	5.2	-21.9	-30.6	-1.0	-0.1		

Fragment-ion (m/z)	419.219	429.204	441.716^{+2}	506.252	569.265	620.291	632.787^{+2}	685.321	714.317^{+2}	882.402	1004.424	1022.431	1086.496
Frac. Inten.(% of TIC)	3.37	4.71	3.82	4.17	4.52	4.99	6.99	5.12	4.77	6.59	3.86	7.33	6.03
Rel. Inten.(% of BP)	45.92	64.31	52.16	56.85	61.66	68.12	95.40	69.87	65.01	89.83	52.62	100.00	82.23
Score	1.50	0.75	0.25	1.50	0.75	1.50	1.50	0.50	1.50	0.25	0.50	1.50	0.50
Ion-type	y_4	kGE	$b_8\text{-}H_2O^{+2}$	y_5	YYk	y_6	y_{11}^{+2}	b_6	y_{12}^{+2}	$b_8\text{-}H_2O$	$y_{10}\text{-}H_2O$	y_{10}	b_{10}
Delta ppm	-13.5	-13.8	15.6	-9.1	-14.8	-14.9	-7.2	-15.3	-9.7	-10.7	-3.8	-7.7	9.4



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Result Summary

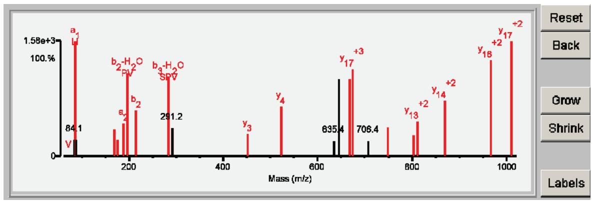
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.23	85.4	8	6/25	K239k	(R)LTSPVINTSLDTkNIAFER(T)	2119.1394	114.0390	-1.8	67619.4/4.94	HUMAN	Q8IZ07	Ankyrin repeat domain-containing protein 13A OS=Homo sapiens GN=ANKRD13A PE=1 SV=3
2	5.92	62.3	4	13/25	None	(R)TLSATSSTGTLSARPPTGTLSAR(S)	2233.1783	0.0001	0.0	59411.9/13.06	HUMAN	RQ9UF83	REVERSE Uncharacterized protein DKFZP434B061 OS=Homo sapiens PE=2 SV=2
3	4.77	54.3	2	13/25	None	(R)TLEPVRPPVVPNDYVPSPTR(N)	2233.1975	-0.0192	-8.6	55663.5/5.82	HUMAN	Q9NYB9	Abl interactor 2 OS=Homo sapiens GN=ABI2 PE=1 SV=1
4	4.41	52.4	2	13/25	None	(K)DVANANANKTLLFEVIEESR(K)	2233.1459	0.0324	14.5	27542.0/8.49	HUMAN	RA7E2S9	REVERSE Putative ankyrin repeat domain-containing protein encoded by NCRNA00164 OS=Homo sapiens GN=NCRNA00164 PE=5 SV=2
5	3.95	58.9	2	15/25	None	(K)TLSEEKLKLTMQLEANKEK(L)	2233.2108	-0.0325	-14.5	158836.1/6.08	HUMAN	RQ9BXX3	REVERSE Ankyrin repeat domain-containing protein 30A OS=Homo sapiens GN=ANKRD30A PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.23	85.4	8	6/25	K239k	(R) L T|S/P V/I/N T S L D T k/N I/A/F E/R (T)	2119.1394	114.0390	-1.8	67619.4/4.94	HUMAN	Q8IZ07	23377	Ankyrin repeat domain-containing protein 13A OS=Homo sapiens GN=ANKRD13A PE=1 SV=3

Fragment-ion (m/z)	70.065	72.080	84.079	86.095	87.097	169.132	175.116	187.143	197.125	215.140	284.159	291.193	451.231
Frac. Inten.(% of TIC)	0.00	0.06	1.42	9.95	1.39	2.36	1.40	2.87	7.17	3.99	6.84	2.39	1.90
Rel. Inten.(% of BP)	0.04	0.62	14.26	100.00	13.92	23.67	14.02	28.87	72.00	40.08	68.71	23.99	19.09
Score	0.20	0.50	-0.14	0.50	-0.14	0.50	1.50	0.50	0.75	0.50	0.75	-0.24	1.50
Ion-type	**PR**	**V**		a_1		**PV**-28	y_1	a_2	$b_2\text{-}H_2O$	b_2	$b_3\text{-}H_2O$		y_3
Delta ppm	-6.1	-6.6		-28.1		-13.2	-16.9	-13.4	-21.6	-2.4	-9.1		3.2
				0.50					**PV**		**SPV**		
				LI					-21.6		-9.1		
				-15.4									

Fragment-ion (m/z)	522.261	635.352^{+3}	644.317^{+3}	667.688^{+3}	673.686^{+3}	706.383^{+2}	749.386	802.904^{+2}	811.904^{+2}	868.440^{+2}	966.509^{+2}	1010.034^{+2}
Frac. Inten.(% of TIC)	4.28	1.35	6.69	6.67	7.50	1.36	2.53	1.84	3.05	4.78	8.31	9.94
Rel. Inten.(% of BP)	43.02	13.55	67.22	66.97	75.34	13.64	25.38	18.44	30.63	48.03	83.46	99.85
Score	1.50	-0.14	-0.67	0.50	1.50	-0.14	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	y_4			$y_{17}\text{-}H_2O^{+3}$	y_{17}^{+3}		y_6	$y_{13}\text{-}H_2O^{+2}$	y_{13}^{+2}	y_{14}^{+2}	y_{16}^{+2}	y_{17}^{+2}
Delta ppm	-12.2			4.4	-3.5		-10.8	-1.0	-7.5	-14.4	-4.2	4.8



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Result Summary

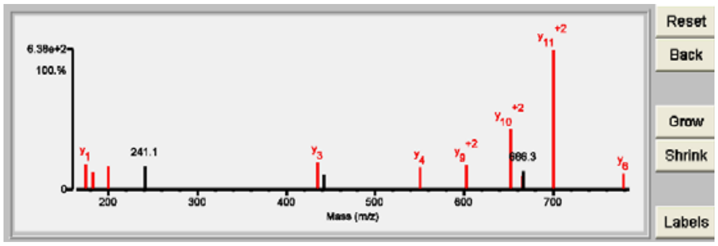
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.19	64.4	9	11/25	K1209k	(K)AQEEPPAkLLDDLFR(K)	1741.9119	114.0707	15.0	151888.2/6.08	HUMAN	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.19	64.4	9	11/25	K1209k	(K) A Q\E E/P/P/A k L/L/D/D/L F/R (K)	1741.9119	114.0707	15.0	151888.2/6.08	HUMAN	Q9UKV3	8007	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.046	84.080	86.099	89.070	90.075	112.079	141.107	175.113	183.073	200.105	241.076
Frac. Inten.(% of TIC)	0.00	0.19	0.20	0.08	4.38	3.04	3.07	2.77	4.47	2.96	4.06	3.98
Rel. Inten.(% of BP)	0.02	0.81	0.84	0.34	18.28	12.70	12.81	11.54	18.65	12.34	16.93	16.62
Score	0.20	1.00	0.50	0.22	-0.18	-0.13	-0.13	-0.12	1.50	0.25	0.50	-0.17
Ion-type	PR	E	KQ	LI					y_1	b_2-NH_3	b_2	
Delta ppm	-11.8	15.6	-11.6	27.6					-32.3	-26.3	2.2	

Fragment-ion (m/z)	435.272	442.246	550.294	602.859^{+2}	651.353^{+2}	665.328	666.329^{+2}	699.886^{+2}	778.414	790.384	849.507	890.529	892.492^{+2}
Frac. Inten.(% of TIC)	4.65	2.63	3.84	4.30	10.38	2.45	3.12	23.98	2.81	3.12	2.26	2.67	4.58
Rel. Inten.(% of BP)	19.38	10.99	16.04	17.93	43.30	10.21	13.01	100.00	11.73	13.01	9.41	11.13	19.09
Score	1.50	-0.11	1.50	1.50	1.50	1.50	-0.13	1.50	1.50	-0.13	-0.09	-0.11	-0.19
Ion-type	y_3		y_4	y_9^{+2}	y_{10}^{+2}	y_5		y_{11}^{+2}	y_6				
Delta ppm	0.8		-7.9	34.9	-17.6	4.5		-6.9	6.3				



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Result Summary

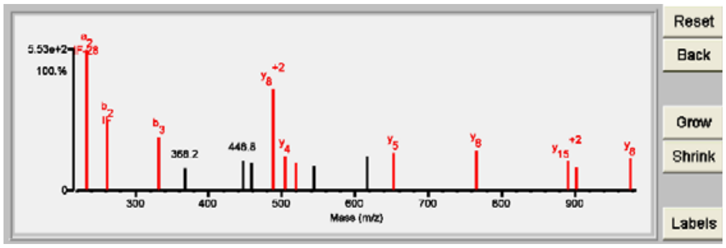
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.81	67.4	7	9/25	K134k	(R)FLAAQkGAYPIIFTAWK(L)	1925.0684	114.0454	1.2	54142.2/5.83	HUMAN	Q6NXE6	Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2
2	6.48	53.1	3	12/25	K1066k	(R)KELTDFLRKLKDAYGk(S)	1925.0855	114.0283	-7.2	138605.0/6.45	HUMAN	Q86Y13	E3 ubiquitin-protein ligase DZIP3 OS=Homo sapiens GN=DZIP3 PE=1 SV=2
3	5.91	54.3	1	11/25	K172k	(R)QLIDYERQLFGKSTVk(M)	1925.0491	114.0647	10.7	22255.1/9.62	HUMAN	O95147	Dual specificity protein phosphatase 14 OS=Homo sapiens GN=DUSP14 PE=1 SV=1
4	5.27	57.9	1	14/25	K117k	(K)ILSESALFADYKKALKk(V)	1925.1106	114.0031	-19.5	24831.5/9.94	HUMAN	RP62906	REVERSE 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2
5	4.18	50.8	2	14/25	K294k	(R)HIRQHMSLTSKQIFAk(G)	1925.0538	114.0600	8.3	98221.8/8.68	HUMAN	RQ5JVG2	REVERSE Zinc finger protein 484 OS=Homo sapiens GN=ZNF484 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.81	67.4	7	9/25	K134k	(R) F L|A\A Q k G A\Y/P I/I/F/T A W K (L)	1925.0684	114.0454	1.2	54142.2/5.83	HUMAN	Q6NXE6	35499	Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2

Fragment-ion (m/z)	70.066	72.081	84.044	86.094	120.078	129.103	136.074	159.082	183.151	233.163	261.161	332.207	368.191
Frac. Inten.(% of TIC)	0.00	3.05	3.44	0.41	0.29	0.08	0.08	4.90	5.62	15.83	7.87	5.98	2.56
Rel. Inten.(% of BP)	0.02	19.25	21.71	2.61	1.86	0.52	0.50	30.98	35.49	100.00	49.72	37.81	16.17
Score	0.20	-0.19	-0.22	0.22	1.00	0.20	1.00	-0.31	-0.35	0.50	0.75	0.50	-0.16
Ion-type	PR			LI	a_1	RKQ	Y			a_2	b_2	b_3	
Delta ppm	9.6			-24.7	-29.8	7.4	-11.7			-14.3	1.7	28.4	
					1.00					IF-28	IF		
					F					-14.3	1.7		
					-20.6								

Fragment-ion (m/z)	446.758^{+2}	459.248	488.284^{+2}	505.275	518.797^{+2}	543.277	616.289	652.337	765.425	889.971^{+2}	901.506	975.558
Frac. Inten.(% of TIC)	3.35	3.14	11.51	3.88	3.24	2.76	3.80	4.21	4.48	3.36	2.62	3.54
Rel. Inten.(% of BP)	21.17	19.86	72.71	24.52	20.48	17.42	23.99	26.63	28.32	21.22	16.55	22.40
Score	-0.21	-0.20	1.50	1.50	0.50	-0.17	-0.24	1.50	1.50	1.50	0.50	1.50
Ion-type			y_8^{+2}	y_4	a_9^{+2}			y_5	y_6	y_{15}^{+2}	b_8	y_8
Delta ppm			-6.4	-3.6	28.0			-12.1	-5.9	-13.5	17.7	-8.5



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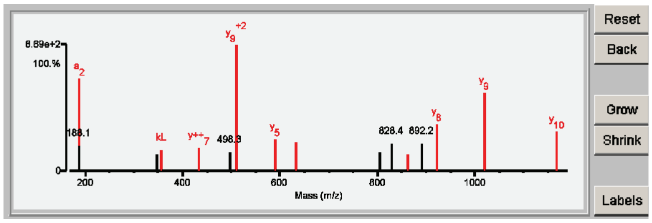
Rank	Score	SPI (%)	BCS	Unmatched Ions	Variable sites	Sequence	Calculated (Da)	Error (Da)	Error (ppm)	MW/pI (Da)	Species	Accession #	Protein Name
1	13.37	72.3	5	9/25	K221k	(R)DVPLHALYDNVEkLFPGFEIETVK(N)	2773.4447	114.0683	8.8	64370.3/6.39	HUMAN	P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4
2	4.22	52.8	1	14/25	K339k	(K)NNGSVGKVQYFKCAPkYGIFAPLSK(I)	2773.4494	114.0636	7.1	76317.0/8.93	HUMAN	Q8N3C7	CAP-Gly domain-containing linker protein 4 OS=Homo sapiens GN=CLIP4 PE=2 SV=1
2	4.22	52.8	1	14/25	K335k	(K)NNGSVGKVQYFkCAPKYGIFAPLSK(I)	2773.4494	114.0636	7.1	76317.0/8.93	HUMAN	Q8N3C7	CAP-Gly domain-containing linker protein 4 OS=Homo sapiens GN=CLIP4 PE=2 SV=1
3	3.85	55.0	1	13/25	None	(K)GKSPQTPELVSALTFREWTCPNLKK(L)	2887.5135	-0.0005	-0.2	120576.7/9.19	HUMAN	Q9NX05	Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=2 SV=2
4	3.56	50.8	2	15/25	M1543m	(K)LPSSVLISGTPNLLSPKSDMPFmRQR(E)	2871.5219	15.9910	-1.3	270211.1/6.67	HUMAN	RO75376	REVERSE Nuclear receptor corepressor 1 OS=Homo sapiens GN=NCOR1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.37	72.3	5	9/25	K221k	(R) D V P L H A L Y D N V E k L|F/P/G/F E/I E T V K (N)	2773.4447	114.0683	8.8	64370.3/6.39	HUMAN	P08243	43793	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4

Fragment-ion (m/z)	70.065	72.080	84.080	86.097	101.064	110.071	120.079	121.083	147.075	187.108	188.112	346.173	356.223
Frac. Inten.(% of TIC)	0.00	0.24	0.08	0.08	2.71	0.07	0.30	3.06	2.97	13.06	3.54	2.35	3.04
Rel. Inten.(% of BP)	0.02	1.36	0.45	0.47	15.18	0.40	1.70	17.11	16.59	73.07	19.78	13.16	17.03
Score	0.20	0.50	0.50	0.22	-0.15	1.00	1.00	-0.17	-0.17	0.50	-0.20	-0.13	0.75
Ion-type	PR	V	KQ	LI		H	F			a_2			kL
Delta ppm	1.1	-9.4	-6.8	10.2		-5.2	-16.5			-2.2			-20.3

Fragment-ion (m/z)	433.239	498.282	510.275^{+2}	589.339	632.335	805.393^{+2}	828.440^{+2}	861.419^{+2}	892.160^{+3}	922.499	1019.548	1166.617
Frac. Inten.(% of TIC)	3.30	2.65	17.88	4.54	4.05	2.64	3.93	2.34	3.86	6.61	11.07	5.61
Rel. Inten.(% of BP)	18.49	14.85	100.00	25.37	22.65	14.78	21.99	13.07	21.58	37.00	61.91	31.39
Score	1.50	-0.15	1.50	1.50	0.75	-0.15	-0.22	0.50	-0.22	1.50	1.50	1.50
Ion-type	$y{+}{+}_7$		y_9^{+2}	y_5	EkLF			b_{14}^{+2}		y_8	y_9	y_{10}
Delta ppm	5.7		1.9	-28.6	-10.0			-32.7		12.1	6.6	6.7



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Result Summary

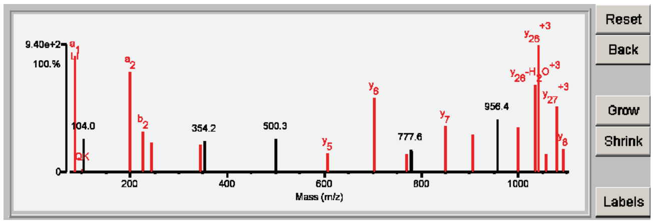
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.98	82.0	11	6/24	K504k	(K)ILQEYVEHQVDDAMMANAAQkFPFNTPK(T)	3235.5551	114.0771	10.2	64370.3/6.39	HUMAN	P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4
2	8.93	63.6	6	11/24	K511k	(K)ILQEYVEHQVDDAMMANAAQKFPFNTPk(T)	3235.5551	114.0771	10.2	64370.3/6.39	HUMAN	P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4
3	5.08	59.4	4	14/24	M1668m K1688k	(R)LLQQDNGmDWLNDTLWVYHPSTSLSSAk(K)	3219.5415	130.0906	15.8	208733.0/4.86	HUMAN	Q9UPS6	Histone-lysine N-methyltransferase SETD1B OS=Homo sapiens GN=SETD1B PE=1 SV=2
4	4.03	58.9	4	14/24	K609k	(R)LLKLDGEPNDNLVYDkCLYCFVYLDR(V)	3235.5802	114.0519	2.7	79198.5/9.37	HUMAN	RQ70CQ1	REVERSE Ubiquitin carboxyl-terminal hydrolase 49 OS=Homo sapiens GN=USP49 PE=2 SV=1
5	3.56	62.2	2	14/24	None	(K)IIHTGEKPYKCEECGKAFIWSSTLTEHK(K)	3349.6344	-0.0022	-0.7	77160.3/9.40	HUMAN	O75437	Zinc finger protein 254 OS=Homo sapiens GN=ZNF254 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.98	82.0	11	6/24	K504k	(K) I/L|Q/E Y V E H Q V/D D A|M M A N A A Q/k/F/P/F N/T/P K (T)	3235.5551	114.0771	10.2	64370.3/6.39	HUMAN	P08243	43793	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4

Fragment-ion (m/z)	84.078	86.095	101.070	104.050	199.179	227.172	244.164	345.203	354.186	500.260	606.324	703.386
Frac. Inten.(% of TIC)	0.13	10.76	0.20	3.12	9.34	3.77	2.77	2.59	2.84	3.05	1.78	6.95
Rel. Inten.(% of BP)	1.11	90.71	1.71	26.28	78.80	31.79	23.39	21.82	23.98	25.71	14.97	58.64
Score		0.50	0.50	-0.26	0.50	0.50	1.50	1.50	-0.24	-0.26	1.50	1.50
Ion-type	QK	a_1	QK		a_2	b_2	y_2	y_3			y_5	y_6
Delta ppm		-34.0 0.50 LI -21.2	-8.3		-14.5	-22.0	-4.8	-30.0			-0.6	11.9

Fragment-ion (m/z)	770.883^{+2}	777.614^{+3}	781.849^{+2}	850.447	905.448	956.445^{+3}	999.152^{+3}	1035.787^{+3}	1041.816^{+3}	1055.993	1079.511^{+3}	1092.615
Frac. Inten.(% of TIC)	1.68	2.06	2.01	4.36	3.52	4.90	4.20	8.15	11.86	1.67	6.13	2.15
Rel. Inten.(% of BP)	14.15	17.38	16.98	36.75	29.71	41.29	35.40	68.70	100.00	14.10	51.68	18.17
Score	0.50	-0.17	-0.17	1.50	1.50	-0.41	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	b_{13}^{+2}			y_7	$y{+}{+}_{15}$		y_{25}^{+3}	$y_{26}\text{-}H_2O^{+3}$	y_{26}^{+3}	$y{+}{+}_{18}$	y_{27}^{+3}	y_8
Delta ppm	19.5			1.9	6.0		23.7	-23.1	1.1	4.9	0.9	28.9



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Result Summary

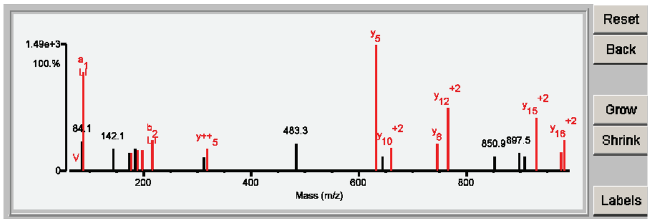
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.15	74.0	8	10/25	K262k	(K)ITSDEPLTkDDIPVFLR(H)	1959.0433	114.0601	8.3	53489.1/5.12	HUMAN	Q9UBB4	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1
2	6.93	57.6	3	14/25	K319k	(K)LFPEDLIDGELVTLkTR(N)	1959.0797	114.0237	-9.3	42052.4/8.16	HUMAN	RP26439	REVERSE 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2 OS=Homo sapiens GN=HSD3B2 PE=1 SV=2
2	6.93	57.6	3	14/25	K169k	(K)LFPEDLIDGELVTLkTR(N)	1959.0797	114.0237	-9.3	24986.9/5.92	HUMAN	RQ6AI10	REVERSE Putative 3-beta-HSD family protein DKFZp686G19280 OS=Homo sapiens PE=5 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.15	74.0	8	10/25	K262k	(K) I/T|S D E/P L/T k/D D/I/P V F L/R (H)	1959.0433	114.0601	8.3	53489.1/5.12	HUMAN	Q9UBB4	62417	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.081	84.080	86.096	142.119	173.123	175.114	183.149	187.149	197.127	215.135
Frac. Inten.(% of TIC)	0.00	0.05	4.00	13.18	2.98	2.39	2.33	2.88	2.87	2.87	4.05
Rel. Inten.(% of BP)	0.01	0.31	23.78	78.43	17.76	14.23	13.84	17.14	17.07	17.07	24.09
Score	0.20	0.50	-0.24	0.50	-0.18	-0.14	1.50	-0.17	0.50	0.75	0.75
Ion-type	PR	V		a_1			y_1		a_2	b_2-H_2O	b_2
Delta ppm	-13.2	0.3		-14.2			-30.0		23.0	-14.0	-25.2
				0.50 LI -1.5					LT-28 23.0	PV -14.0 LT-H_2O -14.0	LT -25.2

Fragment-ion (m/z)	311.113	316.200	483.263	631.397	643.415^{+2}	659.372^{+2}	744.467	764.432^{+2}	850.928^{+2}	897.470	907.993	929.975^{+2}	974.542	980.498^{+2}
Frac. Inten.(% of TIC)	1.85	2.90	3.71	16.81	1.99	3.09	3.68	8.44	1.88	2.44	1.89	7.11	2.50	4.10
Rel. Inten.(% of BP)	10.99	17.27	22.04	100.00	11.85	18.41	21.88	50.18	11.15	14.50	11.26	42.31	14.89	24.41
Score	-0.11	1.50	-0.22	1.50	-0.12	1.50	1.50	1.50	-0.11	-0.14	-0.11	1.50	1.50	1.50
Ion-type		y++$_5$		y_5		y_{10}^{+2}	y_6	y_{12}^{+2}				y_{15}^{+2}	y_8	y_{16}^{+2}
Delta ppm		1.8		6.3		15.3	-12.9	2.2				-6.2	11.6	-7.0



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Result Summary

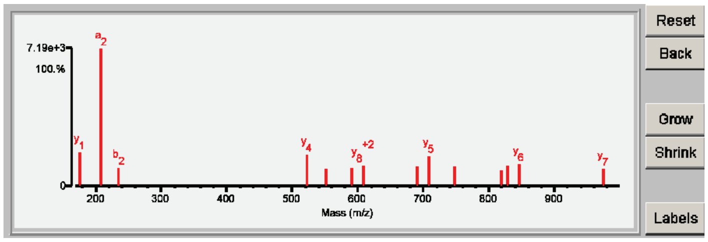
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.10	77.8	10	4/25	K117k	(R)SFICNYkEHWFTVR(K)	1886.9007	114.0543	5.7	43417.8/4.86	HUMAN	P54252	Ataxin-3 OS=Homo sapiens GN=ATXN3 PE=1 SV=3
2	8.88	50.5	4	13/25	M99m M100m	(K)SFLGPLSPSCKMVQmmR(Q)	1968.9526	32.0023	6.3	57915.4/8.35	HUMAN	Q8N8W4	Patatin-like phospholipase domain-containing protein 1 OS=Homo sapiens GN=PNPLA1 PE=2 SV=2
3	7.88	50.5	3	13/25	M96m M100m	(K)SFLGPLSPSCKmVQMmR(Q)	1968.9526	32.0023	6.3	57915.4/8.35	HUMAN	Q8N8W4	Patatin-like phospholipase domain-containing protein 1 OS=Homo sapiens GN=PNPLA1 PE=2 SV=2
3	7.88	50.5	3	13/25	M96m M99m	(K)SFLGPLSPSCKmVQmMR(Q)	1968.9526	32.0023	6.3	57915.4/8.35	HUMAN	Q8N8W4	Patatin-like phospholipase domain-containing protein 1 OS=Homo sapiens GN=PNPLA1 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.10	77.8	10	4/25	K117k	(R) S F|I/C/N/Y/k/E/H/W/F T V/R (K)	1886.9007	114.0543	5.7	43417.8/4.86	HUMAN	P54252	62477	Ataxin-3 OS=Homo sapiens GN=ATXN3 PE=1 SV=3

Fragment-ion (m/z)	60.044	84.080	86.096	87.055	110.069	120.080	131.117	133.040	136.074	159.089	162.089	175.117	207.112
Frac. Inten.(% of TIC)	5.66	11.58	0.79	0.14	0.13	0.46	3.53	3.94	0.16	0.09	3.11	5.67	23.11
Rel. Inten.(% of BP)	24.51	50.12	3.40	0.63	0.57	1.99	15.28	17.07	0.71	0.40	13.45	24.54	100.00
Score	0.50	-0.50	0.22	0.33	1.00	1.00	-0.15	-0.17	1.00	2.00	-0.13	1.50	0.50
Ion-type	a_1		LI	NR	H	F			Y	W		y_1	a_2
Delta ppm	-18.1		-9.6	-3.3	-19.7	-9.0			-9.5	-16.2		-11.7	-10.1

Fragment-ion (m/z)	235.108	522.302	551.933^{+3}	589.620^{+3}	608.818^{+2}	690.343^{+2}	708.387	747.370^{+2}	818.873^{+2}	827.390^{+2}	845.436	974.490
Frac. Inten.(% of TIC)	3.00	5.19	2.79	3.02	3.48	3.24	5.07	3.23	2.74	3.41	3.67	2.79
Rel. Inten.(% of BP)	12.96	22.47	12.06	13.09	15.06	14.02	21.95	13.96	11.84	14.77	15.88	12.09
Score	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	b_2	y_4	y_{11}^{+3}	y_{12}^{+3}	y_8^{+2}	y_9^{+2}	y_5	y_{10}^{+2}	y_{11}-NH_3^{+2}	y_{11}^{+2}	y_6	y_7
Delta ppm	-4.7	-3.6	16.3	0.6	5.7	-4.8	5.7	2.5	4.2	7.7	-6.6	5.4



Result Summary

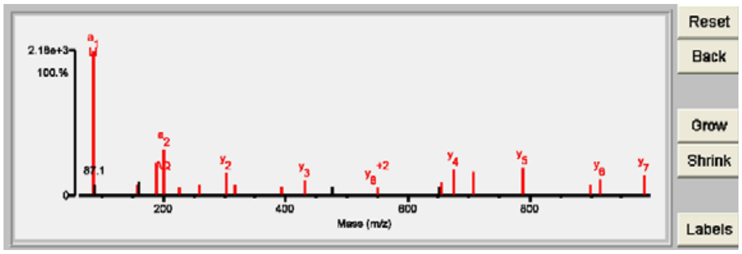
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.91	91.8	8	4/25	K200k	(K)LIGEELAQLkEQR(V)	1526.8537	114.0533	6.3	43417.8/4.86	HUMAN	P54252	Ataxin-3 OS=Homo sapiens GN=ATXN3 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.91	91.8	8	4/25	K200k	(K) L I|G E E/L|A/Q/L/k/E/Q R (V)	1526.8537	114.0533	6.3	43417.8/4.86	HUMAN	P54252	62477	Ataxin-3 OS=Homo sapiens GN=ATXN3 PE=1 SV=3

Fragment-ion (m/z)	70.066	84.080	86.098	87.102	158.089	159.070	187.074	199.182	200.101	227.176	259.089	303.181
Frac. Inten.(% of TIC)	0.00	0.12	28.13	2.00	1.99	2.65	6.38	9.14	2.91	1.57	2.08	4.35
Rel. Inten.(% of BP)	0.01	0.44	100.00	7.11	7.06	9.44	22.69	32.48	10.36	5.57	7.39	15.45
Score	0.20	0.50	0.50 0.50	-0.07	0.50	-0.09	0.75	0.50	0.75	0.50	0.75	1.50
Ion-type	PR	KQ	a_1 LI		y_1-NH$_3$		GE	a_2	AQ	b_2	EE	y_2
Delta ppm	8.2	-11.6	3.2 16.0		-22.2		8.4	4.1	-15.3	-4.4	-16.1	10.1

Fragment-ion (m/z)	316.117	394.228^{+2}	432.207	476.244	550.304^{+2}	650.850^{+2}	655.361	674.348	707.875^{+2}	787.433	898.483	915.505	986.524
Frac. Inten.(% of TIC)	2.11	1.74	3.10	1.76	1.58	1.76	2.41	5.16	4.69	5.31	1.97	3.16	3.94
Rel. Inten.(% of BP)	7.51	6.19	11.01	6.26	5.62	6.26	8.55	18.35	16.68	18.87	7.01	11.23	14.02
Score	0.75	1.50	1.50	-0.06	1.50	-0.06	0.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	GEE	y_5^{+2}	y_3		y_8^{+2}		b_6	y_4	y_{11}^{+2}	y_5	y_6-NH$_3$	y_6	y_7
Delta ppm	5.0	7.9	-29.9		-18.5		-9.9	-15.3	10.6	-11.3	9.9	4.7	-14.3



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Result Summary

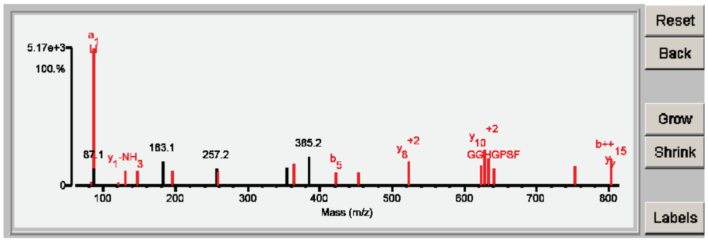
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.38	80.1	7	5/25	K195k	(R)LGGHGPSFPLkGITEQQK(E)	1894.0181	114.0588	7.9	82705.0/5.55	HUMAN	P13010	ATP-dependent DNA helicase 2 subunit 2 OS=Homo sapiens GN=XRCC5 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.38	80.1	7	5/25	K195k	(R) L G G H G\P S F|P L/k/G I/T E\Q Q/K (E)	1894.0181	114.0588	7.9	82705.0/5.55	HUMAN	P13010	347305	ATP-dependent DNA helicase 2 subunit 2 OS=Homo sapiens GN=XRCC5 PE=1 SV=3

Fragment-ion (m/z)	70.065	84.080	86.096	87.054	110.069	120.080	129.101	130.090	147.109	183.149	195.088	257.158
Frac. Inten.(% of TIC)	0.02	0.81	25.96	3.11	0.17	0.46	0.20	2.74	2.74	4.57	2.71	3.24
Rel. Inten.(% of BP)	0.07	3.12	100.00	12.00	0.65	1.78	0.76	10.55	10.54	17.59	10.44	12.48
Score	0.20	0.50	0.50 0.50	-0.12	1.00	1.00	0.20	0.50	1.50	-0.18	0.75	-0.12
Ion-type	**PR**	**KQ**	a_1 **LI**		**H**	**F**	**RKQ**	y_1-NH_3	y_1		**HG**	
Delta ppm	-3.2	-4.5	-17.7 -4.9		-17.0	-9.8	-10.4	30.3	-28.6		-5.9	

Fragment-ion (m/z)	258.147	354.182	363.187^{+2}	385.230	422.212	453.284	523.298^{+2}	622.286	628.353^{+2}	633.321	640.287	753.372	803.427
Frac. Inten.(% of TIC)	2.85	3.47	4.09	5.47	2.52	2.52	4.61	3.78	6.76	5.17	3.32	3.58	5.14
Rel. Inten.(% of BP)	10.98	13.36	15.75	21.09	9.72	9.71	17.78	14.57	26.03	19.91	12.80	13.79	19.81
Score	0.50	-0.13	0.50	-0.21	0.50	0.75	1.50	0.50	1.50	1.50	0.75	0.50	1.50
Ion-type	y_2-NH_3		a_8^{+2}		b_5	**PLk**	y_8^{+2}	**GGHGPSF**-H_2O	y_{10}^{+2}	y_5	**GGHGPSF**	b_8	$b{+}{+}_{15}$ y_7
Delta ppm	9.6		-9.8		-9.8	1.3	23.8	18.8	-1.6	1.4	3.0	4.2	4.6 1.7



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Result Summary

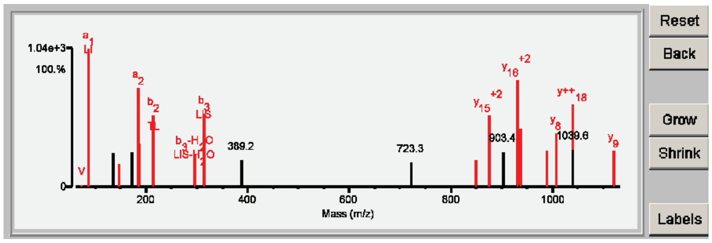
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.37	81.6	9	8/25	K137k	(R)LVTLISQQATLLASNEAFkK(Q)	2175.2383	114.0586	6.8	27991.8/8.44	HUMAN	P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3
2	14.71	79.8	8	9/25	K138k	(R)LVTLISQQATLLASNEAFKk(Q)	2175.2383	114.0586	6.8	27991.8/8.44	HUMAN	P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3
3	5.37	58.4	2	13/25	None	(K)LVLTSRSGIRTGYQAKQVRR(W)	2289.3262	-0.0293	-12.8	273401.0/5.99	HUMAN	P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=2
4	4.65	52.5	3	13/25	None	(R)SILLKTLCKLVDVGSDSLSLK(L)	2289.3098	-0.0128	-5.6	96867.1/8.53	HUMAN	Q8NEN0	Armadillo repeat-containing protein 2 OS=Homo sapiens GN=ARMC2 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.37	81.6	9	8/25	K137k	(R) L V|T|L/I/S Q Q A T L/L/A/S/N E A F k/K (Q)	2175.2383	114.0586	6.8	27991.8/8.44	HUMAN	P51572	64683	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3

Fragment-ion (m/z)	70.065	72.079	86.095	136.072	147.109	173.124	185.165	187.142	213.158	215.137	296.195	314.207	389.170
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.11 1.02 -0.01	0.12 1.05 0.50 V -19.1	11.28 100.00 0.50 a1 -29.3 0.50 LI -16.6	2.74 24.31 -0.24	1.86 16.53 1.50 y1 -26.5	2.88 25.50 -0.26	8.07 71.51 0.50 a2 -5.1	3.49 30.94 0.50 TL-28 -16.6	5.85 51.88 0.50 b2 -13.8	3.80 33.72 0.75 TL -15.4	2.69 23.83 0.50 b3-H2O -11.0 LIS-H2O -11.0	5.94 52.66 0.75 b3 -5.2 LIS -5.2	2.19 19.40 -0.19

Fragment-ion (m/z)	723.326	850.449	875.463^{+2}	903.430^{+2}	903.683^{+2}	931.999^{+2}	937.477	988.521^{+2}	1008.513	1039.074	1039.575	1121.585
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.93 17.13 -0.17	2.18 19.34 1.50 y6 8.5	5.81 51.46 1.50 y15^{+2} 3.3	2.81 24.90 -0.25	2.67 23.64 -0.24	8.78 77.79 1.50 y16^{+2} -3.7	4.80 42.53 1.50 y7 3.4	2.95 26.17 1.50 y17^{+2} -23.4	4.40 38.97 1.50 y8 2.4	6.68 59.22 1.50 y++18 5.3	3.03 26.90 -0.27	2.93 25.95 1.50 y9 -8.4



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Result Summary

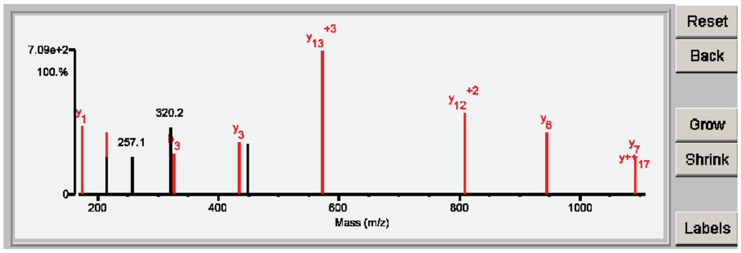
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.62	69.4	8	7/23	K95k	(K)VNLQNNPGAMEHFHMkLFR(A)	2283.1274	114.0650	9.2	27991.8/8.44	HUMAN	P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.62	69.4	8	7/23	K95k	(K) V N|L\Q N N/P/G A M E H/F/H M k/L F/R (A)	2283.1274	114.0650	9.2	27991.8/8.44	HUMAN	P51572	32342	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3

Fragment-ion (m/z)	70.028	70.065	72.081	84.044	84.080	86.097	87.055	104.051	110.071	120.080	156.078
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	7.85 54.49 -0.22	0.02 0.17 0.20 PR -4.6	1.09 7.59 0.50 a_1 -13.5 0.50 V 1.7	0.23 1.58 1.00 E 0.1	0.23 1.63 0.50 KQ -14.0	0.69 4.78 0.22 LI 0.9	0.36 2.51 0.33 NR -2.2	10.58 73.39 -0.29	0.52 3.60 1.00 H -4.3	0.27 1.84 1.00 F -6.5	3.78 26.21 -0.10

Fragment-ion (m/z)	175.119	214.116	215.119	257.134	320.183	327.204	435.276	449.467	572.278^{+3}	809.414^{+2}	945.513	1092.553
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	6.78 47.02 1.50 y_1 -0.9	6.26 43.43 0.50 b_2 -18.8	3.73 25.86 -0.10	3.77 26.17 -0.10	6.68 46.32 -0.18	4.14 28.75 0.50 b_3 -0.2	5.30 36.75 1.50 y_3 10.7	5.09 35.33 -0.14	14.41 100.00 1.50 y_{13}^{+3} -6.2	8.23 57.12 1.50 y_{12}^{+2} 26.7	6.23 43.21 1.50 y_6 4.8	3.75 26.04 1.50 y_7 -22.3 $y{+}{+}_{17}$ 18.0



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Result Summary

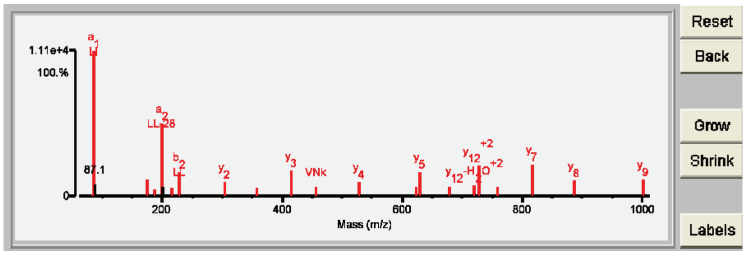
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.06	96.0	12	2/25	K1460k	(R)LIVNkNAGETLLQR(A)	1568.9119	114.0614	11.0	192189.6/6.06	HUMAN	Q6W2J9	BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.06	96.0	12	2/25	K1460k	(R) L I|V/N/k/N/A/G/E/T/L/L/Q/R (A)	1568.9119	114.0614	11.0	192189.6/6.06	HUMAN	Q6W2J9	65703	BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1

Fragment-ion (m/z)	70.066	72.080	84.080	86.096	87.098	175.117	187.145	199.180	200.187	215.141	227.175	303.178
Frac. Inten.(% of TIC)	0.00	0.09	0.30	27.78	2.30	3.22	1.34	13.85	1.71	1.47	4.53	2.75
Rel. Inten.(% of BP)	0.01	0.33	1.07	100.00	8.29	11.60	4.84	49.87	6.15	5.30	16.31	9.89
Score	0.20	0.50	0.50	0.50 0.50	-0.08	1.50	0.50	0.50	-0.06	0.75	0.75	1.50
Ion-type	PR	V	KQ	a_1 LI		y_1	TL-28	a_2 LL-28		TL	b_2 LL	y_2
Delta ppm	9.6	-5.2	-9.2	-2.6 -2.6		-10.6	2.6	-3.5 -3.5		6.9	-1.3 -1.3	0.6

Fragment-ion (m/z)	357.192	416.262	456.261	529.347	622.324	630.396	679.376^{+2}	719.899^{+2}	728.904^{+2}	759.438	816.465	887.495	1001.539
Frac. Inten.(% of TIC)	1.54	4.83	1.68	2.78	1.67	4.57	1.74	2.02	5.85	1.84	6.03	2.98	3.14
Rel. Inten.(% of BP)	5.53	17.39	6.03	10.01	6.00	16.46	6.25	7.26	21.05	6.63	21.69	10.75	11.31
Score	0.75	1.50	0.75	1.50	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	kN	y_3	VNk	y_4	$y{++}_{10}$	y_5	y_{11}^{+2}	$y_{12}\text{-}H_2O^{+2}$	y_{12}^{+2}	y_6	y_7	y_8	y_9
Delta ppm	11.8	0.7	9.8	3.1	-28.1	3.7	19.3	10.2	9.4	3.1	8.7	0.8	1.3



Result Summary

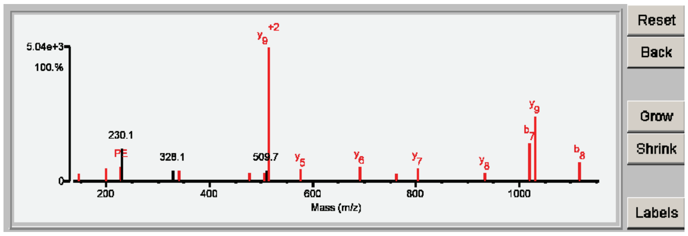
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.07	81.6	9	5/25	K509k	(K)WkALFEEVPELLTEAEK(K)	2032.0637	114.0327	-4.8	64616.2/6.27	HUMAN	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3
2	8.81	60.5	2	12/25	K333k K335k	(R)ATkSkMELSQVTPELQK(A)	1918.0314	228.0651	-9.7	94048.1/7.99	HUMAN	RQ5TYW2	REVERSE Ankyrin repeat domain-containing protein 20A1 OS=Homo sapiens GN=ANKRD20A1 PE=2 SV=1
2	8.81	60.5	2	12/25	K333k K335k	(R)ATkSkMELSQVTPELQK(A)	1918.0314	228.0651	-9.7	94087.1/8.13	HUMAN	RQ5SQ80	REVERSE Ankyrin repeat domain-containing protein 20A2 OS=Homo sapiens GN=ANKRD20A2 PE=2 SV=1
2	8.81	60.5	2	12/25	K333k K335k	(R)ATkSkMELSQVTPELQK(A)	1918.0314	228.0651	-9.7	94108.1/8.13	HUMAN	RQ5VUR7	REVERSE Ankyrin repeat domain-containing protein 20A3 OS=Homo sapiens GN=ANKRD20A3 PE=4 SV=1
2	8.81	60.5	2	12/25	K333k K335k	(R)ATkSkMELSQVTPELQK(A)	1918.0314	228.0651	-9.7	94149.2/8.13	HUMAN	RQ4UJ75	REVERSE Ankyrin repeat domain-containing protein 20A4 OS=Homo sapiens GN=ANKRD20A4 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.07	81.6	9	5/25	K509k	(K) W k A L F\E E\V|P/E/L/L/T/E A E/K (K)	2032.0637	114.0327	-4.8	64616.2/6.27	HUMAN	P31939	538719	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3

Fragment-ion (m/z)	70.062	72.079	84.041	84.077	86.093	102.051	120.078	147.111	199.101	227.096	230.107	328.150
Frac. Inten.(% of TIC)	0.01	0.42	0.06	2.01	4.72	0.10	0.07	1.67	2.89	2.98	6.96	2.43
Rel. Inten.(% of BP)	0.02	1.46	0.21	6.93	16.29	0.34	0.23	5.75	9.95	10.27	24.00	8.38
Score	0.20	0.50		-0.07	-0.16	1.00	1.00	1.50	0.50	0.75	-0.24	-0.08
Ion-type	PR	V	E			E	F	y_1	PE-28	PE		
Delta ppm	-38.9	-30.2				-38.8	-20.6	-11.6	-38.3	-34.5		

Fragment-ion (m/z)	340.179	476.223	506.269^{+2}	509.745	515.269^{+2}	577.273	690.360	760.414	803.439	932.471	1018.484	1029.530	1117.555
Frac. Inten.(% of TIC)	2.28	1.77	1.81	2.25	29.00	2.55	3.22	1.55	2.97	1.81	8.38	14.11	4.00
Rel. Inten.(% of BP)	7.88	6.10	6.24	7.76	100.00	8.78	11.09	5.34	10.23	6.24	28.88	48.66	13.80
Score	0.75	1.50	0.50	-0.08	1.50	1.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50
Ion-type	PEL	y_4	y_9-H_2O^{+2}		y_9^{+2}	y_5	y_6	b_5	y_7	y_8	b_7	y_9	b_8
Delta ppm	-25.0	-26.0	-4.5		-15.5	-16.4	-10.1	-1.8	-15.1	-24.2	-15.9	-15.8	-12.7



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Result Summary

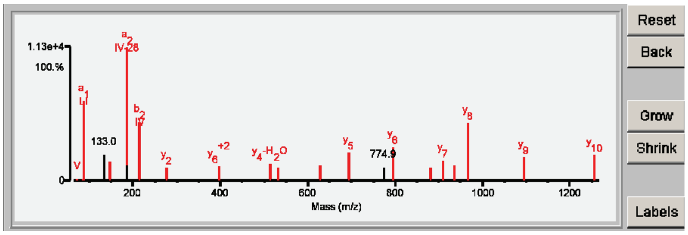
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.35	91.6	10	3/25	K381k K385k	(R)LVASkTDGkIVQYECEGDTCQEEK(I)	2787.2812	228.1150	9.7	67291.0/5.64	HUMAN	Q7Z569	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=1
2	6.51	53.7	1	12/25	M184m	(R)CFNLYTSFESPYGKCLVEIPTSmKK(E)	2999.4351	15.9610	-11.2	47315.4/9.68	HUMAN	RP49674	REVERSE Casein kinase I isoform epsilon OS=Homo sapiens GN=CSNK1E PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.35	91.6	10	3/25	K381k K385k	(R) L V|A S k T D G k I V Q Y E|C/E/G/D/T/C/Q E/E/K (I)	2787.2812	228.1150	9.7	67291.0/5.64	HUMAN	Q7Z569	70829	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=1

Fragment-ion (m/z)	72.080	84.044	84.080	86.097	102.054	133.042	136.076	147.111	185.165	186.168	213.160	276.155	397.672^{+2}
Frac. Inten.(% of TIC)	0.23	0.10	0.19	12.33	0.18	4.06	0.13	2.88	20.83	2.34	9.23	2.09	2.21
Rel. Inten.(% of BP)	1.11	0.49	0.93	59.20	0.84	19.51	0.63	13.84	100.00	11.25	44.32	10.03	10.60
Score	0.50		0.50	0.50	1.00	-0.20	1.00	1.50	0.50	-0.11	0.75	1.50	1.50
Ion-type	V	E	KQ	a_1	E		Y	y_1	a_2		b_2	y_2	y_6^{+2}
Delta ppm	-6.6		-8.0	-10.7	-6.4		1.5	-10.2	-5.6		-4.9	-2.2	2.1
				0.50					IV-28		IV		
				LI					-5.6		-4.9		
				2.0									

Fragment-ion (m/z)	515.263	533.261	628.227	693.292	774.873^{+2}	794.336	880.962^{+2}	909.364	935.083^{+3}	966.385	1095.426	1255.456
Frac. Inten.(% of TIC)	2.55	2.05	2.45	4.44	1.97	5.23	2.14	3.13	2.49	9.07	3.73	3.96
Rel. Inten.(% of BP)	12.22	9.82	11.74	21.32	9.45	25.10	10.26	15.01	11.94	43.55	17.91	19.04
Score	0.50	1.50	1.50	1.50	-0.09	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_4-H_2O	y_4	y^{++}_{10}	y_5		y_6	b_{14}^{+2}	y_7	y_{22}^{+3}	y_8	y_9	y_{10}
Delta ppm	33.6	8.1	-8.0	6.6		1.5	-1.1	2.8	7.3	2.3	0.3	-0.2



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Result Summary

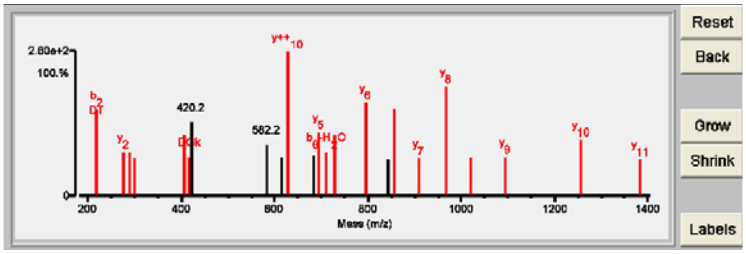
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.31	82.4	12	5/25	K385k	(K)TDGkIVQYECEGDTCQEEK(I)	2288.9646	114.0459	1.2	67291.0/5.64	HUMAN	Q7Z569	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.31	82.4	12	5/25	K385k	(K) T D\G k I V\Q\Y|E/C/E/G/D/T/C Q/E/E K (I)	2288.9646	114.0459	1.2	67291.0/5.64	HUMAN	Q7Z569	70829	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=1

Fragment-ion (m/z)	86.094	136.075	217.081	276.155	290.076	300.164	405.187	415.189	420.197	582.246	615.294	628.241
Frac. Inten.(% of TIC)	0.12	0.10	6.26	3.24	3.24	2.73	4.48	2.86	5.35	3.77	2.82	10.57
Rel. Inten.(% of BP)	1.17	0.98	59.28	30.68	30.64	25.87	42.38	27.10	50.65	35.68	26.67	100.00
Score	0.22	1.00	0.75	1.50	0.75	0.75	1.50	0.75	-0.51	-0.36	-0.27	1.50
Ion-type	LI	Y	b$_2$ DT	y$_2$	CE	Gk	y$_3$	DGk				y++$_{10}$
Delta ppm	-24.7	-8.7	-8.7 -8.7	-0.4	-19.0	-11.4	-26.1	-13.7				14.2

Fragment-ion (m/z)	684.237	693.279	710.397	728.401	794.324	841.428	856.440	909.342	966.377	1019.503	1095.421	1255.453	1384.461
Frac. Inten.(% of TIC)	2.98	4.63	3.25	4.50	6.81	2.69	6.36	2.74	8.03	2.82	2.86	4.13	2.64
Rel. Inten.(% of BP)	28.21	43.84	30.72	42.61	64.47	25.48	60.16	25.94	76.02	26.67	27.10	39.11	24.98
Score	-0.28	1.50	0.25	0.50	1.50	-0.25	0.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type		y$_5$	b$_6$-H$_2$O	b$_6$	y$_6$		b$_7$	y$_7$	y$_8$	b$_8$	y$_9$	y$_{10}$	y$_{11}$
Delta ppm		-11.3	17.8	7.9	-13.8		-16.1	-21.4	-6.7	-13.4	-4.7	-3.0	-27.7



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Result Summary

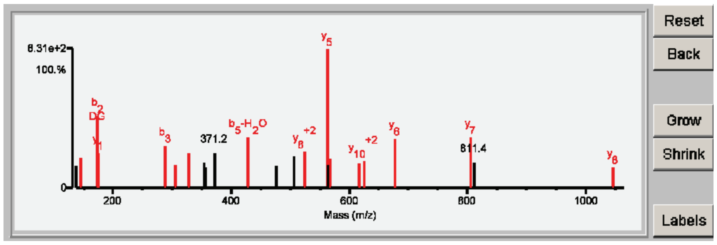
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.41	69.9	9	9/25	K31k	(K)DGDGTITTkELGTVMR(S)	1693.8425	114.0528	5.5	16837.7/4.09	HUMAN	P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.41	69.9	9	9/25	K31k	(K) D G\D\G T I/T T/k/E/L/G T V/M/R (S)	1693.8425	114.0528	5.5	16837.7/4.09	HUMAN	P62158	77191	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2

Fragment-ion (m/z)	84.081	86.095	136.076	145.058	173.055	175.117	288.078	306.156	327.087	353.104	356.164	371.191	428.143
Frac. Inten.(% of TIC)	8.69	0.23	2.33	3.12	7.51	3.65	4.37	2.46	3.69	2.64	2.20	3.70	5.30
Rel. Inten.(% of BP)	59.58	1.54	15.99	21.43	51.52	25.02	29.96	16.87	25.31	18.07	15.08	25.36	36.33
Score	-0.60	0.22	-0.16	0.50	0.75	1.50	0.50	1.50	0.25	-0.18	-0.15	-0.25	0.25
Ion-type		LI		a_2 DG-28	b_2 DG	y_1	b_3	y_2	b_4-H_2O				b_5-H_2O
Delta ppm		-11.9		-26.0 -26.0	-12.6 -12.6	-14.0	-19.2	-10.9	-23.3				0.7

Fragment-ion (m/z)	477.212	506.275^{+2}	524.269^{+2}	563.296	565.284^{+2}	566.288^{+2}	616.318^{+2}	625.339^{+2}	676.377	805.433	811.413	1047.582
Frac. Inten.(% of TIC)	2.27	3.25	3.81	14.58	2.42	3.06	2.54	2.84	5.24	5.29	2.64	2.21
Rel. Inten.(% of BP)	15.56	22.30	26.10	100.00	16.58	20.96	17.39	19.45	35.92	36.27	18.11	15.17
Score	-0.16	-0.22	1.50	1.50	-0.17	0.50	0.50	1.50	1.50	1.50	-0.18	1.50
Ion-type			y_8^{+2}	y_5		y_9-NH_3^{+2}	y_{10}-H_2O^{+2}	y_{10}^{+2}	y_6	y_7		y_8
Delta ppm			-29.2	-1.4		-12.0	-13.6	11.7	-5.6	11.7		19.2



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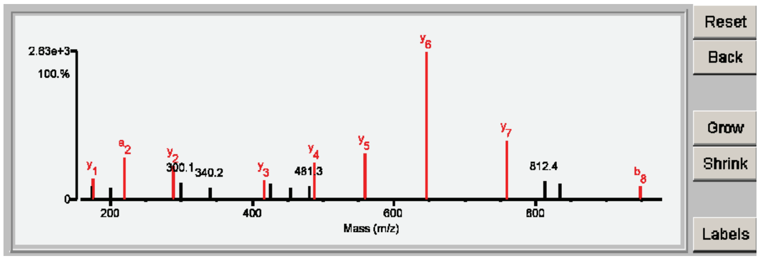
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.06	70.8	8	11/25	K95k	(R)VFDkDGNGYISAAELR(H)	1754.8708	114.0479	2.6	16837.7/4.09	HUMAN	P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.06	70.8	8	11/25	K95k	(R) V F D k D G N G\Y/I/S/A/A/E/L/R (H)	1754.8708	114.0479	2.6	16837.7/4.09	HUMAN	P62158	77191	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2

Fragment-ion (m/z)	70.067	72.081	84.080	86.096	120.081	136.076	173.123	175.117	199.177	219.145	288.203	300.078	340.165	417.245	426.168	454.208	481.288	488.279	559.322	646.356	759.439	812.380^{+2}	834.329	947.417	1111.462
Frac. Inten.(% of TIC)	0.00	0.30	8.59	0.48	0.17	0.22	2.20	3.30	1.89	6.64	5.32	2.77	1.97	3.20	2.51	1.89	2.16	5.98	7.37	23.51	9.38	2.98	2.49	2.11	2.57
Rel. Inten.(% of BP)	0.01	1.27	36.56	2.04	0.73	0.92	9.37	14.02	8.05	28.23	22.64	11.79	8.40	13.59	10.67	8.06	9.19	25.43	31.36	100.00	39.88	12.69	10.57	8.98	10.95
Score	0.20	0.50 0.50	-0.37	0.22	1.00	1.00	-0.09	1.50	-0.08	0.50	1.50	-0.12	-0.08	1.50	-0.11	-0.08	-0.09	1.50	1.50	1.50	1.50	-0.13	-0.11	0.50	-0.11
Ion-type	PR	a_1 V		LI	F	Y		y_1		a_2	y_2			y_3				y_4	y_5	y_6	y_7			b_8	
Delta ppm	28.2	-13.5 1.7		-10.8	1.9	-0.7		-10.6		-23.2	-0.4			-1.9				-7.2	3.3	5.8	4.6			-5.8	



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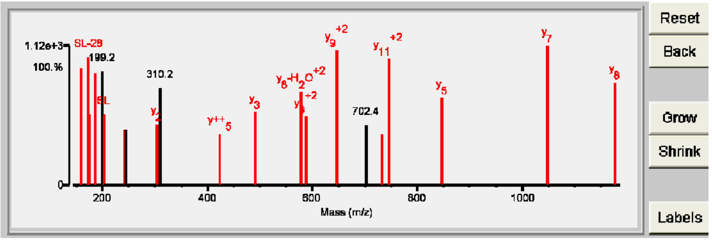
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.92	82.7	10	6/25	K261k	(K)VSILESLDkWER(L)	1474.7900	114.0471	2.6	43210.1/5.27	HUMAN	P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.92	82.7	10	6/25	K261k	(K) V/S\I/L/E/S L/D/k/W/E/R (L)	1474.7900	114.0471	2.6	43210.1/5.27	HUMAN	P10644	333703	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1

Fragment-ion (m/z)	72.080	86.096	87.100	120.079	159.111	173.127	175.117	187.106	199.177	201.123	243.134	244.089	304.161	310.164	424.216	490.239	579.781^{+2}	588.793^{+2}	645.325^{+2}	702.366	732.375	745.384^{+2}	847.409	1047.519	1176.563
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.82 11.89 0.50 a_1 -5.2 0.50 V -5.2	0.81 11.67 0.22 LI -4.9	2.44 35.29 -0.09	3.28 47.59 -0.12	5.82 84.27 0.50 a_2 -11.3	6.32 91.53 0.50 SL-28 -10.7	3.50 50.76 1.50 y_1 -14.0	5.56 80.54 0.50 b_2 -7.0	5.65 81.89 -0.21	3.54 51.23 0.75 SL -3.3	2.73 39.60 0.75 LE 1.1	2.73 39.49 -0.10	3.03 43.84 1.50 y_2 -3.1	4.79 69.43 -0.18	2.58 37.39 1.50 $y{+}{+}_5$ 23.4	3.60 52.15 1.50 y_3 -3.6	4.65 67.42 0.50 y_8-H_2O^{+2} 1.3	3.37 48.79 1.50 y_8^{+2} 11.9	6.67 96.65 1.50 y_9^{+2} -4.6	2.99 43.30 -0.11	2.56 37.08 1.50 y_4 -4.8	6.26 90.69 1.50 y_{11}^{+2} -2.3	4.31 62.42 1.50 y_5 3.9	6.90 100.00 1.50 y_7 -2.8	5.11 74.01 1.50 y_8 -1.0



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Result Summary

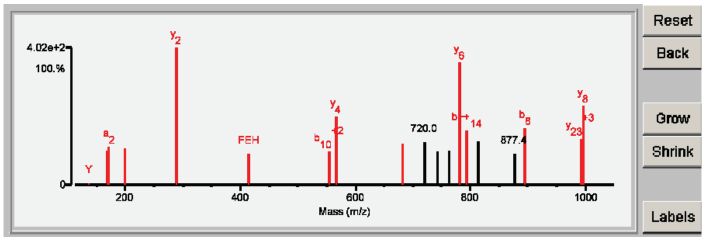
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.26	77.7	10	6/25	K122k	(R)TPALVFEHVNNTDFkQLYQTLTDYDIR(F)	3241.6164	114.0726	8.8	45143.8/7.29	HUMAN	P68400	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.26	77.7	10	6/25	K122k	(R) T P\A L/V F E H\V N\N T D F\k Q L Y Q/T L/T/D/Y D/I R (F)	3241.6164	114.0726	8.8	45143.8/7.29	HUMAN	P68400	128017	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1

Fragment-ion (m/z)	70.063	84.080	86.095	110.067	120.080	136.071	169.096	171.110	199.104	288.202	414.178	554.791^{+2}
Frac. Inten.(% of TIC)	0.01	0.32	0.32	0.11	0.10	0.12	3.42	3.69	3.64	13.46	3.09	3.28
Rel. Inten.(% of BP)	0.04	2.39	2.39	0.81	0.77	0.92	25.40	27.39	27.06	100.00	22.99	24.35
Score	0.20	0.50	0.22	1.00	1.00	1.00	0.75	0.50	0.50	1.50	0.75	0.50
Ion-type	PR	KQ	LI	H	F	Y	PA	a_2	b_2	y_2	FEH	b_{10}^{+2}
Delta ppm	-28.9	-14.0	-15.4	-38.8	-9.0	-38.1	-13.3	-24.0	-22.2	-5.3	-1.2	-5.0

Fragment-ion (m/z)	566.292	681.334	719.977	744.056	762.888^{+2}	782.380	793.406	814.656^{+2}	877.374	895.497	991.814^{+3}	996.501	1287.562
Frac. Inten.(% of TIC)	6.71	4.10	4.19	3.30	3.38	12.04	5.39	4.31	3.03	5.53	4.59	7.75	4.11
Rel. Inten.(% of BP)	49.83	30.47	31.12	24.55	25.12	89.48	40.02	32.04	22.49	41.07	34.13	57.59	30.55
Score	1.50	1.50	-0.31	-0.25	-0.25	1.50	0.50	-0.32	-0.22	0.50	1.50	1.50	-0.31
Ion-type	y_4	y_5				y_6	$b{+}{+}_{14}$			b_8	y_{23}^{+3}	y_8	
Delta ppm	-1.9	19.9				15.6	24.4			32.5	-3.1	1.2	



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Result Summary

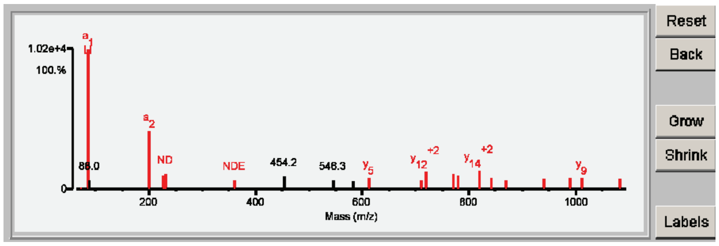
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.73	91.0	12	4/25	K170k	(K)LLNDEDQVVVNkAAVMVHQLSK(K)	2450.3072	114.0674	9.5	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1
2	14.26	75.8	6	10/25	K180k	(K)LLNDEDQVVVNKAAVMVHQLSk(K)	2450.3072	114.0674	9.5	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.73	91.0	12	4/25	K170k	(K) L L|N D E/D Q/V/V/V/N k/A/A/V/M/V/H Q L S K (K)	2450.3072	114.0674	9.5	85497.1/5.53	HUMAN	P35222	130857	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Fragment-ion (m/z)	72.080	84.044	84.080	86.096	88.040	110.070	199.180	227.174	230.075	359.118	454.207	546.282^{+3}
Frac. Inten.(% of TIC)	0.37	0.07	0.23	32.70	2.22	0.06	13.64	3.09	3.59	2.23	2.87	2.03
Rel. Inten.(% of BP)	1.13	0.21	0.71	100.00	6.80	0.19	41.72	9.44	10.97	6.83	8.77	6.21
Score	0.50	1.00	0.50	0.50 0.50	-0.07	1.00	0.50	0.50	0.75	0.75	-0.09	-0.06
Ion-type	V	E	KQ	a_1 LI		H	a_2	b_2	ND	NDE		
Delta ppm	-14.9	1.3	-4.5	-15.4 -2.6		-14.3	-7.5	-9.7	-13.7	-8.5		

Fragment-ion (m/z)	584.213	612.345	711.410	720.398^{+2}	769.932^{+2}	780.048^{+3}	819.460^{+2}	842.458	868.990^{+2}	941.513	990.551^{+2}	1012.567	1083.583
Frac. Inten.(% of TIC)	1.87	2.76	2.17	4.19	3.50	3.24	4.25	2.76	2.02	2.34	2.62	2.72	2.45
Rel. Inten.(% of BP)	5.72	8.44	6.63	12.82	10.71	9.92	13.01	8.44	6.17	7.16	8.00	8.32	7.50
Score	-0.06	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type		y_5	y_6	y_{12}^{+2}	y_{13}^{+2}	y_{20}^{+3}	y_{14}^{+2}	y_7	y_{15}^{+2}	y_8	y_{17}^{+2}	y_9	y_{10}
Delta ppm		-2.4	-7.3	6.4	6.3	-22.2	-1.9	3.5	-6.5	-10.9	12.4	6.4	-14.1



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Result Summary

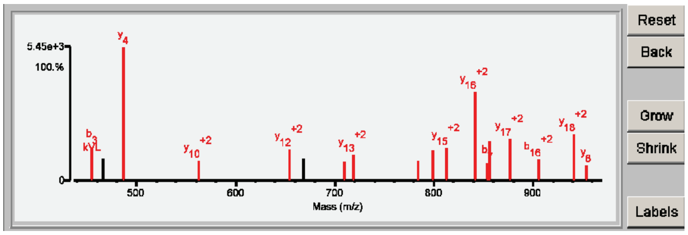
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.20	91.8	14	3/25	K345k	(R)VLkVLSVCSSNKPAIVEAGGMQALGLHLTDPSQR(L)	3575.9036	114.0898	12.7	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1
2	18.57	85.2	12	5/25	K354k	(R)VLKVLSVCSSNkPAIVEAGGMQALGLHLTDPSQR(L)	3575.9036	114.0898	12.7	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.20	91.8	14	3/25	K345k	(R) V L k\V L S V\C S S N K P A\I\V|E/A/G/G/M/Q/A L/G L/H L T D/P S Q R (L)	3575.9036	114.0898	12.7	85497.1/5.53	HUMAN	P35222	130857	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.044	84.080	86.095	102.053	104.052	455.292	466.326	487.261	562.300^{+2}	654.357^{+2}	668.095^{+4}
Frac. Inten.(% of TIC)	0.00	0.37	0.07	0.17	0.24	0.08	2.65	4.89	3.23	19.48	2.94	4.55	3.32
Rel. Inten.(% of BP)	0.01	1.92	0.38	0.89	1.23	0.39	13.59	25.09	16.60	100.00	15.09	23.35	17.05
Score	0.20	0.50		0.50	0.22	1.00	-0.14	0.75	-0.17	1.50	1.50	1.50	-0.17
Ion-type	PR	a_1	E	KQ	LI	E		b_3		y_4	y_{10}^{+2}	y_{12}^{+2}	
Delta ppm	-4.6	-21.8 0.50 V -6.6		-4.5	-11.9	-19.2		-13.9 kVL -13.9		-2.1	7.2	0.7	

Fragment-ion (m/z)	709.878^{+2}	718.395^{+2}	783.920^{+2}	799.434^{+2}	812.420^{+2}	840.923^{+2}	853.558	855.983^{+2}	876.443^{+2}	905.518^{+2}	940.971^{+2}	953.480
Frac. Inten.(% of TIC)	2.76	3.78	2.88	4.37	4.73	12.91	2.50	5.73	6.05	3.14	6.81	2.33
Rel. Inten.(% of BP)	14.18	19.42	14.79	22.45	24.27	66.25	12.83	29.42	31.05	16.10	34.96	11.95
Score	0.50	1.50	1.50	0.50	1.50	1.50	0.50	0.50	1.50	0.50	1.50	1.50
Ion-type	$y_{13}\text{-}NH_3^{+2}$	y_{13}^{+2}	y_{14}^{+2}	b_{14}^{+2}	y_{15}^{+2}	y_{16}^{+2}	b_7	b_{15}^{+2}	y_{17}^{+2}	b_{16}^{+2}	y_{18}^{+2}	y_8
Delta ppm	6.4	12.5	17.5	-8.3	4.0	-5.3	7.9	0.3	-3.4	0.7	3.6	0.4



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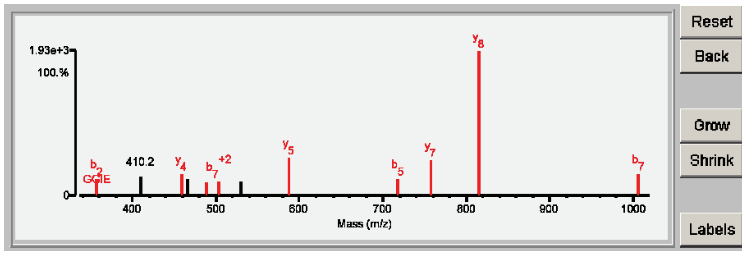
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.37	64.8	9	11/25	K435k	(K)NkMMVCQVGGIEALVR(T)	1804.9230	114.0710	14.6	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.37	64.8	9	11/25	K435k	(K) N k\M\M V\C Q\V/G/G I/E/A L V/R (T)	1804.9230	114.0710	14.6	85497.1/5.53	HUMAN	P35222	130857	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.080	86.096	104.050	133.045	136.075	141.100	159.091	175.116	187.144	215.145	237.119	357.184	410.223	458.296	466.710^{+2}	488.222	503.730^{+2}	530.277^{+2}	587.344	718.339	757.451	814.472	1006.444
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -0.4	0.59 2.19 0.50 V -14.9	0.22 0.83 0.50 KQ -12.8	0.44 1.62 0.22 LI -9.6	2.88 10.62 -0.11	2.76 10.17 -0.10	3.98 14.67 -0.15	2.93 10.79 -0.11	3.75 13.84 -0.14	3.14 11.59 1.50 y_1 -16.9	3.80 14.01 -0.14	2.86 10.56 -0.11	2.91 10.72 -0.11	3.16 11.64 0.75 b_2 -14.3 GGIE 17.2	3.62 13.34 -0.13	4.04 14.90 1.50 y_4 -26.5	3.16 11.65 -0.12	2.46 9.07 0.50 b_3 -16.1	2.73 10.06 0.50 b_7^{+2} 25.2	2.56 9.45 -0.09	7.01 25.84 1.50 y_5 -12.3	3.14 11.57 0.50 b_5 0.3	6.65 24.53 1.50 y_7 -7.9	27.12 100.00 1.50 y_8 -8.0	4.09 15.07 0.50 b_7 15.9



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Result Summary

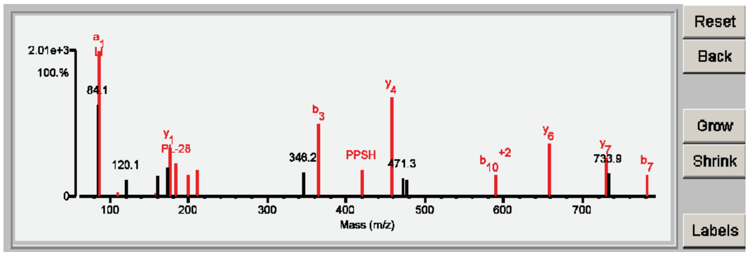
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.75	72.0	7	8/25	K508k	(K)LLHPPSHWPLIkATVGLIR(N)	2148.2804	114.0653	9.9	85497.1/5.53	HUMAN	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.75	72.0	7	8/25	K508k	(K) L L H\P P S H\W P L\I k/A/T V/G L I/R (N)	2148.2804	114.0653	9.9	85497.1/5.53	HUMAN	P35222	130857	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.079	84.079	86.095	110.070	120.080	129.100	159.089	160.091	173.128	175.118	183.146	199.183
Frac. Inten.(% of TIC)	0.01	0.13	10.69	16.95	0.45	1.99	0.06	0.36	2.38	3.34	5.67	3.83	2.48
Rel. Inten.(% of BP)	0.05	0.74	63.08	100.00	2.68	11.76	0.35	2.13	14.07	19.72	33.48	22.60	14.64
Score	0.20	0.50	-0.63	0.50 0.50	1.00	-0.12	0.20	2.00	-0.14	-0.20	1.50	0.50	0.50
Ion-type	PR	V		a_1 LI	H		RKQ	W			y_1	PL-28	a_2
Delta ppm	-14.6	-23.2		-25.8 -13.1	-8.8		-15.0	-14.3			-3.2	-26.1	9.1

Fragment-ion (m/z)	211.139	346.228	364.233	419.207	458.308	471.268	476.745^{+2}	589.822^{+2}	658.423	729.464	733.906^{+2}	782.432
Frac. Inten.(% of TIC)	3.14	2.77	8.51	3.12	11.45	2.17	1.97	2.57	6.13	4.59	2.63	2.58
Rel. Inten.(% of BP)	18.54	16.35	50.22	18.41	67.55	12.82	11.63	15.14	36.18	27.06	15.51	15.22
Score	0.75	-0.16	0.50	0.75	1.50	-0.13	-0.12	0.50	1.50	1.50	-0.16	0.50
Ion-type	PL		b_3	PPSH	y_4			b_{10}^{+2}	y_6	y_7		b_7
Delta ppm	-29.8		-8.0	4.0	-1.2			-10.3	-2.3	2.5		0.5



Result Summary

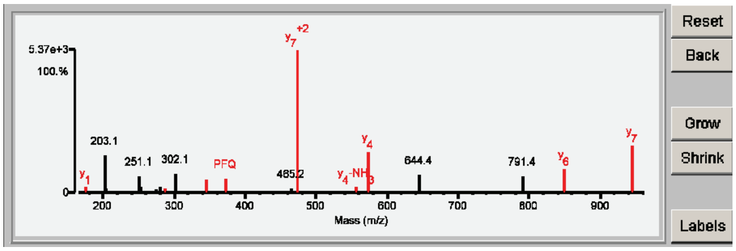
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.33	65.2	4	13/25	K220k	(K)DYPFQGkVR(A)	1109.5738	114.0569	11.4	42099.3/7.16	HUMAN	P56202	Cathepsin W OS=Homo sapiens GN=CTSW PE=1 SV=1
2	6.22	54.2	2	16/25	M353m	(R)mNKNFERLR(S)	1207.6364	15.9943	-0.5	161737.3/8.78	HUMAN	Q5JU85	IQ motif and SEC7 domain-containing protein 2 OS=Homo sapiens GN=IQSEC2 PE=2 SV=1
3	5.71	61.4	1	15/25	None	(K)FLPRVGYTDR(G)	1223.6531	-0.0224	-18.3	64370.3/6.40	HUMAN	RP08243	REVERSE Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4
4	3.66	52.3	1	18/25	None	(K)KPFDYQALNK(Y)	1223.6419	-0.0112	-9.1	479394.8/5.01	HUMAN	Q9NYQ8	Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=1
5	3.39	50.1	2	20/25	M214m	(R)mLDGVLIFDGK(T)	1207.6391	15.9916	-2.7	126968.6/5.14	HUMAN	RQ16531	REVERSE DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.33	65.2	4	13/25	K220k	(K) D Y/P/F Q/G k V/R (A)	1109.5738	114.0569	11.4	42099.3/7.16	HUMAN	P56202	81077	Cathepsin W OS=Homo sapiens GN=CTSW PE=1 SV=1

Fragment-ion (m/z)	70.065	71.070	120.080	127.085	155.081	158.095	175.122	203.117	204.119	251.120	252.126	274.161
Frac. Inten.(% of TIC)	0.01	0.89	0.11	1.60	4.13	0.72	1.20	8.14	1.03	3.51	1.17	0.75
Rel. Inten.(% of BP)	0.02	2.88	0.35	5.15	13.32	2.31	3.86	26.27	3.32	11.34	3.78	2.40
Score	0.20	-0.03	1.00	-0.05	-0.13	0.50	1.50	-0.26	-0.03	-0.11	-0.04	-0.02
Ion-type	PR		F			y_1-NH$_3$	y_1					
Delta ppm	-1.8		-6.5			15.8	17.4					

Fragment-ion (m/z)	279.117	287.171	302.147	345.189	373.183	465.244	473.262^{+2}	556.304	573.335	644.375	791.437	848.463	945.516
Frac. Inten.(% of TIC)	1.09	0.92	4.15	2.86	2.94	0.82	30.99	1.07	8.97	3.84	3.67	5.17	10.26
Rel. Inten.(% of BP)	3.50	2.98	13.38	9.24	9.49	2.63	100.00	3.45	28.94	12.37	11.84	16.69	33.10
Score	-0.04	1.50	-0.13	0.50	0.75	-0.03	1.50	0.50	1.50	-0.12	-0.12	1.50	1.50
Ion-type		y^{++}_4		PFQ-28	PFQ		y_7^{+2}	y_4-NH$_3$	y_4			y_6	y_7
Delta ppm		-19.8		-12.8	-14.3		-9.5	-28.3	-20.3			-12.9	-11.2



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Result Summary

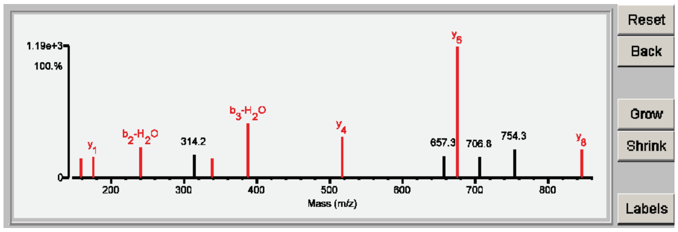
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.78	69.5	4	6/24	K166k	(R)EQFYHSCkQYGITGENVR(G)	2216.0189	114.0668	10.3	56921.0/4.68	HUMAN	Q96JB5	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2
2	6.66	54.2	2	12/24	None	(R)LAGGESSSNESGRRIGPSPCPSK(A)	2330.1153	-0.0296	-12.7	128109.8/6.02	HUMAN	RO15068	REVERSE Guanine nucleotide exchange factor DBS OS=Homo sapiens GN=MCF2L PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.78	69.5	4	6/24	K166k	(R) E Q F Y H S C k Q Y/G I/T G/E N V/R (G)	2216.0189	114.0668	10.3	56921.0/4.68	HUMAN	Q96JB5	102879	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2

Fragment-ion (m/z)	72.080	74.060	84.043	84.079	86.095	87.053	87.095	102.053	110.071	120.081	129.066	136.073
Frac. Inten.(% of TIC)	0.15	8.39	0.33	0.46	1.00	0.16	4.14	0.29	0.21	0.25	0.30	0.47
Rel. Inten.(% of BP)	0.59	33.72	1.32	1.85	4.04	0.65	16.62	1.15	0.83	0.99	1.20	1.89
Score	0.50	-0.34	1.00	0.50	0.22	0.33	-0.17	1.00	1.00	1.00	0.20	1.00
Ion-type	V		E	KQ	LI	NR		a_1	H	F	QKR	Y
Delta ppm	-6.6		-11.8	-19.9	-11.9	-30.9		-32.8 E	1.1	-1.5	2.7	-19.8

Fragment-ion (m/z)	159.073	175.117	240.099	314.171	338.172^{+2}	387.163	517.273	657.299	675.338	706.787^{+2}	754.339	845.428
Frac. Inten.(% of TIC)	3.82	3.95	5.82	4.41	3.76	10.37	7.77	4.21	24.88	3.93	5.41	5.52
Rel. Inten.(% of BP)	15.37	15.88	23.40	17.72	15.09	41.67	31.23	16.94	100.00	15.77	21.75	22.19
Score	0.75	1.50	0.25	-0.18	1.50	0.25	1.50	-0.17	1.50	-0.16	-0.22	1.50
Ion-type	TG	y_1	b_2-H_2O		y_6^{+2}	b_3-H_2O	y_4		y_6			y_8
Delta ppm	-25.9	-9.4	-0.3		-7.0	-11.9	1.0		-6.0			-23.2



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Result Summary

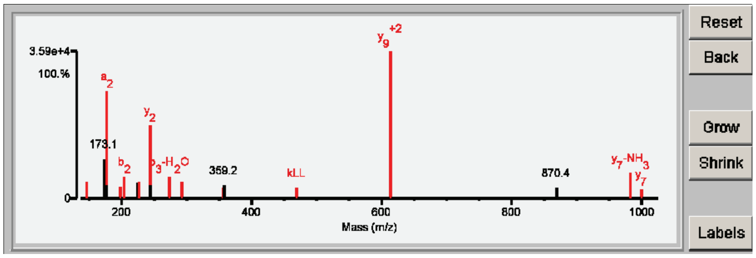
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.07	80.8	7	7/25	K103k	(R)GFSIPECQkLLPK(A)	1516.8192	114.0557	7.9	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2
2	7.06	62.6	4	11/25	K107k	(R)GFSIPECQKLLPk(A)	1516.8192	114.0557	7.9	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.07	80.8	7	7/25	K103k	(R) G F\S\I/P E/C Q k L/L/P/K (A)	1516.8192	114.0557	7.9	51712.7/8.45	HUMAN	O75390	101769	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Fragment-ion (m/z)	70.065	84.080	86.096	120.080	121.084	129.102	147.111	173.128	177.102	178.104	199.108	205.096
Frac. Inten.(% of TIC)	0.01	0.18	0.22	0.66	1.99	0.10	2.67	6.36	17.42	2.13	1.85	3.50
Rel. Inten.(% of BP)	0.04	0.73	0.90	2.75	8.30	0.43	11.13	26.57	72.75	8.89	7.74	14.63
Score	0.20	0.50	0.22	1.00	-0.08	0.20	1.50	-0.27	0.50	-0.09	0.50	0.50
Ion-type	**PR**	**KQ**	**LI**	**F**		**RKQ**	**y_1**		**a_2**		**PE**-28	**b_2**
Delta ppm	-3.2	-8.0	-10.8	-6.5		-5.0	-10.9		-9.8		-3.1	-8.5

Fragment-ion (m/z)	226.155	227.105	244.166	245.168	274.120	292.130	357.249	359.209	469.314	613.834^{+2}	870.418	983.505	1000.563
Frac. Inten.(% of TIC)	2.57	2.67	12.01	2.17	3.55	2.77	1.77	2.19	1.80	23.95	1.80	4.12	1.55
Rel. Inten.(% of BP)	10.73	11.15	50.15	9.07	14.82	11.58	7.38	9.14	7.51	100.00	7.50	17.18	6.49
Score	-0.11	0.75	1.50	-0.09	0.25	0.50	1.50	-0.09	0.75	1.50	-0.07	0.50	1.50
Ion-type		**PE**	**y_2**		**b_3**-H_2O	**b_3**	**y_3**		**kLL**	**y_9**$^{+2}$		**y_7**-NH_3	**y_7**
Delta ppm		4.3	0.1		0.7	-0.3	-0.9		-0.6	4.0		-29.5	1.9



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Result Summary

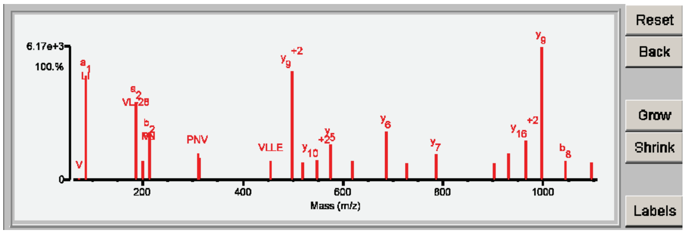
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.20	100.0	9	0/25	K382k	(K)LVAQLYkIVPNVLLEQGK(A)	2025.2107	114.0701	12.7	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2
2	9.17	62.1	4	10/25	K393k	(K)LVAQLYKIVPNVLLEQGk(A)	2025.2107	114.0701	12.7	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2
3	5.74	62.8	4	14/25	K261k K264k	(K)VIkISkDLDLVVGTAAIR(F)	1911.1637	228.1170	14.6	145808.0/6.04	HUMAN	RQ14692	REVERSE Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1
4	3.11	55.9	0	14/25	K1424k	(R)ENIIkVLSIQLNITKGNK(L)	2025.2067	114.0741	14.6	170545.1/7.01	HUMAN	RQ14146	REVERSE Unhealthy ribosome biogenesis protein 2 homolog OS=Homo sapiens GN=URB2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.20	100.0	9	0/25	K382k	(K) L V|A Q L Y/k\I|V/P/N/V/L/L E Q G K (A)	2025.2107	114.0701	12.7	51712.7/8.45	HUMAN	O75390	101769	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Fragment-ion (m/z)	70.064	72.080	84.079	86.096	185.164	200.103	212.102	213.158	311.171	313.188	455.298	499.290^{+2}
Frac. Inten.(% of TIC)	0.00	0.16	0.12	11.70	8.75	2.16	3.37	4.88	3.06	2.53	2.11	12.20
Rel. Inten.(% of BP)	0.02	1.10	0.83	78.16	58.48	14.40	22.51	32.60	20.46	16.93	14.10	81.49
Score	0.20	0.50	0.50	0.50	0.50	0.75	0.75	0.75	0.75	0.75	0.75	1.50
Ion-type	**PR**	**V**	**KQ**	a_1	a_2	**AQ**	**PN**	b_2	**PNV**	**AQL**	**VLLE**	y_9^{+2}
Delta ppm	-8.9	-5.2	-15.2	-16.5 0.50 **LI** -3.8	-12.1 **VL**-28 -12.1	-7.3	-11.2	-15.7 **VL** -15.7	-3.8	-0.4	23.5	4.7

Fragment-ion (m/z)	519.296	548.828^{+2}	574.323	618.358	687.411	726.443^{+2}	786.471	900.513	930.546	964.053^{+2}	997.570	1043.636	1096.630
Frac. Inten.(% of TIC)	1.97	2.24	4.09	2.17	5.44	1.88	2.85	1.89	2.96	4.48	14.97	2.09	1.93
Rel. Inten.(% of BP)	13.13	14.99	27.32	14.48	36.33	12.53	19.05	12.63	19.75	29.92	100.00	13.99	12.87
Score	0.75	1.50	1.50	0.75	1.50	1.50	1.50	1.50	0.50	1.50	1.50	0.50	1.50
Ion-type	**YkI**	y_{10}^{+2}	y_5	**YkIV**	y_6	y_{12}^{+2}	y_7	y_8	b_7	y_{16}^{+2}	y_9	b_8	y_{10}
Delta ppm	4.9	12.1	6.4	-6.7	10.7	14.2	-0.6	-2.7	4.8	-0.7	2.5	9.7	-5.8



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Result Summary

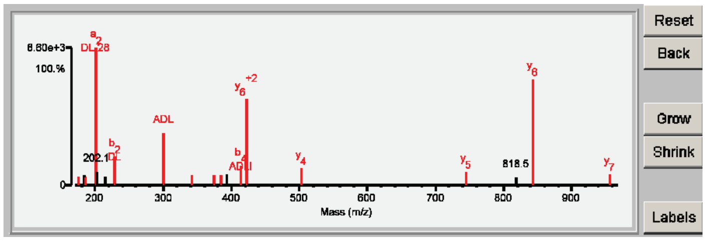
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.56	86.2	9	8/25	K43k	(K)DILADLIPkEQAR(I)	1481.8322	114.0456	1.7	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2
2	8.06	69.2	2	13/25	None	(R)VQNALEVNLRHFR(R)	1595.8765	0.0014	0.9	337856.6/5.90	HUMAN	Q9Y485	DmX-like protein 1 OS=Homo sapiens GN=DMXL1 PE=1 SV=2
3	6.95	78.0	1	12/25	None	(R)SRHKNLAIDEKER(E)	1595.8612	0.0166	10.4	79417.7/6.44	HUMAN	RO94844	REVERSE Rho-related BTB domain-containing protein 1 OS=Homo sapiens GN=RHOBTB1 PE=1 SV=2
4	6.92	66.1	3	13/25	None	(R)NTALLSELNKVTHR(E)	1595.8864	-0.0085	-5.3	133504.9/5.87	HUMAN	RQ66GS9	REVERSE Centrosomal protein of 135 kDa OS=Homo sapiens GN=CEP135 PE=1 SV=1
5	6.64	73.4	2	14/25	None	(K)LPSPLDITAERVER(L)	1595.8751	0.0027	1.7	125430.4/5.66	HUMAN	Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.56	86.2	9	8/25	K43k	(K) D I\L\A\D L/I/P/k/E/Q A/R (I)	1481.8322	114.0456	1.7	51712.7/8.45	HUMAN	O75390	101769	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Fragment-ion (m/z)	70.064	84.080	86.096	87.099	141.102	156.101	175.116	183.111	185.127	201.123	202.125	215.141
Frac. Inten.(% of TIC)	0.00	0.07	0.78	1.28	1.93	2.30	1.41	1.62	1.45	22.61	2.23	1.45
Rel. Inten.(% of BP)	0.01	0.30	3.43	5.65	8.52	10.19	6.25	7.15	6.42	100.00	9.86	6.40
Score	0.20	0.50	0.22	-0.06	-0.09	-0.10	1.50	-0.07	0.75	0.50	-0.10	-0.06
Ion-type	PR	KQ	LI				y_1		LA	a_2		
Delta ppm	-13.2	-11.6	-9.6				-16.9		-13.2	-9.8		
										DL-28		
										-9.8		

Fragment-ion (m/z)	229.118	300.155	342.201	374.216	385.244	393.214^{+2}	413.237	421.729^{+2}	503.254	745.399	818.485	842.448	955.536
Frac. Inten.(% of TIC)	4.73	8.65	1.56	1.69	1.56	1.76	3.21	14.27	2.79	2.13	1.23	17.55	1.74
Rel. Inten.(% of BP)	20.94	38.23	6.88	7.49	6.89	7.77	14.21	63.12	12.35	9.41	5.45	77.62	7.70
Score	0.75	0.75	0.75	1.50	0.50	-0.08	0.75	1.50	1.50	1.50	-0.05	1.50	1.50
Ion-type	b_2	ADL	b_3	y_3	a_4		b_4	y_6^{+2}	y_4	y_5		y_6	y_7
Delta ppm	-4.7	-3.6	-6.6	3.6	-3.2		-8.9	3.8	-6.8	4.8		0.6	4.5
	DL		DLI		ADLI-28		ADLI						
	-4.7		-6.6		-3.2		-8.9						



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Result Summary

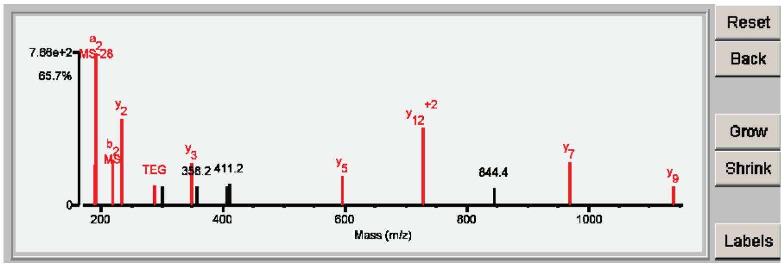
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.38	56.3	6	10/24	K459k	(K)SMSTEGLMkFVDSK(S)	1559.7444	114.0501	4.3	51712.7/8.45	HUMAN	O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.38	56.3	6	10/24	K459k	(K) S M|S T E/G L/M k/F V/D/S K (S)	1559.7444	114.0501	4.3	51712.7/8.45	HUMAN	O75390	101769	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

Fragment-ion (m/z)	60.043	72.081	84.079	86.095	87.052	104.053	129.097	143.079	144.082	189.080	191.083	219.081
Frac. Inten.(% of TIC)	5.06	0.11	0.35	0.33	3.99	3.35	5.07	20.91	1.84	3.73	13.74	4.15
Rel. Inten.(% of BP)	24.21	0.52	1.67	1.56	19.10	16.03	24.24	100.00	8.81	17.81	65.68	19.83
Score	0.50	0.50	0.50	0.22	-0.19	-0.16	-0.24	-1.00	-0.09	0.75	0.50	0.75
Ion-type	a_1	V	KQ	LI						ST	a_2 MS-28	b_2 MS
Delta ppm	-39.8	1.7	-24.7	-17.7						-41.1	-17.6 -17.6	-1.3 -1.3

Fragment-ion (m/z)	234.142	288.115	300.119	349.175	358.216^{+2}	406.267	411.206	595.289	728.353^{+2}	844.447	968.484	1138.569
Frac. Inten.(% of TIC)	7.79	1.87	1.73	3.81	1.66	1.65	1.97	2.63	7.01	1.56	3.97	1.72
Rel. Inten.(% of BP)	37.27	8.96	8.25	18.21	7.93	7.90	9.44	12.57	33.52	7.46	18.97	8.21
Score	1.50	0.75	-0.08	1.50	-0.08	-0.08	-0.09	1.50	1.50	-0.07	1.50	1.50
Ion-type	y_2	TEG		y_3				y_5	y_{12}^{+2}		y_7	y_9
Delta ppm	-11.2	-16.3		10.4				-33.8	-10.8		-3.4	-20.3



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Result Summary

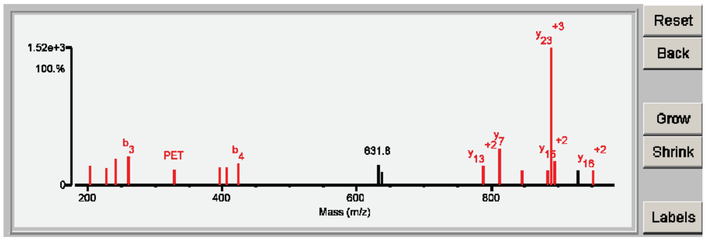
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.74	87.8	8	4/25	K265k	(K)DSGYPETLVNLIVLSQHLGkPPEVTNR(Y)	2976.5789	114.0629	6.4	34482.2/4.98	HUMAN	O14579	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.74	87.8	8	4/25	K265k	(K) D S\G\Y|P E T L V N L/I/V/L/S Q H L G k/P P E V T N R (Y)	2976.5789	114.0629	6.4	34482.2/4.98	HUMAN	O14579	118159	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3

Fragment-ion (m/z)	70.066	72.079	84.079	86.097	110.070	136.073	203.068	227.098	242.081	260.090	328.144	395.156
Frac. Inten.(% of TIC)	0.01	0.12	0.11	0.29	0.11	0.27	3.90	3.43	5.28	5.93	3.26	3.74
Rel. Inten.(% of BP)	0.02	0.43	0.39	1.05	0.40	0.95	13.98	12.27	18.91	21.22	11.67	13.40
Score	0.20	0.50	0.50	0.22	1.00	1.00	0.50	0.75	0.25	0.50	0.75	0.50
Ion-type	PR	V	KQ	LI	H	Y	b_2	PE	b_3-H_2O	b_3	PET	a_4
Delta ppm	6.8	-20.5	-24.7	3.2	-13.4	-22.0	3.2	-26.6	11.0	3.0	-21.1	-2.3

Fragment-ion (m/z)	406.726^{+2}	423.142	631.808^{+2}	637.293	788.904^{+2}	812.433	845.473^{+2}	884.491^{+3}	890.169^{+3}	894.981^{+2}	929.093^{+2}	951.530^{+2}	1112.621
Frac. Inten.(% of TIC)	3.76	4.33	4.11	2.66	3.85	7.57	2.87	3.06	27.92	4.97	2.87	3.06	2.52
Rel. Inten.(% of BP)	13.47	15.51	14.74	9.51	13.81	27.12	10.28	10.95	100.00	17.82	10.28	10.97	9.01
Score	1.50	0.50	-0.15	-0.10	1.50	1.50	1.50	0.50	1.50	1.50	-0.10	1.50	-0.09
Ion-type	y_7^{+2}	b_4			y_{13}^{+2}	y_7	y_{14}^{+2}	$y_{23}-NH_3^{+3}$	y_{23}^{+3}	y_{15}^{+2}		y_{16}^{+2}	
Delta ppm	22.2	-23.5			-11.7	8.4	21.6	3.1	5.5	-8.8		-1.2	



Result Summary

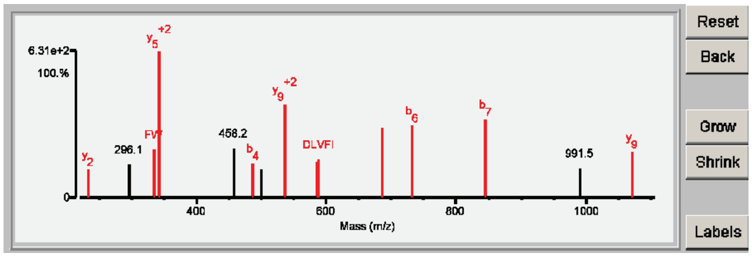
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.52	71.7	7	8/25	K112k	(K)KEDLVFIFWAPESAPLkSK(M)	2205.1954	114.0636	8.9	18502.6/8.22	HUMAN	P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3
1	13.52	71.7	7	8/25	K112k	(K)KEDLVFIFWAPESAPLkSK(M)	2205.1954	114.0636	8.9	18736.7/7.66	HUMAN	Q9Y281	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1
2	11.82	68.8	6	9/25	K114k	(K)KEDLVFIFWAPESAPLKSk(M)	2205.1954	114.0636	8.9	18502.6/8.22	HUMAN	P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3
2	11.82	68.8	6	9/25	K114k	(K)KEDLVFIFWAPESAPLKSk(M)	2205.1954	114.0636	8.9	18736.7/7.66	HUMAN	Q9Y281	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.52	71.7	7	8/25	K112k	(K) K E D L\V\F\I\F W A/P E S A/P L k/S K (M)	2205.1954	114.0636	8.9	18502.6/8.22	HUMAN	P23528	116581	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3
1	13.52	71.7	7	8/25	K112k	(K) K E D L\V\F\I\F W A/P E S A/P L k/S K (M)	2205.1954	114.0636	8.9	18736.7/7.66	HUMAN	Q9Y281	116601	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.081	84.081	86.096	120.080	121.083	130.071	159.092	185.162	199.100	234.150	296.124	334.154
Frac. Inten.(% of TIC)	0.01	0.17	0.32	0.53	0.73	3.62	2.80	0.09	3.09	4.62	2.92	3.34	4.86
Rel. Inten.(% of BP)	0.07	1.17	2.15	3.59	4.89	24.33	18.84	0.62	20.76	31.08	19.66	22.47	32.67
Score	0.20	0.50	0.50	0.22	1.00	-0.24	-0.19	2.00	-0.21	-0.31	1.50	-0.22	0.75
Ion-type	PR	V	KQ	LI	F			W			y_2		FW
Delta ppm	-13.2	1.7	1.5	-10.8	-10.6			1.4			24.2		-7.2

Fragment-ion (m/z)	343.715^{+2}	458.242	486.270	500.236	535.798^{+2}	585.317	588.318	686.422	732.386	845.464	991.515	1070.593
Frac. Inten.(% of TIC)	14.86	5.03	3.52	2.85	9.48	3.57	3.83	7.04	7.31	7.89	2.94	4.58
Rel. Inten.(% of BP)	100.00	33.86	23.69	19.19	63.76	24.04	25.75	47.38	49.19	53.09	19.79	30.80
Score	1.50	-0.34	0.50	-0.19	1.50	0.50	0.75	1.50	0.50	0.50	-0.20	1.50
Ion-type	y_5^{+2}		b_4		y_9^{+2}	b_5	DLVFI	y_5	b_6	b_7		y_9
Delta ppm	5.2		26.7		4.9	-14.1	-38.7	3.1	-10.7	-16.4		8.1



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Result Summary

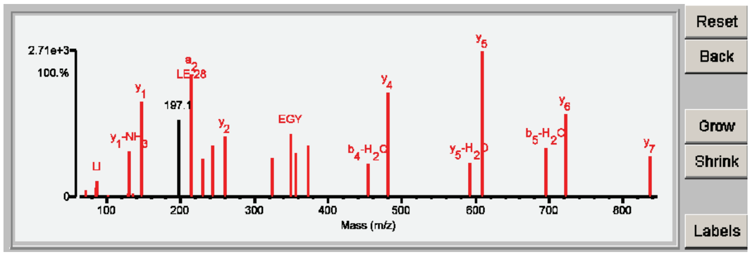
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.40	93.7	7	1/25	K63k	(K)ELVEkLLEGYLK(E)	1433.8250	114.0498	4.5	39446.9/4.93	HUMAN	Q96G28	Coiled-coil domain-containing protein 104 OS=Homo sapiens GN=CCDC104 PE=1 SV=2
2	6.29	56.6	2	9/25	None	(K)AAAKSEHITKNIHK(A)	1547.8653	0.0096	6.2	111631.0/8.76	HUMAN	Q9Y2L6	FERM domain-containing protein 4B OS=Homo sapiens GN=FRMD4B PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.40	93.7	7	1/25	K63k	(K) E L\V E k/L/L/E/G Y/L/K (E)	1433.8250	114.0498	4.5	39446.9/4.93	HUMAN	Q96G28	84057	Coiled-coil domain-containing protein 104 OS=Homo sapiens GN=CCDC104 PE=1 SV=2

Fragment-ion (m/z)	72.080	84.044	84.080	86.096	102.055	129.101	130.084	136.074	147.111	197.128	215.140	229.120	243.135
Frac. Inten.(% of TIC)	0.53	0.13	0.79	1.23	0.13	0.23	3.72	0.30	7.86	6.30	10.11	3.13	4.24
Rel. Inten.(% of BP)	4.40	1.08	6.58	10.27	1.12	1.93	31.10	2.48	65.79	52.71	84.60	26.19	35.49
Score	0.50		0.50	0.22	1.00	0.20	0.50	1.00	1.50	-0.53	0.50	0.75	0.75
Ion-type	V	E	KQ	LI	a_1	RKQ	y_1-NH$_3$	Y	y_1		a_2	VE	b_2
Delta ppm	-5.2		-8.0	-8.4	-12.3	-8.8	-19.6	-9.5	-13.6		-1.9	1.4	-1.8
					1.00						LE-28		LE
					E						-1.9		-1.8
					-1.5								

Fragment-ion (m/z)	260.197	324.189	350.137	356.229	372.187	453.242	480.285	591.321	609.325	695.371	722.410	835.489
Frac. Inten.(% of TIC)	4.90	3.18	5.15	3.64	4.24	2.74	8.54	2.77	11.95	4.04	6.82	3.36
Rel. Inten.(% of BP)	41.04	26.62	43.12	30.46	35.46	22.95	71.49	23.18	100.00	33.78	57.08	28.13
Score	1.50	0.25	0.75	0.75	0.75	0.25	1.50	0.50	1.50	0.25	1.50	1.50
Ion-type	y_2	b_3-H$_2$O	EGY	LLE	Ek	b_4-H$_2$O	y_4	y_5-H$_2$O	y_5	b_5-H$_2$O	y_6	y_7
Delta ppm	1.3	-10.7	4.4	29.2	-5.8	14.0	7.2	11.5	0.9	-2.8	1.8	-3.7



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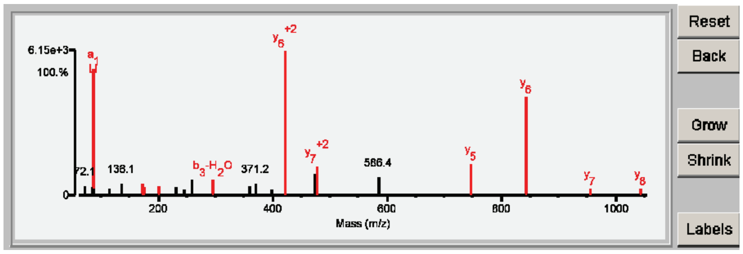
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.75	77.9	5	13/25	K289k	(R)ISLPESLkR(I)	1042.6255	114.0282	-12.7	187149.1/6.02	HUMAN	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2
2	11.56	74.7	4	11/25	None	(R)VTLQIEGLQR(R)	1156.6684	-0.0147	-12.7	100036.0/8.68	HUMAN	RA0FGR9	REVERSE Extended synaptotagmin-3 OS=Homo sapiens GN=FAM62C PE=2 SV=1
3	11.21	76.8	4	12/25	None	(R)LSLAQTGLTPR(G)	1156.6684	-0.0147	-12.7	154689.8/6.31	HUMAN	Q6F5E8	Leucine-rich repeat-containing protein 16C OS=Homo sapiens GN=RLTPR PE=1 SV=2
4	10.19	76.7	4	14/25	K1665k K1669k	(K)LSLPkAGDk(V)	928.5462	228.1075	18.7	226356.8/8.39	HUMAN	RO60293	REVERSE Zinc finger C3H1 domain-containing protein OS=Homo sapiens GN=ZFC3H1 PE=1 SV=3
5	9.03	72.6	3	14/25	None	(R)LSLEGERQPK(S)	1156.6321	0.0217	18.7	213620.7/7.15	HUMAN	P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.75	77.9	5	13/25	K289k	(R) I/S|L/P/E S L k/R (I)	1042.6255	114.0282	-12.7	187149.1/6.02	HUMAN	P01024	111117	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Fragment-ion (m/z)	70.064	72.079	84.080	86.095	87.100	115.087	136.073	173.128	175.120	201.122	230.091	246.142	258.087	296.197	360.200	371.179	399.160	422.229^{+2}	473.283	478.771^{+2}	586.364	746.407	843.452	956.526	1043.580
Frac. Inten.(% of TIC)	0.01	1.47	1.20	20.23	1.11	1.01	1.91	1.86	1.23	1.45	1.20	0.97	2.38	2.44	1.55	1.91	0.97	23.13	3.52	4.65	2.88	4.98	15.81	1.07	1.08
Rel. Inten.(% of BP)	0.02	6.37	5.20	87.48	4.79	4.37	8.26	8.04	5.31	6.25	5.20	4.19	10.31	10.55	6.69	8.25	4.19	100.00	15.21	20.10	12.46	21.53	68.35	4.64	4.66
Score	0.20	-0.06	-0.05	0.50	-0.05	-0.04	-0.08	0.50	1.50	0.75	-0.05	-0.04	-0.10	0.25	-0.07	-0.08	-0.04	1.50	-0.15	1.50	-0.12	1.50	1.50	1.50	1.50
Ion-type	PR			a_1				a_2	y_1	b_2				b_3-H_2O				y_6^{+2}		y_7^{+2}		y_5	y_6	y_7	y_8
Delta ppm	-17.5			-24.7				-7.8	8.3	-11.8				-4.3				-19.6		-18.9		-11.2	-19.8	-27.4	-4.3
				0.50				SL-28		SL															
				LI				-7.8		-11.8															
				-11.9																					



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Result Summary

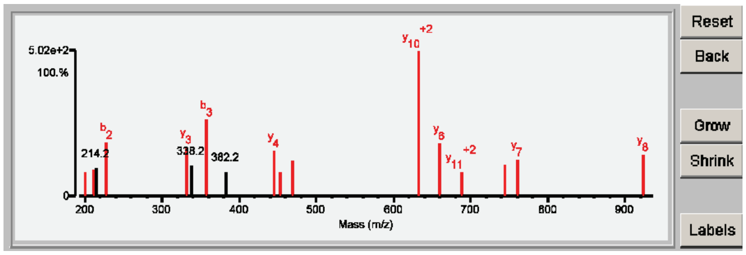
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.83	78.5	8	8/25	K243k	(K)VQQLPkYTSQIVGR(F)	1616.9119	114.0425	-0.3	47873.4/6.19	HUMAN	Q9UNS2	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.83	78.5	8	8/25	K243k	(K) V Q\Q|L|P k/Y/T/S Q/I/V G R (F)	1616.9119	114.0425	-0.3	47873.4/6.19	HUMAN	Q9UNS2	64255	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3

Fragment-ion (m/z)	72.079	84.041	84.078	86.094	121.078	132.084	141.099	185.154	200.134	211.103	214.150	228.132	331.206
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.22 1.32 0.50 a_1 -42.6 0.50 V -27.4	2.52 15.21 -0.15	0.33 2.01 0.50 KQ -28.3	0.19 1.14 0.22 LI -22.4	2.53 15.31 -0.15	2.49 15.03 -0.15	3.32 20.08 -0.20	2.80 16.90 -0.17	2.71 16.36 0.50 a_2 -30.2	3.09 18.68 0.25 b_2-NH_3 -26.1	3.13 18.92 -0.19	6.16 37.20 0.50 b_2 -13.9	5.66 34.20 1.50 y_3 -8.5

Fragment-ion (m/z)	338.160	356.188	382.211	444.282	453.278	469.280	631.847^{+2}	659.408	688.394^{+2}	743.418^{+2}	760.431	923.483
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.47 20.93 -0.21	8.71 52.60 0.50 b_3 -15.6	2.74 16.52 -0.17	5.14 31.03 1.50 y_4 -23.8	2.82 17.04 0.75 LPk -12.1	4.09 24.69 0.50 b_4 3.8	16.55 100.00 1.50 y_{10}^{+2} 1.9	6.09 36.76 1.50 y_6 36.9	2.72 16.44 1.50 y_{11}^{+2} 8.2	3.58 21.61 0.50 y_{12}-H_2O^{+2} 7.9	4.22 25.48 1.50 y_7 0.0	4.73 28.60 1.50 y_8 -12.0



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Result Summary

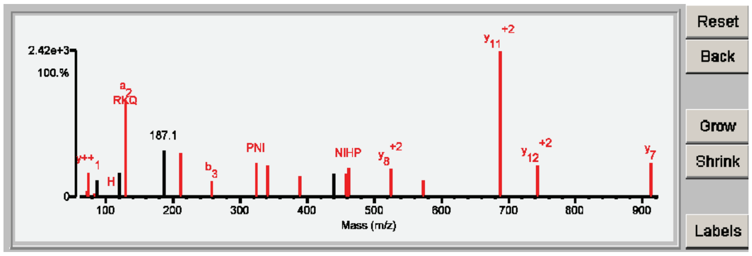
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.49	84.5	9	4/25	K116k	(K)GVTIASGGVLPNIHPELLAkK(R)	2114.2332	114.0746	14.2	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4
2	17.82	81.0	8	5/25	K117k	(K)GVTIASGGVLPNIHPELLAKk(R)	2114.2332	114.0746	14.2	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.49	84.5	9	4/25	K116k	(K) G V T\I A S G G V/L/P N I/H/P E L/L/A/k/K (R)	2114.2332	114.0746	14.2	39617.3/9.80	HUMAN	O75367	271841	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4

Fragment-ion (m/z)	70.065	72.081	74.061	84.081	86.097	87.058	87.098	110.069	120.078	129.101	187.145	212.104	258.143
Frac. Inten.(% of TIC)	0.01	0.70	3.45	0.39	0.68	0.08	2.39	0.14	3.43	13.33	6.54	6.09	2.23
Rel. Inten.(% of BP)	0.04	3.46	17.07	1.95	3.34	0.37	11.82	0.69	16.98	65.95	32.34	30.14	11.05
Score	0.20	0.50	1.50	0.50	0.22	0.33	-0.12	1.00	-0.17	0.50 0.50	-0.32	0.75	0.50
Ion-type	PR	V	y^{++}_1	KQ	LI	NR		H		a_2 RKQ		PN	b_3
Delta ppm	-6.1	-2.4	7.6	-2.1	2.0	27.7		-18.8		-17.3 -8.8		-2.7	-10.6

Fragment-ion (m/z)	325.185	340.182	389.254	440.252	458.611^{+3}	460.285	462.249	525.322^{+2}	573.385	687.402^{+2}	743.934^{+2}	912.556
Frac. Inten.(% of TIC)	4.75	4.43	2.80	3.18	3.15	2.60	4.03	3.86	2.27	20.22	4.48	4.78
Rel. Inten.(% of BP)	23.47	21.91	13.83	15.72	15.60	12.84	19.93	19.08	11.24	100.00	22.17	23.62
Score	0.75	0.75	1.50	-0.16	1.50	1.50	0.75	1.50	1.50	1.50	1.50	1.50
Ion-type	PNI	PEL	y_2		y_{11}^{+3}	y_3	NIHP	y_8^{+2}	y_4	y_{11}^{+2}	y_{12}^{+2}	y_7
Delta ppm	-8.4	-17.9	8.5		21.4	-6.1	3.4	25.5	22.4	5.1	-9.5	5.0



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Result Summary

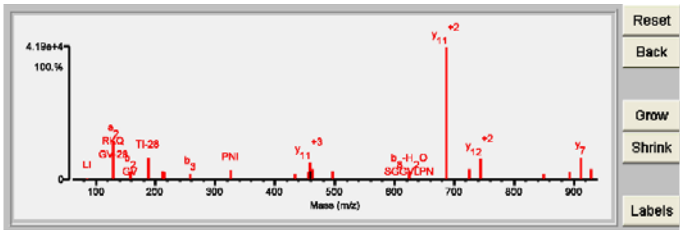
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.61	97.7	8	1/25	K117k	(K)GVTIASGGVLPNIHPELLAKk(R)	2114.2332	114.0382	-2.1	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4
1	21.61	97.7	8	1/25	K116k	(K)GVTIASGGVLPNIHPELLAkK(R)	2114.2332	114.0382	-2.1	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4
2	9.02	67.0	2	12/25	K629k K630k	(R)EkkQIQPFQVLTTRKR(K)	2000.1764	228.0950	4.1	101736.6/5.49	HUMAN	P18858	DNA ligase 1 OS=Homo sapiens GN=LIG1 PE=1 SV=1
3	8.47	71.0	2	13/25	K634k	(R)IkGEVTLLSRLHHENIVR(Y)	2114.2193	114.0521	4.1	186839.5/5.90	HUMAN	Q9P2K8	Eukaryotic translation initiation factor 2-alpha kinase 4 OS=Homo sapiens GN=EIF2AK4 PE=1 SV=2
4	7.66	65.3	1	12/25	None	(K)VRLDNEKEGFPITAIREIK(I)	2228.2397	0.0316	14.2	164924.0/9.71	HUMAN	Q14004	Cell division cycle 2-like protein kinase 5 OS=Homo sapiens GN=CDC2L5 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.61	97.7	8	1/25	K117k	(K) G V\T\I/A/S/G G V/L/P N I H/P E L L A K k (R)	2114.2332	114.0382	-2.1	39617.3/9.80	HUMAN	O75367	271841	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4

Fragment-ion (m/z)	70.065	72.082	84.081	86.097	129.102	157.098	187.144	212.102	215.137	258.146	325.190	434.252
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -0.4	0.21 0.60 0.50 V 11.4	0.08 0.22 0.50 KQ 7.4	0.57 1.64 0.22 LI 7.8	10.28 29.60 0.50 a_2 -7.3 0.50 RKQ 1.2 GV-28 -7.3	2.33 6.72 0.75 b_2 -1.6 GV -1.6	5.70 16.43 0.50 TI-28 -5.9	2.19 6.32 0.75 PN -10.2	1.98 5.71 0.75 TI -15.4	1.55 4.46 0.50 b_3 1.8	2.55 7.36 0.75 PNI 7.0	1.74 5.02 0.50 NIHP-28 -1.4

Fragment-ion (m/z)	456.777^{+2}	458.604^{+3}	459.271	462.248	496.298^{+3}	625.329	687.397^{+2}	724.397	743.939^{+2}	850.490^{+2}	894.019^{+2}	912.548	929.534^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.92 5.53 1.50 y_7^{+2} -6.1	4.64 13.37 1.50 y_{11}^{+3} 4.6	2.33 6.70 -0.07	2.69 7.76 0.75 NIHP 1.4	2.22 6.40 1.50 y_{12}^{+3} 3.8	2.14 6.16 0.75 b_8-H_2O -3.8 SGGVLPN -3.8	34.71 100.00 1.50 y_{11}^{+2} -2.2	2.87 8.26 0.25 b_9-H_2O -3.6	5.52 15.90 1.50 y_{12}^{+2} -2.0	1.55 4.47 1.50 y_{15}^{+2} -8.0	1.79 5.16 1.50 y_{16}^{+2} 7.2	5.72 16.46 1.50 y_7 -3.1	2.71 7.81 1.50 b_{19}+H_2O^{+2} 9.2 y_{17}^{+2} 3.8



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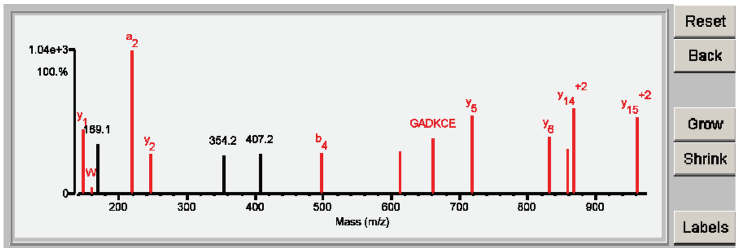
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.55	77.5	8	5/25	K292k	(K)FVIHCNSPVWGADKCEELLEkTVK(N)	2859.4168	114.0591	5.4	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4
2	13.83	67.2	6	7/25	K295k	(K)FVIHCNSPVWGADKCEELLEKTVk(N)	2859.4168	114.0591	5.4	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4
3	13.62	64.1	6	7/25	K285k	(K)FVIHCNSPVWGADkCEELLEKTVK(N)	2859.4168	114.0591	5.4	39617.3/9.80	HUMAN	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.55	77.5	8	5/25	K292k	(K) F V I H\C N S\P V/W/G A D K C E E L/L/E k T/V/K (N)	2859.4168	114.0591	5.4	39617.3/9.80	HUMAN	O75367	271841	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4

Fragment-ion (m/z)	60.044	70.065	72.080	84.081	86.096	102.055	110.069	120.079	129.100	130.073	147.110	159.089	169.132	219.148	246.183	354.184	407.196^{+2}	497.281	612.253	661.270	718.406	831.489	858.397	867.438^{+2}	960.489^{+2}
Frac. Inten.(% of TIC)	4.27	0.02	0.39	0.42	1.47	0.26	0.30	0.88	0.32	5.36	6.42	0.72	4.97	14.35	3.93	3.90	3.99	4.16	4.23	5.53	7.75	5.66	4.53	8.51	7.66
Rel. Inten.(% of BP)	29.78	0.14	2.69	2.92	10.26	1.80	2.07	6.16	2.24	37.36	44.75	5.03	34.65	100.00	27.40	27.17	27.78	29.00	29.44	38.54	54.00	39.43	31.56	59.31	53.36
Score	-0.30	0.20	0.50	0.50	0.22	1.00	1.00	1.00 1.00	0.20	-0.37	1.50	2.00	-0.35	0.50	1.50	-0.27	-0.28	0.50	0.75	0.75	1.50	1.50	0.50	1.50	1.50
Ion-type		**PR**	**V**	**KQ**	**LI**	**E**	**H**	**a_1** **F**	**RKQ**		**y_1**	**W**		**a_2**	**y_2**			**b_4**	**IHCNS**	**GADKCE**	**y_5**	**y_6**	**b_7**	**y_{14}^{+2}**	**y_{15}^{+2}**
Delta ppm		-7.5	-5.2	-3.3	-2.6	1.4	-22.5	-23.1 -14.0	-18.1		-17.0	-20.0		-11.3	7.6			-14.2	-6.0	12.7	-4.8	-5.0	3.9	-2.9	9.2



Result Summary

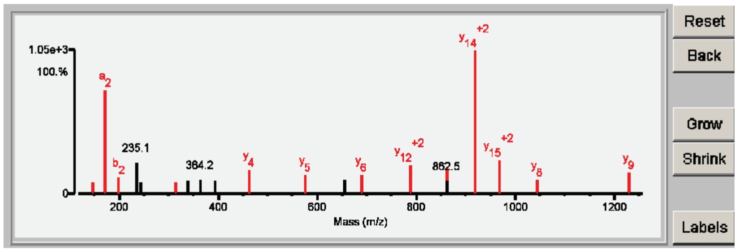
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.63	83.6	10	8/25	K16k	(R)VVDFDETWNkLLTTIK(A)	1922.0270	114.0529	4.9	86983.6/6.46	HUMAN	Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2
2	12.98	75.3	6	11/25	K22k	(R)VVDFDETWNKLLTTIk(A)	1922.0270	114.0529	4.9	86983.6/6.46	HUMAN	Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2
3	7.40	63.6	3	15/25	K849k	(R)VVKDMLKWCkEVMKK(D)	1922.0424	114.0374	-2.7	99647.4/6.10	HUMAN	RP22681	REVERSE E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=1
3	7.40	63.6	3	15/25	K853k	(R)VVKDMLKWCKEVMkK(D)	1922.0424	114.0374	-2.7	99647.4/6.10	HUMAN	RP22681	REVERSE E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=1
3	7.40	63.6	3	15/25	K842k	(R)VVkDMLKWCKEVMKK(D)	1922.0424	114.0374	-2.7	99647.4/6.10	HUMAN	RP22681	REVERSE E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.63	83.6	10	8/25	K16k	(R) V/V|D|F/D E T/W/N k/L/L/T T I/K (A)	1922.0270	114.0529	4.9	86983.6/6.46	HUMAN	Q13617	132065	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2

Fragment-ion (m/z)	72.079	73.082	86.098	129.101	147.114	159.087	171.146	199.138	235.103	242.185	314.170	340.166
Frac. Inten.(% of TIC)	0.77	1.98	0.06	0.07	1.96	0.07	17.27	2.73	5.23	2.02	1.94	2.24
Rel. Inten.(% of BP)	3.24	8.31	0.24	0.30	8.19	0.30	72.34	11.42	21.90	8.46	8.12	9.38
Score	0.50 0.50	-0.08	0.22	0.20	1.50	2.00	0.50	0.50	-0.20	-0.08	0.50	-0.09
Ion-type	a_1 V		LI	RKQ	y_1	W	a_2	b_2			b_3	
Delta ppm	-35.7 -20.5		16.0	-6.5	5.4	-29.4	-22.7	-33.7			-6.8	

Fragment-ion (m/z)	364.158	392.185	462.287	575.382	655.846	688.459	788.441^{+2}	861.974	862.459	919.470^{+2}	969.008^{+2}	1044.621	1230.723
Frac. Inten.(% of TIC)	2.33	2.24	3.96	3.18	2.29	3.27	4.73	4.16	2.15	23.87	5.65	2.25	3.58
Rel. Inten.(% of BP)	9.74	9.38	16.59	13.34	9.61	13.68	19.82	17.43	8.99	100.00	23.69	9.44	15.01
Score	-0.09	-0.09	1.50	1.50	-0.09	1.50	1.50	1.50	-0.08	1.50	1.50	1.50	1.50
Ion-type			y_4	y_5		y_6	y_{12}^{+2}	y^{++}_{13}		y_{14}^{+2}	y_{15}^{+2}	y_8	y_9
Delta ppm			-10.7	9.6		-2.3	22.9	20.0		0.0	4.2	-19.3	1.9



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Result Summary

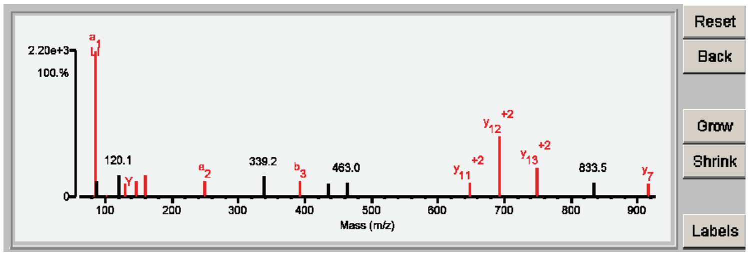
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pl (Da)	Species	Accession #	Protein Name
1	13.59	77.7	6	7/25	K63k	(R)IYDAQNELSAATHLTSkLLK(E)	2216.1921	114.0720	12.5	79663.9/5.28	HUMAN	Q9UKG1	DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1
2	11.39	71.2	5	9/25	K66k	(R)IYDAQNELSAATHLTSKLLk(E)	2216.1921	114.0720	12.5	79663.9/5.28	HUMAN	Q9UKG1	DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pl (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.59	77.7	6	7/25	K63k	(R) I Y D\A Q N E/L/S/A A T H/L T S k L L/K (E)	2216.1921	114.0720	12.5	79663.9/5.28	HUMAN	Q9UKG1	169043	DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.044	84.081	86.097	87.055	87.101	101.072	102.055	110.071	120.082	129.102	130.084
Frac. Inten.(% of TIC)	0.15	0.22	0.29	32.14	0.13	3.53	0.09	0.31	0.15	4.94	0.15	2.92
Rel. Inten.(% of BP)	0.47	0.67	0.89	100.00	0.41	10.99	0.27	0.96	0.45	15.36	0.46	9.10
Score	-0.00		0.50	0.50 0.50	0.33	-0.11		1.00	1.00	-0.15	0.20	0.50
Ion-type		E	KQ	a_1 LI	NR		KQ	E	H		RKQ	y_1-NH_3
Delta ppm			5.0	-10.7 2.0	2.4			-1.5	-5.2		-2.6	-17.3

Fragment-ion (m/z)	136.074	147.112	159.078	249.159	339.161	392.178	436.249	462.972^{+4}	648.889^{+2}	692.413^{+2}	748.957^{+2}	833.472	916.582
Frac. Inten.(% of TIC)	0.21	3.54	4.78	3.53	4.54	3.35	3.02	3.06	3.04	13.37	6.50	3.07	2.98
Rel. Inten.(% of BP)	0.64	11.02	14.87	10.99	14.12	10.42	9.40	9.52	9.46	41.61	20.23	9.56	9.26
Score	1.00	1.50	0.75	0.50	-0.14	0.50	-0.09	-0.10	1.50	1.50	1.50	-0.10	1.50
Ion-type	Y	y_1	SA	a_2		b_3			y_{11}^{+2}	y_{12}^{+2}	y_{13}^{+2}		y_7
Delta ppm	-13.2	-8.9	4.9	-8.6		-12.3			5.2	16.7	18.6		-0.2



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Result Summary

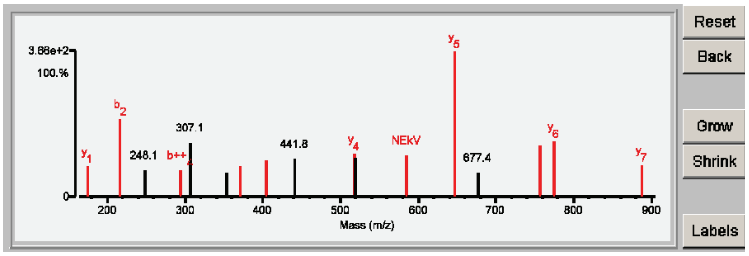
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.91	66.2	9	8/25	K109k	(R)TNEkVELQELNDR(F)	1587.7973	114.0409	-1.2	53536.0/5.21	HUMAN	P17661	Desmin OS=Homo sapiens GN=DES PE=1 SV=3
1	12.91	66.2	9	8/25	K104k	(R)TNEkVELQELNDR(F)	1587.7973	114.0409	-1.2	53651.9/5.06	HUMAN	P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.91	66.2	9	8/25	K109k	(R) T\N\E k\V E/L/Q/E/L/N D/R (F)	1587.7973	114.0409	-1.2	53536.0/5.21	HUMAN	P17661	157549	Desmin OS=Homo sapiens GN=DES PE=1 SV=3
1	12.91	66.2	9	8/25	K104k	(R) T\N\E k\V E/L/Q/E/L/N D/R (F)	1587.7973	114.0409	-1.2	53651.9/5.06	HUMAN	P08670	837031	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Fragment-ion (m/z)	70.062	72.079	84.047	84.080	86.093	101.070	102.052	155.039	175.115	216.105	248.127	294.152
Frac. Inten.(% of TIC)	0.01	0.23	0.14	0.11	6.19	0.19	0.23	3.82	3.49	8.83	3.07	3.07
Rel. Inten.(% of BP)	0.03	1.38	0.86	0.65	37.27	1.12	1.36	23.00	21.03	53.15	18.48	18.46
Score	0.20	0.50	1.00		-0.37	0.50	1.00	-0.23	1.50	0.50	-0.18	0.50
Ion-type	PR	V	b_1-H_2O	QK		QK	b_1		y_1	b_2		$b{+}{+}_4$
Delta ppm	-38.9	-23.2	14.4			-12.3	-40.7		-22.0	27.4		30.0
							1.00					
			E				E					
							-29.9					

Fragment-ion (m/z)	307.115	354.168	371.183	404.191	441.750^{+2}	517.283	519.790^{+2}	585.298	646.316	677.361^{+2}	756.355	774.382	887.439
Frac. Inten.(% of TIC)	6.26	2.78	3.48	4.20	4.38	4.96	4.53	4.72	16.61	2.81	5.85	6.39	3.68
Rel. Inten.(% of BP)	37.65	16.73	20.95	25.27	26.34	29.85	27.25	28.40	100.00	16.89	35.21	38.44	22.15
Score	-0.38	-0.17	0.75	1.50	-0.26	1.50	-0.27	0.75	1.50	-0.17	0.50	1.50	1.50
Ion-type			QEL	y_3		y_4		NEkV	y_5		y_6-H_2O	y_6	y_7
Delta ppm			-29.1	4.4		19.7		-3.2	0.2		-11.5	10.4	-22.0



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Result Summary

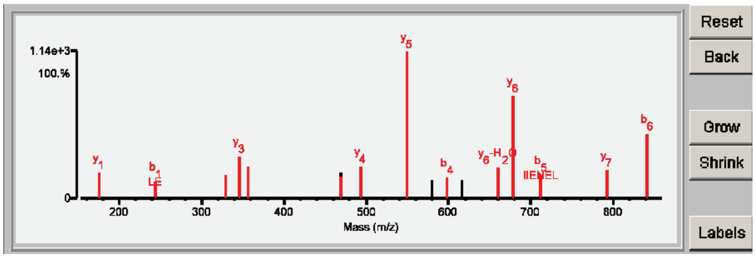
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.55	72.4	11	6/25	K159k	(K)kIIENELEGFGIR(L)	1517.8322	114.0561	8.1	40542.4/9.00	HUMAN	Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.55	72.4	11	6/25	K159k	(K) k\I\I\E\N\E|L/E/G/F/G I/R (L)	1517.8322	114.0561	8.1	40542.4/9.00	HUMAN	Q9Y295	85945	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.044	84.081	86.096	89.060	102.054	116.066	120.080	175.122	243.136	328.221	345.223
Frac. Inten.(% of TIC)	0.00	0.08	13.64	0.98	3.74	0.25	3.22	0.17	3.03	1.90	2.63	4.93
Rel. Inten.(% of BP)	0.02	0.48	80.11	5.74	21.93	1.49	18.89	1.01	17.81	11.14	15.44	28.96
Score	0.20		-0.80	0.22	-0.22	1.00	-0.19	1.00	1.50	0.75	0.50	1.50
Ion-type	PR	E		LI		E		F	y_1	b_1 LE	IIE-28	y_3
Delta ppm	-1.8			-10.8		-11.3		-4.8	16.8	-41.4 4.8	-10.6	-5.2

Fragment-ion (m/z)	356.229	469.200^{+2}	469.303	492.295	549.316	579.203	598.354	616.331	660.337	678.353	712.393	791.432	841.442
Frac. Inten.(% of TIC)	3.78	2.94	2.52	3.76	17.03	2.05	2.37	2.06	3.59	11.86	2.67	3.21	7.56
Rel. Inten.(% of BP)	22.20	17.28	14.83	22.10	100.00	12.04	13.91	12.08	21.10	69.66	15.69	18.85	44.40
Score	0.75	-0.17	0.50	1.50	1.50	-0.12	0.50	-0.12	0.50	1.50	0.75	1.50	0.50
Ion-type	b_2 IIE		b_3	y_4	y_5		b_4		y_6-H_2O	y_6	b_5 IIENEL	y_7	b_6
Delta ppm	-5.1 26.4		-24.3	4.1	3.4		-5.3		-14.2	-5.2	-9.4 6.3	-11.3	-1.2



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Result Summary

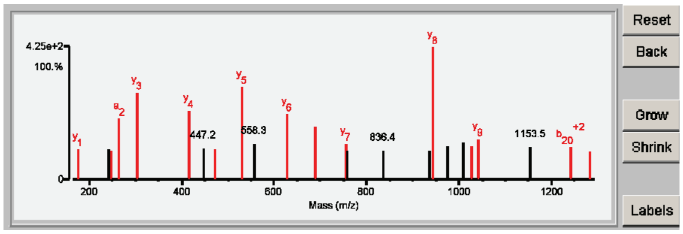
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.62	72.2	9	10/25	K123k	(R)QYTSLLGkMNSEEEDEVWQVIIGAR(A)	2895.4193	114.0591	5.4	27131.0/5.68	HUMAN	Q9NR28	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.62	72.2	9	10/25	K123k	(R) Q Y T S L L G k M N S E E E D E/V/W/Q/V|I/I/G/A/R (A)	2895.4193	114.0591	5.4	27131.0/5.68	HUMAN	Q9NR28	148915	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1

Fragment-ion (m/z)	175.118	243.142	246.165	264.128	303.172	416.268	447.218^{+2}	471.789^{+2}	529.342	558.250	628.414	688.352	756.467
Frac. Inten.(% of TIC)	2.64	2.64	2.56	5.34	7.67	6.06	2.79	2.64	8.17	3.11	5.79	4.69	3.14
Rel. Inten.(% of BP)	22.56	22.53	21.92	45.61	65.55	51.75	23.83	22.58	69.86	26.61	49.52	40.10	26.87
Score	1.50	-0.23	1.50	0.50	1.50	1.50	-0.24	1.50	1.50	-0.27	1.50	0.25	1.50
Ion-type	y_1		y_2	a_2	y_3	y_4		y_8^{+2}	y_5		y_6	b_6-H_2O	y_7
Delta ppm	-3.7		35.1	-26.4	-17.6	15.6		19.9	-7.7		0.7	-22.7	-7.5

Fragment-ion (m/z)	757.464^{+3}	836.445	935.492	942.556	975.981^{+2}	1010.332	1025.476^{+2}	1041.605	1153.548	1241.016^{+2}	1283.587^{+2}	1360.182^{+2}
Frac. Inten.(% of TIC)	2.52	2.59	2.55	11.70	2.92	3.21	2.94	3.55	2.87	2.82	2.46	2.63
Rel. Inten.(% of BP)	21.57	22.16	21.78	100.00	24.98	27.43	25.10	30.30	24.49	24.09	21.03	22.46
Score	-0.22	-0.22	-0.22	1.50	-0.25	-0.27	0.25	1.50	-0.24	0.50	0.50	-0.22
Ion-type				y_8			b_{17}-H_2O^{+2}	y_9		b_{20}^{+2}	a_{21}^{+2}	
Delta ppm				4.7			18.0	-14.4		-40.1	-18.8	



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Result Summary

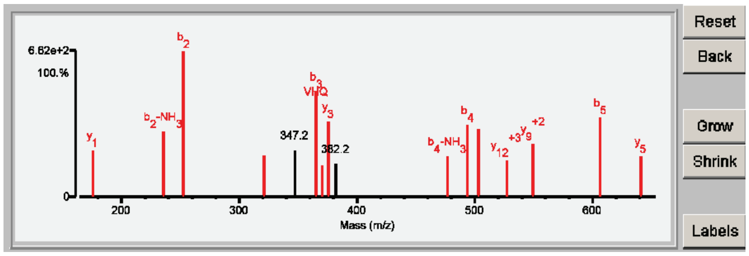
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.80	82.4	11	5/25	K191k	(R)NHIQLVkLQVEEVHQLSR(K)	2170.2091	114.0568	6.1	27131.0/5.68	HUMAN	Q9NR28	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.80	82.4	11	5/25	K191k	(R) N H\I\Q\L\V/k L Q/V E E/V/H/Q/L S/R (K)	2170.2091	114.0568	6.1	27131.0/5.68	HUMAN	Q9NR28	148915	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1

Fragment-ion (m/z)	72.080	84.045	84.080	86.096	110.070	129.100	136.077	141.101	175.117	235.078	252.109	320.691^{+2}
Frac. Inten.(% of TIC)	0.64	0.40	0.96	0.74	0.44	0.10	4.02	3.30	4.11	5.78	12.79	3.62
Rel. Inten.(% of BP)	5.00	3.10	7.53	5.78	3.41	0.77	31.44	25.79	32.12	45.19	100.00	28.33
Score	0.50	1.00	0.50	0.22	1.00	0.20	-0.31	-0.26	1.50	0.25	0.50	1.50
Ion-type	V	E	KQ	LI	H	RKQ			y_1	b_2-NH_3	b_2	y_5^{+2}
Delta ppm	-6.6	4.9	-9.2	-4.9	-10.7	-18.9			-14.0	-23.2	-3.6	34.7

Fragment-ion (m/z)	347.189	365.197	370.210	375.231	382.216	476.240	493.246	502.600	503.300	527.299^{+3}	548.795^{+2}	606.333	640.369
Frac. Inten.(% of TIC)	4.15	9.27	2.84	6.62	2.94	3.51	6.28	3.20	5.92	3.22	4.68	6.98	3.52
Rel. Inten.(% of BP)	32.42	72.48	22.20	51.73	22.96	27.44	49.12	25.03	46.26	25.21	36.56	54.61	27.49
Score	-0.32	0.75	1.50	1.50	-0.23	0.25	0.50	-0.25	1.50	1.50	1.50	0.50	1.50
Ion-type		b_3 VHQ	y^{++}_6	y_3		b_4-NH_3	b_4		y_4	y_{12}^{+3}	y_9^{+2}	b_5	y_5
Delta ppm		8.6 8.6	-10.0	-10.8		28.3	-13.5		11.7	17.7	7.1	-6.3	25.1



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Result Summary

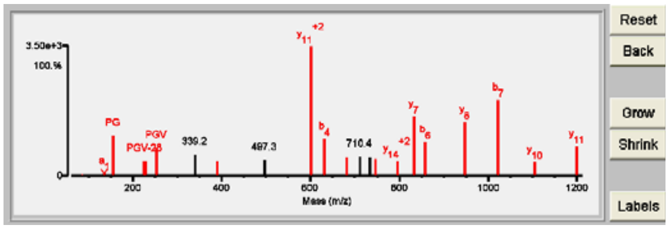
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.34	88.9	7	4/25	K158k	(K)YkLLPEYPGVLSDVQEEK(G)	2107.0958	114.0640	9.5	21452.9/6.85	HUMAN	P00374	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=2
2	5.84	50.1	1	12/25	M4936m K4935k	(K)VKPGkmHLDVDPMSIKPAK(I)	2091.1453	130.0144	-10.5	629104.8/5.80	HUMAN	RQ09666	REVERSE Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
3	4.63	53.9	1	14/25	None	(R)KQHPYTFPGGSGTVFARNTR(R)	2221.1261	0.0336	15.1	64733.1/8.63	HUMAN	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.34	88.9	7	4/25	K158k	(K) Y k L L|P E|Y|P/G V/L/S/D V Q E E K (G)	2107.0958	114.0640	9.5	21452.9/6.85	HUMAN	P00374	177907	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=2

Fragment-ion (m/z)	70.064	72.080	84.080	86.095	136.075	155.079	226.152	227.102	254.150	339.237	390.168	497.298^{+2}	600.811^{+2}
Frac. Inten.(% of TIC)	0.01	0.16	0.05	0.18	0.39	5.99	2.27	2.18	4.21	3.16	2.22	2.36	19.03
Rel. Inten.(% of BP)	0.03	0.82	0.29	0.97	2.05	31.50	11.94	11.47	22.15	16.59	11.66	12.42	100.00
Score	0.20	0.50	0.50	0.22	1.00 1.00	0.75	0.50	0.75	0.75	-0.17	0.75	-0.12	1.50
Ion-type	PR	V	KQ	LI	a_1 Y	PG	PGV-28	PE	PGV		EYP		y_{11}^{+2}
Delta ppm	-13.2	-10.8	-6.8	-13.1	-14.6 -6.5	-21.9	-16.4	-8.1	-2.0		3.7		3.4

Fragment-ion (m/z)	632.371	682.345^{+2}	710.397^{+2}	734.037	747.375	795.371^{+2}	834.387	858.470	947.471	1021.537	1103.560	1200.617
Frac. Inten.(% of TIC)	5.52	2.76	2.87	2.70	2.50	2.20	8.63	5.03	7.89	11.21	2.08	4.37
Rel. Inten.(% of BP)	29.00	14.52	15.09	14.17	13.15	11.58	45.35	26.45	41.49	58.92	10.93	22.98
Score	0.50	1.50	-0.15	-0.14	1.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	b_4	y_{12}^{+2}			y_6	y_{14}^{+2}	y_7	b_6	y_8	b_7	y_{10}	y_{11}
Delta ppm	-10.3	6.0			30.6	-21.9	3.9	-3.1	2.8	0.7	2.2	5.6



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Result Summary

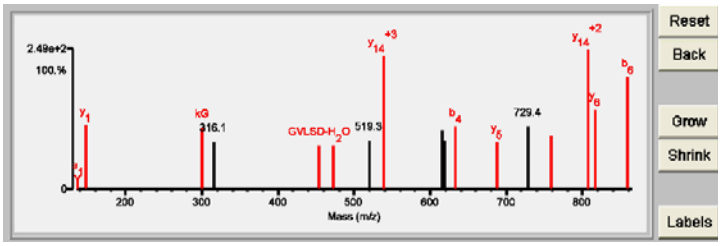
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.30	68.7	7	7/25	K158k K174k	(K)YkLLPEYPGVLSDVQEEkGIK(Y)	2405.2963	228.0943	3.2	21452.9/6.85	HUMAN	P00374	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=2
2	9.15	58.7	6	9/25	K158k K177k	(K)YkLLPEYPGVLSDVQEEKGIk(Y)	2405.2963	228.0943	3.2	21452.9/6.85	HUMAN	P00374	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.30	68.7	7	7/25	K158k K174k	(K) Y k L L\P E\Y/P/G V L S D V Q/E/E k G I/K (Y)	2405.2963	228.0943	3.2	21452.9/6.85	HUMAN	P00374	177907	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=2

Fragment-ion (m/z)	70.066	72.079	84.079	86.097	101.072	120.080	129.099	136.073	147.107	300.177	316.124
Frac. Inten.(% of TIC)	0.01	0.28	0.28	0.40	0.12	6.75	0.15	0.76	5.07	4.92	3.71
Rel. Inten.(% of BP)	0.07	2.53	2.49	3.59	1.07	60.80	1.33	6.86	45.68	44.27	33.45
Score	0.20	0.50	0.50	0.22		-0.61	0.20	1.00	1.50	0.75	-0.33
Ion-type	PR	V	KQ	LI	KQ		RKQ	a_1	y_1	kG	
Delta ppm	12.5	-19.1	-22.3	3.2			-22.8	-19.0	-36.7	33.2	
								1.00			
								Y			
								-19.0			

Fragment-ion (m/z)	454.242	472.238	519.261	538.289^{+3}	616.362	619.327	632.366	688.385	729.412^{+2}	758.396^{+2}	806.934^{+2}	817.433	858.482	888.951
Frac. Inten.(% of TIC)	3.46	3.46	3.84	10.55	4.75	3.86	4.99	3.71	4.99	4.22	11.10	6.33	8.88	3.42
Rel. Inten.(% of BP)	31.16	31.16	34.58	95.01	42.74	34.74	44.95	33.41	44.91	38.00	100.00	57.02	80.02	30.84
Score	0.50	0.75	-0.35	1.50	-0.43	-0.35	0.50	1.50	-0.45	1.50	1.50	1.50	0.50	-0.31
Ion-type	GVLSD-H_2O	GVLSD		y_{14}^{+3}			b_4	y_5		y_{13}^{+2}	y_{14}^{+2}	y_6	b_6	
Delta ppm	26.6	-3.6		-0.8			-17.4	-19.8		-11.3	4.4	-10.4	11.2	



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Result Summary

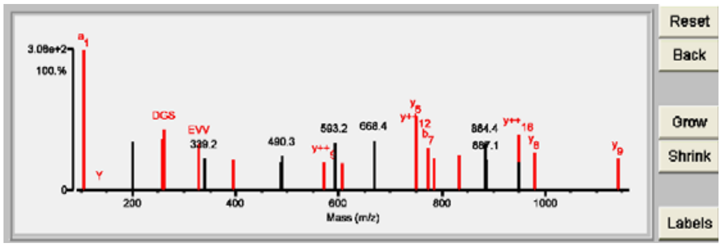
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.32	64.8	8	10/25	K1121k	(K)MQEVVANLQYDDGSGMkR(E)	2040.9477	114.0569	6.5	126968.6/5.14	HUMAN	Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.32	64.8	8	10/25	K1121k	(K) M Q/E V/V/A/N\L Q/Y/D D/G S/G M k R (E)	2040.9477	114.0569	6.5	126968.6/5.14	HUMAN	Q16531	152761	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1

Fragment-ion (m/z)	86.090	104.051	136.071	201.119	258.105	260.096	328.185	339.159	394.126	488.216^{+2}	490.256	571.736	593.228
Frac. Inten.(% of TIC)	2.89	13.13	0.10	4.58	4.75	5.64	4.32	2.97	2.84	2.60	3.22	2.64	4.44
Rel. Inten.(% of BP)	21.98	100.00	0.75	34.85	36.15	42.91	32.87	22.59	21.65	19.83	24.54	20.09	33.81
Score	-0.22	0.50	1.00	-0.35	0.75	0.75	0.75	-0.23	0.75	-0.20	-0.25	1.50	-0.34
Ion-type		a_1	Y		QE	DGS	EVV		YDD			y^{++}_9	
Delta ppm		-22.5	-32.3		-14.5	31.1	-3.6		3.8			-22.2	

Fragment-ion (m/z)	605.310	668.354	749.366	772.348	784.831	834.388^{+2}	884.427^{+2}	887.126^{+2}	948.426	948.942^{+2}	979.436	1142.481
Frac. Inten.(% of TIC)	2.51	4.63	6.96	3.97	2.98	3.27	4.41	2.85	5.20	2.62	3.55	2.95
Rel. Inten.(% of BP)	19.08	35.27	52.99	30.23	22.69	24.90	33.58	21.72	39.56	19.96	27.02	22.43
Score	1.50	-0.35	1.50	0.50	1.50	1.50	-0.34	-0.22	1.50	-0.20	1.50	1.50
Ion-type	y_4		y_6 y^{++}_{12}	b_7	y^{++}_{13}	y_{14}^{+2}			y^{++}_{16}		y_8	y_9
Delta ppm	-14.2		-8.0 33.5	-23.4	-37.1	-7.6			-24.5		10.3	-7.2



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Result Summary

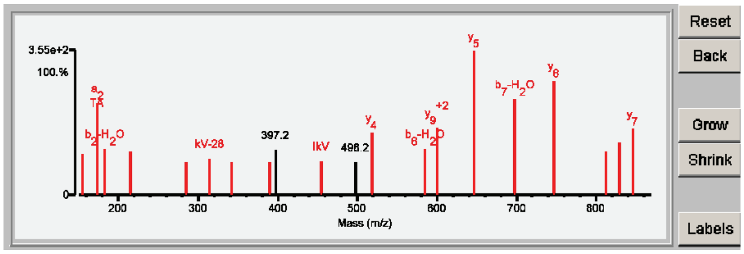
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.96	80.8	7	5/25	K1131k	(R)EATADDLIkVVEELTR(I)	1801.9542	114.0537	5.6	126968.6/5.14	HUMAN	Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.96	80.8	7	5/25	K1131k	(R) E A T A D D L/I\k/V/V/E/E/L T R (I)	1801.9542	114.0537	5.6	126968.6/5.14	HUMAN	Q16531	152761	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1

Fragment-ion (m/z)	72.078	84.079	102.055	141.106	155.082	173.095	183.079	215.135	284.122	314.223	342.217	389.236	397.166	455.301
Frac. Inten.(% of TIC)	0.31	6.55	0.15	4.48	3.09	6.83	3.42	3.26	2.42	2.68	2.41	2.39	3.36	2.54
Rel. Inten.(% of BP)	2.93	61.14	1.41	41.82	28.82	63.76	31.87	30.46	22.56	24.96	22.45	22.34	31.36	23.69
Score	0.50	-0.61	1.00	-0.42	0.50	0.75	0.25	0.75	0.25	0.50	0.75	1.50	-0.31	0.75
Ion-type	V		a_1		TA-H_2O	a_2	b_2-H_2O	LT	b_3-H_2O	kV-28	kV	y_3		IkV
Delta ppm	-38.5		-12.3		-5.8	7.7	5.9	-22.4	-12.3	10.6	7.7	-37.2		5.0
			1.00			TA								
			E			7.7								
			-1.5											

Fragment-ion (m/z)	498.232^{+3}	518.290	585.208	600.839^{+2}	647.337	698.304	746.407	811.376	829.398	845.484	953.503
Frac. Inten.(% of TIC)	2.42	4.61	3.39	4.96	10.72	7.08	8.47	3.28	3.87	4.87	2.42
Rel. Inten.(% of BP)	22.62	43.03	31.67	46.31	100.00	66.07	79.02	30.60	36.07	45.40	22.56
Score	-0.23	1.50	0.25	1.50	1.50	0.25	1.50	0.25	0.50	1.50	-0.23
Ion-type		y_4	b_6-H_2O	y_9^{+2}	y_5	b_7-H_2O	y_6	b_8-H_2O	b_8	y_7	
Delta ppm		-6.7	-13.8	-20.6	1.6	5.4	4.2	-10.5	3.3	12.9	



Result Summary

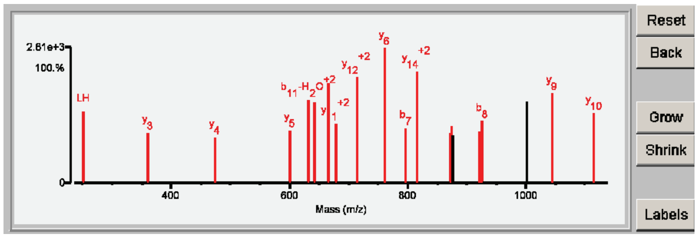
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.81	87.6	15	3/25	K600k	(R)SVLHEVMEQQTLSIAkAGIICQLNAR(T)	2909.5336	114.0870	14.6	96558.4/6.28	HUMAN	P33991	DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.81	87.6	15	3/25	K600k	(R) S V L H E V\M\E\Q Q/T|L/S I/A/k/A/G I/I/C/Q/L/N A R (T)	2909.5336	114.0870	14.6	96558.4/6.28	HUMAN	P33991	381743	DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5

Fragment-ion (m/z)	72.080	84.044	84.081	86.096	166.084	251.152	360.200	473.288	601.345	632.811^{+2}	641.810^{+2}	665.366	679.382^{+2}
Frac. Inten.(% of TIC)	0.24	0.13	0.22	0.33	3.99	4.62	3.30	2.98	3.44	5.35	5.20	6.55	3.88
Rel. Inten.(% of BP)	2.70	1.42	2.46	3.74	45.26	52.41	37.42	33.79	39.10	60.72	58.98	74.36	44.05
Score	0.50	1.00	0.50	0.22	-0.45	0.75	1.50	1.50	1.50	0.25	0.50	0.50	1.50
Ion-type	V	E	KQ	LI		LH	y_3	y_4	y_5	$b_{11}-H_2O^{+2}$	b_{11}^{+2}	b_6	y_{11}^{+2}
Delta ppm	-13.5	-3.5	-3.3	-6.1		2.6	3.3	9.6	5.9	11.4	2.2	5.3	14.6

Fragment-ion (m/z)	714.894^{+2}	761.380	796.409	814.956^{+2}	871.500^{+2}	874.464	875.476^{+2}	922.036^{+2}	925.464	1001.000^{+2}	1044.574	1115.612
Frac. Inten.(% of TIC)	6.88	8.81	3.58	7.30	3.27	3.73	3.14	3.34	4.02	5.31	5.87	4.55
Rel. Inten.(% of BP)	78.15	100.00	40.64	82.87	37.09	42.34	35.68	37.86	45.64	60.22	66.62	51.64
Score	1.50	1.50	0.50	1.50	1.50	1.50	-0.36	1.50	0.50	-0.60	1.50	1.50
Ion-type	y_{12}^{+2}	y_6	b_7	y_{14}^{+2}	y_{15}^{+2}	y_7		y_{16}^{+2}	b_8		y_9	y_{10}
Delta ppm	5.1	10.0	7.8	8.6	11.0	8.5		23.3	19.3		11.1	11.9



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Result Summary

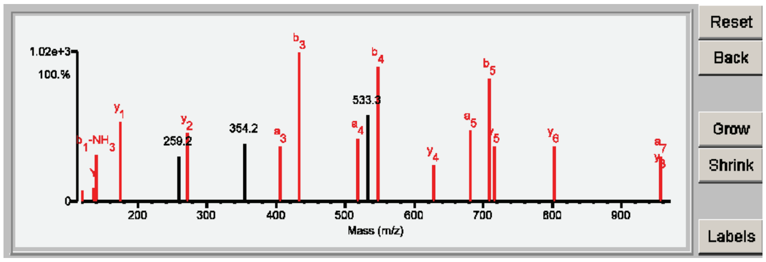
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.11	76.9	9	5/25	K145k	(R)RFELYFQGPSSNkPR(V)	1825.9344	114.0614	9.5	81308.4/6.08	HUMAN	P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.11	76.9	9	5/25	K145k	(R) R F E\L\Y\F Q/G P/S/S/N k/P/R (V)	1825.9344	114.0614	9.5	81308.4/6.08	HUMAN	P33993	190904	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.080	84.045	84.080	86.095	101.069	103.053	120.080	136.074	140.081	175.117	259.154
Frac. Inten.(% of TIC)	0.02	5.07	0.25	0.47	0.57	0.16	3.77	0.81	0.98	3.45	5.98	3.39
Rel. Inten.(% of BP)	0.15	45.25	2.25	4.23	5.05	1.44	33.64	7.27	8.76	30.80	53.35	30.23
Score	0.20	-0.45	1.00	0.50	0.22		-0.34	1.00	1.00	0.25	1.50	-0.30
Ion-type	PR		E	KQ	LI	KQ		F	Y	b_1-NH_3	y_1	
Delta ppm	-7.5		2.5	-5.7	-18.9			-5.6	-10.2	-17.4	-11.7	

Fragment-ion (m/z)	272.167	354.173	405.223	433.219	518.308	533.259^{+2}	546.301	628.343	681.375	709.370	715.382	802.420	956.500
Frac. Inten.(% of TIC)	5.11	4.36	4.13	11.20	4.74	6.47	10.13	2.76	5.28	9.20	4.15	4.13	3.42
Rel. Inten.(% of BP)	45.65	38.95	36.89	100.00	42.32	57.78	90.48	24.61	47.15	82.17	37.01	36.84	30.50
Score	1.50	-0.39	0.50	0.50	0.50	-0.58	0.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	y_2		a_3	b_3	a_4		b_4	y_4	a_5	b_5	y_5	y_6	a_7 y_8
Delta ppm	-16.2		-6.4	-2.3	-2.4		-7.2	-14.5	3.1	2.4	-3.0	3.8	0.0 9.6



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.54	67.0	6	7/25	K75k	(R)YAkLFADAVQELLPQYK(E)	1997.0742	114.0605	8.3	81308.4/6.08	HUMAN	P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH$^+$ Calculated (Da)</th><th>MH$^+$ Error (Da)</th><th>MH$^+$ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>12.54</td><td>67.0</td><td>6</td><td>7/25</td><td>K75k</td><td>(R) Y A k L F A D\A\V Q/E|L/L/P Q Y K (E)</td><td>1997.0742</td><td>114.0605</td><td>8.3</td><td>81308.4/6.08</td><td>HUMAN</td><td>P33993</td><td>381807</td><td>DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4</td></tr>
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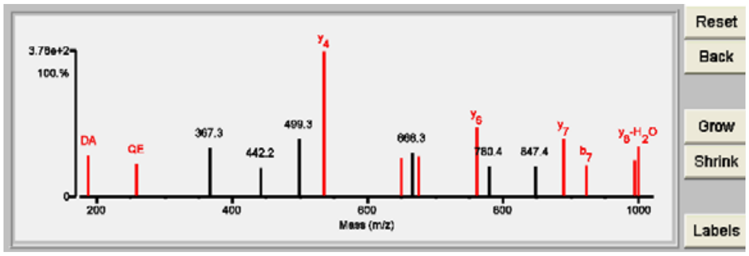
Fragment-ion (m/z)	70.064	72.080	84.043	84.078	86.097	101.069	120.082	136.080	143.120	187.072	258.106	367.276	442.222
Frac. Inten.(% of TIC)	0.01	0.22	0.14	0.23	0.45	0.11	0.18	0.14	3.91	4.97	4.05	5.85	3.58
Rel. Inten.(% of BP)	0.04	1.23	0.80	1.30	2.59	0.65	1.03	0.82	22.30	28.37	23.09	33.40	20.41
Score	0.20	0.50	1.00	0.50	0.22		1.00	1.00 1.00	-0.22	0.75	0.75	-0.33	-0.20
Ion-type	PR	V	E	KQ	LI	KQ	F	a_1 Y		DA	QE		
Delta ppm	-23.2	-10.8	-16.5	-30.6	6.7		6.9	26.5 34.6		0.4	-13.7		

Fragment-ion (m/z)	499.282	535.285	648.391	666.332^{+2}	675.837^{+2}	761.464	780.403	847.438^{+2}	890.492	923.448	994.470	1000.519
Frac. Inten.(% of TIC)	6.97	17.52	4.70	5.28	4.83	8.29	3.68	3.69	6.93	3.78	4.43	6.08
Rel. Inten.(% of BP)	39.77	100.00	26.83	30.14	27.55	47.35	21.02	21.05	39.58	21.55	25.27	34.70
Score	-0.40	1.50	1.50	-0.30	0.50	1.50	-0.21	-0.21	1.50	0.50	0.50	0.50
Ion-type		y_4	y_5		b_{11}^{+2}	y_6			y_7	b_7	b_8	y_8-H_2O
Delta ppm		-4.1	29.7		-1.6	11.6			-7.0	-16.3	-31.0	-27.5



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Result Summary

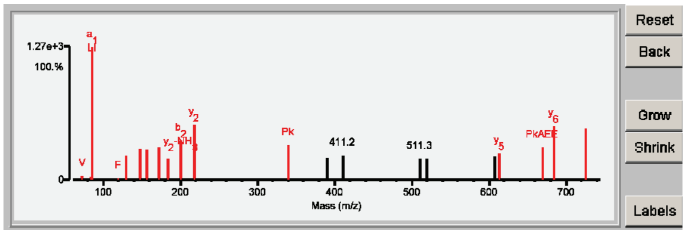
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.63	81.0	5	6/25	K252k	(K)LSPkAEEVATFFAK(M)	1537.8261	114.0582	9.2	90726.2/9.33	HUMAN	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2
2	9.14	57.5	2	8/25	K44k K49k	(R)LLEPLVTQVTTLVNTSNkGPSGkK(K)	2524.4345	228.0344	-18.7	105313.5/5.52	HUMAN	P26232	Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5
3	8.17	63.7	2	8/25	M560m K555k	(R)RNLAESSGVGRVGAGSRPkPEAPmAK(G)	2622.3893	130.0796	15.2	97502.7/9.63	HUMAN	Q8IY33	MICAL-like protein 2 OS=Homo sapiens GN=MICALL2 PE=1 SV=1
4	6.80	52.1	3	9/25	K71k	(K)KLEPIWNEVGLEMkSIGSPVKVGK(M)	2638.4637	114.0052	-13.7	51872.3/4.80	HUMAN	Q96JJ7	Protein disulfide-isomerase TXNDC10 OS=Homo sapiens GN=TXNDC10 PE=1 SV=2
5	6.42	55.5	1	7/25	None	(K)HQMNLLEARSIIPMVIFELSVPSK(E)	2752.4888	-0.0199	-7.2	115192.6/6.30	HUMAN	Q3MIS4	Uncharacterized protein C6orf224 OS=Homo sapiens GN=C6orf224 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.63	81.0	5	6/25	K252k	(K) L S|P k A E E V/A/T F F/A/K (M)	1537.8261	114.0582	9.2	90726.2/9.33	HUMAN	P11387	394331	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2

Fragment-ion (m/z)	70.064	72.080	84.043	84.081	86.095	120.079	129.099	130.087	147.111	157.095	173.127	185.093
Frac. Inten.(% of TIC)	0.01	0.56	0.10	0.44	18.60	0.30	0.15	3.39	4.41	4.26	4.54	3.01
Rel. Inten.(% of BP)	0.05	3.01	0.54	2.36	100.00	1.62	0.82	18.22	23.71	22.89	24.40	16.18
Score	0.20	0.50	1.00	0.50	0.50 0.50	1.00	0.20	0.50	1.50	0.50	0.50	0.75
Ion-type	PR	V	E	KQ	a_1 LI	F	RKQ	y_1-NH$_3$	y_1	SP-28	a_2	SP
Delta ppm	-11.8	-13.5	-18.9	6.2	-24.7 -11.9	-15.6	-28.2	1.9	-15.0	-23.2	-17.0	-0.4

Fragment-ion (m/z)	201.122	218.150	340.196	390.188	411.229^{+3}	511.272	520.284	607.353	613.334	669.322	684.376	726.380^{+2}	835.443
Frac. Inten.(% of TIC)	5.52	7.77	4.93	3.07	3.45	2.97	2.96	3.20	3.71	4.51	7.53	7.28	3.33
Rel. Inten.(% of BP)	29.66	41.78	26.50	16.49	18.55	15.96	15.93	17.19	19.92	24.23	40.45	39.16	17.89
Score	0.50	1.50	0.75	-0.16	-0.19	-0.16	-0.16	-0.17	1.50	0.75	1.50	1.50	-0.18
Ion-type	b_2 y_2-NH$_3$	y_2	Pk						y_5	PkAEE	y_6	y_{12}^{+2}	
Delta ppm	-11.3 -5.8	1.8	-7.7						-1.3	0.6	6.4	0.0	



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Result Summary

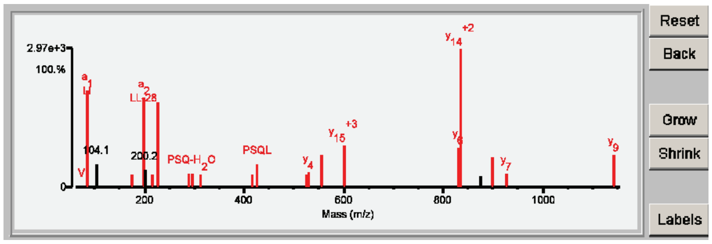
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.58	93.5	8	3/25	K129k	(R)LLMPSQLVSQVGkELLR(L)	1911.1096	114.0560	6.4	25370.7/4.87	HUMAN	Q9NX09	DNA-damage-inducible transcript 4 protein OS=Homo sapiens GN=DDIT4 PE=1 SV=1
2	11.77	61.1	4	9/25	K104k	(R)LLEkGVQSVLQSPMLLR(A)	1911.1096	114.0560	6.4	25370.7/4.87	HUMAN	RQ9NX09	REVERSE DNA-damage-inducible transcript 4 protein OS=Homo sapiens GN=DDIT4 PE=1 SV=1
3	6.17	64.6	2	16/25	K276k	(K)ILMANkINENLKPERK(E)	1911.0844	114.0811	18.9	35583.1/10.00	HUMAN	RQ9H7B2	REVERSE Brix domain-containing protein 1 OS=Homo sapiens GN=BXDC1 PE=1 SV=2
3	6.17	64.6	2	16/25	K282k	(K)ILMANKINENLkPERK(E)	1911.0844	114.0811	18.9	35583.1/10.00	HUMAN	RQ9H7B2	REVERSE Brix domain-containing protein 1 OS=Homo sapiens GN=BXDC1 PE=1 SV=2
3	6.17	64.6	2	16/25	K286k	(K)ILMANKINENLKPERk(E)	1911.0844	114.0811	18.9	35583.1/10.00	HUMAN	RQ9H7B2	REVERSE Brix domain-containing protein 1 OS=Homo sapiens GN=BXDC1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.58	93.5	8	3/25	K129k	(R) L L|M/P S Q L V/S Q/V/G k/E L/L/R (L)	1911.1096	114.0560	6.4	25370.7/4.87	HUMAN	Q9NX09	154071	DNA-damage-inducible transcript 4 protein OS=Homo sapiens GN=DDIT4 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.079	86.096	101.068	104.052	175.120	199.181	200.181	216.094	227.174	288.201	295.136
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 **PR** -1.8	0.07 0.40 0.50 **V** -30.2	12.35 69.25 0.50 a_1 -23.5 0.50 **LI** -10.8	0.05 0.26 0.50 **QK** -25.1	2.94 16.50 -0.16	1.62 9.08 1.50 y_1 3.7	11.47 64.32 0.50 a_2 -5.0 **LL**-28 -5.0	2.18 12.23 -0.12	1.53 8.57 0.75 **SQ** -22.6	10.93 61.28 0.75 b_2 -9.3 **LL** -9.3	1.75 9.83 1.50 y_2 -7.0	1.76 9.84 0.50 **PSQ**-H_2O -18.6

Fragment-ion (m/z)	313.156	415.259^{+2}	426.243	525.306	530.333	556.651^{+3}	600.334^{+3}	829.493	834.483^{+2}	874.417	899.991^{+2}	928.561	1143.640
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.66 9.30 0.75 **PSQ** 14.9	1.68 9.39 1.50 y_6^{+2} 26.2	2.95 16.54 0.75 **PSQL** 16.6	1.60 8.95 0.75 **PSQLV** 3.4	1.89 10.58 1.50 y_4 6.5	4.20 23.53 1.50 y_{14}^{+3} -3.1	5.40 30.27 1.50 y_{15}^{+3} 2.2	5.04 28.25 1.50 y_6 4.8	17.84 100.00 1.50 y_{14}^{+2} 9.1	1.42 7.96 -0.08	3.83 21.49 1.50 y_{15}^{+2} -4.9	1.71 9.57 1.50 y_7 4.0	4.14 23.23 1.50 y_9 -7.3



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Result Summary

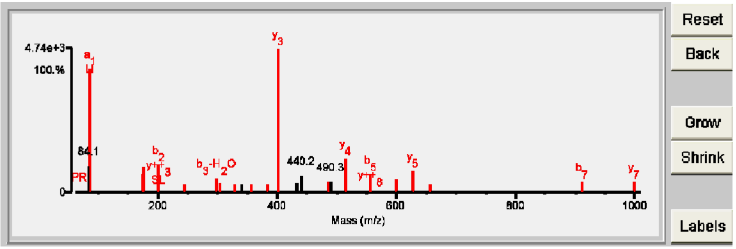
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.95	87.9	10	5/25	K344k	(K)LSLLEkLLPER(K)	1310.8042	114.0505	5.3	45610.1/6.65	HUMAN	P31689	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2
2	7.68	69.0	4	13/25	None	(R)LRGAAERPRRSR(D)	1424.8305	0.0242	17.0	103656.7/8.57	HUMAN	Q9Y2I9	TBC1 domain family member 30 OS=Homo sapiens GN=TBC1D30 PE=2 SV=2
3	6.01	63.2	3	16/25	None	(R)LRLQLGSPGSLQR(K)	1424.8332	0.0215	15.1	178278.3/6.19	HUMAN	Q9Y6N6	Laminin subunit gamma-3 OS=Homo sapiens GN=LAMC3 PE=2 SV=2
4	5.53	63.9	2	16/25	None	(K)LNGVKLWITAGPR(E)	1424.8372	0.0175	12.3	49991.9/5.14	HUMAN	Q9Y366	Intraflagellar transport protein 52 homolog OS=Homo sapiens GN=IFT52 PE=2 SV=3
5	5.05	64.2	1	15/25	K620k	(K)LPVADIKAVVTGk(D)	1310.8042	114.0505	5.3	84571.6/5.89	HUMAN	Q92556	Engulfment and cell motility protein 1 OS=Homo sapiens GN=ELMO1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.95	87.9	10	5/25	K344k	(K) L/S\L/L/E\k/L|L/P/E/R (K)	1310.8042	114.0505	5.3	45610.1/6.65	HUMAN	P31689	83416	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2

Fragment-ion (m/z)	70.065	84.078	86.096	173.128	175.118	201.117	243.136	296.194	304.163	328.224	341.205	356.220
Frac. Inten.(% of TIC)	0.00	4.54	21.04	2.93	4.17	4.63	1.36	2.48	1.61	1.27	1.35	1.42
Rel. Inten.(% of BP)	0.00	18.61	86.27	12.00	17.10	18.98	5.56	10.15	6.61	5.21	5.55	5.81
Score	0.20	-0.19	0.50	0.50	1.50	1.50	0.75	0.25	1.50	0.50	-0.06	0.75
Ion-type	PR		a_1	a_2	y_1	b_2	LE	b_3-H_2O	y_2	kL-28		kL
Delta ppm	-7.5		-7.3	-0.3	-3.2	-30.2	7.3	-8.7	3.1	-32.3		-24.8
			0.50	SL-28		$y{+}{+}_3$						
			LI	-0.3		32.4						
			-7.3			SL						
						-30.2						

Fragment-ion (m/z)	384.196	401.213	433.295	440.246	485.280	490.316^{+2}	514.300	556.337	598.354	627.386	656.378^{+2}	911.562	998.578
Frac. Inten.(% of TIC)	1.46	24.39	1.61	2.72	1.75	1.87	5.82	3.08	2.09	3.56	1.39	1.67	1.79
Rel. Inten.(% of BP)	5.97	100.00	6.59	11.13	7.16	7.69	23.88	12.63	8.59	14.62	5.71	6.85	7.35
Score	0.50	1.50	-0.07	-0.11	0.75	-0.08	1.50	1.50	0.75	1.50	1.50	0.50	1.50
Ion-type	y_3-NH_3	y_3			EkL		y_4	b_5	EkLL	y_5	y_{10}^{+2}	b_7	y_7
Delta ppm	22.0	-2.8			17.1		3.0	5.2	-4.0	5.4	-10.5	6.2	15.1
								$y{+}{+}_8$					
								17.7					



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Result Summary

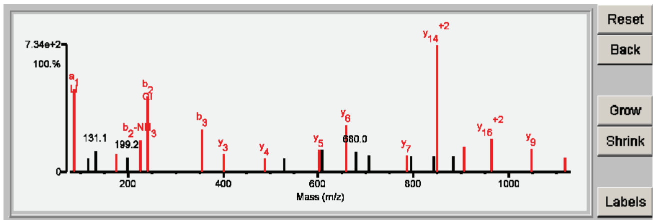
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.18	77.9	11	10/25	K82k	(R)IQINPQNkADFQGISPER(A)	2055.0618	114.0624	9.0	12496.8/6.52	HUMAN	P61803	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.18	77.9	11	10/25	K82k	(R) I Q|I|N/P Q N k/A/D F/Q/G/I/S/P E/R (A)	2055.0618	114.0624	9.0	12496.8/6.52	HUMAN	P61803	144453	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=3

Fragment-ion (m/z)	86.097	116.071	131.117	175.120	199.179	225.119	242.148	355.230	401.228	488.245	529.208	601.320	608.818	658.350
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	10.99 65.70 0.50 a_1 -9.6 0.50 LI 3.2	1.80 10.78 -0.11	2.74 16.35 -0.16	2.35 14.04 1.50 y_1 4.3	1.97 11.76 -0.12	4.22 25.24 0.25 b_2-NH_3 -24.3	9.94 59.40 0.75 b_2 -11.2 QI -11.2	5.66 33.81 0.50 b_3 -13.7	2.29 13.71 1.50 y_3 34.4	1.83 10.96 1.50 y_4 -2.9	1.77 10.60 -0.11	2.95 17.61 1.50 y_5 -16.8	2.88 17.21 -0.17	6.16 36.79 1.50 y_6 -2.2

Fragment-ion (m/z)	680.049	706.726	786.413	794.889	842.944^{+2}	850.924^{+2}	884.419	907.954^{+2}	964.520^{+2}	1048.507	1119.579
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.63 15.73 -0.16	2.21 13.22 -0.13	2.19 13.10 1.50 y_7 3.4	2.02 12.05 -0.12	2.06 12.31 -0.12	16.73 100.00 1.50 y_{14}^{+2} 3.6	2.02 12.06 -0.12	3.31 19.76 1.50 y_{15}^{+2} 12.1	4.36 26.04 1.50 y_{16}^{+2} 36.5	3.02 18.07 1.50 y_9 1.6	1.91 11.42 1.50 y_{10} 32.4



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Result Summary

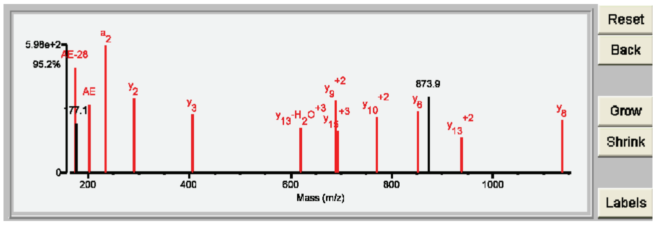
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.04	66.9	9	6/25	K67k	(R)FLAEEGFYkFHNWFDDR(A)	2221.0138	114.0632	8.7	80530.1/8.28	HUMAN	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.04	66.9	9	6/25	K67k	(R) F L/A E/E G F/Y/k/F H/N W F/D/D/R (A)	2221.0138	114.0632	8.7	80530.1/8.28	HUMAN	P46977	737579	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2

Fragment-ion (m/z)	84.042	84.081	86.096	102.054	110.074	120.080	121.082	136.075	155.094	157.133	173.091	175.115	177.095	201.086
Frac. Inten.(% of TIC)	0.07	9.63	0.93	0.08	0.08	1.19	7.66	0.20	2.84	3.94	7.57	6.78	3.55	4.90
Rel. Inten.(% of BP)	0.76	100.00	9.67	0.85	0.87	12.38	79.54	2.06	29.45	40.92	78.54	70.40	36.89	50.88
Score		-1.00	0.22	1.00	1.00	1.00 1.00	-0.80	1.00	-0.29	-0.41	0.50	1.50	-0.37	0.75
Ion-type	E		LI	E	H	a$_1$ F		Y			AE-28	y$_1$		AE
Delta ppm			-7.3	-9.4	22.0	-5.6 -5.6		-8.0			-5.6	-23.1		-7.4

Fragment-ion (m/z)	233.165	290.149	405.168	619.605^{+3}	689.821^{+2}	692.327^{+3}	771.357^{+2}	852.366	873.891^{+2}	937.901^{+2}	1136.506
Frac. Inten.(% of TIC)	9.16	5.41	4.22	3.26	5.20	3.03	4.03	4.44	5.48	2.52	3.82
Rel. Inten.(% of BP)	95.10	56.12	43.75	33.80	53.96	31.41	41.79	46.09	56.87	26.13	39.69
Score	0.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	-0.57	1.50	1.50
Ion-type	a$_2$	y$_2$	y$_3$	y$_{13}$-H$_2$O^{+3}	y$_9$$^{+2}$	y$_{15}$$^{+3}$	y$_{10}$$^{+2}$	y$_6$		y$_{13}$$^{+2}$	y$_8$
Delta ppm	1.1	12.4	-11.7	-6.8	3.8	29.8	9.8	2.6		-15.9	13.5



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Result Summary

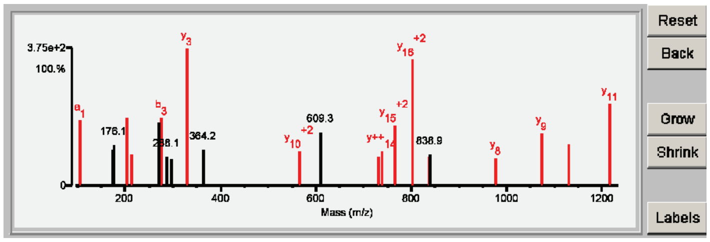
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.97	69.9	10	10/25	K255k	(R)MAAAGGTVSGPSSACkPGR(S)	1761.8371	114.0539	5.8	289596.3/5.29	HUMAN	Q9ULT8	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.97	69.9	10	10/25	K255k	(R) M A|A|A/G/G T V/S/G/P/S S A/C k/P G R (S)	1761.8371	114.0539	5.8	289596.3/5.29	HUMAN	Q9ULT8	277349	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=2

Fragment-ion (m/z)	84.079	104.052	173.125	175.098	176.095	203.083	214.117	269.154	274.120	288.110	296.173	329.194	364.172
Frac. Inten.(% of TIC)	3.08	5.10	2.14	2.80	3.22	5.30	2.44	4.99	5.36	2.30	2.12	10.81	2.79
Rel. Inten.(% of BP)	28.52	47.15	19.78	25.93	29.80	49.00	22.56	46.16	49.61	21.28	19.59	100.00	25.80
Score	-0.29	0.50	-0.20	-0.26	-0.30	0.50	0.75	-0.46	0.50	-0.21	-0.20	1.50	-0.26
Ion-type		a_1				b_2	AAA		b_3			y_3	
Delta ppm		-18.7				-14.6	-13.6		-12.4			1.9	

Fragment-ion (m/z)	565.761^{+2}	609.323^{+2}	731.354	737.859	766.364^{+2}	801.917^{+2}	837.408^{+2}	838.919^{+2}	976.447	1073.526	1130.537	1217.570
Frac. Inten.(% of TIC)	2.75	4.17	2.25	2.77	4.80	9.96	2.28	2.47	2.18	4.17	3.29	6.45
Rel. Inten.(% of BP)	25.39	38.60	20.82	25.63	44.37	92.11	21.12	22.88	20.13	38.55	30.47	59.61
Score	1.50	-0.39	1.50	1.50	1.50	1.50	1.50	-0.23	1.50	1.50	1.50	1.50
Ion-type	y_{10}^{+2}		y_5	$y{++}_{14}$	y_{15}^{+2}	y_{16}^{+2}	a_{18}^{+2} y_{17}^{+2}		y_8	y_9	y_{10}	y_{11}
Delta ppm	-19.6		-11.2	2.5	-4.3	38.3	20.8 4.1		-16.6	9.4	0.3	0.7



Result Summary

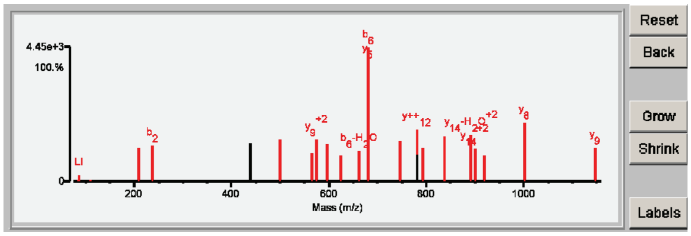
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.48	92.2	11	2/25	K3345k	(R)HVLDTLIQLAkVFPSHFTQQR(T)	2478.3616	114.0586	6.0	481893.3/5.10	HUMAN	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.48	92.2	11	2/25	K3345k	(R) H V\L D T\L\I|Q|L/A/k/V/F/P S H/F T Q Q R (T)	2478.3616	114.0586	6.0	481893.3/5.10	HUMAN	Q7Z6Z7	304349	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3

Fragment-ion (m/z)	84.079	86.096	101.071	110.071	120.080	209.137	237.135	438.274^{+2}	500.753^{+2}	566.294	574.287^{+2}	594.983^{+3}
Frac. Inten.(% of TIC)	0.25	0.75	0.11	0.20	0.08	3.96	4.17	4.56	4.85	3.29	4.92	4.38
Rel. Inten.(% of BP)	1.59	4.75	0.70	1.25	0.52	25.17	26.54	29.05	30.85	20.97	31.32	27.88
Score	0.50	0.22		1.00 1.00	1.00	0.50	0.50	-0.29	1.50	0.50	1.50	0.50
Ion-type	KQ	LI	KQ	a_1 H	F	a_2	b_2		y_8^{+2}	b_5	y_9^{+2}	y_{14}-H_2O^{+3}
Delta ppm	-16.4	-9.6		-15.2 -5.2	-6.5	-17.1	-2.1		3.6	-0.2	1.4	-3.3

Fragment-ion (m/z)	623.820^{+2}	661.369	679.374	744.898^{+2}	780.405	780.914	792.464	836.948^{+2}	891.979^{+2}	900.977^{+2}	920.525	1000.502	1147.566
Frac. Inten.(% of TIC)	2.97	3.51	15.71	4.71	6.07	3.19	3.95	5.32	5.43	3.81	2.97	6.94	3.90
Rel. Inten.(% of BP)	18.89	22.37	100.00	30.00	38.66	20.29	25.13	33.87	34.58	24.25	18.88	44.17	24.81
Score	1.50	0.25	1.50	1.50	1.50	-0.20	0.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y_{10}^{+2}	b_6-H_2O	b_6 y_5	y_{11}^{+2}	y++12		b_7	b_{14}-NH_3^{+2} y_{13}^{+2}	y_{14}-H_2O^{+2}	y_{14}^{+2}	b_8	y_8	y_9
Delta ppm	0.5	1.1	-6.0 32.7	11.6	-3.5		1.9	-32.3 -1.6	5.6	-2.0	4.5	6.0	1.6



Nature Biotechnology: doi: 10.1038/nbt.1654

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Result Summary

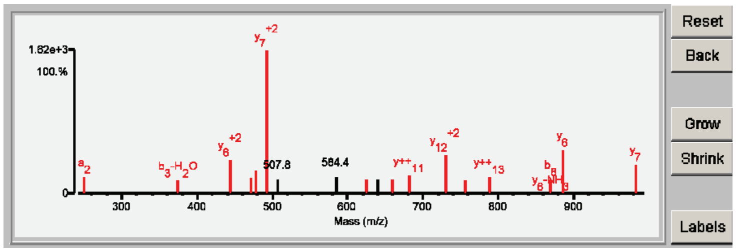
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.92	76.2	8	6/25	K446k	(K)EFDPLGPLPPGWEkR(T)	1737.8959	114.0602	9.3	102803.3/5.94	HUMAN	Q96J02	E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.92	76.2	8	6/25	K446k	(K) E F/D/P/L/G\P\L|P/P G W E k R (T)	1737.8959	114.0602	9.3	102803.3/5.94	HUMAN	Q96J02	328773	E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH PE=1 SV=2

Fragment-ion (m/z)	70.064	84.081	86.096	120.079	183.145	231.112	249.121	374.142	443.735^{+2}	471.180	478.305	492.258^{+2}	507.790
Frac. Inten.(% of TIC)	0.02	7.31	0.24	0.08	5.58	3.67	2.76	2.04	5.50	2.57	3.83	23.68	2.36
Rel. Inten.(% of BP)	0.08	30.87	1.03	0.36	23.57	15.49	11.67	8.62	23.25	10.87	16.18	100.00	9.95
Score	0.20	-0.31	0.22	1.00	-0.24	-0.15	0.50	0.25	1.50	0.25	0.75	1.50	-0.10
Ion-type	PR		LI	F			a_2	b_3-H_2O	y_6^{+2}	b_4-H_2O	LGPLP	y_7^{+2}	
Delta ppm	-21.8		-9.6	-11.5			-15.1	16.4	10.8	-17.2	3.6	3.2	

Fragment-ion (m/z)	584.272	584.369	625.821^{+2}	640.374	659.316	682.352	730.932^{+2}	756.371	788.390	869.414	886.456	983.518
Frac. Inten.(% of TIC)	2.20	2.64	2.41	2.24	2.38	2.85	6.35	2.18	2.72	2.40	7.24	4.75
Rel. Inten.(% of BP)	9.31	11.13	10.16	9.47	10.04	12.03	26.82	9.19	11.47	10.15	30.57	20.08
Score	0.25	-0.11	1.50	-0.09	0.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	b_5-H_2O		y_{10}^{+2}		b_6	y^{++}_{11}	y_{12}^{+2}	b_7	y^{++}_{13}	b_8 y_6-NH_3	y_6	y_7
Delta ppm	-1.5		-23.4		17.4	-36.9	38.5	17.9	-34.8	-32.0 -14.8	3.6	12.7



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Result Summary

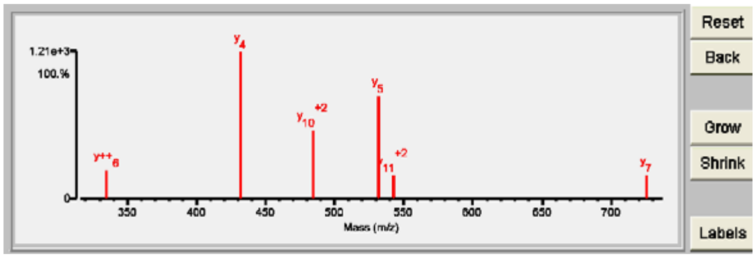
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.40	63.8	7	6/25	K28k	(K)WGkQDGGEGHVGTVR(S)	1582.7721	114.0489	3.5	110136.6/6.47	HUMAN	Q86YT6	E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.40	63.8	7	6/25	K28k	(K) W G k Q/D/G G E/G/H/V/G T V/R (S)	1582.7721	114.0489	3.5	110136.6/6.47	HUMAN	Q86YT6	395271	E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=2 SV=1

Fragment-ion (m/z)	72.081	84.043	84.081	87.054	88.037	101.069	110.070	115.049	129.100	130.062	132.080	141.102	142.093
Frac. Inten.(% of TIC)	0.17	0.18	0.59	4.32	3.13	0.08	0.59	2.86	0.08	0.14	6.71	3.93	2.87
Rel. Inten.(% of BP)	1.07	1.17	3.77	27.43	19.86	0.49	3.73	18.15	0.50	0.90	42.53	24.93	18.19
Score	0.50	1.00	0.50	0.50	-0.20		1.00	0.75	0.20		-0.43	-0.25	-0.18
Ion-type	V	E	KQ	NR GG-28		KQ	H	GG	RKQ	W			
Delta ppm	4.5	-16.5	-0.9	-11.4 -11.4			-8.8	-12.2	-19.7				

Fragment-ion (m/z)	159.088	167.094	170.058	175.115	195.086	227.075	334.702	432.255	484.753^{+2}	531.326	542.275^{+2}	725.419
Frac. Inten.(% of TIC)	0.40	2.51	15.74	6.32	3.33	3.84	3.06	15.77	7.31	11.03	2.52	2.51
Rel. Inten.(% of BP)	2.56	15.94	99.79	40.06	21.14	24.35	19.41	100.00	46.39	69.98	15.96	15.89
Score	2.00 2.00	0.50	-1.00	1.50	0.75	-0.24	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	a_1 W	GH-28		y_1	GH		y^{++}_6	y_4	y_{10}^{+2}	y_5	y_{11}^{+2}	y_7
Delta ppm	-21.2 -21.2	7.0		-20.9	-8.0		19.9	-4.2	7.7	1.1	24.0	18.5



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Result Summary

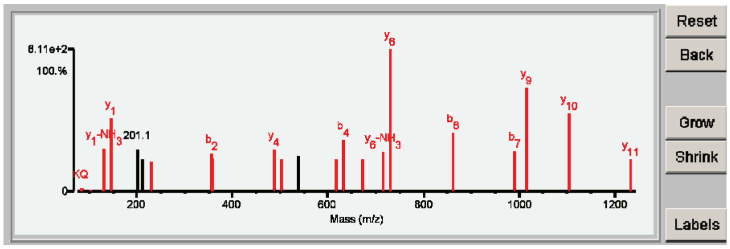
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.90	89.2	11	3/25	K421k	(K)kLFETQESGDLNEELVK(A)	1978.9968	114.0606	8.4	110136.6/6.47	HUMAN	Q86YT6	E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=2 SV=1
2	6.25	58.8	3	12/25	K533k	(K)IKIEHAPSPSSGGTLkNDK(A)	1979.0556	114.0017	-19.7	164924.0/9.71	HUMAN	Q14004	Cell division cycle 2-like protein kinase 5 OS=Homo sapiens GN=CDC2L5 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.90	89.2	11	3/25	K421k	(K) k L\F\E\T Q|E|S/G D L/N/E/E/L V/K (A)	1978.9968	114.0606	8.4	110136.6/6.47	HUMAN	Q86YT6	395271	E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=2 SV=1

Fragment-ion (m/z)	84.042	84.081	86.097	102.053	129.100	130.091	147.112	201.119	213.084	230.112	356.225	359.255	488.310
Frac. Inten.(% of TIC)	0.10	0.34	0.24	0.13	0.17	4.24	7.23	4.15	3.16	2.89	3.69	3.26	4.05
Rel. Inten.(% of BP)	0.75	2.46	1.72	0.97	1.25	30.55	52.10	29.89	22.81	20.84	26.58	23.48	29.21
Score		0.50	0.22	1.00	0.20	0.50	1.50	-0.30	-0.23	0.75	0.50	1.50	1.50
Ion-type	E	KQ	LI	E	RKQ	y_1-NH$_3$	y_1			TQ	b_2	y_3	y_4
Delta ppm		-2.1	3.2	-18.2	-14.2	33.4	-6.8			-11.4	-16.1	-28.1	3.3

Fragment-ion (m/z)	503.301	537.272	617.350	632.347	672.326^{+2}	714.378	731.404	861.458	990.482	1016.535	1103.568	1232.605
Frac. Inten.(% of TIC)	3.17	3.44	3.11	4.99	3.18	3.90	13.87	5.77	3.92	10.15	7.69	3.15
Rel. Inten.(% of BP)	22.86	24.83	22.44	35.94	22.92	28.10	100.00	41.62	28.27	73.17	55.46	22.74
Score	0.50	-0.25	1.50	0.50	0.50	0.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	b_3		y_5	b_4	y_{12}-NH$_3^{+2}$	y_6-NH$_3$	y_6	b_6	b_7	y_9	y_{10}	y_{11}
Delta ppm	3.5		-0.9	9.0	9.1	14.9	13.8	12.4	-8.6	9.2	9.2	3.7



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Result Summary

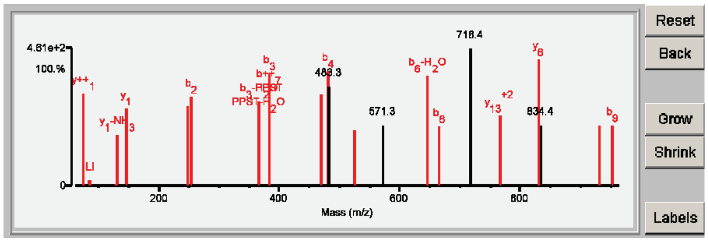
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.52	80.5	9	4/25	K197k	(K)RPEPPSTSTLkQVTK(V)	1668.9279	114.0488	3.3	56194.9/7.17	HUMAN	Q9NS91	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1
2	6.33	64.1	7	8/25	K201k	(K)RPEPPSTSTLKQVTk(V)	1668.9279	114.0488	3.3	56194.9/7.17	HUMAN	Q9NS91	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.52	80.5	9	4/25	K197k	(K) R P|E\P\P S\T\S/T|L/k Q V/T/K (V)	1668.9279	114.0488	3.3	56194.9/7.17	HUMAN	Q9NS91	277676	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1

Fragment-ion (m/z)	70.065	74.059	84.080	86.095	129.101	130.083	147.111	248.163	254.161	365.194	383.201	468.231^{+2}
Frac. Inten.(% of TIC)	0.01	5.01	0.26	0.27	0.10	2.80	4.22	4.36	4.82	4.61	6.10	4.99
Rel. Inten.(% of BP)	0.17	66.83	3.48	3.59	1.31	37.29	56.31	58.13	64.32	61.52	81.38	66.55
Score	0.20	1.50	0.50	0.22	0.20	0.50	1.50	1.50	0.50	0.50	0.75	0.25
Ion-type	PR	y^{++}_1	KQ	LI	RKQ	y_1-NH_3	y_1	y_2	b_2	b_3-H_2O	b_3	b_9-H_2O^{+2}
Delta ppm	3.9	-16.7	-6.8	-21.2	-12.7	-25.0	-15.7	10.1	-6.5	-0.8	-10.3	-4.6
										PPST-H_2O	b^{++}_7	
										30.0	5.8	
											PPST	
											19.0	

Fragment-ion (m/z)	480.255	483.284^{+2}	524.771^{+2}	571.321^{+3}	646.324	664.352	717.424	718.434^{+2}	765.392^{+2}	830.518	834.415^{+2}	931.572	953.458
Frac. Inten.(% of TIC)	6.23	5.44	3.07	3.29	5.97	3.24	7.11	7.50	3.82	6.92	3.29	3.28	3.29
Rel. Inten.(% of BP)	83.09	72.52	40.94	43.89	79.64	43.26	94.77	100.00	50.94	92.23	43.87	43.76	43.89
Score	0.50	-0.73	0.25	-0.44	0.25	0.50	1.50	-1.00	1.50	1.50	-0.44	1.50	0.50
Ion-type	b_4		b_{10}-H_2O^{+2}		b_6-H_2O	b_6	y_5		y_{13}^{+2}	y_6		y_7	b_9
Delta ppm	-5.0		-7.4		-12.3	15.2	-2.2		-26.0	10.7		16.5	-12.1



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.47	100.0	11	0/25	K309k	(K)SAAEIVQEIENIEkTR(M)	1829.9603	114.0639	10.8	56194.9/7.17	HUMAN	Q9NS91	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1
2	8.35	59.2	2	11/25	None	(K)QLTEKEARIAELSAQTR(V)	1944.0509	-0.0266	-13.7	76068.7/5.58	HUMAN	RQ8N6Y0	REVERSE USH1C-binding protein 1 OS=Homo sapiens GN=USHBP1 PE=1 SV=1
3	7.66	60.4	3	11/25	K626k	(R)LEVQVMQGTQkSQTPR(V)	1829.9538	114.0704	14.2	70519.5/5.60	HUMAN	A4FU49	SH3 domain-containing protein C1orf113 OS=Homo sapiens GN=C1orf113 PE=1 SV=2
4	6.96	55.6	1	11/25	None	(K)EPLSAEAELDNLVYPKR(V)	1944.0073	0.0170	8.7	21188.5/9.94	HUMAN	RQ9Y3C1	REVERSE Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2
5	6.72	51.8	3	13/25	None	(K)DCPVVVSAGNSELSLQLR(L)	1943.9855	0.0387	19.9	52901.5/7.07	HUMAN	Q15036	Sorting nexin-17 OS=Homo sapiens GN=SNX17 PE=1 SV=1

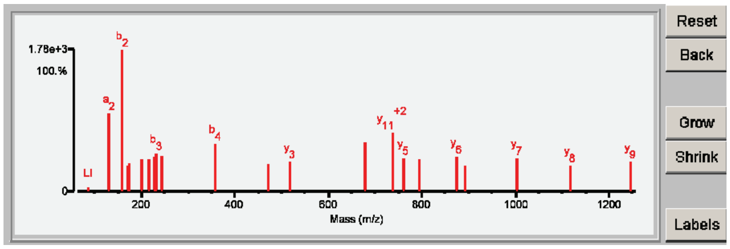
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.47	100.0	11	0/25	K309k	(K) S A|A\E|I|V Q/E/I/E/N/I E/k T/R (M)	1829.9603	114.0639	10.8	56194.9/7.17	HUMAN	Q9NS91	555351	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1

Fragment-ion (m/z)	72.080	84.041	84.081	86.095	131.082	159.077	173.094	175.116
Frac. Inten.(% of TIC)	0.10	0.09	0.09	0.46	8.84	16.04	2.98	3.20
Rel. Inten.(% of BP)	0.61	0.55	0.57	2.88	55.08	100.00	18.60	19.96
Score	0.50	1.00	0.50	0.22	0.50	0.50	0.50	1.50
Ion-type	V	E	KQ	LI	a_2	b_2	AE-28	y_1
Delta ppm	-10.8	-39.1	7.4	-14.2	-3.8	-1.4	4.8	-14.6

Fragment-ion (m/z)	201.088	215.139	228.138	230.116	243.139	359.157	472.254	518.301
Frac. Inten.(% of TIC)	3.65	3.70	3.88	4.29	4.07	5.39	3.15	3.40
Rel. Inten.(% of BP)	22.78	23.05	24.20	26.77	25.36	33.62	19.63	21.19
Score	0.75	0.50	0.75	0.50	0.75	0.50	0.50	1.50
Ion-type	AE	IE-28	NI	b_3	IE	b_4	b_5	y_3
Delta ppm	-1.9	-3.8	12.0	3.8	18.0	-0.3	26.9	-6.6

Fragment-ion (m/z)	678.346^{+2}	736.896^{+2}	760.440	793.420^{+2}	874.471	893.451^{+2}	1003.513	1116.597	1245.625
Frac. Inten.(% of TIC)	5.62	6.64	3.75	3.57	3.96	2.95	3.78	2.99	3.39
Rel. Inten.(% of BP)	35.02	41.43	23.38	22.25	24.71	18.41	23.56	18.66	21.14
Score	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_{10}-H_2O^{+2}	y_{11}^{+2}	y_5	y_{12}^{+2}	y_6	y_{14}^{+2}	y_7	y_8	y_9
Delta ppm	-5.3	10.2	11.1	-13.8	-3.7	-22.5	-4.1	-3.6	-14.7



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Result Summary

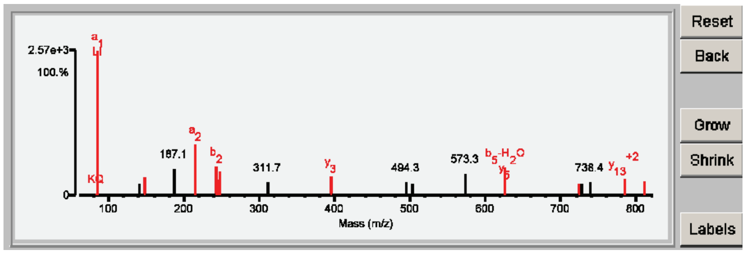
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.42	75.1	7	9/25	K318k	(R)LEASkLNESVMVFTK(D)	1695.8986	114.0584	8.5	56194.9/7.17	HUMAN	Q9NS91	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.42	75.1	7	9/25	K318k	(R) L E|A S k L N E/S/V/M V/F/T/K (D)	1695.8986	114.0584	8.5	56194.9/7.17	HUMAN	Q9NS91	555351	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.080	84.080	86.097	87.056	102.054	129.099	141.100	147.111	187.142	215.139	243.132
Frac. Inten.(% of TIC)	0.13	0.21	0.33	28.93	0.08	0.12	0.12	2.42	3.64	5.33	10.15	5.85
Rel. Inten.(% of BP)	0.44	0.73	1.16	100.00	0.29	0.40	0.42	8.37	12.60	18.42	35.08	20.22
Score	-0.00	0.50	0.50	0.50 0.50	0.33	1.00	0.20	-0.08	1.50	-0.18	0.50	0.50
Ion-type		V	KQ	a_1 LI	NR	E	RKQ		y_1		a_2	b_2
Delta ppm		-13.5	-9.2	-8.4 4.3	5.9	-6.4	-22.8		-9.5		-6.6	-10.8

Fragment-ion (m/z)	244.085	248.160	311.685^{+2}	395.233	494.292^{+2}	502.255	573.328	625.323	724.429	727.396^{+2}	738.362	784.409^{+2}	811.448
Frac. Inten.(% of TIC)	3.03	4.86	2.59	3.78	2.69	2.45	4.24	5.49	2.27	2.41	2.59	3.40	2.87
Rel. Inten.(% of BP)	10.46	16.81	8.94	13.07	9.30	8.48	14.66	18.99	7.85	8.33	8.96	11.76	9.92
Score	0.75	1.50	-0.09	1.50	-0.09	-0.08	-0.15	1.50	1.50	-0.08	-0.09	1.50	1.50
Ion-type	NE	y_2		y_3				b_5-H_2O y_5	y_6			y_{13}^{+2}	y_7
Delta ppm	-38.1	-1.9		11.1				-13.0 -23.0	31.9			-2.3	12.6



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Result Summary

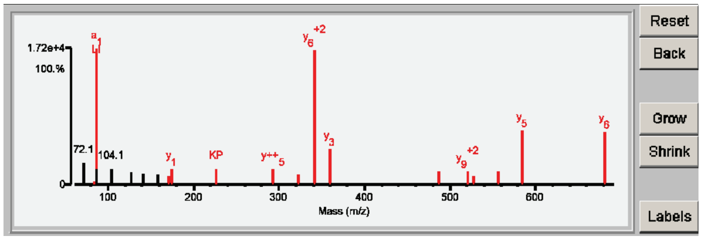
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.78	86.4	9	6/24	K334k	(R)LGETQkAMLDPPKPSR(G)	1767.9422	114.0784	18.8	51219.0/6.10	HUMAN	Q96BH1	E3 ubiquitin-protein ligase RNF25 OS=Homo sapiens GN=RNF25 PE=1 SV=1
2	9.76	74.1	3	12/24	None	(R)LWSRSLESLEPIPQVK(L)	1882.0433	-0.0227	-12.1	233116.3/5.96	HUMAN	RQ92614	REVERSE Myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3
3	6.84	50.9	3	13/24	None	(K)TLDPKLNPASAEIMLLR(K)	1882.0466	-0.0261	-13.9	84648.3/5.09	HUMAN	Q9UJC3	Protein Hook homolog 1 OS=Homo sapiens GN=HOOK1 PE=1 SV=2
4	6.51	61.0	2	12/24	K672k	(K)GkLAPQQEESVAKNIR(N)	1767.9712	114.0494	3.4	95926.2/6.41	HUMAN	RQ8NE71	REVERSE ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2
5	6.48	61.8	1	12/24	None	(R)HKKYEDERDAIKPPR(H)	1881.9930	0.0276	14.7	145816.2/6.59	HUMAN	RO75533	REVERSE Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.78	86.4	9	6/24	K334k	(R) L G\E/T Q k/A/M L D/P/P/K/P S/R (G)	1767.9422	114.0784	18.8	51219.0/6.10	HUMAN	Q96BH1	639369	E3 ubiquitin-protein ligase RNF25 OS=Homo sapiens GN=RNF25 PE=1 SV=1

Fragment-ion (m/z)	70.066	72.081	84.081	86.097	87.100	102.057	104.052	127.087	129.102	141.099	159.076	171.116
Frac. Inten.(% of TIC)	0.01	3.40	0.52	22.00	2.52	0.05	2.45	1.93	0.16	1.70	1.62	1.50
Rel. Inten.(% of BP)	0.07	15.46	2.37	100.00	11.46	0.24	11.15	8.79	0.73	7.72	7.36	6.80
Score	0.20	-0.15	0.50	0.50	-0.11	1.00	-0.11	-0.09	0.20	-0.08	-0.07	0.50
Ion-type	PR		KQ	a_1		E			RKQ			b_2
Delta ppm	6.8		5.0	-9.6		15.1			1.2			9.9
				0.50								
				LI								
				3.2								

Fragment-ion (m/z)	175.117	226.156	292.683	323.203	341.209^{+2}	359.207	487.301	520.789^{+2}	528.289^{+3}	556.303^{+2}	584.356	681.408
Frac. Inten.(% of TIC)	2.57	2.56	2.63	1.65	21.64	5.80	2.16	2.25	1.49	2.10	8.68	8.59
Rel. Inten.(% of BP)	11.69	11.64	11.94	7.48	98.34	26.36	9.80	10.23	6.79	9.56	39.46	39.04
Score	1.50	0.75	1.50	0.75	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_1	KP	y^{++}_5	PKP	y_6^{+2}	y_3	y_4	y_9^{+2}	y_{13}^{+3}	y_{10}^{+2}	y_5	y_6
Delta ppm	-11.1	-0.0	13.4	-19.1	8.9	9.3	4.7	14.4	10.3	6.0	6.9	5.7



Result Summary

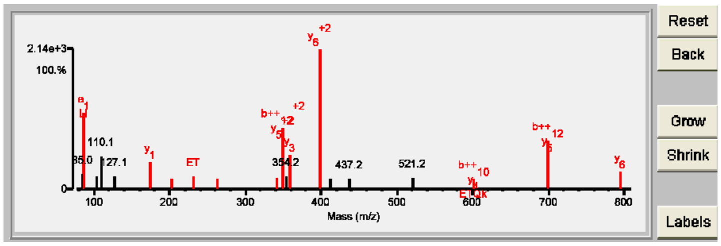
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.45	77.7	6	9/24	K334k K341k	(R)LGETQkAMLDPPkPSR(G)	1767.9422	228.1000	7.1	51219.0/6.10	HUMAN	Q96BH1	E3 ubiquitin-protein ligase RNF25 OS=Homo sapiens GN=RNF25 PE=1 SV=1
2	8.81	75.8	4	10/24	None	(K)KQSKQPDMTHLTELALR(L)	1996.0644	-0.0223	-11.1	109563.3/6.82	HUMAN	Q7Z3J2	UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2
3	8.27	66.7	3	12/24	K114k	(R)KSSTLEVkDVQLHLER(Q)	1882.0393	114.0029	-20.0	17924.6/7.78	HUMAN	Q16514	Transcription initiation factor TFIID subunit 12 OS=Homo sapiens GN=TAF12 PE=1 SV=1
4	7.89	56.1	2	12/24	K239k	(R)IHRkNAPAGGSGMASAKTK(T)	1882.0076	114.0346	-4.2	51486.9/9.26	HUMAN	P35348	Alpha-1A adrenergic receptor OS=Homo sapiens GN=ADRA1A PE=2 SV=2
5	7.23	62.6	4	13/24	K267k	(K)VEIVCPPQSPPkNCTR(N)	1881.9310	114.1112	34.2	31076.3/9.45	HUMAN	Q8WXH6	Ras-related protein Rab-40A OS=Homo sapiens GN=RAB40A PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.45	77.7	6	9/24	K334k K341k	(R) LGETQkAMLD|P/P|k/P/S/R (G)	1767.9422	228.1000	7.1	51219.0/6.10	HUMAN	Q96BH1	319685	E3 ubiquitin-protein ligase RNF25 OS=Homo sapiens GN=RNF25 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.079	84.081	85.024	86.099	104.053	110.072	127.086	129.102	175.123	203.095	231.095	262.152
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.06 0.20 PR -4.6	2.65 11.22 -0.11	0.50 2.10 0.50 KQ -0.9	2.44 10.33 -0.10	12.71 53.88 0.50 a_1 24.1 0.50 LI 24.1	2.10 8.90 -0.09	5.60 23.74 -0.24	2.17 9.19 -0.09	0.06 0.27 0.20 RKQ -4.2	4.44 18.84 1.50 y_1 24.8	1.66 7.02 0.75 AM 48.4 ET-28 -39.1	2.07 8.76 0.75 ET -12.3	1.71 7.25 1.50 y_2 3.5

Fragment-ion (m/z)	341.190^{+2}	349.700^{+2}	354.159	359.205	398.224^{+2}	412.416	437.236^{+2}	521.248	601.327	698.382	795.449
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.99 8.45 0.50 $y_5\text{-NH}_3^{+2}$ 5.7	10.37 43.98 1.50 b++$_{12}^{+2}$ 60.5 y_5^{+2} -2.4	2.05 8.69 -0.09	5.74 24.33 1.50 y_3 3.2	23.58 100.00 1.50 y_6^{+2} -8.8	1.70 7.20 -0.07	1.77 7.50 -0.07	1.85 7.87 -0.08	1.76 7.48 1.50 b++$_{10}$ 49.4 y_4 -23.7 ETQk 55.5	8.22 34.87 1.50 b++$_{12}$ 44.6 y_5 -18.3	2.87 12.16 1.50 y_6 2.8



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Result Summary

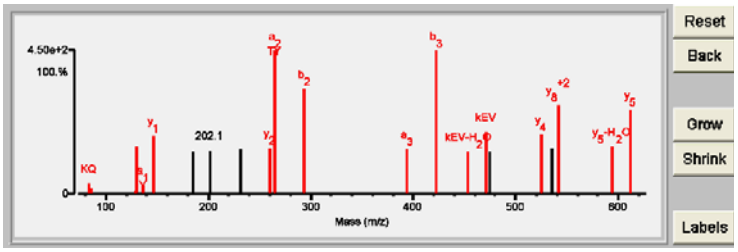
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.33	72.9	7	7/25	K172k	(R)YEEIVkEVSTYIK(K)	1600.8469	114.0515	5.0	50141.1/9.10	HUMAN	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	12.33	72.9	7	7/25	K172k	(R)YEEIVkEVSTYIK(K)	1600.8469	114.0515	5.0	50185.3/9.15	HUMAN	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.33	72.9	7	7/25	K172k	(R) Y E\E\I V/k E V/S/T Y/I/K (K)	1600.8469	114.0515	5.0	50141.1/9.10	HUMAN	P68104	180287	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	12.33	72.9	7	7/25	K172k	(R) Y E\E\I V/k E V/S/T Y/I/K (K)	1600.8469	114.0515	5.0	50185.3/9.15	HUMAN	Q5VTE0	180333	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Fragment-ion (m/z)	72.082	84.080	86.096	129.098	130.083	136.074	147.113	185.121	202.079	231.089	260.194	265.115
Frac. Inten.(% of TIC)	0.14	0.72	0.42	0.21	3.44	0.63	4.24	3.12	3.13	3.30	3.38	10.45
Rel. Inten.(% of BP)	1.33	6.91	3.99	1.96	32.95	6.07	40.56	29.86	29.97	31.61	32.32	100.00
Score	0.50	0.50	0.22	0.20	0.50	1.00	1.50	-0.30	-0.30	-0.32	1.50	0.75
Ion-type	V	KQ	LI	RKQ	y_1-NH_3	a_1	y_1				y_2	a_2
Delta ppm	22.5	-12.8	-0.3	-30.5	-24.3	-19.0	-0.7				-12.2	-15.4
						1.00						TY
						Y						-15.4
						-11.0						

Fragment-ion (m/z)	293.102	394.169	422.150	453.248	471.259	474.203	524.300	535.240^{+2}	541.291^{+2}	593.326	611.351	710.404^{+2}	840.467
Frac. Inten.(% of TIC)	7.61	3.25	10.37	3.09	4.49	3.08	4.36	3.33	6.52	3.44	6.17	6.74	4.40
Rel. Inten.(% of BP)	72.84	31.08	99.29	29.54	42.96	29.45	41.74	31.86	62.40	32.88	59.02	64.54	42.09
Score	0.50	0.50	0.50	0.50	0.75	-0.29	1.50	-0.32	1.50	0.50	1.50	-0.65	-0.42
Ion-type	b_2	a_3	b_3	kEV-H_2O	kEV		y_4		y_8^{+2}	y_5-H_2O	y_5		
Delta ppm	-40.6	17.1	-15.6	2.6	3.9		-14.8		-13.0	-5.3	18.6		



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Result Summary

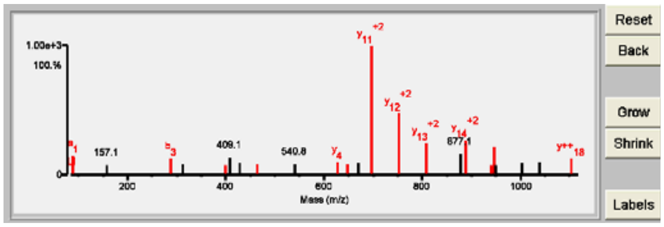
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.43	74.4	10	11/25	K244k	(K)DGNASGTTLLEALDCILPPTRPTDkPLR(L)	3021.5674	114.0760	10.6	50141.1/9.10	HUMAN	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	15.43	74.4	10	11/25	K244k	(K)DGNASGTTLLEALDCILPPTRPTDkPLR(L)	3021.5674	114.0760	10.6	50185.3/9.15	HUMAN	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1
2	4.95	50.2	4	19/25	M103m M110m	(R)GADEQRRSVPFQmLLLLEKmQDSRQK(A)	3103.6139	32.0294	12.6	43011.1/8.04	HUMAN	Q9UMW8	Ubl carboxyl-terminal hydrolase 18 OS=Homo sapiens GN=USP18 PE=1 SV=1
2	4.95	50.2	4	19/25	M103m M110m	(R)GADEQRRSVPFQmLLLLEKmQDSRQK(A)	3103.6139	32.0294	12.6	41394.4/8.36	HUMAN	Q3LFD5	Putative ubiquitin carboxyl-terminal hydrolase 41 OS=Homo sapiens GN=USP41 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.43	74.4	10	11/25	K244k	(K) D G N\A S G T T L L/E A L/D/C/I/L/P/P T R/P T D/k P L R (L)	3021.5674	114.0760	10.6	50141.1/9.10	HUMAN	P68104	180287	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	15.43	74.4	10	11/25	K244k	(K) D G N\A S G T T L L/E A L/D/C/I/L/P/P T R/P T D/k P L R (L)	3021.5674	114.0760	10.6	50185.3/9.15	HUMAN	Q5VTE0	180333	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Fragment-ion (m/z)	70.062	86.094	88.038	157.132	287.096	313.109	400.175^{+2}	409.148	428.264	464.602^{+3}	540.787^{+2}	627.391	647.875^{+2}
Frac. Inten.(% of TIC)	1.72	0.16	3.64	1.82	3.14	1.92	1.80	3.21	2.23	2.06	2.06	2.36	2.06
Rel. Inten.(% of BP)	6.99	0.65	14.75	7.37	12.72	7.76	7.32	13.02	9.03	8.36	8.36	9.58	8.35
Score	-0.07	0.22	0.50	-0.07	0.50	-0.08	0.25	-0.13	-0.09	1.50	-0.08	1.50	1.50
Ion-type		LI	a_1		b_3		$b_9\text{-}H_2O^{+2}$			y_{11}^{+3}		y_4	y_{10}^{+2}
Delta ppm		-25.9	-28.4		-14.0		-20.3			10.7		-4.4	14.9

Fragment-ion (m/z)	670.350^{+2}	696.393^{+2}	752.930^{+2}	809.474^{+2}	877.083	889.501^{+2}	940.519	947.009^{+2}	948.970^{+2}	1004.060^{+2}	1039.558^{+2}	1103.590
Frac. Inten.(% of TIC)	2.29	24.67	11.74	5.97	3.82	6.65	1.89	5.30	1.74	2.31	2.47	2.96
Rel. Inten.(% of BP)	9.28	100.00	47.60	24.22	15.48	26.98	7.65	21.49	7.05	9.37	10.03	12.01
Score	-0.09	1.50	1.50	1.50	-0.15	1.50	1.50	1.50	-0.07	-0.09	-0.10	1.50
Ion-type		y_{11}^{+2}	y_{12}^{+2}	y_{13}^{+2}		y_{14}^{+2}	y_7	y_{15}^{+2}				$y{+}{+}_{18}$
Delta ppm		2.0	-4.6	-1.2		11.6	-2.7	4.8				3.4



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Result Summary

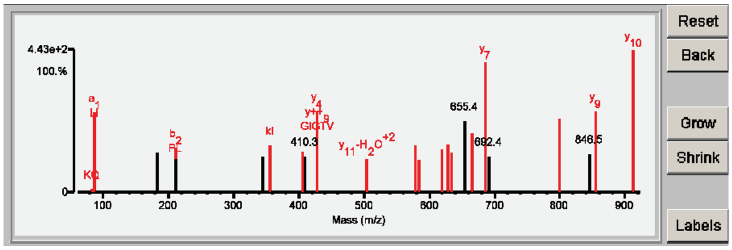
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.91	77.9	9	7/25	K255k	(R)LPLQDVYkIGGIGTVPVGR(V)	1982.1433	114.0484	2.6	50141.1/9.10	HUMAN	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	14.91	77.9	9	7/25	K255k	(R)LPLQDVYkIGGIGTVPVGR(V)	1982.1433	114.0484	2.6	50470.4/9.11	HUMAN	Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1
1	14.91	77.9	9	7/25	K255k	(R)LPLQDVYkIGGIGTVPVGR(V)	1982.1433	114.0484	2.6	50185.3/9.15	HUMAN	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.91	77.9	9	7/25	K255k	(R) L P\L Q D V\Y/k I/G/G/I/G/T V/P V G R (V)	1982.1433	114.0484	2.6	50141.1/9.10	HUMAN	P68104	180287	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	14.91	77.9	9	7/25	K255k	(R) L P\L Q D V\Y/k I/G/G/I/G/T V/P V G R (V)	1982.1433	114.0484	2.6	50470.4/9.11	HUMAN	Q05639	180317	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1
1	14.91	77.9	9	7/25	K255k	(R) L P\L Q D V\Y/k I/G/G/I/G/T V/P V G R (V)	1982.1433	114.0484	2.6	50185.3/9.15	HUMAN	Q5VTE0	180333	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Fragment-ion (m/z)	70.065	84.081	86.096	183.106	211.141	212.144	344.183	356.224	406.207	410.263	428.253	504.292^{+2}
Frac. Inten.(% of TIC)	0.00	0.24	6.02	3.02	3.34	2.52	2.72	3.59	3.06	2.73	6.12	2.55
Rel. Inten.(% of BP)	0.03	2.17	55.66	27.93	30.85	23.25	25.13	33.13	28.25	25.20	56.59	23.59
Score	0.20	0.50	0.50	-0.28	0.75	-0.23	-0.25	0.75	0.75	-0.25	1.50	0.50
Ion-type	PR	KQ	a_1		b_2			kI	Yk		y_4	y_{11}-H_2O^{+2}
Delta ppm	-3.2	-2.1	-15.4		-18.5			-17.2	-5.4		-21.2	-23.1
			0.50		PL						$y{+}{+}_9$	
			LI		-18.5						-8.1	
			-2.6								GIGTV	
											2.4	

Fragment-ion (m/z)	578.847^{+2}	583.355	619.311	628.362	634.376^{+2}	655.366^{+3}	666.394	685.397	692.402	798.501	846.469	855.508	912.526
Frac. Inten.(% of TIC)	3.56	2.50	3.28	3.68	3.04	5.45	4.51	9.88	2.71	5.58	2.91	6.17	10.82
Rel. Inten.(% of BP)	32.93	23.10	30.31	33.99	28.09	50.40	41.67	91.25	25.04	51.55	26.92	56.99	100.00
Score	0.50	0.75	0.75	1.50	1.50	-0.50	0.50	1.50	-0.25	1.50	-0.27	1.50	1.50
Ion-type	a_9^{+2}	kIGGI	LQDVY	y_6	y_{12}^{+2}		b_6	y_7		y_8		y_9	y_{10}
Delta ppm	11.9	-4.3	1.3	-24.8	-2.2		16.1	-3.1		22.9		3.6	-0.4



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Result Summary

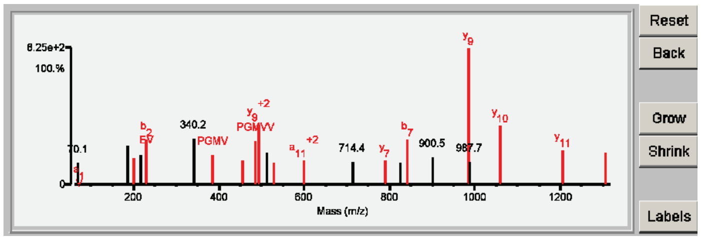
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.04	71.2	7	9/25	K273k	(R)VETGVLkPGMVVTFAPVNVTTEVK(S)	2515.3840	114.0586	6.0	50141.1/9.10	HUMAN	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	13.04	71.2	7	9/25	K273k	(R)VETGVLkPGMVVTFAPVNVTTEVK(S)	2515.3840	114.0586	6.0	50185.3/9.15	HUMAN	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.04	71.2	7	9/25	K273k	(R) V E\T G V L k\P G M V V/T/F/A/P V/N V T T E V K (S)	2515.3840	114.0586	6.0	50141.1/9.10	HUMAN	P68104	180287	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
1	13.04	71.2	7	9/25	K273k	(R) V E\T G V L k\P G M V V/T/F/A/P V/N V T T E V K (S)	2515.3840	114.0586	6.0	50185.3/9.15	HUMAN	Q5VTE0	180333	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1

Fragment-ion (m/z)	70.062	72.080	86.097	187.145	201.119	215.135	229.118	340.213	385.190	456.260
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.45 15.62 -0.16	0.16 1.01 0.50 a_1 -20.4 0.50 V -5.2	0.11 0.69 0.22 LI 4.3	4.53 28.89 -0.29	2.98 19.02 0.75 a_2 -29.7 VT -29.7 EV-28 -29.7	3.42 21.84 -0.22	5.10 32.53 0.75 b_2 -5.6 EV -5.6	5.33 34.00 -0.34	3.44 21.98 0.75 PGMV -4.9	2.76 17.62 0.50 PGMVV-28 -11.4

Fragment-ion (m/z)	484.255	493.783^{+2}	511.257	528.257	599.332^{+2}	714.378	790.420	825.623^{+3}	841.481	900.465^{+2}	986.549	987.690	1057.578	1204.639	1305.683
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	4.97 31.70 0.75 PGMVV -9.3	6.88 43.91 1.50 y_9^{+2} 6.1	3.72 23.74 -0.24	2.50 15.92 0.75 kPGM -7.0	2.76 17.63 0.50 a_{11}^{+2} -8.8	2.61 16.65 -0.17	2.75 17.55 1.50 y_7 -13.8	2.47 15.73 -0.16	5.13 32.75 0.50 b_7 2.9	3.13 20.00 -0.20	15.67 100.00 1.50 y_9 -2.4	2.64 16.82 -0.17	6.82 43.54 1.50 y_{10} -9.8	3.93 25.07 1.50 y_{11} -15.5	3.73 23.78 1.50 y_{12} -16.9



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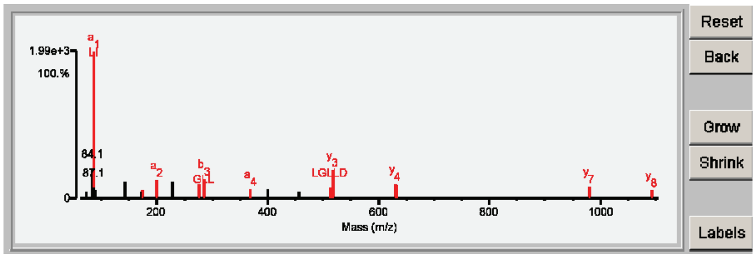
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.09	71.7	8	10/25	K147k	(R)ILGLLDAYLkTR(T)	1375.8308	114.0550	8.1	50119.1/6.25	HUMAN	P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.09	71.7	8	10/25	K147k	(R) I L/G\L/L/D A Y/L/k/T/R (T)	1375.8308	114.0550	8.1	50119.1/6.25	HUMAN	P26641	180797	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3

Fragment-ion (m/z)	70.066	72.084	84.081	86.095	87.100	89.059	129.102	136.073	143.115	171.106	175.119	199.179	228.179	229.131	276.161	284.194	369.287	399.218^{+2}	457.297	512.308	518.310	631.385	632.375^{+2}	980.522	1093.585
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR 16.8	1.65 4.76 -0.05	7.12 20.47 -0.20	34.75 100.00 0.50 a_1 -28.1 0.50 LI -15.4	2.48 7.14 -0.07	1.99 5.73 -0.06	0.06 0.17 0.20 RKQ 1.2	0.21 0.61 1.00 Y -19.8	3.91 11.26 -0.11	1.71 4.93 -0.05	1.83 5.28 1.50 y_1 -0.3	4.26 12.26 0.50 a_2 -14.5	3.90 11.21 -0.11	1.73 4.98 -0.05	3.37 9.69 1.50 y_2 -21.1	4.59 13.22 0.75 b_3 -15.0 GLL -15.0	2.14 6.16 0.50 a_4 -0.9	2.10 6.04 -0.06	1.69 4.86 -0.05	2.38 6.84 0.75 LGLLD -0.9	6.79 19.52 1.50 y_3 10.2	3.41 9.82 1.50 y_4 -5.5	3.09 8.89 1.50 y_{10}^{+2} 29.2	2.81 8.08 1.50 y_7 6.3	2.03 5.83 1.50 y_8 -13.8



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Result Summary

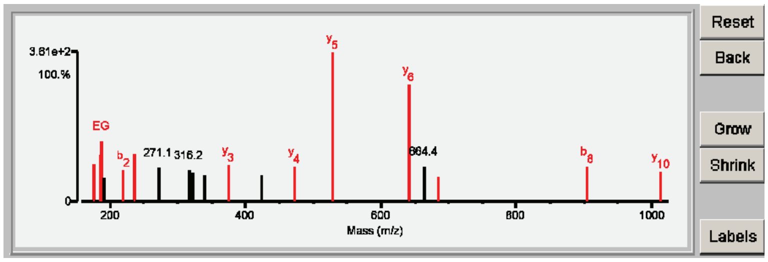
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.38	73.7	7	8/24	K239k	(K)FAAkGEGQLGPAER(A)	1430.7387	114.0549	7.7	95338.7/6.41	HUMAN	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.38	73.7	7	8/24	K239k	(K) F A\A k/G E G Q|L/G/P/A E/R (A)	1430.7387	114.0549	7.7	95338.7/6.41	HUMAN	P13639	180869	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Fragment-ion (m/z)	84.042	84.079	86.097	120.080	141.104	175.118	186.084	187.068	191.110	219.119	236.632
Frac. Inten.(% of TIC)	0.15	0.61	0.26	0.52	3.45	4.13	5.20	6.79	2.66	3.41	5.36
Rel. Inten.(% of BP)	0.93	3.67	1.56	3.13	20.88	24.96	31.42	41.07	16.08	20.60	32.42
Score	1.00	0.50	0.22	1.00	-0.21	1.50	0.75	0.75	-0.16	0.50	1.50
Ion-type	E	KQ	LI	a_1		y_1	GQ	EG		b_2	y^{++}_4
Delta ppm	-24.9	-21.1	2.0	-17.3		-6.0	-25.3	-25.3		24.6	13.3
				1.00							
				F							
				-8.1							

Fragment-ion (m/z)	271.134	316.215	321.666	339.681^{+2}	375.208	424.217	472.250	529.273	642.362	664.361^{+2}	685.333	903.462	1013.471
Frac. Inten.(% of TIC)	3.78	3.47	3.24	2.92	4.08	2.85	3.85	16.54	12.98	3.89	2.72	3.83	3.32
Rel. Inten.(% of BP)	22.85	20.97	19.58	17.64	24.68	17.22	23.29	100.00	78.51	23.54	16.42	23.13	20.05
Score	-0.23	-0.21	-0.20	-0.18	1.50	-0.17	1.50	1.50	1.50	-0.24	0.75	0.50	1.50
Ion-type					y_3		y_4	y_5	y_6		AkGEGQ	b_8	y_{10}
Delta ppm					25.2		-2.0	-0.5	8.0		7.9	31.9	-30.0



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Result Summary

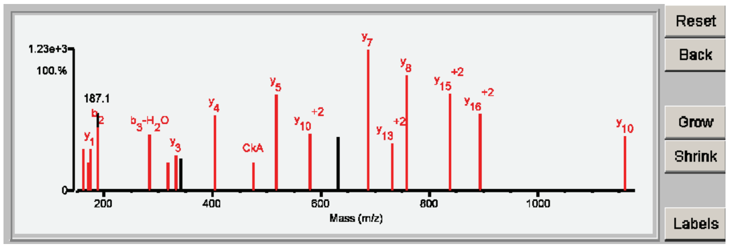
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.65	77.4	10	6/25	K42k	(K)STLTDSLVCkAGIIASAR(A)	1863.0004	114.0574	7.3	95338.7/6.41	HUMAN	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.65	77.4	10	6/25	K42k	(K) S T|L/T D/S L V/C k/A/G I/I/A/S A/R (A)	1863.0004	114.0574	7.3	95338.7/6.41	HUMAN	P13639	180869	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Fragment-ion (m/z)	70.064	84.081	86.097	116.068	120.080	161.091	171.079	175.120	187.142	189.085	284.161
Frac. Inten.(% of TIC)	0.00	5.16	0.66	3.57	2.32	2.90	2.04	2.96	5.51	4.47	3.93
Rel. Inten.(% of BP)	0.03	51.77	6.63	35.77	23.27	29.13	20.51	29.70	55.28	44.81	39.39
Score	0.20	-0.52	0.22	-0.36	-0.23	0.50	0.25	1.50	-0.55	0.50	0.25
Ion-type	**PR**		**LI**			a_2	b_2-H_2O	y_1		b_2	b_3-H_2O
Delta ppm	-10.4		5.5			-15.9	7.5	4.8		-14.2	-2.7

Fragment-ion (m/z)	316.152	333.183	341.220	404.227	474.211	517.314	580.815^{+2}	630.376^{+2}	687.417	730.423^{+2}	758.452	838.452^{+2}	894.985^{+2}	1160.628
Frac. Inten.(% of TIC)	2.04	2.55	2.26	5.29	2.02	6.80	4.08	3.81	9.97	3.33	8.18	6.86	5.41	3.88
Rel. Inten.(% of BP)	20.43	25.60	22.65	53.05	20.26	68.16	40.89	38.20	100.00	33.39	82.06	68.79	54.24	38.91
Score	0.75	1.50	-0.23	1.50	0.75	1.50	1.50	-0.38	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_3-NH_3 **DSL**	y_3		y_4	**CkA**	y_5	y_{10}^{+2}		y_7	y_{13}^{+2}	y_8	y_{15}^{+2}	y_{16}^{+2}	y_{10}
Delta ppm	-28.6 3.4	-15.3		3.4	-6.2	10.1	2.6		3.8	23.8	0.2	9.6	-0.2	6.1



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Result Summary

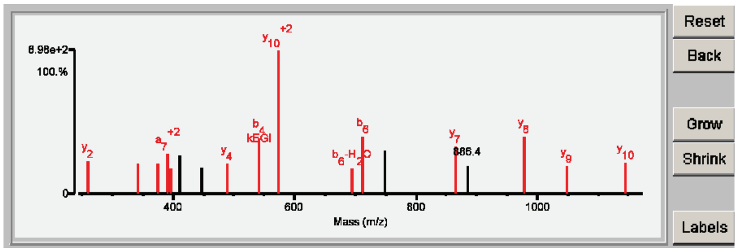
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.58	71.4	8	7/25	K845k	(K)GLkEGIPALDNFLDKL(-)	1742.9687	114.0570	7.6	95338.7/6.41	HUMAN	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.58	71.4	8	7/25	K845k	(K) G L k E\G I|P/A/L/D/N F/L/D/K L (-)	1742.9687	114.0570	7.6	95338.7/6.41	HUMAN	P13639	180869	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Fragment-ion (m/z)	70.064	84.079	86.096	129.101	141.101	169.090	226.116	260.193	342.714^{+2}	375.223	391.244^{+2}	397.202	411.206	446.211
Frac. Inten.(% of TIC)	0.01	0.14	0.58	0.17	4.84	4.44	4.19	3.59	3.34	3.41	4.38	2.83	4.34	2.92
Rel. Inten.(% of BP)	0.06	0.86	3.61	1.09	30.29	27.82	26.23	22.48	20.93	21.36	27.45	17.74	27.16	18.28
Score	0.20	0.50	0.22	0.20	-0.30	-0.28	-0.26	1.50	0.50	1.50	0.50	0.75	-0.27	-0.18
Ion-type	PR	KQ	LI	RKQ				y_2	a_6^{+2}	y_3 $y{+}{+}_6$	a_7^{+2}	PALD		
Delta ppm	-20.3	-17.5	-6.1	-11.9				-16.0	22.4	-1.6 26.5	30.2	-17.8		

Fragment-ion (m/z)	488.308	542.293	573.308^{+2}	694.399	712.404	748.436	864.427	886.429	977.530	1048.586	1145.597
Frac. Inten.(% of TIC)	3.30	6.28	15.96	2.86	6.36	4.82	5.23	3.03	6.36	3.12	3.52
Rel. Inten.(% of BP)	20.68	39.31	100.00	17.93	39.81	30.21	32.76	18.97	39.81	19.54	22.04
Score	1.50	0.75	1.50	0.25	0.50	-0.30	1.50	-0.19	1.50	1.50	1.50
Ion-type	y_4	b_4 kEGI	y_{10}^{+2}	b_6-H_2O	b_6		y_7		y_8	y_9	y_{10}
Delta ppm	-0.6	-2.4 -2.4	-9.6	14.6	5.0		-22.3		-0.2	17.6	-20.1



Result Summary

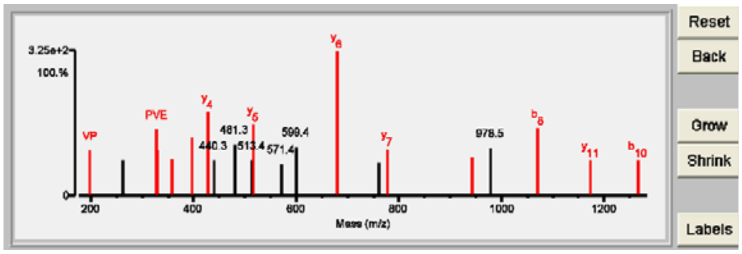
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.86	65.3	8	10/25	K256k	(R)DLEkPFLLPVEAVYSVPGR(G)	2129.1641	114.0525	4.3	49541.8/7.26	HUMAN	P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.86	65.3	8	10/25	K256k	(R) D L E/k P F L L|P V\E A/V/Y/S/V/P G R (G)	2129.1641	114.0525	4.3	49541.8/7.26	HUMAN	P49411	186445	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2

Fragment-ion (m/z)	86.095	102.047	120.077	143.117	197.129	262.156	326.164	329.191	358.217	397.212	428.259	440.250	481.253
Frac. Inten.(% of TIC)	0.33	2.96	0.18	5.07	3.74	2.91	5.56	3.80	3.02	4.91	7.03	2.99	4.31
Rel. Inten.(% of BP)	2.71	24.44	1.45	41.87	30.89	24.00	45.88	31.32	24.90	40.48	58.04	24.65	35.54
Score	0.22	-0.24	1.00	-0.42	0.75	-0.24	0.75	1.50	0.75	0.75	1.50	-0.25	-0.36
Ion-type	LI		F		VP		PVE	y3	PFL	PVEA	y4		
Delta ppm	-17.7		-32.3		-5.3		-25.0	-6.0	10.6	7.7	-6.5		

Fragment-ion (m/z)	513.439^{+3}	515.290	571.368	599.375	678.350	759.860	777.430	943.514	978.523	1070.584	1173.636	1266.700
Frac. Inten.(% of TIC)	2.94	5.93	2.68	4.05	12.12	2.70	3.92	3.23	4.03	5.68	2.98	2.93
Rel. Inten.(% of BP)	24.28	48.90	22.09	33.45	100.00	22.31	32.30	26.63	33.29	46.90	24.62	24.16
Score	-0.24	1.50	-0.22	-0.33	1.50	-0.22	1.50	1.50	-0.33	0.50	1.50	0.50
Ion-type		y5			y6		y7	y++16		b8	y11	b10
Delta ppm		-7.6			-9.7		6.3	-17.9		-4.8	8.6	-7.9



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Result Summary

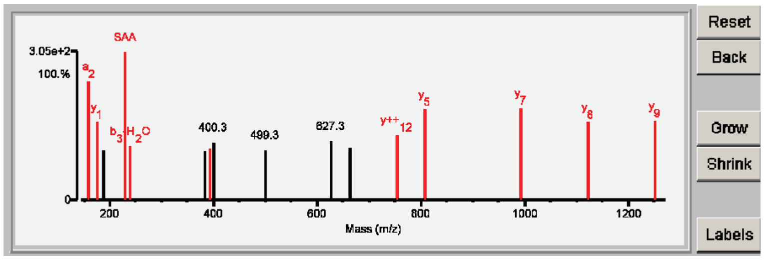
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.84	67.1	6	10/24	K133k	(R)VSAALEEADkMFLR(T)	1579.8149	114.0547	6.9	20875.7/3.89	HUMAN	Q9Y6B2	EP300-interacting inhibitor of differentiation 1 OS=Homo sapiens GN=EID1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.84	67.1	6	10/24	K133k	(R) V S/A A L/E/E/A D/k M F L/R (T)	1579.8149	114.0547	6.9	20875.7/3.89	HUMAN	Q9Y6B2	187729	EP300-interacting inhibitor of differentiation 1 OS=Homo sapiens GN=EID1 PE=1 SV=1

Fragment-ion (m/z)	72.081	84.081	86.097	87.056	115.085	120.079	129.095	136.070	159.107	175.118	187.145	230.113
Frac. Inten.(% of TIC)	0.86	9.35	0.49	0.10	3.57	0.14	4.66	3.46	7.80	5.16	3.31	9.75
Rel. Inten.(% of BP)	8.81	95.86	4.99	1.03	36.57	1.40	47.75	35.51	80.04	52.94	33.97	100.00
Score	0.50	-0.33	0.22	0.33	-0.12	1.00	-0.16	-0.12	0.50	1.50	-0.12	0.75
Ion-type	a_1		LI	NR		F			a_2	y_1		SAA
Delta ppm	-9.3		12.5	11.6		-16.5			-43.4	-7.7		-6.2
	0.50											
	V											
	5.9											

Fragment-ion (m/z)	240.131	384.254	392.199	400.270	499.318	627.311	663.335	754.362	808.449	994.511	1123.541	1252.604
Frac. Inten.(% of TIC)	3.56	3.24	3.34	3.82	3.31	3.85	3.50	4.32	5.94	6.07	5.18	5.23
Rel. Inten.(% of BP)	36.50	33.18	34.30	39.20	33.94	39.46	35.91	44.29	60.90	62.28	53.11	53.60
Score	0.25	-0.11	0.75	-0.13	-0.12	-0.13	-0.12	1.50	1.50	1.50	1.50	1.50
Ion-type	b_3-H_2O		MFL					y^{++}_{12}	y_5	y_7	y_8	y_9
Delta ppm	-19.4		-7.0					-27.5	-0.4	-2.6	-13.8	4.1



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Result Summary

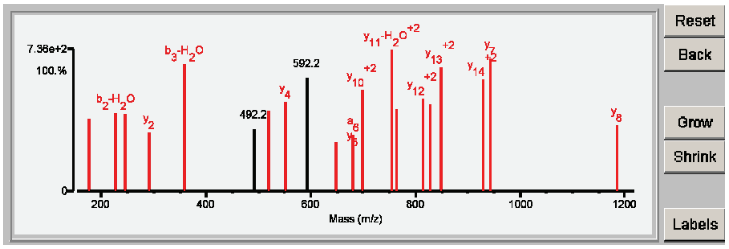
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.25	83.8	14	4/24	K107k	(K)ENMYAVQTLkDFQYVDR(D)	2120.0117	114.0558	5.8	57575.6/4.77	HUMAN	Q9Y6I3	Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.25	83.8	14	4/24	K107k	(K) E N\M/Y/A/V/Q/T/L/k/D/F/Q/Y V/D/R (D)	2120.0117	114.0558	5.8	57575.6/4.77	HUMAN	Q9Y6I3	195733	Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=1

Fragment-ion (m/z)	84.048	86.095	104.053	136.073	175.117	226.083	244.094	290.142	357.117	492.189	520.183	552.274
Frac. Inten.(% of TIC)	4.61	0.09	2.57	0.16	3.73	4.02	3.93	3.04	6.51	3.17	4.14	4.58
Rel. Inten.(% of BP)	63.42	1.18	35.39	2.19	51.31	55.33	54.00	41.87	89.49	43.65	56.97	62.96
Score	-0.63	0.22	-0.35	1.00	1.50	0.25	0.50	1.50	0.25	-0.44	0.25	1.50
Ion-type		LI		Y	y_1	b_2-H_2O	b_2	y_2	b_3-H_2O		b_4-H_2O	y_4
Delta ppm		-21.2		-22.7	-10.0	-0.6	-1.6	-14.5	-18.0		-8.3	-7.5

Fragment-ion (m/z)	592.228^{+2}	649.348^{+2}	680.316	699.872^{+2}	754.893^{+2}	763.868^{+2}	813.428^{+2}	827.400	848.949^{+2}	930.464^{+2}	942.423	1184.588
Frac. Inten.(% of TIC)	5.81	2.53	2.92	5.18	7.27	4.19	4.73	4.45	6.37	5.76	6.83	3.41
Rel. Inten.(% of BP)	79.92	34.75	40.10	71.22	100.00	57.59	65.08	61.20	87.67	79.24	93.96	46.85
Score	-0.80	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type		y_9^{+2}	a_6 y_5	y_{10}^{+2}	y_{11}-H_2O^{+2}	a_{12}^{+2} y_{11}^{+2}	y_{12}^{+2}	y_6	y_{13}^{+2}	y_{14}^{+2}	y_7	y_8
Delta ppm		26.7	11.4 -29.6	25.3	19.6	-2.5 -20.7	13.1	-6.0	15.2	-4.0	-8.7	15.2



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.52	81.4	10	4/25	K146k	(R)AEVQkLQMEAPHIIVGTPGR(V)	2174.1750	114.0707	12.2	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

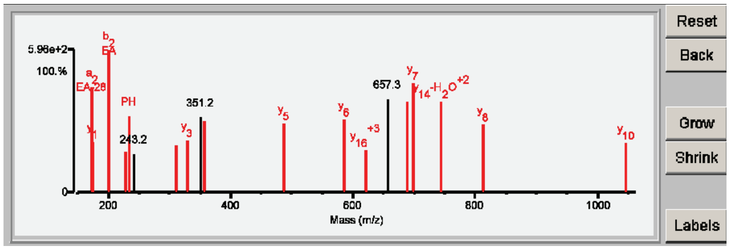
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.52	81.4	10	4/25	K146k	(R) A E\V Q/k L Q/M E A/P H/I/I/V/G T/P G/R (V)	2174.1750	114.0707	12.2	46154.2/5.32	HUMAN	P60842	312285	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.081	84.044	84.080	86.096	102.059	173.092	175.119	201.088
Frac. Inten.(% of TIC)	0.00	0.19	0.09	0.23	0.27	4.49	7.19	3.43	9.76
Rel. Inten.(% of BP)	0.05	1.93	0.89	2.33	2.77	45.95	73.68	35.17	100.00
Score	0.20	0.50	1.00	0.50	0.22	-0.46	0.50	1.50	0.75
Ion-type	PR	V	E	KQ	LI		a_2	y_1	b_2
Delta ppm	-6.1	3.1	-7.0	-9.2	-2.6		-9.0	2.0	0.1
							EA-28		EA
							-9.0		0.1

Fragment-ion (m/z)	228.135	235.119	243.152	312.171	329.197	351.173	356.224^{+2}	487.275	586.330
Frac. Inten.(% of TIC)	2.77	5.26	2.65	3.20	3.53	5.13	4.90	4.72	5.01
Rel. Inten.(% of BP)	28.38	53.83	27.14	32.82	36.18	52.54	50.24	48.39	51.33
Score	0.75	0.75	-0.27	0.50	1.50	-0.53	0.75	1.50	1.50
Ion-type	VQ	PH		y_3-NH_3	y_3		VQkLQ^{+2}	y_5	y_6
Delta ppm	0.2	-5.7		13.7	13.1		35.5	25.2	-0.9

Fragment-ion (m/z)	621.009^{+3}	657.323^{+3}	689.375^{+2}	699.430	744.395^{+2}	812.519	1046.640
Frac. Inten.(% of TIC)	2.86	6.35	6.19	7.45	6.25	4.66	3.41
Rel. Inten.(% of BP)	29.24	65.07	63.37	76.28	63.97	47.75	34.88
Score	1.50	-0.65	1.50	1.50	0.50	1.50	1.50
Ion-type	y_{16}^{+3}		y_{13}^{+2}	y_7	y_{14}-H_2O^{+2}	y_8	y_{10}
Delta ppm	-0.0		8.7	21.2	2.1	24.5	27.7



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Result Summary

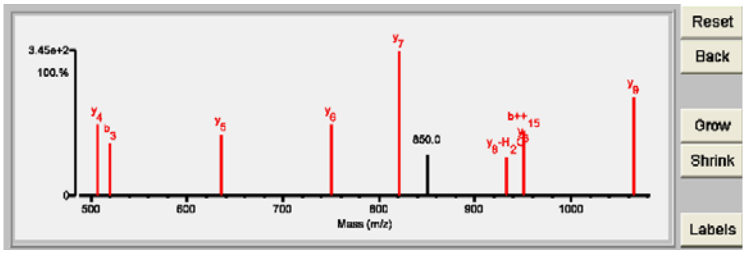
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.08	65.9	9	8/25	K177k	(K)YIkMFVLDEADEMLSR(G)	1959.9554	114.0642	10.3	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.08	65.9	9	8/25	K177k	(K) Y I k\M F V L/D/E/A/D/E/M L/S\R (G)	1959.9554	114.0642	10.3	46154.2/5.32	HUMAN	P60842	312285	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

Fragment-ion (m/z)	72.080	84.044	84.080	86.096	102.057	120.082	136.076	217.070	245.076	249.156	250.163	262.149	374.226
Frac. Inten.(% of TIC)	0.37	0.12	7.11	0.40	0.09	0.22	0.32	4.14	3.08	6.61	3.41	5.54	3.17
Rel. Inten.(% of BP)	3.15	0.98	60.23	3.40	0.73	1.83	2.71	35.12	26.12	56.01	28.88	46.95	26.87
Score	0.50	1.00	-0.60	0.22		1.00	1.00 1.00	-0.35	0.75	0.50	-0.29	1.50	-0.27
Ion-type	V	E		LI	E	F	a_1 Y		DE	a_2		y_2	
Delta ppm	-8.0	-5.8		-8.4		7.7	-1.4 -1.4		-4.5	-15.5		-9.1	

Fragment-ion (m/z)	384.214^{+2}	445.325^{+2}	474.230	506.277	519.293	635.304	750.353	821.381	849.968^{+2}	932.388	950.426	1065.462
Frac. Inten.(% of TIC)	6.64	2.90	3.37	5.76	4.26	5.01	5.76	11.80	3.36	3.23	5.35	8.00
Rel. Inten.(% of BP)	56.25	24.55	28.53	48.84	36.08	42.48	48.84	100.00	28.47	27.37	45.32	67.81
Score	-0.56	-0.25	-0.29	1.50	0.50	1.50	1.50	1.50	-0.28	0.50	1.50	1.50
Ion-type				y_4	b_3	y_5	y_6	y_7		y_8-H_2O	b++$_{15}$ y_8	y_9
Delta ppm				1.9	0.8	-22.4	10.3	-1.1		-28.5	-22.4 1.0	9.3



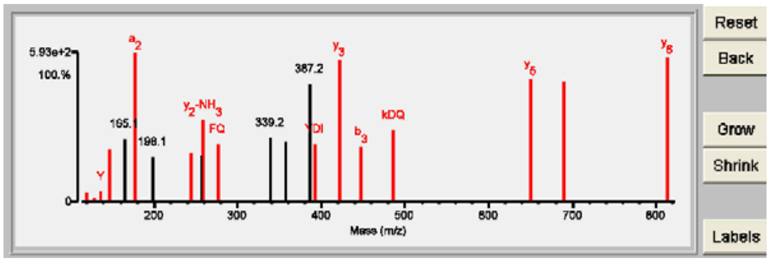
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.53	69.6	6	8/25	K193k	(R)GFkDQIYDIFQK(L)	1501.7686	114.0614	11.4	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.53	69.6	6	8/25	K193k	(R) G F k\D Q\I/Y/D I/F Q/K (L)	1501.7686	114.0614	11.4	46154.2/5.32	HUMAN	P60842	312285	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

Fragment-ion (m/z)	84.042	84.080	86.096	91.055	120.081	129.099	136.075	147.111	165.097	177.101	198.120	244.092	257.165	258.146	276.133	339.180	358.149	387.203	392.185	422.244	447.248	486.232	650.350	690.309	813.428
Frac. Inten.(% of TIC)	3.86	0.44	1.18	2.59	0.56	0.19	0.65	3.16	3.79	8.97	2.75	2.95	2.79	4.93	3.45	3.84	3.68	7.08	3.50	8.59	3.33	4.35	7.39	7.28	8.70
Rel. Inten.(% of BP)	43.07	4.93	13.15	28.88	6.27	2.10	7.28	35.21	42.28	100.00	30.65	32.91	31.07	54.94	38.51	42.89	41.03	78.99	39.09	95.80	37.18	48.52	82.45	81.22	97.01
Score	-0.43	0.50	0.22	-0.29	1.00	0.20	1.00	1.50	-0.42	0.50	-0.31	0.75	-0.31	0.50	0.75	-0.43	-0.41	-0.79	0.75	1.50	0.50	0.75	1.50	0.50	1.50
Ion-type		KQ	LI		F	RKQ	Y	y_1		a_2		DQ		y_2-NH$_3$	FQ				YDI	y_3	b_3	kDQ	y_5	b_5	y_6
Delta ppm		-8.0	-3.8		4.4	-28.2	-4.3	-15.7		-14.3		-7.4		6.1	-8.6				5.8	10.7	25.6	-0.2	-1.1	-17.8	16.8



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Result Summary

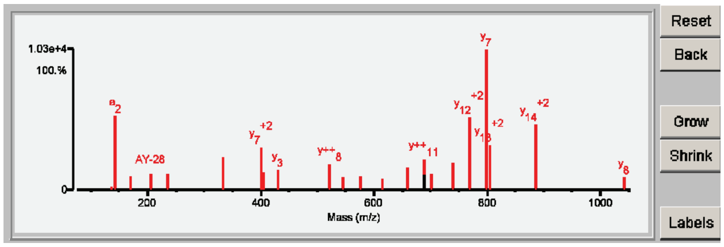
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	25.87	98.1	11	1/25	K54k	(R)GIYAYGFEkPSAIQQR(A)	1827.9388	114.0436	0.4	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1
1	25.87	98.1	11	1/25	K55k	(R)GIYAYGFEkPSAIQQR(A)	1827.9388	114.0436	0.4	46402.5/5.33	HUMAN	Q14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2
1	25.87	98.1	11	1/25	K60k	(R)GIYAYGFEkPSAIQQR(A)	1827.9388	114.0436	0.4	46871.3/6.30	HUMAN	P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4
2	9.39	56.2	2	11/25	K353k	(R)QQIASPkEFGYAYIGR(L)	1827.9388	114.0436	0.4	46154.2/5.32	HUMAN	RP60842	REVERSE Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1
2	9.39	56.2	2	11/25	K353k	(R)QQIASPkEFGYAYIGR(L)	1827.9388	114.0436	0.4	46402.5/5.33	HUMAN	RQ14240	REVERSE Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	25.87	98.1	11	1/25	K54k	(R) G I|Y|A|Y/G/F E/k/P/S/A/I/Q Q R (A)	1827.9388	114.0436	0.4	46154.2/5.32	HUMAN	P60842	312285	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1
1	25.87	98.1	11	1/25	K55k	(R) G I|Y|A|Y/G/F E/k/P/S/A/I/Q Q R (A)	1827.9388	114.0436	0.4	46402.5/5.33	HUMAN	Q14240	312305	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2
1	25.87	98.1	11	1/25	K60k	(R) G I|Y|A|Y/G/F E/k/P/S/A/I/Q Q R (A)	1827.9388	114.0436	0.4	46871.3/6.30	HUMAN	P38919	312323	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4

Fragment-ion (m/z)	84.081	86.097	136.076	143.118	171.113	207.114	235.106	334.174	400.224^{+2}	405.213	431.233	521.297
Frac. Inten.(% of TIC)	0.10	0.12	0.39	9.82	1.77	2.23	2.15	4.39	5.73	2.37	2.69	3.49
Rel. Inten.(% of BP)	0.53	0.64	2.06	52.29	9.43	11.89	11.46	23.40	30.49	12.62	14.29	18.60
Score	0.50	0.22	1.00	0.50	0.50	0.50	0.75	0.50	1.50	0.50	1.50	1.50
Ion-type	KQ	LI	Y	a_2	b_2	AY-28	AY	b_3	y_7^{+2}	b_4	y_3	y^{++}_8
Delta ppm	6.2	3.2	3.0	-10.4	-5.9	-1.0	-10.7	-8.8	-1.9	-4.1	-6.3	6.5

Fragment-ion (m/z)	544.320	576.272	615.355	659.345^{+2}	687.857	688.366	702.386	739.331	769.392^{+2}	799.440	804.904^{+2}	886.434^{+2}	1041.575
Frac. Inten.(% of TIC)	1.73	1.82	1.56	2.90	4.07	1.94	2.14	3.60	9.76	18.78	6.04	8.73	1.66
Rel. Inten.(% of BP)	9.20	9.70	8.32	15.45	21.69	10.31	11.40	19.16	51.97	100.00	32.13	46.49	8.86
Score	1.50	0.75	1.50	1.50	1.50	-0.10	1.50	0.75	1.50	1.50	1.50	1.50	1.50
Ion-type	y_4	GFEk	y_5	y_{10}^{+2}	y^{++}_{11}		y_6	YGFEk	y_{12}^{+2}	y_7	y_{13}^{+2}	y_{14}^{+2}	y_8
Delta ppm	-0.7	-11.3	-3.6	-6.6	-4.2		-5.3	-14.7	1.0	-2.7	-7.9	-8.7	-4.6



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.96	89.4	10	5/25	K69k	(R)AIIPCIkGYDVIAQAQSGTGK(T)	2190.1587	114.0659	10.0	46402.5/5.33	HUMAN	Q14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2
1	19.96	89.4	10	5/25	K68k	(R)AILPCIkGYDVIAQAQSGTGK(T)	2190.1587	114.0659	10.0	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1
2	5.49	53.6	2	15/25	K83k	(R)AIIPCIKGYDVIAQAQSGTGk(T)	2190.1587	114.0659	10.0	46402.5/5.33	HUMAN	Q14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2
2	5.49	53.6	2	15/25	K82k	(R)AILPCIKGYDVIAQAQSGTGk(T)	2190.1587	114.0659	10.0	46154.2/5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1
3	4.96	52.9	3	16/25	None	(R)AILLEMLNHTAHLRQLSDTK(L)	2304.2493	-0.0246	-10.7	193080.5/7.34	HUMAN	RQ149N8	REVERSE E3 ubiquitin-protein ligase SHPRH OS=Homo sapiens GN=SHPRH PE=1 SV=2

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>19.96</td><td>89.4</td><td>10</td><td>5/25</td><td>K69k</td><td>(R) A I|I|P C I k G Y D V|I/A/Q/A/Q/S/G T/G K (T)</td><td>2190.1587</td><td>114.0659</td><td>10.0</td><td>46402.5/5.33</td><td>HUMAN</td><td>Q14240</td><td>312305</td><td>Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2</td></tr>
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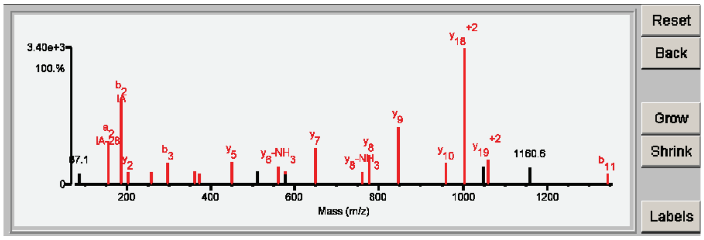
Fragment-ion (m/z)	84.078	86.095	87.097	157.133	185.128	204.132	258.085	298.214	362.204	371.176	449.228
Frac. Inten.(% of TIC)	0.07	0.33	1.64	6.65	13.07	1.92	1.91	3.28	2.04	1.72	3.46
Rel. Inten.(% of BP)	0.32	1.60	7.88	32.00	62.89	9.24	9.19	15.78	9.79	8.29	16.63
Score	0.50	0.22	-0.08	0.50	0.75	1.50	0.75	0.50	1.50	0.75	1.50
Ion-type	KQ	LI		a_2 IA-28	b_2 IA	y_2	PC	b_3	y_4	PCI	y_5
Delta ppm	-36.6	-18.9		-10.4 -10.4	-8.9 -8.9	-12.6	-25.5	1.3	1.9	-0.4	-17.4

Fragment-ion (m/z)	510.251^{+2}	560.263	577.288	577.364	648.330	759.360	776.387	847.427	960.515	1004.012^{+2}	1047.476	1060.554^{+2}	1160.572	1344.685
Frac. Inten.(% of TIC)	2.13	2.74	2.01	1.58	5.65	1.81	4.46	8.73	3.27	20.78	2.70	3.82	2.60	1.64
Rel. Inten.(% of BP)	10.23	13.18	9.67	7.62	27.19	8.72	21.47	41.98	15.71	100.00	13.01	18.38	12.51	7.88
Score	-0.10	0.50	1.50	-0.08	1.50	0.50	1.50	1.50	1.50	1.50	-0.13	1.50	-0.13	0.50
Ion-type		y_6-NH$_3$	y_6		y_7	y_8-NH$_3$	y_8	y_9	y_{10}	y_{18}^{+2}		y_{19}^{+2}		b_{11}
Delta ppm		-8.7	-9.9		-1.9	-3.9	-3.2	-0.4	4.3	10.0		9.3		-10.7



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Result Summary

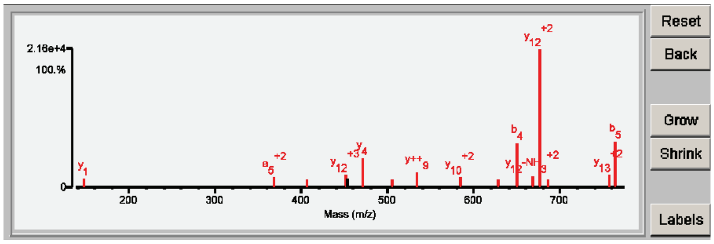
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.38	78.3	10	5/25	K68k	(K)kYEDICPSTHNMDVPNIK(R)	2161.0053	114.0509	3.5	16832.4/5.08	HUMAN	P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2
1	18.38	78.3	10	5/25	K68k	(K)kYEDICPSTHNMDVPNIK(R)	2161.0053	114.0509	3.5	16793.3/5.38	HUMAN	Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3
1	18.38	78.3	10	5/25	K68k	(K)kYEDICPSTHNMDVPNIK(R)	2161.0053	114.0509	3.5	16773.3/4.85	HUMAN	Q6IS14	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=2 SV=2
2	6.88	50.0	2	14/25	K55k	(R)ASQSFGKGCEECkFLKER(T)	2161.0165	114.0397	-1.4	92033.5/9.11	HUMAN	RQ86WZ6	REVERSE Zinc finger protein 227 OS=Homo sapiens GN=ZNF227 PE=2 SV=1
2	6.88	50.0	2	14/25	K58k	(R)ASQSFGKGCEECKFLkER(T)	2161.0165	114.0397	-1.4	92033.5/9.11	HUMAN	RQ86WZ6	REVERSE Zinc finger protein 227 OS=Homo sapiens GN=ZNF227 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.38	78.3	10	5/25	K68k	(K) k Y\E D\I|C/P/S/T/H N M/D V/P N I/K (R)	2161.0053	114.0509	3.5	16832.4/5.08	HUMAN	P63241	312563	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2
1	18.38	78.3	10	5/25	K68k	(K) k Y\E D\I|C/P/S/T/H N M/D V/P N I/K (R)	2161.0053	114.0509	3.5	16793.3/5.38	HUMAN	Q9GZV4	312591	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3
1	18.38	78.3	10	5/25	K68k	(K) k Y\E D\I|C/P/S/T/H N M/D V/P N I/K (R)	2161.0053	114.0509	3.5	16773.3/4.85	HUMAN	Q6IS14	312619	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=2 SV=2

Fragment-ion (m/z)	70.066	72.082	84.081	86.097	116.017	129.103	133.043	147.114	368.189^{+2}	406.203	451.560^{+3}	452.229	471.292
Frac. Inten.(% of TIC)	0.00	0.05	0.18	0.42	2.30	0.05	12.85	1.89	2.03	1.62	2.64	1.76	6.02
Rel. Inten.(% of BP)	0.01	0.19	0.61	1.44	7.84	0.18	43.89	6.44	6.93	5.52	9.03	6.02	20.55
Score	0.20	0.50	0.50	0.22	-0.08	0.20	-0.44	1.50	0.50	0.50	1.50	-0.06	1.50
Ion-type	PR	V	KQ	LI		RKQ		y_1	a_5^{+2}	b_2	y_{12}^{+3}		y_4
Delta ppm	18.2	12.8	7.4	6.7		2.8		11.5	2.2	-16.2	0.9		-0.6

Fragment-ion (m/z)	504.902^{+3}	534.272	584.793^{+2}	628.304^{+2}	650.276	668.325^{+2}	676.836^{+2}	685.388	756.856^{+2}	763.361	783.311	882.376
Frac. Inten.(% of TIC)	1.68	3.08	2.09	1.74	9.29	2.27	29.29	1.60	2.61	9.71	2.47	2.35
Rel. Inten.(% of BP)	5.75	10.53	7.12	5.93	31.73	7.75	100.00	5.48	8.90	33.15	8.45	8.03
Score	1.50	1.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50	0.50	-0.08	-0.08
Ion-type	y_{13}^{+3}	$y{+}{+}_9$	y_{10}^{+2}	y_{11}^{+2}	b_4	$y_{12}\text{-}NH_3^{+2}$	y_{12}^{+2}	y_6	y_{13}^{+2}	b_5		
Delta ppm	-1.1	6.6	0.0	-7.0	-4.5	5.1	0.7	0.6	7.4	-3.0		



Result Summary

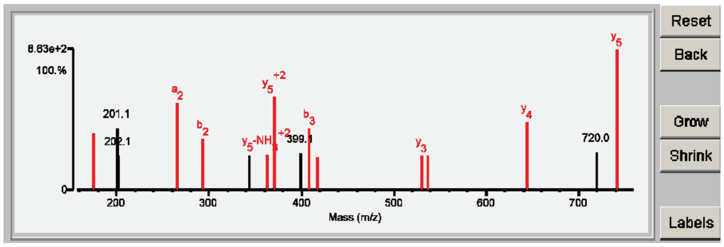
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.40	64.6	7	9/25	K85k	(K)YEDICPSTHNMDVPNIkR(N)	2189.0114	114.0508	3.4	16832.4/5.08	HUMAN	P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2
1	12.40	64.6	7	9/25	K85k	(K)YEDICPSTHNMDVPNIkR(N)	2189.0114	114.0508	3.4	16793.3/5.38	HUMAN	Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3
1	12.40	64.6	7	9/25	K85k	(K)YEDICPSTHNMDVPNIkR(N)	2189.0114	114.0508	3.4	16773.3/4.85	HUMAN	Q6IS14	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.40	64.6	7	9/25	K85k	(K) Y E\D\I C P S T H N M D V/P/N/I/k/R (N)	2189.0114	114.0508	3.4	16832.4/5.08	HUMAN	P63241	312563	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2
1	12.40	64.6	7	9/25	K85k	(K) Y E\D\I C P S T H N M D V/P/N/I/k/R (N)	2189.0114	114.0508	3.4	16793.3/5.38	HUMAN	Q9GZV4	312591	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3
1	12.40	64.6	7	9/25	K85k	(K) Y E\D\I C P S T H N M D V/P/N/I/k/R (N)	2189.0114	114.0508	3.4	16773.3/4.85	HUMAN	Q6IS14	312619	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=2 SV=2

Fragment-ion (m/z)	70.065	72.082	84.080	86.097	110.071	136.076	137.077	175.116	201.120	202.091	265.118	293.117	343.209
Frac. Inten.(% of TIC)	0.02	0.23	4.48	0.25	0.22	0.68	3.47	5.20	5.64	3.11	7.93	4.68	3.11
Rel. Inten.(% of BP)	0.12	1.77	35.16	1.92	1.71	5.34	27.24	40.84	44.30	24.38	62.23	36.69	24.39
Score	0.20	0.50	-0.35	0.22	1.00	1.00 1.00	-0.27	1.50	-0.44	-0.24	0.50	0.50	-0.24
Ion-type	PR	V		LI	H	a_1 Y		y_1			a_2	b_2	
Delta ppm	2.5	10.0		11.3	-7.0	-7.3 0.8		-14.6			-6.0	10.3	

Fragment-ion (m/z)	362.709^{+2}	371.222^{+2}	399.132	408.141	417.265	530.337	537.237	644.386	720.049	741.435	783.311	943.348
Frac. Inten.(% of TIC)	3.26	8.43	3.30	5.65	2.96	3.14	3.06	6.20	3.43	12.74	5.05	3.78
Rel. Inten.(% of BP)	25.58	66.20	25.88	44.33	23.19	24.61	24.02	48.66	26.94	100.00	39.60	29.65
Score	0.50	1.50	-0.26	0.50	1.50	1.50	0.75	1.50	-0.27	1.50	-0.40	-0.30
Ion-type	$y_5\text{-}NH_3^{+2}$	y_5^{+2}		b_3	y_2	y_3	PSTHN	y_4		y_5		
Delta ppm	1.2	-0.6		-1.3	20.0	-8.1	-9.8	3.5		-2.6		



Result Summary

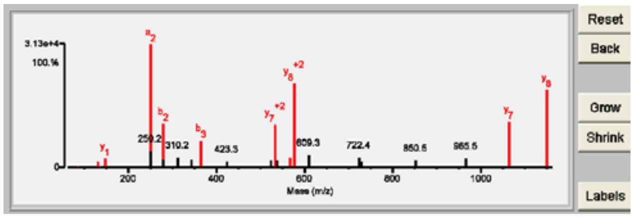
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.09	82.0	3	12/25	K224k	(K)YLSFLEkRQK(L)	1311.7419	114.0270	-11.2	58305.1/5.50	HUMAN	Q8NHP7	Exonuclease 3'-5' domain-like-containing protein 1 OS=Homo sapiens GN=EXDL1 PE=2 SV=3
2	8.97	79.6	2	14/25	K227k	(K)YLSFLEKRQk(L)	1311.7419	114.0270	-11.2	58305.1/5.50	HUMAN	Q8NHP7	Exonuclease 3'-5' domain-like-containing protein 1 OS=Homo sapiens GN=EXDL1 PE=2 SV=3
3	8.97	79.6	2	14/25	M92m K97k	(K)YLSAFmIPLIk(D)	1295.7432	130.0257	-8.5	56194.0/6.29	HUMAN	RQ15172	REVERSE Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Homo sapiens GN=PPP2R5A PE=1 SV=1
4	8.88	77.5	5	13/25	K1969k K1971k	(K)AYIPDLFkSk(T)	1197.6849	228.0840	11240.7	305413.8/5.90	HUMAN	Q8TD26	Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=3
5	7.70	72.6	2	15/25	None	(K)YLSNSLDAKITGK(Y)	1425.7919	-0.0229	-16.1	116454.0/7.92	HUMAN	RO76041	REVERSE Nebulette OS=Homo sapiens GN=NEBL PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.09	82.0	3	12/25	K224k	(K) Y L|S|F L E k R Q/K (L)	1311.7419	114.0270	-11.2	58305.1/5.50	HUMAN	Q8NHP7	201371	Exonuclease 3'-5' domain-like-containing protein 1 OS=Homo sapiens GN=EXDL1 PE=2 SV=3

Fragment-ion (m/z)	70.066	86.098	130.089	136.078	147.115	249.166	250.170	277.161	278.164	310.184	341.152	364.193
Frac. Inten.(% of TIC)	0.00	0.20	0.95	0.34	1.53	21.47	2.91	7.69	1.31	1.79	1.33	4.62
Rel. Inten.(% of BP)	0.00	0.93	4.40	1.56	7.11	100.00	13.53	35.79	6.08	8.33	6.19	21.52
Score	0.20	0.22	0.50	1.00 1.00	1.50	0.50	-0.14	0.50	-0.06	-0.08	-0.06	0.50
Ion-type	PR	LI	y_1-NH$_3$	a_1 Y	y_1	a_2		b_2				b_3
Delta ppm	18.2	13.6	17.3	8.9 17.0	17.6	18.7		18.5				15.4

Fragment-ion (m/z)	423.270	523.276	531.792^{+2}	538.301	566.307^{+2}	575.307^{+2}	609.342	722.421	727.342	850.486	965.524	1062.567	1149.600
Frac. Inten.(% of TIC)	0.99	1.11	7.45	1.11	1.67	14.51	2.17	1.70	0.96	1.14	1.47	8.06	13.55
Rel. Inten.(% of BP)	4.59	5.17	34.68	5.18	7.79	67.60	10.10	7.92	4.45	5.32	6.84	37.51	63.11
Score	-0.05	-0.05	1.50	-0.05	0.50	1.50	-0.10	-0.08	-0.04	-0.05	-0.07	1.50	1.50
Ion-type			y_7^{+2}		y_8-H$_2$O^{+2}	y_8^{+2}						y_7	y_8
Delta ppm			-27.2		-17.5	-27.3						-35.8	-32.5



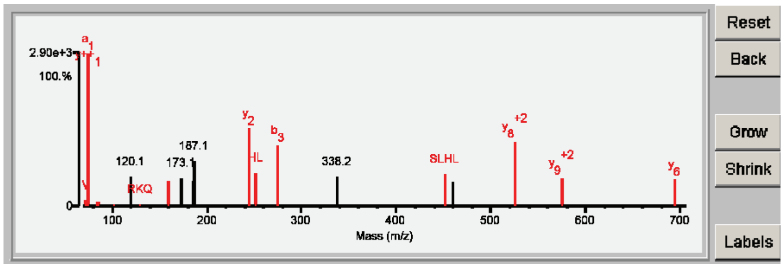
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.97	70.9	8	7/24	K157k	(K)TGDVEDSTVLkSLHLPK(N)	1838.9858	114.0584	7.9	73954.5/4.81	HUMAN	Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2
2	8.28	56.7	5	9/24	K163k	(K)TGDVEDSTVLKSLHLPk(N)	1838.9858	114.0584	7.9	73954.5/4.81	HUMAN	Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.97	70.9	8	7/24	K157k	(K) T\G\D\V E D S T/V/L k/S L H L/P/K (N)	1838.9858	114.0584	7.9	73954.5/4.81	HUMAN	Q9UNN5	208781	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2

Fragment-ion (m/z)	60.043	70.065	72.080	74.060	84.044	84.080	86.095	102.054	110.069	120.079	129.101	159.075	173.126	185.163	187.108	244.165	251.150	274.104	338.183^{+2}	451.262	459.292	525.330^{+2}	574.868^{+2}	694.428
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	4.50 21.73 -0.22	0.01 0.03 0.20 PR -7.5	0.82 3.94 0.50 V -8.0	20.70 100.00 1.50 a_1 -18.1 y^{++}_1 -3.2	0.31 1.52 1.00 b_1-H_2O -17.7 1.00 E -4.6	0.69 3.34 0.50 KQ -5.7	0.65 3.15 0.22 LI -11.9	0.19 0.90 1.00 b_1 -19.1 E	0.16 0.78 1.00 H -20.7	4.04 19.51 -0.20	0.19 0.93 0.20 RKQ -8.8	3.45 16.64 0.50 b_2 -16.4	3.76 18.18 -0.18	3.46 16.70 -0.17	6.16 29.73 -0.30	10.59 51.17 1.50 y_2 -4.4	4.51 21.78 0.75 HL -7.0	8.23 39.74 0.50 b_3 -2.0	3.90 18.82 -0.19	4.35 21.02 0.75 SLHL -12.5	3.32 16.04 -0.16	8.70 42.04 1.50 y_8^{+2} 6.6	3.76 18.17 1.50 y_9^{+2} 11.4	3.56 17.18 1.50 y_6 4.3



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Result Summary

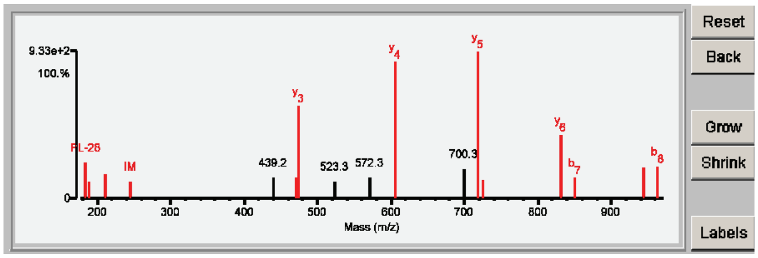
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.98	79.2	6	7/25	K457k	(K)TDQFPLFLIIMGkR(S)	1678.9349	114.0552	6.9	73954.5/4.81	HUMAN	Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2
2	5.97	62.5	2	14/25	K386k	(R)ISLIFEKISkSEER(R)	1678.9374	114.0527	5.5	78569.0/8.45	HUMAN	Q8IZF7	Probable G-protein coupled receptor 111 OS=Homo sapiens GN=GPR111 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.98	79.2	6	7/25	K457k	(K) T D Q/F P L F|L|I/I/M/G k R (S)	1678.9349	114.0552	6.9	73954.5/4.81	HUMAN	Q9UNN5	208781	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2

Fragment-ion (m/z)	70.065	84.080	86.095	101.069	104.051	120.079	171.078	175.111	183.151	189.083	211.140	245.133	439.245
Frac. Inten.(% of TIC)	0.00	0.14	0.83	0.14	3.77	0.18	2.53	3.96	4.21	2.06	2.90	2.05	2.46
Rel. Inten.(% of BP)	0.03	0.83	4.74	0.83	21.64	1.03	14.54	22.73	24.17	11.80	16.64	11.74	14.11
Score	0.20		0.22	0.50	-0.22	1.00	-0.15	-0.23	0.50	0.50	0.75	0.75	-0.14
Ion-type	**PR**	**QK**	**LI**	**QK**		**F**			**PL**-28	a_2	**PL**	**IM**	
Delta ppm	-6.1		-20.0	-21.2		-14.8			2.8	-29.0	-25.1	-1.3	

Fragment-ion (m/z)	471.303	474.278	523.287	572.273	605.320	700.348	718.404	724.933^{+2}	831.498	849.409	944.587	962.527
Frac. Inten.(% of TIC)	2.41	10.98	2.05	2.44	16.21	3.56	17.43	2.17	7.48	2.52	3.63	3.87
Rel. Inten.(% of BP)	13.83	62.98	11.74	13.99	93.00	20.44	100.00	12.47	42.91	14.46	20.80	22.18
Score	0.75	1.50	-0.12	-0.14	1.50	-0.20	1.50	1.50	1.50	0.50	1.50	0.50
Ion-type	**LIIM**	y_3			y_4		y_5	y_{11}^{+2}	y_6	b_7	y_7	b_8
Delta ppm	3.1	-0.0			2.2		1.7	10.4	13.2	-6.9	16.9	29.1



Result Summary

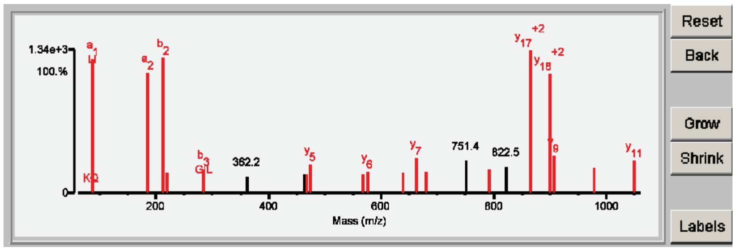
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.54	91.2	12	4/25	K28k	(R)IVAPGkGILAADESTGSIAK(R)	1898.0593	114.0544	5.7	39420.2/8.30	HUMAN	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
2	3.67	63.0	2	16/25	K42k	(R)IVAPGKGILAADESTGSIAk(R)	1898.0593	114.0544	5.7	39420.2/8.30	HUMAN	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.54	91.2	12	4/25	K28k	(R) I V|A|P G k\G/I L/A/A/D/E/S/T/G S I/A K (R)	1898.0593	114.0544	5.7	39420.2/8.30	HUMAN	P04075	9442	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2

Fragment-ion (m/z)	70.064	72.079	84.079	86.096	185.163	213.158	218.156	284.195	362.218	462.743^{+2}	468.252
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -14.6	0.05 0.38 0.50 V -30.2	0.08 0.62 0.50 KQ -17.5	12.50 94.00 0.50 a_1 -23.5 0.50 LI -10.8	11.18 84.05 0.50 a_2 -13.7	12.62 94.91 0.50 b_2 -14.3	1.89 14.19 1.50 y_2 27.9	2.19 16.49 0.75 b_3 -9.0 GIL -9.0	1.56 11.72 -0.12	1.82 13.66 -0.14	1.77 13.31 0.75 APGk -12.8

Fragment-ion (m/z)	475.283	567.317	576.346	638.364	663.360	680.411	751.433	792.426	822.486	864.965^{+2}	900.477^{+2}	907.450	978.467	1049.507
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.71 20.38 1.50 y_5 -9.6	1.77 13.28 0.75 PGkGI -15.7	1.95 14.67 1.50 y_6 19.3	1.89 14.20 1.50 y++$_{13}$ 31.8 APGkGI 0.6	3.20 24.07 1.50 y_7 -10.2	1.97 14.83 0.75 b_6 1.3 PGkGIL 1.3	3.07 23.09 -0.23	2.19 16.49 1.50 y_8 20.4	2.40 18.03 -0.18	13.30 100.00 1.50 y_{17}^{+2} 5.9	11.11 83.53 1.50 y_{18}^{+2} -1.1	3.51 26.41 1.50 y_9 14.7	2.30 17.28 1.50 y_{10} -6.6	2.99 22.47 1.50 y_{11} -3.7



Result Summary

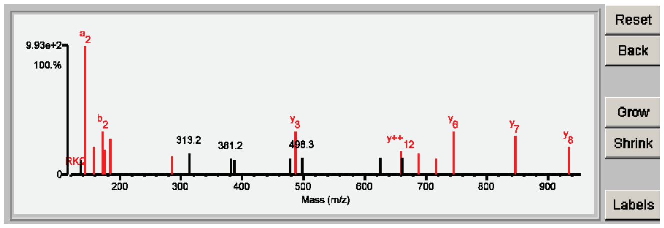
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.70	72.6	8	10/25	K42k	(K)GILAADESTGSIAkR(L)	1488.8016	114.0539	6.8	39420.2/8.30	HUMAN	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
2	5.75	59.6	3	16/25	None	(K)IGVSEAAEFALLLNR(K)	1602.8850	-0.0294	-18.4	118585.6/6.29	HUMAN	RQ5M775	REVERSE Sperm antigen with calponin homology and coiled-coil domains 1 OS=Homo sapiens GN=SPECC1 PE=1 SV=1
3	4.48	51.9	1	14/25	M180m	(R)FGPTmQLAVAVLSPR(V)	1586.8723	15.9832	-7.3	77188.4/6.18	HUMAN	RO15228	REVERSE Dihydroxyacetone phosphate acyltransferase OS=Homo sapiens GN=GNPAT PE=1 SV=1
4	3.79	53.2	2	15/25	K74k	(K)MVkPVASQFVINR(I)	1488.8355	114.0200	-14.3	70384.6/5.18	HUMAN	RQ9UJY5	REVERSE ADP-ribosylation factor-binding protein GGA1 OS=Homo sapiens GN=GGA1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.70	72.6	8	10/25	K42k	(K) G I|L|A A D E/S/T/G/S I/A k/R (L)	1488.8016	114.0539	6.8	39420.2/8.30	HUMAN	P04075	18883	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2

Fragment-ion (m/z)	84.079	86.096	87.098	129.101	136.072	143.116	157.132	171.112	175.118	185.127	284.192	313.204	381.155
Frac. Inten.(% of TIC)	5.47	0.93	2.22	0.06	2.19	18.66	4.14	6.31	3.63	5.14	2.59	3.12	2.35
Rel. Inten.(% of BP)	29.34	4.96	11.92	0.34	11.72	100.00	22.21	33.81	19.45	27.53	13.88	16.72	12.59
Score	-0.29	0.22	-0.12	0.20	-0.12	0.50	0.50	0.50	1.50	0.75	0.50	-0.17	-0.13
Ion-type		LI		RKQ		a_2	IA-28	b_2	y_1	IA	b_3		
Delta ppm		-4.9		-13.5		-20.2	-17.4	-14.0	-4.3	-12.2	-21.3		

Fragment-ion (m/z)	387.143^{+2}	478.245	488.291	498.320^{+2}	625.304	660.337	661.296^{+2}	688.392	716.886^{+2}	745.440	846.479	933.513
Frac. Inten.(% of TIC)	2.22	2.39	6.35	2.54	2.48	3.44	2.46	3.04	2.33	6.23	5.61	4.10
Rel. Inten.(% of BP)	11.90	12.81	34.02	13.64	13.30	18.41	13.18	16.31	12.47	33.39	30.09	21.98
Score	-0.12	-0.13	1.50	-0.14	-0.13	1.50	-0.13	1.50	1.50	1.50	1.50	1.50
Ion-type			y_3			$y{+}{+}_{12}$		y_5	y_{13}^{+2}	y_6	y_7	y_8
Delta ppm			-6.1			8.3		-25.9	18.2	11.1	0.1	1.9



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Result Summary

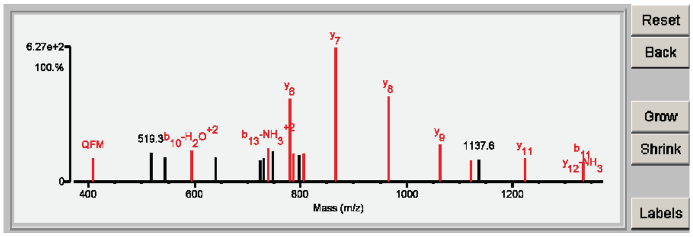
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.39	69.3	7	10/25	K55k	(R)GFFkVLGQLTETGVVSPEQFMK(S)	2442.2737	114.0616	7.3	20749.2/8.17	HUMAN	Q96EK6	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens GN=GNPNAT1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.39	69.3	7	10/25	K55k	(R) G F F k V L\G Q L T E|T/G/V/V/S/P E Q F M K (S)	2442.2737	114.0616	7.3	20749.2/8.17	HUMAN	Q96EK6	256965	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens GN=GNPNAT1 PE=1 SV=1

Fragment-ion (m/z)	72.079	85.044	86.097	102.097	120.079	407.189	519.292	543.781^{+2}	594.325^{+2}	640.375^{+2}	724.362	729.458
Frac. Inten.(% of TIC)	0.15	2.49	0.23	2.91	0.14	2.91	3.63	3.07	3.97	3.11	2.68	2.87
Rel. Inten.(% of BP)	0.90	14.84	1.39	17.34	0.84	17.36	21.65	18.33	23.69	18.52	15.97	17.12
Score	0.50	-0.15	0.22	-0.17	1.00	0.75	-0.22	-0.18	0.25	-0.19	-0.16	-0.17
Ion-type	V		LI		F	QFM			b_{10}-H_2O^{+2}			
Delta ppm	-21.9		3.2		-11.5	31.6			-13.6			

Fragment-ion (m/z)	738.406^{+2}	746.947^{+2}	779.361	787.420^{+2}	796.933	806.441	866.415	965.475	1064.554	1121.539	1137.553^{+2}	1222.592	1334.679
Frac. Inten.(% of TIC)	4.20	3.75	10.44	3.57	3.35	3.56	16.77	10.74	4.59	2.58	2.83	2.96	2.49
Rel. Inten.(% of BP)	25.05	22.38	62.24	21.28	19.99	21.22	100.00	64.02	27.39	15.40	16.90	17.65	14.84
Score	0.25	-0.22	1.50	0.25	-0.20	0.50	1.50	1.50	1.50	1.50	-0.17	1.50	0.50
Ion-type	b_{13}-NH_3^{+2}		y_6	b_{14}-H_2O^{+2}		b_6	y_7	y_8	y_9	y_{10}		y_{11}	b_{11} y_{12}-NH_3
Delta ppm	34.2		-19.0	-3.4		-19.8	8.2	-1.4	9.3	-23.9		-17.5	-24.4 36.8



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Result Summary

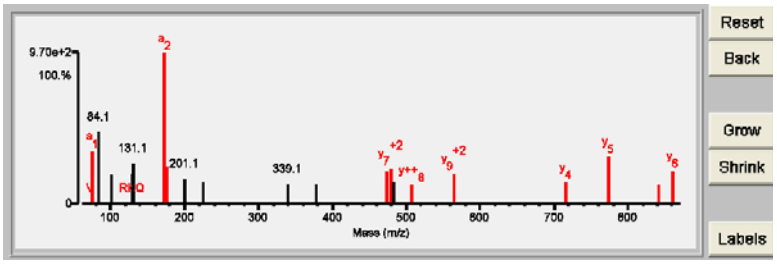
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.77	63.1	8	9/24	K194k	(K)TVDGPSGkLWR(D)	1215.6480	114.0506	5.8	36053.4/8.57	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.77	63.1	8	9/24	K194k	(K) T V/D/G/P/S/G/k/L W/R (D)	1215.6480	114.0506	5.8	36053.4/8.57	HUMAN	P04406	230149	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

Fragment-ion (m/z)	70.063	72.081	74.058	84.079	86.094	101.069	128.103	129.104	131.125	173.127	175.119	201.110
Frac. Inten.(% of TIC)	0.01	0.14	6.85	9.44	0.09	3.79	4.01	0.11	5.37	19.93	4.84	3.29
Rel. Inten.(% of BP)	0.06	0.69	34.37	47.38	0.44	19.03	20.11	0.57	26.96	100.00	24.26	16.51
Score	0.20	0.50	0.50	-0.47	0.22	-0.19	-0.20	0.20	-0.27	0.50	1.50	-0.17
Ion-type	PR	V	a_1		LI			RKQ		a_2	y_1	
Delta ppm	-27.5	7.3	-41.0		-23.5			10.5		-13.6	2.0	

Fragment-ion (m/z)	225.110	339.133	378.133	474.271	479.273^{+2}	483.274	507.767	565.290^{+2}	716.418	773.426	842.433	860.462
Frac. Inten.(% of TIC)	2.86	2.67	2.66	4.36	4.64	2.78	2.46	3.95	2.84	6.14	2.51	4.26
Rel. Inten.(% of BP)	14.36	13.38	13.33	21.85	23.26	13.95	12.34	19.82	14.24	30.81	12.59	21.40
Score	-0.14	-0.13	-0.13	1.50	1.50	-0.14	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type				y_3	y_7^{+2}		$y{+}{+}_8$	y_9^{+2}	y_4	y_5	y_6-H_2O	y_6
Delta ppm				-24.1	12.0		-20.3	-2.3	-2.8	-19.9	-35.7	-13.8



Result Summary

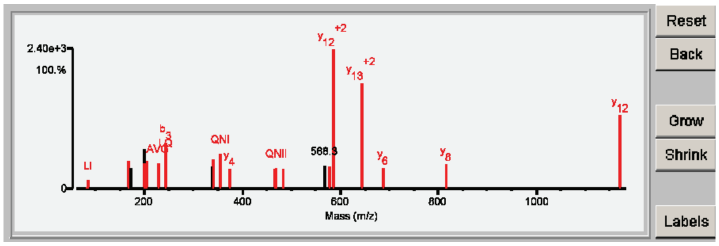
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.41	87.2	8	4/25	K215k	(R)GALQNIIPASTGAAkAVGK(V)	1767.0123	114.0566	7.3	36053.4/8.57	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
2	14.32	81.4	6	6/25	K219k	(R)GALQNIIPASTGAAKAVGk(V)	1767.0123	114.0566	7.3	36053.4/8.57	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
3	8.29	63.2	2	12/25	K679k	(R)ISVPAkRTGILQEAKR(R)	1767.0599	114.0090	-18.0	117514.7/8.75	HUMAN	Q9UMS6	Synaptopodin-2 OS=Homo sapiens GN=SYNPO2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.41	87.2	8	4/25	K215k	(R) G A L\Q N\I/I/P A S T/G A/A k/A V/G K (V)	1767.0123	114.0566	7.3	36053.4/8.57	HUMAN	P04406	115075	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

Fragment-ion (m/z)	70.065	84.081	86.096	101.071	169.096	173.128	199.180	200.146	204.135	228.133	242.150	339.167
Frac. Inten.(% of TIC)	0.01	0.26	1.05	0.12	3.52	2.55	4.97	3.16	3.57	3.13	5.73	2.77
Rel. Inten.(% of BP)	0.04	1.51	6.03	0.68	20.21	14.64	28.50	18.14	20.48	17.96	32.88	15.90
Score	0.20	0.50	0.22	0.50	0.75	-0.15	-0.28	0.50	1.50	0.75	0.75	-0.16
Ion-type	PR	KQ	LI	a_2	PA			AVG-28	y_2	AVG	b_3	
Delta ppm	-0.4	0.3	-3.8	-15.2	-13.3			29.2	4.6	-11.2	-4.6	
											LQ	
				KQ							-4.6	

Fragment-ion (m/z)	341.219	356.191	374.240	467.227	469.277	484.268	568.317	577.326^{+2}	586.330^{+2}	642.867^{+2}	687.423	815.482	1171.646
Frac. Inten.(% of TIC)	3.59	4.33	2.47	2.47	2.68	2.49	2.96	2.74	17.43	13.18	2.61	3.04	9.15
Rel. Inten.(% of BP)	20.60	24.84	14.19	14.17	15.38	14.29	16.98	15.73	100.00	75.62	14.95	17.43	52.47
Score	0.75	0.75	1.50	0.25	0.75	0.50	-0.17	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	NII	QNI	y_4	b_5-NH_3	QNII	b_5		y_{12}-H_2O^{+2}	y_{12}^{+2}	y_{13}^{+2}	y_6	y_8	y_{12}
Delta ppm	0.2	-9.1	1.3	2.2	-2.4	32.8		10.9	8.5	0.1	12.4	10.9	2.8



Result Summary

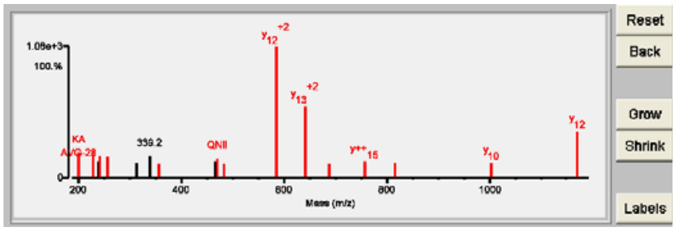
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.01	80.1	8	7/25	K219k	(R)GALQNIIPASTGAAKAVGk(V)	1767.0123	114.0548	6.3	36053.4/8.57	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
2	15.76	80.1	8	7/25	K215k	(R)GALQNIIPASTGAAkAVGK(V)	1767.0123	114.0548	6.3	36053.4/8.57	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
3	8.05	71.1	3	13/25	None	(K)LIQQNLAARQNQLKSR(G)	1881.0777	-0.0106	-5.6	76993.7/6.36	HUMAN	RQ8IUC4	REVERSE Rhophilin-2 OS=Homo sapiens GN=RHPN2 PE=1 SV=1
4	5.73	54.6	2	15/25	None	(R)EPIEKIAIRVQNSLDR(G)	1881.0552	0.0119	6.3	147437.9/5.42	HUMAN	RQ6ZN16	REVERSE Mitogen-activated protein kinase kinase kinase 15 OS=Homo sapiens GN=MAP3K15 PE=2 SV=2
4	5.73	54.6	2	15/25	None	(R)EPIEKIAIRVQNSLDR(G)	1881.0552	0.0119	6.3	154537.7/5.52	HUMAN	RQ99683	REVERSE Mitogen-activated protein kinase kinase kinase 5 OS=Homo sapiens GN=MAP3K5 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.01	80.1	8	7/25	K219k	(R) G A L\Q/N\I/I/P A/S T/G A/A K A V G k (V)	1767.0123	114.0548	6.3	36053.4/8.57	HUMAN	P04406	230149	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

Fragment-ion (m/z)	70.065	84.042	84.080	86.096	87.101	101.069	129.096	200.135	228.134	240.136	242.147
Frac. Inten.(% of TIC)	0.01	2.88	0.20	1.00	2.76	0.11	2.95	4.41	4.17	2.85	3.81
Rel. Inten.(% of BP)	0.03	12.65	0.87	4.41	12.14	0.49	12.96	19.37	18.32	12.52	16.75
Score	0.20	-0.13	0.50	0.22	-0.12	0.50	-0.13	0.75	0.75	-0.13	0.75
Ion-type	PR		KQ	LI		a_2		KA	AVG		b_3
Delta ppm	-7.5		-14.0	-4.9		-27.1		-26.7	-4.2		-18.6
								AVG-28	PAS-28		LQ
						KQ		-26.7	-4.2		-18.6

Fragment-ion (m/z)	256.122	313.174	339.163	356.190	466.224	469.272	484.264	586.322^{+2}	642.873^{+2}	687.427	756.443	815.469	1003.559	1171.643
Frac. Inten.(% of TIC)	3.57	2.61	3.70	2.42	2.90	3.39	2.44	22.75	12.32	2.48	2.89	2.69	2.64	8.05
Rel. Inten.(% of BP)	15.70	11.48	16.25	10.63	12.75	14.89	10.72	100.00	54.16	10.90	12.72	11.83	11.61	35.38
Score	0.75	-0.11	-0.16	0.75	-0.13	0.75	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	PAS			QNI		QNII	b_5	y_{12}^{+2}	y_{13}^{+2}	y_6	$y{++}_{15}$	y_8	y_{10}	y_{12}
Delta ppm	-30.8			-9.9		-13.9	24.1	-4.8	8.5	17.9	15.8	-5.7	6.3	0.4



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Result Summary

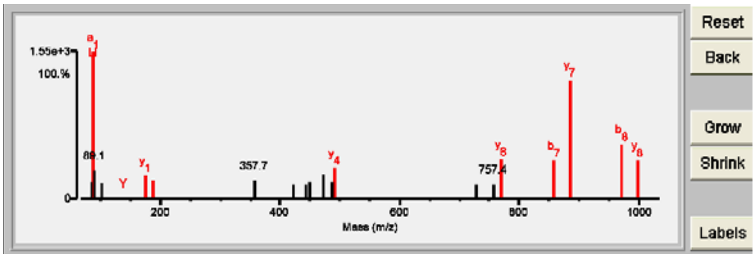
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.02	67.4	6	14/25	K216k	(K)LTkAICGLIDDYSMVR(F)	1854.9452	114.0660	11.7	32761.5/4.38	HUMAN	Q9UHW5	GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.02	67.4	6	14/25	K216k	(K) L T k A I C G\L|I/D/D Y/S M V/R (F)	1854.9452	114.0660	11.7	32761.5/4.38	HUMAN	Q9UHW5	261527	GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 PE=1 SV=2

Fragment-ion (m/z)	70.065	84.044	84.082	86.095	89.057	102.052	136.076	175.117	187.150	357.713^{+2}
Frac. Inten.(% of TIC)	0.00	1.81	2.21	19.43	3.77	2.13	0.09	3.05	2.36	2.39
Rel. Inten.(% of BP)	0.02	9.32	11.35	100.00	19.40	10.97	0.48	15.70	12.14	12.31
Score	0.20	-0.09	-0.11	0.50	-0.19	-0.11	1.00	1.50	0.50	-0.12
Ion-type	PR			a_1			Y	y_1	a_2	
Delta ppm	-0.4			-24.7			3.0	-12.3	27.2	
				0.50						
				LI						
				-11.9						

Fragment-ion (m/z)	421.236	442.229	450.296^{+2}	472.277	472.777	486.261	492.268	728.323	757.411	770.350	858.450	885.381	971.541	998.458	1110.586
Frac. Inten.(% of TIC)	1.90	1.87	2.29	3.20	3.15	2.26	4.13	1.85	1.99	5.20	5.06	15.72	7.29	5.03	1.79
Rel. Inten.(% of BP)	9.79	9.63	11.80	16.48	16.22	11.64	21.24	9.52	10.24	26.78	26.05	80.92	37.51	25.90	9.23
Score	-0.10	-0.10	-0.12	-0.16	-0.16	-0.12	1.50	-0.10	-0.10	1.50	0.50	1.50	0.50	1.50	-0.09
Ion-type							y_4			y_6	b_7	y_7	b_8	y_8	
Delta ppm							16.9			0.2	-1.5	4.8	5.4	-3.4	



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Result Summary

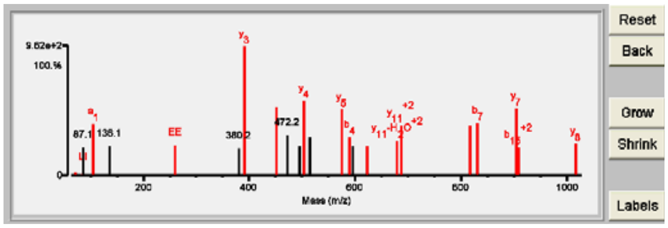
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.26	78.5	10	7/25	K18k K29k	(R)MDkVGDALEEVLSkALSQR(T)	2089.0958	228.0976	5.1	18335.9/4.36	HUMAN	P24522	Growth arrest and DNA-damage-inducible protein GADD45 alpha OS=Homo sapiens GN=GADD45A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.26	78.5	10	7/25	K18k K29k	(R) M D k V\G D A\L/E/E V/L/S/k/A|L/S Q R (T)	2089.0958	228.0976	5.1	18335.9/4.36	HUMAN	P24522	231797	Growth arrest and DNA-damage-inducible protein GADD45 alpha OS=Homo sapiens GN=GADD45A PE=1 SV=1

Fragment-ion (m/z)	72.081	84.081	86.097	87.101	104.052	136.075	259.094	380.207^{+2}	390.210	452.253^{+2}	472.232^{+2}	496.015^{+4}	503.294
Frac. Inten.(% of TIC)	0.25	0.18	0.64	2.69	4.98	2.84	2.94	2.61	12.51	6.58	3.95	2.80	7.21
Rel. Inten.(% of BP)	2.00	1.47	5.09	21.48	39.79	22.72	23.50	20.86	100.00	52.65	31.57	22.38	57.65
Score	0.50	0.50	0.22	-0.21	0.50	-0.23	0.75	-0.21	1.50	1.50	-0.32	-0.22	1.50
Ion-type	V	KQ	LI		a_1		EE		y_3	y_7^{+2}			y_4
Delta ppm	-1.0	-2.1	6.7		-14.8		0.9		0.4	-1.9			-0.0

Fragment-ion (m/z)	514.287^{+2}	574.331	588.278	594.815^{+2}	622.842^{+2}	678.386^{+2}	687.369^{+2}	816.464	831.363	903.501	907.928^{+2}	1016.593
Frac. Inten.(% of TIC)	3.74	6.40	3.72	2.84	2.82	3.33	4.88	4.82	5.04	6.50	2.73	3.02
Rel. Inten.(% of BP)	29.90	51.18	29.73	22.75	22.51	26.62	39.02	38.51	40.29	52.00	21.81	24.14
Score	-0.30	1.50	0.50	-0.23	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type		y_5	b_4		y_{10}^{+2}	y_{11}-H_2O^{+2}	y_{11}^{+2}	y_6	b_7	y_7	b_{15}^{+2}	y_8
Delta ppm		0.6	-7.8		-15.6	26.8	-5.2	-5.3	-5.9	-0.1	-25.8	7.9



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Result Summary

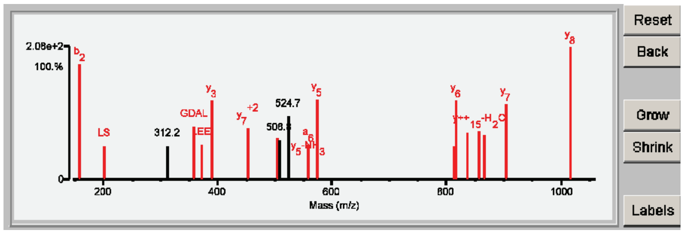
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.20	82.9	8	6/24	K29k	(K)VGDALEEVLSkALSQR(T)	1714.9334	114.0535	5.8	18335.9/4.36	HUMAN	P24522	Growth arrest and DNA-damage-inducible protein GADD45 alpha OS=Homo sapiens GN=GADD45A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.20	82.9	8	6/24	K29k	(K) V/G|D A L E E V|L/S/k/A/L/S Q R (T)	1714.9334	114.0535	5.8	18335.9/4.36	HUMAN	P24522	231797	Growth arrest and DNA-damage-inducible protein GADD45 alpha OS=Homo sapiens GN=GADD45A PE=1 SV=1

Fragment-ion (m/z)	72.081	86.095	98.092	142.101	157.094	201.117	312.153	357.163	372.183	390.221	452.244^{+2}	503.299
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.46 4.32 0.50 a_1 -14.9 0.50 V 0.3	0.14 1.33 0.22 LI -16.6	2.94 27.35 -0.19	2.89 26.91 -0.19	9.34 86.95 0.50 b_2 -26.4	2.75 25.57 0.75 LS -35.6	2.70 25.13 -0.17	4.25 39.58 0.75 GDAL -41.0	2.85 26.48 0.75 LEE 15.3	6.38 59.41 1.50 y_3 29.6	4.15 38.66 1.50 y_7^{+2} -21.8	3.33 30.96 1.50 y_4 9.9

Fragment-ion (m/z)	508.751^{+2}	524.669	557.310	574.315	813.383	816.464	836.948^{+2}	856.455	865.451	903.507	1016.591	1245.714
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.18 29.61 -0.21	5.13 47.76 -0.33	2.80 26.05 0.50 a_6 29.3 y_5-NH_3 11.1	6.47 60.18 1.50 y_5 -27.2	2.72 25.32 0.50 b_8 -21.1	6.43 59.85 1.50 y_6 -5.8	3.80 35.39 1.50 $b_{15}+H_2O^{+2}$ 7.2 y_{14}^{+2} 1.1	3.92 36.45 0.50 $y{+}{+}_{15}$-H_2O 2.7	3.64 33.90 1.50 $y{+}{+}_{15}$ -7.8	6.12 56.91 1.50 y_7 6.7	10.75 100.00 1.50 y_8 5.7	2.85 26.53 -0.18



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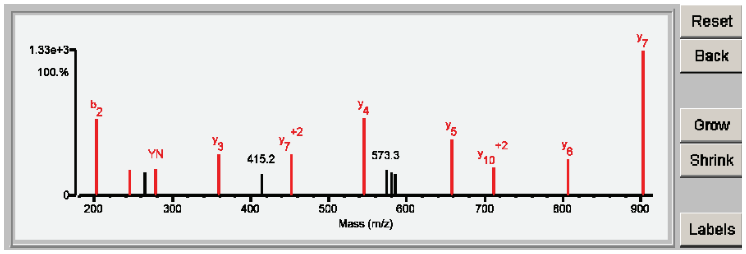
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.97	69.7	8	8/25	K159k	(K)SNYNFEkPFLWLAR(K)	1784.9119	114.0557	6.7	24423.2/7.01	HUMAN	P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.97	69.7	8	8/25	K159k	(K) S N\Y N/F E k/P/F/L/W/L/A R (K)	1784.9119	114.0557	6.7	24423.2/7.01	HUMAN	P62826	556919	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3

Fragment-ion (m/z)	60.043	70.063	72.078	84.080	86.095	115.049	120.078	136.075	159.089	202.081	245.127	246.149	264.652	278.105	359.241	415.214	451.761^{+2}	545.315	573.331^{+2}	580.766^{+2}	584.321	658.394	710.892^{+2}	805.480	902.526
Frac. Inten.(% of TIC)	7.14	0.00	2.35	13.28	0.24	2.45	0.15	0.14	0.08	8.17	2.54	2.79	2.44	2.85	4.49	2.26	4.42	8.32	2.73	2.45	2.35	6.05	2.92	3.86	15.54
Rel. Inten.(% of BP)	45.97	0.02	15.10	85.45	1.55	15.78	0.99	0.89	0.50	52.58	16.37	17.93	15.73	18.37	28.89	14.56	28.43	53.54	17.59	15.75	15.10	38.93	18.82	24.85	100.00
Score	0.50	0.20	-0.15	-0.85	0.22	-0.16	1.00	1.00	2.00	0.50	0.75	1.50	-0.16	0.75	1.50	-0.15	1.50	1.50	-0.18	-0.16	-0.15	1.50	1.50	1.50	1.50
Ion-type	a_1	PR			LI		F	Y	W	b_2	PF	y_2		YN	y_3		y_7^{+2}	y_4				y_5	y_{10}^{+2}	y_6	y_7
Delta ppm	-38.1	-28.9			-17.7		-23.1	-4.3	-14.9	-13.0	-12.0	-27.5		-36.1	2.4		-11.0	-7.4				-14.6	2.4	9.8	1.9



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Result Summary

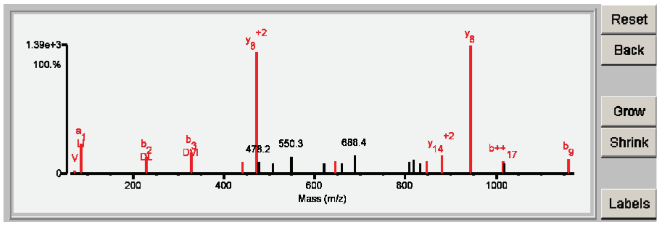
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.23	76.4	8	10/25	K829k	(K)IDVIkQADYVPSDQDLLR(C)	2088.0972	114.0654	10.2	111025.1/4.91	HUMAN	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	12.23	76.4	8	10/25	K186k	(K)IDVIkQADYVPSDQDLLR(C)	2088.0972	114.0654	10.2	45664.8/5.59	HUMAN	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1
2	7.85	72.3	5	12/25	K226k	(R)VLDLFSPNLkKGTEEELR(L)	2088.1335	114.0290	-6.3	62565.0/8.68	HUMAN	RO15244	REVERSE Solute carrier family 22 member 2 OS=Homo sapiens GN=SLC22A2 PE=1 SV=1
3	6.43	57.3	3	16/25	M236m	(R)mNDLGSLSIRRPVLTCEPK(K)	2186.1420	16.0205	11.6	65588.9/6.83	HUMAN	RQ8WWW8	REVERSE GRB2-associated-binding protein 3 OS=Homo sapiens GN=GAB3 PE=2 SV=1
4	5.57	60.9	2	15/25	None	(K)DSSKTTIVKTVVEEIDPRGK(V)	2202.1976	-0.0351	-15.9	49823.6/5.06	HUMAN	Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.23	76.4	8	10/25	K829k	(K) I D\V\I|k Q A D Y\V/P/S D/Q D L L\R (C)	2088.0972	114.0654	10.2	111025.1/4.91	HUMAN	Q5JWF2	257093	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	12.23	76.4	8	10/25	K186k	(K) I D\V\I|k Q A D Y\V/P/S D/Q D L L\R (C)	2088.0972	114.0654	10.2	45664.8/5.59	HUMAN	P63092	257101	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

Fragment-ion (m/z)	70.064	72.080	84.079	86.095	136.078	229.119	328.180	441.265	472.246^{+2}	478.183^{+2}	508.243	550.301
Frac. Inten.(% of TIC)	0.01	0.52	0.17	5.63	0.15	3.17	4.08	2.08	22.83	2.19	2.02	3.27
Rel. Inten.(% of BP)	0.04	2.14	0.68	23.17	0.60	13.06	16.80	8.58	94.05	9.03	8.31	13.47
Score	0.20	0.50	0.50	0.50 0.50	1.00	0.75	0.75	0.50	1.50	-0.09	-0.08	-0.13
Ion-type	PR	V	KQ	a_1 LI	Y	b_2 DL	b_3 DVI	b_4	y_8^{+2}			
Delta ppm	-14.6	-9.4	-25.9	-27.0 -14.2	19.2	0.1 0.1	-24.1 -24.1	-16.4	1.3			

Fragment-ion (m/z)	620.818^{+2}	644.381	658.851^{+2}	688.405	809.476^{+2}	819.401	833.394	846.438	881.437^{+2}	943.479	1014.519	1017.565	1160.607
Frac. Inten.(% of TIC)	1.98	2.46	1.93	3.39	2.23	2.67	1.98	2.44	3.40	24.28	2.45	1.92	2.76
Rel. Inten.(% of BP)	8.17	10.14	7.93	13.98	9.19	11.01	8.14	10.07	14.01	100.00	10.07	7.91	11.37
Score	-0.08	1.50	-0.08	-0.14	-0.09	-0.11	-0.08	1.50	1.50	1.50	0.50	-0.08	0.50
Ion-type		y_5						y_7	y_{14}^{+2}	y_8	b++17		b_9
Delta ppm		12.9						7.0	-5.8	-5.7	0.5		9.3



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Result Summary

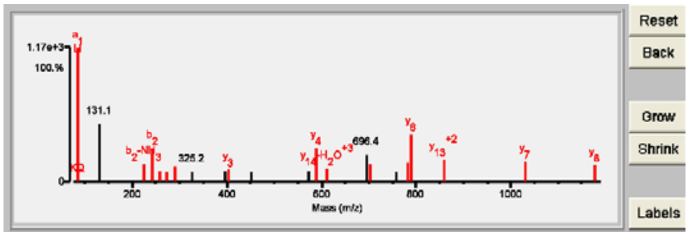
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.33	76.0	8	7/25	K917k	(R)LQEALNLFkSIWNNR(W)	1845.9970	114.0581	7.7	111025.1/4.91	HUMAN	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	16.33	76.0	8	7/25	K274k	(R)LQEALNLFkSIWNNR(W)	1845.9970	114.0581	7.7	45664.8/5.59	HUMAN	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.33	76.0	8	7/25	K917k	(R) L Q|E A L N L|F/k/S/I/W/N/N R (W)	1845.9970	114.0581	7.7	111025.1/4.91	HUMAN	Q5JWF2	257093	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	16.33	76.0	8	7/25	K274k	(R) L Q|E A L N L|F/k/S/I/W/N/N R (W)	1845.9970	114.0581	7.7	45664.8/5.59	HUMAN	P63092	257101	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

Fragment-ion (m/z)	84.079	86.096	87.058	120.079	131.116	225.127	242.147	258.108	272.136	289.166	325.184	397.215
Frac. Inten.(% of TIC)	0.17	23.93	0.07	0.14	10.24	3.16	5.96	2.01	1.69	2.86	1.73	1.86
Rel. Inten.(% of BP)	0.73	100.00	0.27	0.58	42.79	13.21	24.90	8.38	7.06	11.95	7.23	7.78
Score	0.50	0.50 0.50	0.33	1.00	-0.43	0.25	0.50	0.75	0.50	1.50	-0.07	-0.08
Ion-type	KQ	a_1 LI	NR	F		b_2-NH_3	b_2	QE	y_2-NH_3	y_2		
Delta ppm	-24.7	-10.8 -10.8	35.7	-17.3		15.2	-14.1	-2.9	2.8	15.3		

Fragment-ion (m/z)	403.195	452.236	572.326	589.282	610.296^{+3}	696.381^{+2}	702.351	758.395	782.441	789.385	859.948^{+2}	1031.527	1178.621
Frac. Inten.(% of TIC)	2.09	1.69	1.99	6.09	2.27	4.76	3.27	1.77	3.34	8.44	3.92	3.65	2.91
Rel. Inten.(% of BP)	8.75	7.05	8.31	25.47	9.47	19.89	13.66	7.42	13.97	35.28	16.36	15.25	12.15
Score	1.50	-0.07	-0.08	1.50	0.50	-0.20	1.50	-0.07	0.50	1.50	1.50	1.50	1.50
Ion-type	y_3			y_4	y_{14}-H_2O^{+3}		y_5		b_7	y_6	y_{13}^{+2}	y_7	y_8
Delta ppm	-23.3			-3.4	-38.8		-24.2		0.0	-18.9	-4.4	-11.0	12.1



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Result Summary

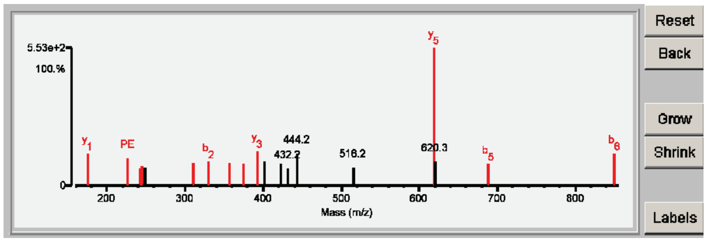
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.77	61.7	6	9/25	K950k	(K)SkIEDYFPEFAR(Y)	1501.7322	114.0630	12.4	111025.1/4.91	HUMAN	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	11.77	61.7	6	9/25	K307k	(K)SkIEDYFPEFAR(Y)	1501.7322	114.0630	12.4	45664.8/5.59	HUMAN	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.77	61.7	6	9/25	K950k	(K) S k\I E D\Y\F/P E/F A/R (Y)	1501.7322	114.0630	12.4	111025.1/4.91	HUMAN	Q5JWF2	257093	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
1	11.77	61.7	6	9/25	K307k	(K) S k\I E D\Y\F/P E/F A/R (Y)	1501.7322	114.0630	12.4	45664.8/5.59	HUMAN	P63092	257101	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

Fragment-ion (m/z)	70.064	72.078	84.079	86.096	120.081	136.074	175.116	227.104	243.143	245.068	249.121	310.171	330.176
Frac. Inten.(% of TIC)	0.01	3.43	11.77	0.26	0.85	0.33	4.65	4.04	2.56	2.79	2.75	3.30	3.50
Rel. Inten.(% of BP)	0.05	17.07	58.52	1.29	4.25	1.62	23.13	20.07	12.71	13.87	13.67	16.42	17.38
Score	0.20	-0.17	-0.59	0.22	1.00	1.00	1.50	0.75	0.75	0.75	-0.14	1.50	0.50
Ion-type	PR			LI	F	Y	y_1	PE	IE	ED		$y{++}_5$	b_2
Delta ppm	-14.6			-1.5	-2.3	-13.2	-17.4	2.9	31.1	-40.8		23.0	-7.5

Fragment-ion (m/z)	356.231	374.172	393.219	402.174	422.205	432.213	444.208	516.209	619.320	620.314	687.335	850.382
Frac. Inten.(% of TIC)	3.39	3.12	5.03	3.52	3.22	2.58	4.78	2.74	20.11	3.50	3.11	4.65
Rel. Inten.(% of BP)	16.87	15.50	25.03	17.50	15.99	12.80	23.78	13.63	100.00	17.40	15.48	23.13
Score	0.75	0.75	1.50	-0.18	-0.16	-0.13	-0.24	-0.14	1.50	-0.17	0.50	0.50
Ion-type	kI	PEF	y_3						y_5		b_5	b_6
Delta ppm	1.9	-0.1	-15.2						-0.2		4.8	-15.2



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Result Summary

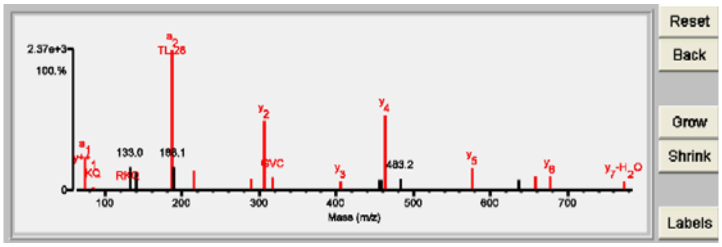
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.17	80.5	7	7/25	K130k	(K)TIkLWNTLGVCK(Y)	1432.7981	114.0517	5.6	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
2	5.91	55.5	2	13/25	None	(K)TLIQPKEGLSWFK(S)	1546.8628	-0.0130	-8.4	312282.1/8.57	HUMAN	RQ9NR99	REVERSE Matrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=2
3	5.59	51.3	4	15/25	None	(R)VSASFGKHLITVCK(S)	1546.8410	0.0087	5.6	47685.0/5.36	HUMAN	RQ01344	REVERSE Interleukin-5 receptor subunit alpha OS=Homo sapiens GN=IL5RA PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.17	80.5	7	7/25	K130k	(K) T I\k L W N/T/L/G/V/C/K (Y)	1432.7981	114.0517	5.6	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	72.079	74.060	84.080	86.094	129.100	130.064	133.043	141.102	159.090	187.143	188.146	215.140
Frac. Inten.(% of TIC)	0.09	5.99	0.63	0.33	0.19	0.12	4.36	3.17	0.12	25.91	4.23	3.66
Rel. Inten.(% of BP)	0.36	23.12	2.44	1.26	0.72	0.45	16.82	12.21	0.45	100.00	16.31	14.11
Score	0.50	1.50	0.50	0.22	0.20		-0.17	-0.12	2.00	0.50	-0.16	0.75
Ion-type	V	a_1 $y{+}{+}_1$	KQ	LI	RKQ	W			W	a_2 TL-28		b_2 TL
Delta ppm	-30.2	-14.0 0.8	-6.8	-22.4	-18.1				-11.8	-12.8 -12.8		-1.9 -1.9

Fragment-ion (m/z)	289.133	307.144	317.134	406.209	455.260	458.275^{+2}	463.230	483.248	576.308	637.342	657.844^{+2}	677.368	773.382
Frac. Inten.(% of TIC)	2.11	12.66	2.34	1.76	1.94	1.82	13.86	2.02	4.09	1.94	2.45	2.46	1.77
Rel. Inten.(% of BP)	8.14	48.87	9.04	6.81	7.48	7.04	53.50	7.80	15.77	7.47	9.45	9.48	6.82
Score	0.50	1.50	0.75	1.50	-0.07	-0.07	1.50	-0.08	1.50	-0.07	0.50	1.50	0.50
Ion-type	GVC-28	y_2	GVC	y_3			y_4		y_5		y_{10}-H_2O^{+2}	y_6	y_7-H_2O
Delta ppm	-4.8	2.1	15.1	-7.8			-6.3		-15.4		-14.0	4.2	-20.5



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Result Summary

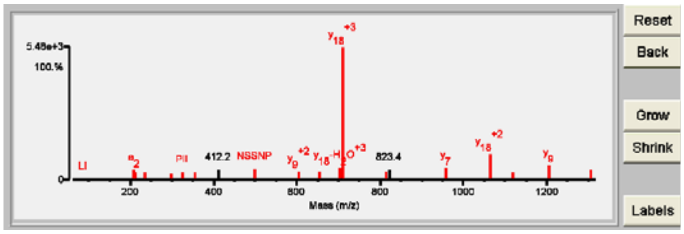
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.03	93.9	7	2/25	K175k	(R)FSPNSSNPIIVSCGWDKLVk(V)	2248.1431	114.0701	11.5	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
1	23.03	93.9	7	2/25	K172k	(R)FSPNSSNPIIVSCGWDkLVK(V)	2248.1431	114.0701	11.5	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
2	9.78	63.2	2	13/25	K29k K31k	(K)FSEWkFkLFRVRSFEK(T)	2134.1596	228.0535	-13.7	119116.8/8.96	HUMAN	P15918	V(D)J recombination-activating protein 1 OS=Homo sapiens GN=RAG1 PE=1 SV=1
3	8.88	68.2	2	12/25	K1373k	(R)FSPGEPSMIVFIHLNkYIR(K)	2248.1947	114.0184	-10.4	399896.9/6.52	HUMAN	RQ0VDD8	REVERSE Dynein heavy chain 14, axonemal OS=Homo sapiens GN=DNAH14 PE=2 SV=3
4	8.36	66.4	2	12/25	K1064k	(K)SFSkSDLVNWFKAHRGPGSK(M)	2248.1622	114.0510	3.4	131572.3/4.89	HUMAN	O43847	Nardilysin OS=Homo sapiens GN=NRD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.03	93.9	7	2/25	K175k	(R) F S|P N/S S N/P I I/V/S/C/G W D K L V k (V)	2248.1431	114.0701	11.5	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	70.065	72.082	84.080	86.095	120.080	207.110	212.110	235.109	299.135	324.221	355.678^{+2}
Frac. Inten.(% of TIC)	0.01	0.06	0.07	0.24	0.09	3.13	2.32	2.18	1.82	2.24	2.24
Rel. Inten.(% of BP)	0.01	0.15	0.17	0.59	0.23	7.59	5.62	5.27	4.41	5.43	5.43
Score	0.20	0.50	0.50	0.22	1.00 1.00	0.50	0.75	0.50	0.75	0.75	0.75
Ion-type	PR	V	KQ	LI	a_1 F	a_2	NP	b_2	SNP	PII	PNSSNPI^{+2}
Delta ppm	-1.8	10.0	-12.8	-14.2	-18.9 -9.8	-20.8	25.6	1.6	-2.7	-24.0	0.6

Fragment-ion (m/z)	412.223^{+2}	500.214	603.799^{+2}	653.320^{+2}	704.037^{+3}	710.039^{+3}	814.964^{+2}	823.440	958.995	959.516	1064.544^{+2}	1119.557	1206.591	1305.682
Frac. Inten.(% of TIC)	3.17	3.36	2.73	2.63	3.83	41.28	2.48	2.89	2.33	3.60	7.78	2.17	4.38	2.96
Rel. Inten.(% of BP)	7.68	8.15	6.60	6.36	9.29	100.00	6.01	7.00	5.65	8.72	18.84	5.27	10.60	7.17
Score	-0.08	0.75	1.50	1.50	0.50	1.50	1.50	-0.07	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type		NSSNP	y_9^{+2}	y_{10}^{+2}	y_{18}-H_2O^{+3}	y_{18}^{+3}	y_{13}^{+2}		y^{++}_{16}	y_7	y_{18}^{+2}	y_8	y_9	y_{10}
Delta ppm		6.3	-3.0	-21.8	9.5	8.4	23.2		-4.0	-15.5	-2.7	-3.9	-2.4	15.3



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Result Summary

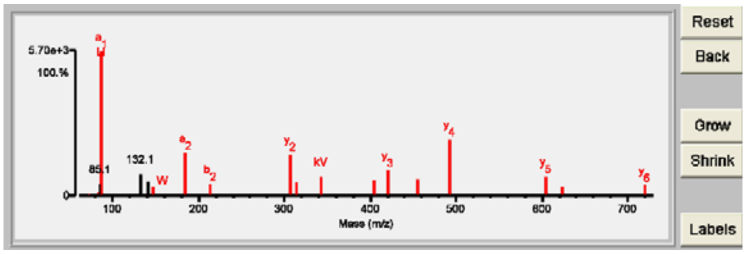
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.36	87.8	8	5/25	K175k	(K)LVkVWNLANCK(L)	1344.7457	114.0679	17.1	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.36	87.8	8	5/25	K175k	(K) L V|k\V W/N/L/A/N/C/K (L)	1344.7457	114.0679	17.1	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	70.064	72.081	84.082	85.084	86.097	87.055	129.101	130.070	132.078	133.045	141.102	147.113
Frac. Inten.(% of TIC)	0.06	0.29	0.70	2.25	28.58	0.07	0.18	0.19	4.38	2.74	2.75	1.93
Rel. Inten.(% of BP)	0.21	1.02	2.46	7.87	100.00	0.25	0.64	0.67	15.31	9.59	9.61	6.76
Score	-0.00	0.50	0.50	-0.08	0.50	0.33	0.20		-0.15	-0.10	-0.10	1.50
Ion-type		**V**	**KQ**		**a_1**	**NR**	**RKQ**	**W**				**y_1**
Delta ppm		3.1	8.6		-10.7	-1.0	-9.6					-2.1
					0.50							
					LI							
					2.0							

Fragment-ion (m/z)	159.093	185.165	213.160	307.146	314.219	342.215	404.166	421.192	455.300	492.232	605.308	623.831	719.361
Frac. Inten.(% of TIC)	0.22	8.40	2.42	8.09	2.65	3.90	3.06	4.90	3.36	11.14	3.91	1.82	2.01
Rel. Inten.(% of BP)	0.78	29.40	8.48	28.31	9.29	13.65	10.70	17.14	11.75	38.97	13.67	6.36	7.03
Score	2.00	0.50	0.50	1.50	0.50	0.75	0.50	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	**W**	**a_2**	**b_2**	**y_2**	**kV**-28	**kV**	y_3-NH_3	**y_3**	**b_3**	**y_4**	**y_5**	**y^{++}_9**	**y_6**
Delta ppm	9.6	-3.4	-6.3	8.6	-1.2	0.4	15.3	12.6	2.5	16.7	1.1	14.1	14.2



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Result Summary

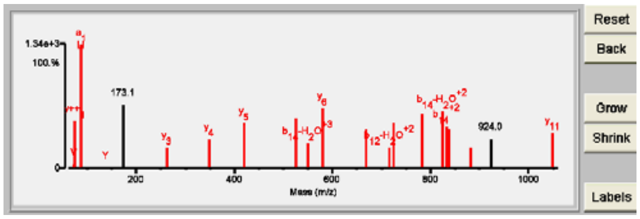
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.40	89.1	12	2/25	K185k	(K)LkTNHIGHTGYLNTVTVSPDGSLCASGGK(D)	2984.4894	114.0774	11.1	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.40	89.1	12	2/25	K185k	(K) L k T N H I G H T G Y\L\N\T\V\T V S/P D/G S L/C/A/S/G G/K (D)	2984.4894	114.0774	11.1	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	70.064	72.079	74.060	84.081	86.095	110.072	129.103	136.077	173.125	261.155	348.181	419.220
Frac. Inten.(% of TIC)	0.01	0.45	5.56	0.24	14.50	0.08	0.12	0.08	7.43	2.43	3.43	5.23
Rel. Inten.(% of BP)	0.04	3.10	38.33	1.63	100.00	0.55	0.82	0.55	51.25	16.77	23.65	36.08
Score	0.20	0.50	1.50	0.50	0.50	1.00	0.20	1.00	-0.51	1.50	1.50	1.50
Ion-type	PR	V	y^{++}_1	KQ	a_1	H	RKQ	Y		y_3	y_4	y_5
Delta ppm	-14.6	-17.7	-5.9	-2.1	-32.8 0.50 LI -20.0	3.0	5.9	11.8		-4.3	-19.1	-12.3

Fragment-ion (m/z)	524.742^{+2}	549.608^{+3}	579.261	668.843	716.364^{+2}	725.381^{+2}	782.405^{+2}	823.924^{+2}	832.940^{+2}	836.396	882.468	923.971	1048.463
Frac. Inten.(% of TIC)	5.91	2.88	7.02	4.52	2.44	5.30	6.43	6.58	4.89	4.48	2.39	3.45	4.13
Rel. Inten.(% of BP)	40.73	19.88	48.44	31.16	16.82	36.57	44.33	45.40	33.73	30.90	16.50	23.82	28.45
Score	1.50	0.25	1.50	0.50	0.25	0.50	0.50	0.25	0.50	1.50	0.50	-0.24	1.50
Ion-type	y_{11}^{+2}	b_{14}-H_2O^{+3}	y_6	b^{++}_{11}	b_{12}-H_2O^{+2}	b_{12}^{+2}	b_{13}^{+2}	b_{14}-H_2O^{+2}	b_{14}^{+2}	y_9	b^{++}_{15}		y_{11}
Delta ppm	4.5	-19.6	9.8	0.9	-21.2	-3.7	-0.3	0.0	12.3	3.9	5.1		-9.5



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Result Summary

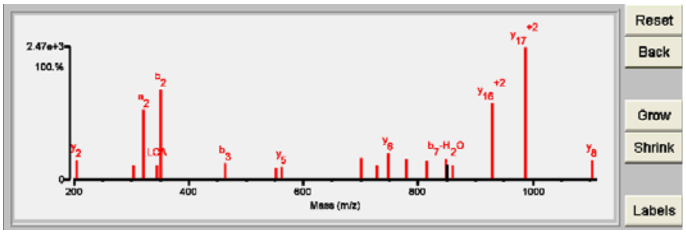
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.95	89.9	11	3/25	K257k	(R)YWLCAATGPSIkIWDLEGK(I)	2208.1158	114.0522	4.0	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
2	18.39	79.2	7	7/25	K264k	(R)YWLCAATGPSIKIWDLEGk(I)	2208.1158	114.0522	4.0	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
3	6.43	62.8	2	14/25	M2102m	(R)LmAMFPLKGNEILEEWVSAK(N)	2306.1923	15.9756	-8.3	290491.5/8.27	HUMAN	RQ99973	REVERSE Telomerase protein component 1 OS=Homo sapiens GN=TEP1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.95	89.9	11	3/25	K257k	(R) Y W|L|C A/A/T/G/P S I/k/I/W/D L E/G K (I)	2208.1158	114.0522	4.0	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	84.079	86.096	136.074	159.090	187.085	191.080	204.134	303.112	322.152	345.154	350.149	463.229
Frac. Inten.(% of TIC)	0.08	0.16	0.17	0.06	1.92	6.00	2.89	2.00	10.06	2.13	13.12	2.39
Rel. Inten.(% of BP)	0.39	0.84	0.87	0.29	9.97	31.18	15.03	10.38	52.29	11.06	68.19	12.41
Score	0.50	0.22	1.00 1.00	2.00	-0.10	-0.31	1.50	0.75	0.50	0.75	0.50	0.50
Ion-type	KQ	LI	a_1 Y	W			y_2	CAA	a_2	LCA	b_2	b_3
Delta ppm	-15.2	-6.1	-23.4 -15.4	-12.4			-1.3	-5.1	-11.2	-18.3	-4.9	-14.2

Fragment-ion (m/z)	551.811^{+2}	561.288	700.385^{+2}	728.902^{+2}	747.365	779.425^{+2}	814.931^{+2}	848.398	850.943	860.460	930.470^{+2}	987.004^{+2}	1102.580
Frac. Inten.(% of TIC)	1.81	1.84	3.15	2.08	3.87	3.09	2.67	3.02	2.14	2.13	11.14	19.24	2.83
Rel. Inten.(% of BP)	9.40	9.56	16.37	10.82	20.12	16.07	13.90	15.70	11.14	11.08	57.87	100.00	14.73
Score	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.25	-0.11	1.50	1.50	1.50	1.50
Ion-type	y_8^{+2}	y_5	y_{11}^{+2}	y_{12}^{+2}	y_6	$b_{13}\text{-}H_2O^{+2}$ y_{13}^{+2}	y_{14}^{+2}	$b_7\text{-}H_2O$		y_7	y_{16}^{+2}	y_{17}^{+2}	y_8
Delta ppm	22.7	0.8	3.0	12.3	-3.6	33.9 9.6	-6.3	24.7		10.5	0.7	-7.6	-8.1



Result Summary

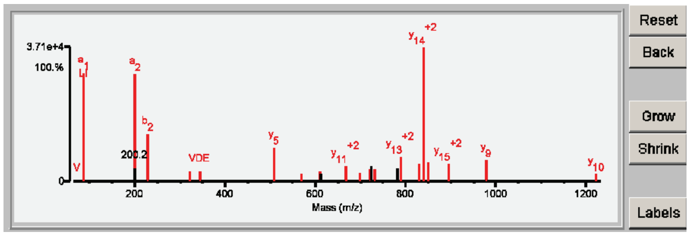
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.88	92.6	11	4/25	K271k	(K)IIVDELkQEVISTSSK(A)	1788.9953	114.0483	2.8	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
2	13.86	77.2	6	10/25	K280k	(K)IIVDELKQEVISTSSk(A)	1788.9953	114.0483	2.8	35076.9/7.60	HUMAN	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3
3	7.46	69.3	3	14/25	None	(R)IIDEVVNKFLDDLGNAK(S)	1903.0171	0.0265	13.9	23772.1/6.25	HUMAN	O95816	BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1
4	7.44	68.9	3	14/25	K36k	(R)LLQELVEDkTRWMK(W)	1788.9677	114.0760	17.4	142507.9/6.73	HUMAN	Q9C0C7	Activating molecule in BECN1-regulated autophagy protein 1 OS=Homo sapiens GN=AMBRA1 PE=1 SV=2
5	6.62	72.5	3	14/25	None	(R)LIVQVQGEGSVLYTLQR(L)	1903.0647	-0.0211	-11.1	446704.2/6.12	HUMAN	RQ8TCZ9	REVERSE Fibrocystin OS=Homo sapiens GN=PKHD1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.88	92.6	11	4/25	K271k	(K) I/I|V/D/E|L/k/Q/E/V I/S T/S S K (A)	1788.9953	114.0483	2.8	35076.9/7.60	HUMAN	P63244	237111	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Fragment-ion (m/z)	72.081	84.081	86.097	199.181	200.184	227.176	321.180	344.147	509.257	570.311	610.828
Frac. Inten.(% of TIC)	0.05	0.05	16.01	15.89	1.95	7.10	1.46	1.52	5.09	1.13	1.49
Rel. Inten.(% of BP)	0.25	0.24	80.38	79.78	9.79	35.68	7.33	7.64	25.58	5.68	7.50
Score	0.50	0.50	0.50 0.50	0.50	-0.10	0.50	1.50	0.75	1.50	0.75	1.50
Ion-type	V	KQ	a$_1$ LI	a$_2$		b$_2$	y$_3$	VDE	y$_5$	b$_5$ IVDEL	y++$_{10}$
Delta ppm	8.7	7.4	-8.4 4.3	-3.4		-1.8	8.5	2.8	0.7	-6.8 -6.8	-0.2

Fragment-ion (m/z)	611.328	667.373^{+2}	699.368	721.406	722.413^{+2}	731.891^{+2}	781.909^{+2}	789.400^{+2}	829.935^{+2}	838.937^{+2}	850.451	895.485^{+2}	978.506	1220.638
Frac. Inten.(% of TIC)	1.19	2.34	1.20	1.80	2.23	1.73	2.04	3.59	2.65	19.91	2.73	2.69	3.11	1.06
Rel. Inten.(% of BP)	5.97	11.75	6.00	9.04	11.18	8.69	10.25	18.05	13.30	100.00	13.70	13.51	15.61	5.30
Score	-0.06	1.50	0.75	1.50	-0.11	1.50	-0.10	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type		y$_{11}^{+2}$	VDELk	y$_7$		y$_{12}^{+2}$		y$_{13}^{+2}$	y$_{14}$-H$_2$O^{+2}	y$_{14}^{+2}$	y$_8$	y$_{15}^{+2}$	y$_9$	y$_{10}$
Delta ppm		4.3	-0.3	-4.4		0.5		-5.4	1.7	-1.9	-1.2	4.4	-4.0	-8.3



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Result Summary

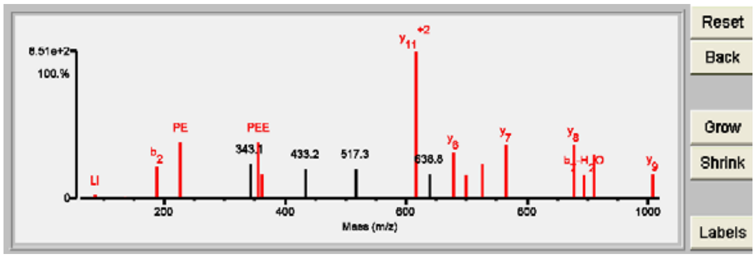
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.82	84.2	8	4/25	K112k	(K)GETkAFYPEEISSMVLTK(M)	2030.0151	114.0684	11.9	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.82	84.2	8	4/25	K112k	(K) G E\T k A F/Y|P E/E/I/S/S M V/L T K (M)	2030.0151	114.0684	11.9	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	70.065	72.079	84.044	84.082	86.097	120.080	129.101	136.073	187.072	227.106	343.124	356.137	361.246
Frac. Inten.(% of TIC)	0.00	0.11	0.11	0.17	0.46	0.16	0.10	0.19	4.34	7.50	4.67	7.50	3.35
Rel. Inten.(% of BP)	0.02	0.54	0.54	0.89	2.35	0.81	0.49	0.99	22.06	38.15	23.72	38.12	17.03
Score	0.20	0.50	1.00	0.50	0.22	1.00	0.20	1.00	0.50	0.75	-0.24	0.75	1.50
Ion-type	PR	V	E	KQ	LI	F	RKQ	Y	b_2	PE		PEE	y_3
Delta ppm	2.5	-21.9	-5.8	13.4	0.9	-5.6	-8.8	-22.0	-3.9	8.2		-27.3	4.3

Fragment-ion (m/z)	433.203	517.317	617.327^{+2}	638.790	678.381	698.858^{+2}	725.360	765.424	878.494	893.420	911.424	1007.564
Frac. Inten.(% of TIC)	3.90	3.94	19.67	3.32	6.22	3.09	4.55	7.21	7.10	3.14	5.96	3.25
Rel. Inten.(% of BP)	19.84	20.05	100.00	16.86	31.64	15.70	23.12	36.63	36.10	15.97	30.28	16.52
Score	-0.20	-0.20	1.50	-0.17	1.50	1.50	0.75	1.50	1.50	0.25	0.50	1.50
Ion-type			y_{11}^{+2}		y_6	y_{12}^{+2}	TkAFY	y_7	y_8	b_7-H_2O	b_7	y_9
Delta ppm			5.2		-7.0	4.6	-4.3	9.1	-8.7	4.6	-3.0	20.1



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Result Summary

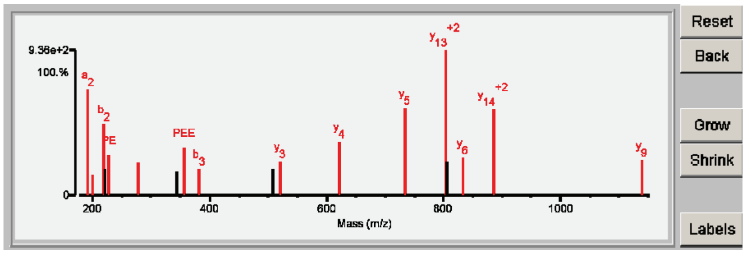
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.96	79.7	8	6/25	K126k	(K)AFYPEEISSMVLTkMK(E)	1873.9438	114.0550	6.1	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
2	15.24	76.6	7	7/25	K128k	(K)AFYPEEISSMVLTKMk(E)	1873.9438	114.0550	6.1	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.96	79.7	8	6/25	K126k	(K) A F|Y|P E E I/S S M/V/L/T/k/M K (E)	1873.9438	114.0550	6.1	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	70.063	72.079	84.077	86.095	104.051	120.079	136.075	191.114	199.107	219.114	220.115	227.103	278.154
Frac. Inten.(% of TIC)	0.00	0.10	7.62	0.25	1.94	0.23	0.30	10.18	2.00	6.77	2.58	3.83	3.10
Rel. Inten.(% of BP)	0.02	0.73	54.89	1.80	13.95	1.63	2.15	73.37	14.43	48.76	18.59	27.55	22.31
Score	0.20	0.50	-0.55	0.22	-0.14	1.00	1.00	0.50	0.50	0.50	-0.19	0.75	1.50
Ion-type	PR	V		LI		F	Y	a_2	PE-28	b_2		PE	y_2
Delta ppm	-27.5	-17.7		-14.2		-13.1	-2.9	-24.0	-9.1	2.7		-1.9	1.1

Fragment-ion (m/z)	343.182	356.140	382.176	507.284	520.296	621.331	734.420	803.913^{+2}	805.434^{+2}	833.503	885.425^{+2}	1138.582
Frac. Inten.(% of TIC)	2.36	4.52	2.51	2.55	3.26	5.21	8.37	13.88	3.21	3.58	8.30	3.34
Rel. Inten.(% of BP)	17.02	32.57	18.07	18.34	23.49	37.56	60.29	100.00	23.12	25.81	59.82	24.05
Score	-0.17	0.75	0.50	-0.18	1.50	1.50	1.50	1.50	-0.23	1.50	1.50	1.50
Ion-type		PEE	b_3		y_3	y_4	y_5	y_{13}^{+2}		y_6	y_{14}^{+2}	y_9
Delta ppm		-17.5	-2.7		9.1	-12.3	-4.5	0.8		13.6	-21.4	-12.1



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Result Summary

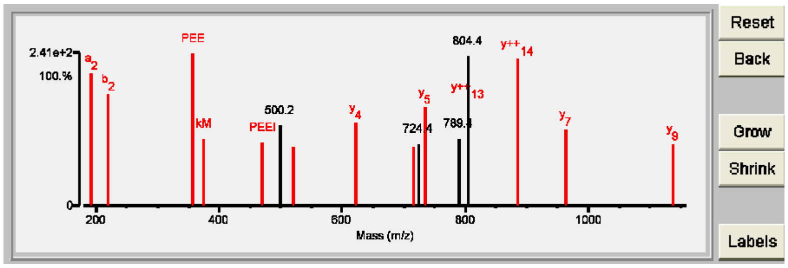
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.85	74.3	7	5/24	K126k	(K)AFYPEEISSMVLTkMK(E)	1873.9438	114.0640	10.6	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
2	13.66	70.2	7	6/24	K128k	(K)AFYPEEISSMVLTKMk(E)	1873.9438	114.0640	10.6	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.85	74.3	7	5/24	K126k	(K) A F|Y/P E E I/S S/M V/L/T/k M K (E)	1873.9438	114.0640	10.6	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	70.064	72.079	84.080	86.096	120.079	132.102	136.076	191.113	219.110	356.142	374.192	469.225
Frac. Inten.(% of TIC)	0.01	0.26	0.12	0.29	0.31	4.24	0.42	7.91	6.66	9.12	4.07	3.79
Rel. Inten.(% of BP)	0.07	2.87	1.36	3.19	3.39	46.48	4.65	86.67	72.97	100.00	44.61	41.57
Score	0.20	0.50	0.50	0.22	1.00	-0.46	1.00	0.50	0.50	0.75	0.75	0.75
Ion-type	PR	V	KQ	LI	F		Y	a_2	b_2	PEE	kM	PEEI
Delta ppm	-16.1	-27.4	-11.6	-7.3	-12.3		4.5	-25.1	-11.4	-9.9	17.5	-8.7

Fragment-ion (m/z)	500.232	520.289	621.338	716.415	724.409	734.413	789.402^{+2}	803.908	804.400	885.455	964.561	1138.591
Frac. Inten.(% of TIC)	4.84	3.53	4.97	3.54	3.68	5.95	4.02	6.25	8.93	8.79	4.56	3.75
Rel. Inten.(% of BP)	53.02	38.73	54.44	38.82	40.36	65.18	44.02	68.47	97.92	96.33	50.02	41.15
Score	-0.53	1.50	1.50	0.50	-0.40	1.50	-0.44	1.50	-0.98	1.50	1.50	1.50
Ion-type		y_3	y_4	y_5-H_2O		y_5		y^{++}_{13}		y^{++}_{14}	y_7	y_9
Delta ppm		-3.4	-0.6	4.2		-13.4		-5.7		12.0	30.3	-4.1



Result Summary

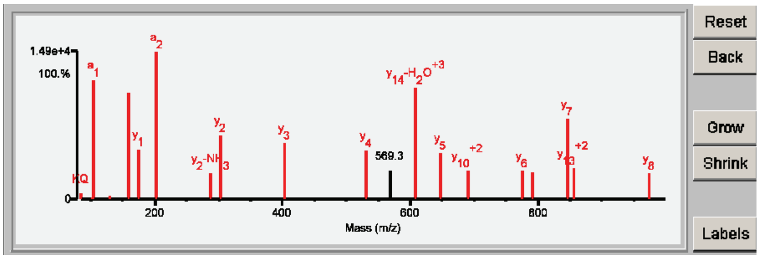
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.79	94.4	11	2/24	K524k	(R)MVQEAEkYKAEDEVQR(E)	1952.9382	114.0664	11.3	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
2	19.12	92.0	10	3/24	K526k	(R)MVQEAEKYkAEDEVQR(E)	1952.9382	114.0664	11.3	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.79	94.4	11	2/24	K524k	(R) M V Q/E/A E/k Y/K/A/E/D/E/V/Q/R (E)	1952.9382	114.0664	11.3	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	61.010	72.080	84.044	84.080	101.070	102.055	104.052	129.102	158.099	175.118	203.121	286.152
Frac. Inten.(% of TIC)	3.00	0.50	0.25	0.52	0.14	0.17	11.13	0.30	9.86	4.61	13.73	2.39
Rel. Inten.(% of BP)	21.86	3.68	1.85	3.76	1.02	1.21	81.10	2.22	71.81	33.58	100.00	17.44
Score	-0.22	0.50	1.00	0.50			0.50	0.20	0.50	1.50	0.50	0.50
Ion-type		V	E	KQ	KQ	E	a_1	RKQ	y_1-NH_3	y_1	a_2	y_2-NH_3
Delta ppm		-6.6	-5.8	-8.0			-15.8	-3.4	39.2	-3.2	-7.2	3.9

Fragment-ion (m/z)	303.179	402.247	531.288	569.280^{+3}	606.963^{+3}	646.320	690.353^{+2}	775.359	790.389^{+2}	846.398	854.914^{+2}	974.490
Frac. Inten.(% of TIC)	5.93	5.18	4.50	2.61	10.42	4.27	2.66	2.61	2.55	7.40	2.93	2.35
Rel. Inten.(% of BP)	43.19	37.72	32.78	19.00	75.88	31.11	19.39	19.04	18.55	53.94	21.34	17.14
Score	1.50	1.50	1.50	-0.19	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_2	y_3	y_4		y_{14}-H_2O^{+3}	y_5	y_{10}^{+2}	y_6	y_{12}^{+2}	y_7	y_{13}^{+2}	y_8
Delta ppm	4.5	3.1	-0.3		7.8	7.5	5.0	0.6	-0.1	3.7	4.6	-0.3



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Result Summary

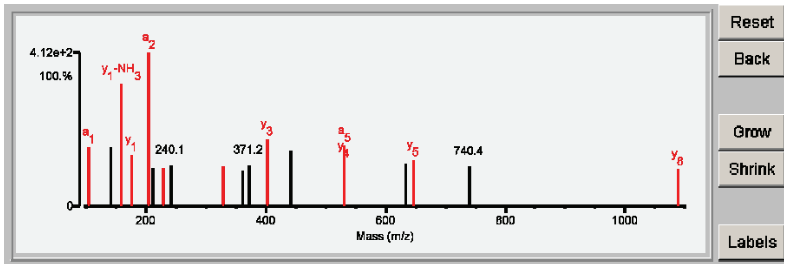
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.09	63.3	5	9/23	K524k K526k	(R)MVQEAEkYkAEDEVQR(E)	1952.9382	228.1036	8.1	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.09	63.3	5	9/23	K524k K526k	(R) M V Q E A E k Y/k A E/D/E/V Q/R (E)	1952.9382	228.1036	8.1	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	70.067	72.082	84.043	84.080	86.095	104.053	141.103	158.099	175.113	203.119	211.110	228.135
Frac. Inten.(% of TIC)	0.00	0.28	0.18	0.50	4.10	5.49	5.49	11.26	4.79	14.09	3.60	3.59
Rel. Inten.(% of BP)	0.03	2.01	1.31	3.56	29.08	38.96	38.96	79.88	34.00	100.00	25.56	25.49
Score	0.20	0.50	1.00	0.50	-0.29	0.50	-0.39	0.50	1.50	0.50	-0.26	0.75
Ion-type	PR	V	E	KQ		a_1		y_1-NH_3	y_1	a_2		VQ
Delta ppm	23.9	15.6	-11.8	-10.4		-9.1		38.6	-34.0	-18.0		-0.7

Fragment-ion (m/z)	240.093	329.136	360.676^{+2}	371.177^{+2}	402.238	441.221	531.274	633.961	646.301	740.368	1088.526
Frac. Inten.(% of TIC)	3.75	3.63	3.33	3.74	6.19	5.08	5.55	3.92	4.25	3.69	3.47
Rel. Inten.(% of BP)	26.63	25.78	23.67	26.58	43.91	36.07	39.39	27.82	30.17	26.21	24.66
Score	-0.27	0.75	-0.24	-0.27	1.50	-0.36	1.50	-0.28	1.50	-0.26	1.50
Ion-type		QEA			y_3		a_5 y_4		y_5		y_8
Delta ppm		-32.4			-19.5		26.1 -26.4		-23.2		-6.8



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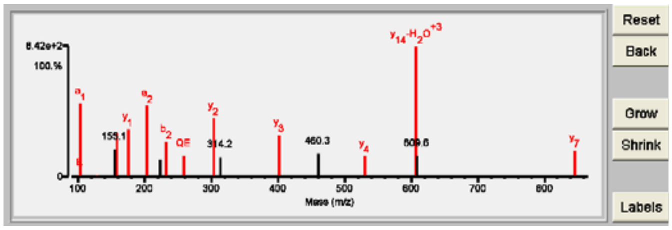
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.78	79.3	6	7/24	K524k	(R)MVQEAEkYKAEDEVQR(E)	1952.9382	114.0604	8.4	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
1	11.78	79.3	6	7/24	K526k	(R)MVQEAEKYkAEDEVQR(E)	1952.9382	114.0604	8.4	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
2	6.53	57.2	3	11/24	M61m	(K)TEDKVRVMADSmQEKQR(M)	2051.0008	15.9977	1.4	43262.5/5.69	HUMAN	P49662	Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1
3	4.64	59.2	2	11/24	None	(-)MVADIKGNEQIEKYSWR(E)	2067.0328	-0.0342	-16.6	22529.6/5.27	HUMAN	Q8N1N2	Uncharacterized protein C18orf26 OS=Homo sapiens GN=C18orf26 PE=2 SV=1
4	3.91	51.3	2	12/24	None	(-)MVRFGDELGGRYGGPGGGER(A)	2066.9825	0.0161	7.8	262497.7/8.78	HUMAN	Q00975	Voltage-dependent N-type calcium channel subunit alpha-1B OS=Homo sapiens GN=CACNA1B PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.78	79.3	6	7/24	K524k	(R) M V\Q E A E k Y K/A E D/E/V/Q/R (E)	1952.9382	114.0604	8.4	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	61.009	72.080	84.043	84.079	101.071	102.053	104.051	129.101	155.079	155.117	158.098	175.118	203.119	224.101	231.115	258.107	303.176	314.166	402.244	460.281	531.305	606.964^{+3}	609.628^{+3}	846.408
Frac. Inten.(% of TIC)	3.58	0.52	0.17	0.45	0.16	0.27	9.91	0.24	2.47	3.74	6.03	6.41	9.63	2.41	4.82	2.85	7.93	2.71	5.74	3.11	2.82	17.72	2.73	3.60
Rel. Inten.(% of BP)	20.22	2.93	0.98	2.52	0.88	1.50	55.97	1.35	13.92	21.11	34.02	36.16	54.35	13.59	27.22	16.08	44.75	15.30	32.43	17.55	15.89	100.00	15.42	20.34
Score	-0.20	0.50		0.50		1.00	0.50	0.20	-0.14	-0.21	0.50	1.50	0.50	-0.14	0.50	0.75	1.50	-0.15	1.50	-0.18	1.50	0.50	-0.15	1.50
Ion-type		V	E	KQ	KQ	E	a_1	RKQ			y_1-NH_3	y_1	a_2		b_2	QE	y_2		y_3		y_4	y_{14}-H_2O^{+3}		y_7
Delta ppm		-5.2		-17.5		-20.1	-27.3	-12.7			37.9	-6.6	-16.5		-9.8	-11.0	-4.4		-4.6		30.8	8.0		15.1



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Result Summary

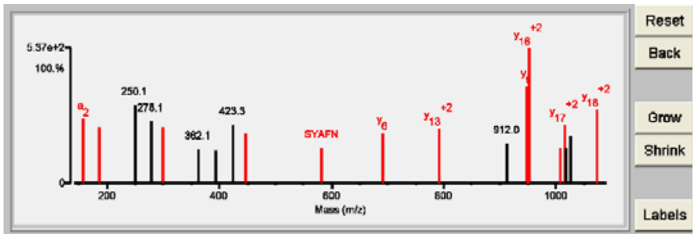
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.21	60.3	7	11/25	K550k	(K)NALESYAFNMkSAVEDEGLK(G)	2216.0540	114.0721	12.5	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.21	60.3	7	11/25	K550k	(K) N A|L|E/S Y A/F N M k/S A V/E D/E G L K (G)	2216.0540	114.0721	12.5	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	84.078	86.095	88.038	99.059	158.091	186.084	250.121	278.113	299.175	362.122	393.137	423.260	446.253	583.273
Frac. Inten.(% of TIC)	0.09	0.29	3.93	2.70	5.04	4.42	6.05	4.81	4.41	2.64	2.59	4.53	3.94	2.74
Rel. Inten.(% of BP)	0.86	2.76	37.21	25.55	47.68	41.80	57.29	45.50	41.76	24.98	24.51	42.86	37.25	25.93
Score	0.50	0.22	-0.37	-0.26	0.50	0.50	-0.57	-0.46	0.50	-0.25	-0.25	-0.43	1.50	0.75
Ion-type	KQ	LI			a_2	b_2			b_3				y_4	SYAFN
Delta ppm	-35.4	-18.9			-11.4	-16.2			11.8				-18.4	37.9

Fragment-ion (m/z)	690.327	791.376^{+2}	911.999^{+2}	947.466	951.948^{+2}	1007.496^{+2}	1016.472^{+2}	1017.069^{+2}	1025.524	1073.014^{+2}	1112.580^{+2}
Frac. Inten.(% of TIC)	3.90	4.33	3.08	7.52	10.57	2.76	4.60	2.73	3.78	5.70	2.87
Rel. Inten.(% of BP)	36.88	41.01	29.11	71.13	100.00	26.15	43.55	25.80	35.76	53.94	27.16
Score	1.50	1.50	-0.29	1.50	1.50	0.50	1.50	-0.26	-0.36	1.50	-0.27
Ion-type	y_6	y_{13}^{+2}		y_9	y_{16}^{+2}	$y_{17}\text{-}H_2O^{+2}$	y_{17}^{+2}			y_{18}^{+2}	
Delta ppm	-5.0	-8.4		-2.3	-1.1	31.2	2.3			1.4	



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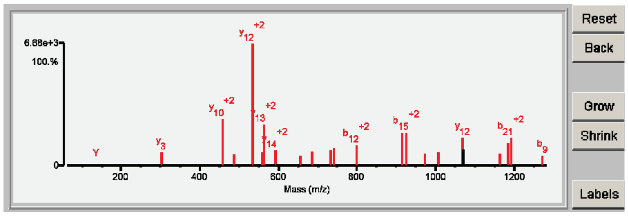
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.54	97.1	15	1/25	K597k	(K)RkELEQVCNPIISGLYQGAGGPGPGGFGAQGPK(G)	3339.6903	114.0591	4.7	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
2	8.37	54.1	5	14/25	K628k	(K)RKELEQVCNPIISGLYQGAGGPGPGGFGAQGPk(G)	3339.6903	114.0591	4.7	70052.6/5.48	HUMAN	P08107	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5
3	6.23	51.1	4	14/25	K68k	(K)TVDLkPDWGKGYSRKAAALEFLNRFEEAK(R)	3339.7484	114.0009	-12.2	62639.6/6.40	HUMAN	P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1
4	3.86	53.9	3	15/25	K397k K413k	(K)DTTPNNAIkYQQLDIIEKMEYNDGkRK(C)	3225.6209	228.1285	12.4	97776.4/6.67	HUMAN	RQ9UKW4	REVERSE Guanine nucleotide exchange factor VAV3 OS=Homo sapiens GN=VAV3 PE=1 SV=1
4	3.86	53.9	3	15/25	K397k K415k	(K)DTTPNNAIkYQQLDIIEKMEYNDGKRk(C)	3225.6209	228.1285	12.4	97776.4/6.67	HUMAN	RQ9UKW4	REVERSE Guanine nucleotide exchange factor VAV3 OS=Homo sapiens GN=VAV3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.54	97.1	15	1/25	K597k	(K) R k E L E Q V C N\P\I\I\S G L\Y\Q/G\A/G|G|P/G/P G G F/G A Q/G P K (G)	3339.6903	114.0591	4.7	70052.6/5.48	HUMAN	P08107	300447	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.064	0.01	0.03	0.20	PR	-11.8
86.095	0.08	0.34	0.22	LI	-17.7
136.074	0.12	0.52	1.00	Y	-9.5
301.187	2.34	10.47	1.50	y_3	0.2
458.237^{+2}	8.53	38.18	1.50	y_{10}^{+2}	-1.1
486.752^{+2}	1.95	8.74	1.50	y_{11}^{+2}	6.8
535.277^{+2}	22.34	100.00	1.50	y_{12}^{+2}	3.6
557.298	2.41	10.77	1.50	y_6	-10.9
563.787^{+2}	7.55	33.81	1.50	y_{13}^{+2}	3.0
592.296^{+2}	2.75	12.33	1.50	y_{14}^{+2}	-0.1
656.331^{+2}	1.90	8.50	1.50	y_{16}^{+2}	8.2
684.845^{+2}	2.50	11.17	0.50	b_{10}^{+2}	9.2
734.040^{+3}	2.73	12.20	0.50	b_{18}^{+3}	-5.5
741.385^{+2}	3.21	14.37	0.50	b_{11}^{+2}	5.6
797.918^{+2}	3.81	17.04	0.50	b_{12}^{+2}	-5.4
915.467	5.97	26.72	1.50	y_{10}	-2.0
926.488^{+2}	6.10	27.30	0.50	b_{15}^{+2}	-4.1
972.495	2.19	9.82	1.50	y_{11}	5.8
1008.014^{+2}	2.32	10.39	0.50	b_{16}^{+2}	-9.3
1069.540	5.07	22.68	1.50	y_{12}	-2.3
1071.547^{+2}	2.90	12.99	-0.13		
1164.585^{+2}	2.25	10.09	0.50	b_{20}^{+2}	-6.0
1184.586^{+2}	4.03	18.04	0.25	$b_{21}\text{-}NH_3^{+2}$	-2.9
1193.111^{+2}	5.05	22.62	0.50	b_{21}^{+2}	6.2
1271.618	1.91	8.54	0.50	b_9	0.9



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Result Summary

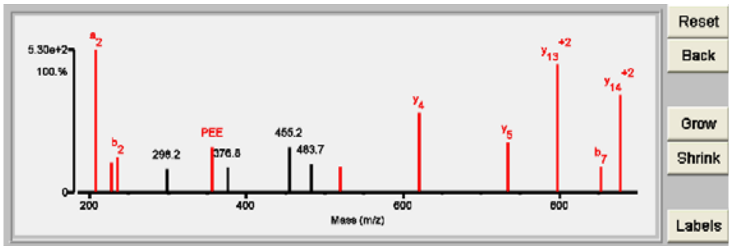
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.43	70.3	6	10/25	K126k	(K)SFYPEEVSSMVLTkMK(E)	1875.9231	114.0624	9.8	70898.4/5.38	HUMAN	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1
1	11.43	70.3	6	10/25	K128k	(K)SFYPEEVSSMVLTKMk(E)	1875.9231	114.0624	9.8	70898.4/5.38	HUMAN	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.43	70.3	6	10/25	K126k	(K) S F|Y/P E E V\S S M V/L/T/k M K (E)	1875.9231	114.0624	9.8	70898.4/5.38	HUMAN	P11142	300597	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.084	84.080	86.096	104.052	120.081	136.074	162.093	207.114	227.104	235.106	298.177	356.144
Frac. Inten.(% of TIC)	0.01	2.73	0.21	0.13	4.15	0.10	0.58	2.81	14.90	3.15	3.75	2.50	4.79
Rel. Inten.(% of BP)	0.04	18.30	1.42	0.85	27.85	0.69	3.92	18.89	100.00	21.17	25.15	16.77	32.13
Score	0.20	-0.18	0.50	0.22	-0.28	1.00	1.00	-0.19	0.50	0.75	0.50	-0.17	0.75
Ion-type	PR		KQ	LI		F	Y		a_2	PE	b_2		PEE
Delta ppm	3.9		-9.2	-0.3		-0.6	-10.2		0.5	-0.6	-14.1		-7.4

Fragment-ion (m/z)	376.836^{+3}	455.219^{+2}	483.747	520.281	621.338	734.428	796.903^{+2}	852.361	878.439^{+2}	1005.961	1138.696	1238.656
Frac. Inten.(% of TIC)	2.58	4.82	2.99	2.77	8.33	5.22	13.39	2.78	10.19	2.32	2.47	2.33
Rel. Inten.(% of BP)	17.34	32.38	20.09	18.57	55.89	35.06	89.87	18.68	68.40	15.57	16.55	15.64
Score	-0.17	-0.32	-0.20	1.50	1.50	1.50	1.50	0.50	1.50	-0.16	-0.17	-0.16
Ion-type				y_3	y_4	y_5	y_{13}^{+2}	b_7	y_{14}^{+2}			
Delta ppm				-20.3	-1.9	7.1	-2.3	-20.1	3.4			



Result Summary

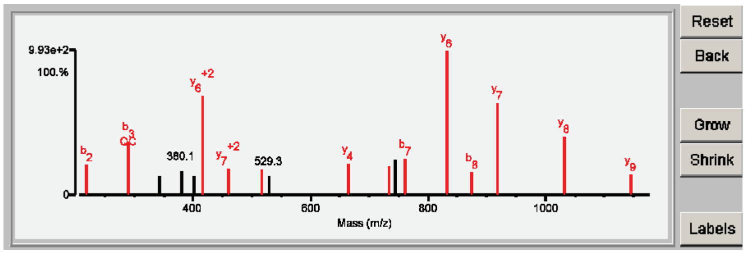
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.15	75.4	9	8/25	K388k	(R)GCALQCAILSPAFkVR(E)	1790.9404	114.0577	7.8	96865.5/5.28	HUMAN	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1
1	15.15	75.4	9	8/25	K388k	(R)GCALQCAILSPAFkVR(E)	1790.9404	114.0577	7.8	94487.0/5.63	HUMAN	O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=2
1	15.15	75.4	9	8/25	K388k	(R)GCALQCAILSPAFkVR(E)	1790.9404	114.0577	7.8	94331.4/5.11	HUMAN	P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.15	75.4	9	8/25	K388k	(R) G C\A\L Q C A|I|L/S/P/A/F/k V R (E)	1790.9404	114.0577	7.8	96865.5/5.28	HUMAN	Q92598	296579	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1
1	15.15	75.4	9	8/25	K388k	(R) G C\A\L Q C A|I|L/S/P/A/F/k V R (E)	1790.9404	114.0577	7.8	94487.0/5.63	HUMAN	O95757	296699	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=2
1	15.15	75.4	9	8/25	K388k	(R) G C\A\L Q C A|I|L/S/P/A/F/k V R (E)	1790.9404	114.0577	7.8	94331.4/5.11	HUMAN	P34932	300517	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4

Fragment-ion (m/z)	70.067	75.054	84.081	86.095	89.059	101.069	198.084	218.053	289.095	343.111	380.077	401.197	416.256^{+2}
Frac. Inten.(% of TIC)	0.00	4.22	0.07	0.37	2.21	0.11	5.18	3.32	6.02	2.11	2.68	2.10	11.05
Rel. Inten.(% of BP)	0.02	26.12	0.44	2.30	13.70	0.67	32.06	20.56	37.30	13.10	16.62	13.00	68.45
Score	0.20	-0.26		0.22	-0.14	0.50	-0.32	0.50	0.75	-0.13	-0.17	-0.13	1.50
Ion-type	PR		QK	LI		QK		b_2	b_3 QC				y_6^{+2}
Delta ppm	26.8			-18.9		-15.2		-35.7	-8.3 -8.3				24.7

Fragment-ion (m/z)	459.773^{+2}	516.327	529.285	663.404	734.434	743.435^{+2}	761.293	831.480	874.393	918.509	1031.605	1144.653
Frac. Inten.(% of TIC)	2.90	2.82	2.15	3.50	3.31	3.92	4.13	16.14	2.54	10.31	6.53	2.31
Rel. Inten.(% of BP)	17.98	17.46	13.33	21.68	20.51	24.28	25.58	100.00	15.75	63.87	40.43	14.29
Score	1.50	1.50	-0.13	1.50	1.50	-0.24	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	y_7^{+2}	y_3		y_4	y_5		b_7	y_6	b_8	y_7	y_8	y_9
Delta ppm	26.1	3.2		15.4	4.7		-19.8	-4.5	0.8	-7.3	5.7	-26.4



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Result Summary

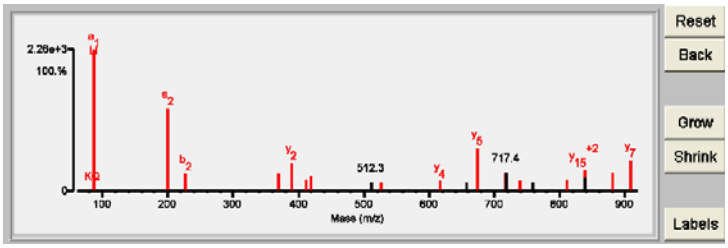
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.65	86.3	10	6/25	K188k	(R)IINEPTAAAIAYGLDkK(G)	1787.9902	114.0536	5.6	70021.3/5.56	HUMAN	P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1
1	16.65	86.3	10	6/25	K189k	(R)IINEPTAAAIAYGLDKk(G)	1787.9902	114.0536	5.6	70021.3/5.56	HUMAN	P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1
1	16.65	86.3	10	6/25	K187k	(R)IINEPTAAAIAYGLDkK(V)	1787.9902	114.0536	5.6	70898.4/5.38	HUMAN	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1
1	16.65	86.3	10	6/25	K188k	(R)IINEPTAAAIAYGLDKk(V)	1787.9902	114.0536	5.6	70898.4/5.38	HUMAN	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.65	86.3	10	6/25	K188k	(R) I I|N E/P T A\A\A\I/A/Y/G/L D/k K (G)	1787.9902	114.0536	5.6	70021.3/5.56	HUMAN	P54652	300485	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1

Fragment-ion (m/z)	70.066	84.081	86.095	136.075	199.181	227.174	370.193	389.251	412.216	419.222^{+2}	512.272	525.299	617.353
Frac. Inten.(% of TIC)	0.00	0.17	24.90	0.15	14.66	2.99	3.15	4.99	1.99	2.77	1.59	1.57	1.74
Rel. Inten.(% of BP)	0.01	0.68	100.00	0.59	58.85	12.00	12.64	20.06	8.01	11.11	6.40	6.31	7.00
Score	0.20	0.50	0.50	1.00	0.50	0.50	0.50	1.50	0.75	1.50	-0.06	0.75	1.50
Ion-type	PR	KQ	a_1	Y	a_2	b_2	b^{++}_7	y_2	PTAAA	y_6^{+2}		PTAAAI	y_4
Delta ppm	11.1	-2.1	-28.1 0.50 LI -15.4	-8.0	-2.9	-11.0	-28.2	1.0	-9.6	-11.4		-10.5	-13.6

Fragment-ion (m/z)	656.370^{+2}	674.379	716.914	717.420	739.399	758.408^{+2}	810.435	837.447^{+2}	838.452^{+2}	838.608	881.476	908.474
Frac. Inten.(% of TIC)	1.70	7.52	3.25	3.39	1.76	1.59	2.07	3.05	3.81	2.40	3.30	5.47
Rel. Inten.(% of BP)	6.84	30.19	13.04	13.60	7.05	6.39	8.32	12.26	15.32	9.64	13.24	21.98
Score	-0.07	1.50	1.50	-0.14	0.50	-0.06	0.50	-0.12	1.50	-0.10	0.50	1.50
Ion-type		y_5	y^{++}_{13}		b_7		b_8		y_{15}^{+2}		b_9	y_7
Delta ppm		-5.7	29.1		-0.1		-2.6		18.3		2.6	-10.2



Result Summary

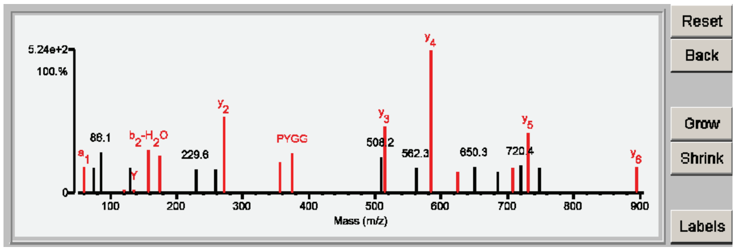
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.40	66.8	7	11/25	K350k	(R)SSGPYGGGGQYFAkPR(N)	1628.7816	114.0567	7.9	38846.0/9.26	HUMAN	P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.40	66.8	7	11/25	K350k	(R) S S G P/Y G G G G Q/Y/F/A/k/P/R (N)	1628.7816	114.0567	7.9	38846.0/9.26	HUMAN	P09651	645661	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=4

Fragment-ion (m/z)	60.043	75.053	86.098	120.083	130.074	136.075	157.060	175.115	229.635	258.137	272.171	357.142
Frac. Inten.(% of TIC)	2.97	2.72	4.50	0.30	2.78	0.38	4.75	4.18	2.70	2.67	8.47	3.50
Rel. Inten.(% of BP)	18.75	17.21	28.48	1.87	17.59	2.40	30.01	26.42	17.09	16.90	53.57	22.16
Score	0.50	-0.17	-0.28	1.00	-0.18	1.00	0.25	1.50	-0.17	-0.17	1.50	0.75
Ion-type	a_1			F		Y	b_2-H_2O	y_1			y_2	GGGGQ
Delta ppm	-36.4			19.4		-5.8	-13.8	-23.7			-1.2	-31.1

Fragment-ion (m/z)	375.163	508.226	514.309	562.271	585.345	624.294	650.289	685.362	707.852^{+2}	720.372^{+2}	732.421	747.293	895.477
Frac. Inten.(% of TIC)	4.34	4.05	7.43	2.78	15.82	2.34	2.87	2.43	2.79	2.98	6.65	2.72	2.86
Rel. Inten.(% of BP)	27.41	25.64	47.01	17.61	100.00	14.82	18.14	15.39	17.66	18.85	42.04	17.22	18.07
Score	0.75	-0.26	1.50	-0.18	1.50	0.75	-0.18	-0.15	1.50	-0.19	1.50	-0.17	1.50
Ion-type	PYGG		y_3		y_4	YFAk			y_{12}^{+2}		y_5		y_6
Delta ppm	-12.5		-1.6		-2.9	-34.2			8.0		8.6		-2.0



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Result Summary

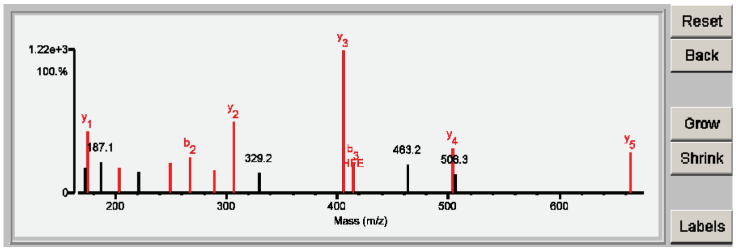
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.18	67.4	7	10/25	K57k	(R)EHFEkWGTLTDCVVMR(D)	2007.9415	114.0578	7.0	39595.1/9.09	HUMAN	P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.18	67.4	7	10/25	K57k	(R) E H\F\E k W G T L T D/C/V/V/M/R (D)	2007.9415	114.0578	7.0	39595.1/9.09	HUMAN	P51991	645687	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2

Fragment-ion (m/z)	70.063	72.080	74.058	84.080	86.096	110.070	116.016	133.048	159.092	173.128	175.118	187.143
Frac. Inten.(% of TIC)	0.00	0.63	2.62	3.98	0.30	0.14	3.99	2.94	0.08	3.28	8.02	4.02
Rel. Inten.(% of BP)	0.02	3.37	13.99	21.24	1.62	0.75	21.27	15.69	0.43	17.52	42.80	21.42
Score	0.20	0.50	-0.14	-0.21	0.22	1.00	-0.21	-0.16	2.00	-0.18	1.50	-0.21
Ion-type	PR	V			LI	H			W		y_1	
Delta ppm	-37.5	-16.3			-8.4	-11.6			2.7		-7.7	

Fragment-ion (m/z)	203.118	221.103	249.098	267.108	289.128	306.161	329.183	405.226	414.177	463.200^{+2}	504.288	506.254^{+2}	664.320
Frac. Inten.(% of TIC)	3.26	2.83	3.88	4.70	3.00	9.41	2.65	18.75	4.01	3.72	5.88	2.56	5.34
Rel. Inten.(% of BP)	17.42	15.10	20.67	25.08	15.98	50.19	14.12	100.00	21.37	19.83	31.37	13.64	28.49
Score	1.50	-0.15	0.25	0.50	0.50	1.50	-0.14	1.50	0.75	-0.20	1.50	-0.14	1.50
Ion-type	y^{++}_3		b_2-H_2O	b_2	y_2-NH_3	y_2		y_3	b_3 HFE		y_4		y_5
Delta ppm	2.6		-4.9	-7.0	-15.5	5.1		-5.6	-4.1 -4.1		-16.2		-10.6



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Result Summary

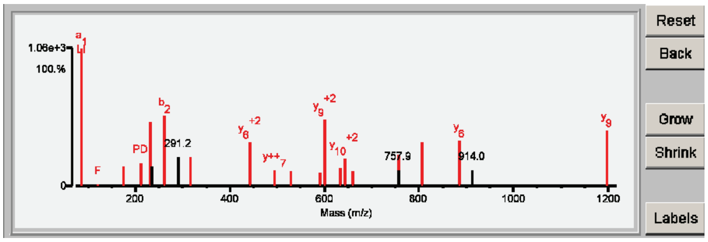
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.93	87.4	9	5/25	K197k	(K)IFVGGLSPDTPEEkIR(E)	1757.9432	114.0552	6.6	38434.4/7.61	HUMAN	Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.93	87.4	9	5/25	K197k	(K) I F|V/G G L/S/P D/T/P E/E/k I/R (E)	1757.9432	114.0552	6.6	38434.4/7.61	HUMAN	Q14103	293629	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1

Fragment-ion (m/z)	70.065	72.078	86.095	120.080	175.113	213.087	233.166	234.163	261.158	291.199	315.156	443.240^{+2}
Frac. Inten.(% of TIC)	0.00	3.14	16.33	0.27	2.31	2.74	7.58	2.32	8.33	3.40	3.36	5.28
Rel. Inten.(% of BP)	0.01	19.21	100.00	1.68	14.16	16.80	46.38	14.19	50.99	20.84	20.55	32.34
Score	0.20	-0.19	0.50 0.50	1.00	1.50	0.75	0.50	-0.14	0.50	-0.21	0.75	1.50
Ion-type	PR		a_1 LI	F	y_1	PD	a_2		b_2		GGLS	y_6^{+2}
Delta ppm	2.5		-30.5 -17.7	-7.3	-31.7	-6.5	-0.6		-10.5		-36.2	-7.4

Fragment-ion (m/z)	493.751	530.346	590.816^{+2}	599.806^{+2}	634.313^{+2}	643.317^{+2}	659.380	756.897^{+2}	757.871^{+2}	806.423^{+2}	885.477	914.007	1198.617
Frac. Inten.(% of TIC)	1.87	1.69	1.58	7.88	2.20	3.34	1.73	3.74	1.87	5.21	5.36	1.89	6.58
Rel. Inten.(% of BP)	11.46	10.34	9.67	48.25	13.47	20.46	10.62	22.93	11.42	31.89	32.81	11.57	40.29
Score	1.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50	-0.11	1.50	1.50	-0.12	1.50
Ion-type	y^{++}_7	y_3	$y_9\text{-}H_2O^{+2}$	y_9^{+2}	$y_{10}\text{-}H_2O^{+2}$	y_{10}^{+2}	y_4	y_{13}^{+2}		y_{14}^{+2}	y_6		y_9
Delta ppm	-32.6	10.2	24.9	-0.6	-7.1	-9.0	-5.9	14.7		2.8	-2.3		9.1



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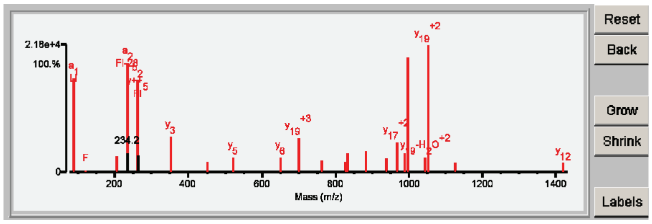
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	28.72	95.9	15	2/25	K22k	(K)LFIGGLNTETNEkALEAVFGK(Y)	2251.1969	114.0682	10.7	42332.0/10.06	HUMAN	P38159	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=RBMX PE=1 SV=3
2	22.30	89.6	11	6/25	None	(K)LFIGGLNRETNEKMLKAVFGK(H)	2365.3060	-0.0410	-17.3	55783.8/9.95	HUMAN	Q15414	RNA-binding motif protein, Y chromosome, family 1 member A1/C OS=Homo sapiens GN=RBMY1A1 PE=1 SV=1
2	22.30	89.6	11	6/25	None	(K)LFIGGLNRETNEKMLKAVFGK(H)	2365.3060	-0.0410	-17.3	55834.9/9.96	HUMAN	A6NDE4	RNA-binding motif protein, Y chromosome, family 1 member B OS=Homo sapiens GN=RBMY1B PE=2 SV=2
2	22.30	89.6	11	6/25	None	(K)LFIGGLNRETNEKMLKAVFGK(H)	2365.3060	-0.0410	-17.3	55774.8/9.95	HUMAN	P0C7P1	RNA-binding motif protein, Y chromosome, family 1 member D OS=Homo sapiens GN=RBMY1D PE=2 SV=1
2	22.30	89.6	11	6/25	None	(K)LFIGGLNRETNEKMLKAVFGK(H)	2365.3060	-0.0410	-17.3	55758.8/9.95	HUMAN	A6NEQ0	RNA-binding motif protein, Y chromosome, family 1 member E OS=Homo sapiens GN=RBMY1E PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	28.72	95.9	15	2/25	K22k	(K) L/F|I/G/G/L/N/T E/T N E k/A/L/E/A/V/F/G K (Y)	2251.1969	114.0682	10.7	42332.0/10.06	HUMAN	P38159	293647	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=RBMX PE=1 SV=3

Fragment-ion (m/z)	84.081	86.096	120.079	204.134	233.165	234.167	261.160	262.164	351.206	450.272	521.307	650.347	702.371^{+3}	763.437	825.926^{+2}	834.472	882.943^{+2}	939.484^{+2}	967.996^{+2}	987.509^{+2}	996.507^{+2}	1044.041^{+2}	1053.056^{+2}	1126.610^{+2}	1420.731
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.06 0.40 0.50 KQ -2.1	10.94 73.89 0.50 a_1 -23.5 0.50 LI -10.8	0.21 1.39 1.00 F -12.3	1.90 12.81 1.50 y_2 -0.8	12.68 85.63 0.50 a_2 -4.4 FI-28 -4.4	2.21 14.90 -0.15	10.68 72.08 1.50 b_2 -3.6 $y{++}_5$ 8.3 FI -3.6	1.92 12.96 -0.13	4.16 28.11 1.50 y_3 8.3	1.25 8.46 1.50 y_4 1.6	1.71 11.55 1.50 y_5 -1.6	1.70 11.50 1.50 y_6 -5.7	4.05 27.35 1.50 y_{19}^{+3} 5.9	1.32 8.92 1.50 y_7 3.3	1.26 8.50 1.50 y_{14}^{+2} 6.8	2.25 15.21 1.50 y_8 0.3	2.46 16.63 1.50 y_{15}^{+2} 1.5	1.55 10.46 1.50 y_{16}^{+2} 0.3	3.43 23.17 1.50 y_{17}^{+2} 1.8	2.21 14.92 0.50 y_{18}-H_2O^{+2} 9.3	13.39 90.39 1.50 y_{18}^{+2} 1.8	1.73 11.65 0.50 y_{19}-H_2O^{+2} -1.3	14.81 100.00 1.50 y_{19}^{+2} 8.6	1.10 7.42 1.50 y_{20}^{+2} 25.2	1.02 6.86 1.50 y_{12} -8.4



Result Summary

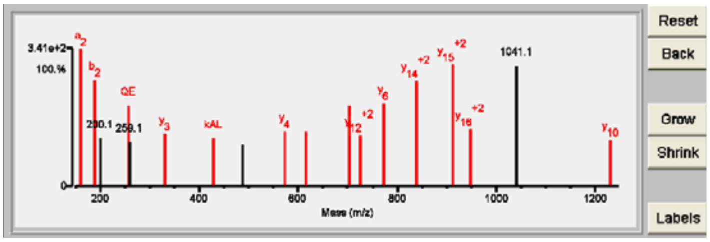
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.01	74.4	10	7/25	K167k	(R)STGEAFVQFASQEIAEkALK(K)	2154.1077	114.0551	5.4	49229.7/5.89	HUMAN	P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4
1	18.01	74.4	10	7/25	K167k	(R)STGEAFVQFASQEIAEkALK(K)	2154.1077	114.0551	5.4	49263.9/5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1
2	16.12	71.1	9	8/25	K170k	(R)STGEAFVQFASQEIAEKALk(K)	2154.1077	114.0551	5.4	49229.7/5.89	HUMAN	P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4
2	16.12	71.1	9	8/25	K170k	(R)STGEAFVQFASQEIAEKALk(K)	2154.1077	114.0551	5.4	49263.9/5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.01	74.4	10	7/25	K167k	(R) S T|G E/A/F/V Q/F A/S Q E I/A/E/k/A L K (K)	2154.1077	114.0551	5.4	49229.7/5.89	HUMAN	P31943	293587	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4
1	18.01	74.4	10	7/25	K167k	(R) S T|G E/A/F/V Q/F A/S Q E I/A/E/k/A L K (K)	2154.1077	114.0551	5.4	49263.9/5.89	HUMAN	P55795	293595	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.078	86.093	120.082	143.078	161.094	189.085	200.137	258.111	259.108	331.234	427.262
Frac. Inten.(% of TIC)	0.08	0.20	0.17	5.63	0.10	4.05	8.56	6.61	2.98	5.01	2.73	3.30	3.00
Rel. Inten.(% of BP)	0.94	2.35	2.04	65.85	1.21	47.37	100.00	77.23	34.85	58.54	31.94	38.52	35.06
Score	-0.01	0.50	0.50	-0.66	1.00	-0.47	0.50	0.50	-0.35	0.75	-0.32	1.50	0.75
Ion-type		V	KQ		F		a_2	b_2		QE		y_3	kAL
Delta ppm		-9.4	-31.8		6.9		5.2	-16.3		6.8		-0.9	-13.4

Fragment-ion (m/z)	488.262	573.361	615.817^{+2}	702.404	724.876^{+2}	773.455	838.460^{+2}	912.001^{+2}	947.521^{+2}	1040.537	1041.052	1230.693
Frac. Inten.(% of TIC)	2.60	3.38	3.38	5.04	3.16	5.17	6.57	7.60	3.52	6.74	7.48	2.92
Rel. Inten.(% of BP)	30.44	39.55	39.55	58.95	36.91	60.42	76.84	88.83	41.11	78.75	87.45	34.18
Score	-0.30	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	-0.87	1.50
Ion-type		y_4	y_{10}^{+2}	y_5	y_{12}^{+2}	y_6	y_{14}^{+2}	y_{15}^{+2}	y_{16}^{+2}	$y{+}{+}_{18}$		y_{10}
Delta ppm		-18.3	-35.0	-15.5	-20.3	4.7	6.4	14.0	15.1	-2.3		19.7



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Result Summary

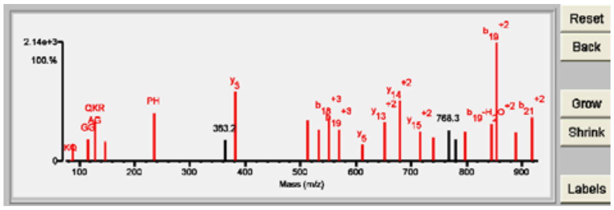
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.38	91.6	13	3/25	K62k	(R)LkTDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK(T)	3222.3816	114.0598	5.1	64133.1/8.46	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.38	91.6	13	3/25	K62k	(R) L k T D N A G D Q H G G G G G\G\G\G\G\A G\A/A/G/G G G G G E/N Y/D D/P H/K (T)	3222.3816	114.0598	5.1	64133.1/8.46	HUMAN	P14866	293671	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2

Fragment-ion (m/z)	84.079	87.056	110.068	115.049	129.065	147.112	235.122	363.214	381.221	512.898^{+3}	531.902^{+3}	550.915^{+3}
Frac. Inten.(% of TIC)	0.18	2.02	0.07	2.53	4.67	2.21	5.56	2.42	7.99	4.71	3.68	5.12
Rel. Inten.(% of BP)	1.29	14.85	0.51	18.56	34.32	16.25	40.86	17.77	58.73	34.63	27.08	37.60
Score	0.50	0.50	1.00	0.75	0.75	1.50	0.75	-0.18	1.50	0.50	0.50	0.50
Ion-type	KQ	NR GG-28	H	GG	QKR AG	y_1	PH		y_3	b_{16}^{+3}	b_{17}^{+3}	b_{18}^{+3}
Delta ppm	-16.4	3.6 3.6	-29.7	-6.1	-3.5 -3.5	-2.7	12.5		-8.6	0.4	-5.0	5.2

Fragment-ion (m/z)	569.931^{+3}	611.269	651.759^{+2}	680.285^{+2}	715.795^{+2}	740.346^{+2}	768.274^{+2}	780.342	797.345^{+2}	845.364^{+2}	854.369^{+2}	888.392	918.427^{+2}
Frac. Inten.(% of TIC)	3.66	1.91	4.50	6.95	3.41	2.76	3.50	2.48	3.44	4.24	13.61	3.30	5.08
Rel. Inten.(% of BP)	26.93	14.05	33.09	51.10	25.05	20.25	25.69	18.26	25.25	31.12	100.00	24.27	37.34
Score	0.50	1.50	1.50	1.50	1.50	0.50	-0.26	-0.18	0.50	0.25	0.50	1.50	0.50
Ion-type	b_{19}^{+3}	y_5	y_{13}^{+2}	y_{14}^{+2}	y_{15}^{+2}	b_{15}^{+2}			b_{17}^{+2}	$b_{19}\text{-}H_2O^{+2}$	b_{19}^{+2}	y_7	b_{21}^{+2}
Delta ppm	19.9	-16.0	-18.7	4.5	-6.7	18.7			-10.4	-7.0	-7.3	8.2	24.7



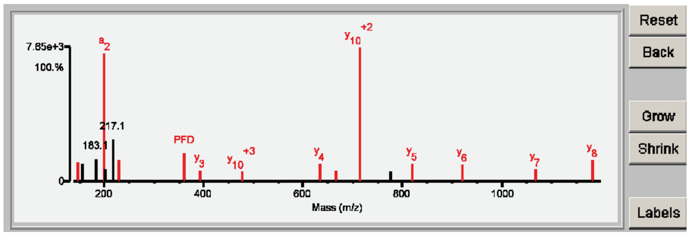
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.08	78.3	9	7/25	K667k	(R)NLPFDFTWkMLK(D)	1539.8028	114.0545	7.0	77516.1/8.85	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3
2	14.85	73.1	7	9/25	K670k	(R)NLPFDFTWKMLk(D)	1539.8028	114.0545	7.0	77516.1/8.85	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3
3	7.68	61.5	3	14/25	None	(R)LNPNTTVKQSYFGGK(R)	1653.8595	-0.0021	-1.3	51260.7/5.88	HUMAN	RQ92484	REVERSE Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2
4	7.66	58.1	3	14/25	K434k	(R)AVGPSPPAGIGGFEkR(T)	1539.8278	114.0295	-8.1	173104.0/7.18	HUMAN	RO43426	REVERSE Synaptojanin-1 OS=Homo sapiens GN=SYNJ1 PE=1 SV=2
5	7.05	63.1	2	15/25	None	(K)LNNLVLFDKATYDK(L)	1653.8846	-0.0273	-16.5	13742.2/10.12	HUMAN	P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.08	78.3	9	7/25	K667k	(R) N L|P/F/D/F/T/W/k/M L/K (D)	1539.8028	114.0545	7.0	77516.1/8.85	HUMAN	P52272	293675	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3

Fragment-ion (m/z)	70.066	84.081	86.097	87.052	89.059	120.082	133.087	147.112	155.119	183.113	200.141	201.140	217.133	228.135	360.153	391.238	476.250^{+3}	633.373	665.329^{+2}	713.861^{+2}	775.422^{+2}	819.455	920.498	1067.566	1182.595
Frac. Inten.(% of TIC)	0.01	0.07	0.38	0.06	2.09	0.10	1.58	3.27	3.01	3.80	22.24	2.09	7.35	3.71	4.85	1.90	1.79	3.00	1.81	23.31	1.76	3.17	2.84	2.08	3.71
Rel. Inten.(% of BP)	0.04	0.31	1.64	0.27	8.98	0.42	6.79	14.04	12.91	16.28	95.41	8.98	31.52	15.92	20.79	8.15	7.67	12.88	7.75	100.00	7.54	13.61	12.19	8.92	15.93
Score	0.20	0.50	0.22	0.33	-0.09	1.00	-0.07	1.50	-0.13	-0.16	0.50	-0.09	-0.32	0.50	0.75	1.50	1.50	1.50	1.50	1.50	-0.08	1.50	1.50	1.50	1.50
Ion-type	PR	KQ	LI	NR		F		y_1			a_2			b_2	PFD	y_3	y_{10}^{+3}	y_4	y_9^{+2}	y_{10}^{+2}		y_5	y_6	y_7	y_8
Delta ppm	18.2	0.3	12.5	-34.3		7.7		-2.7			1.7			0.2	-9.4	2.4	12.5	-3.9	-11.8	-2.6		-0.1	-4.6	-3.9	-1.8



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Result Summary

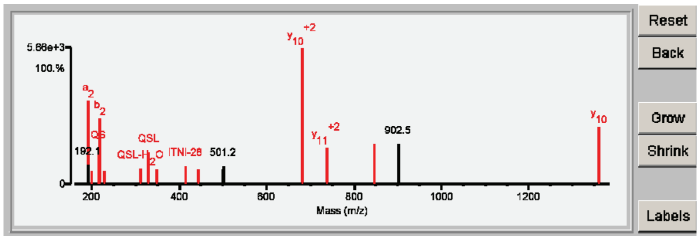
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.11	84.4	5	6/25	K83k	(R)AFITNIPFDVkWQSLK(D)	1907.0425	114.0511	4.0	77516.1/8.85	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3
2	14.50	82.5	4	7/25	K88k	(R)AFITNIPFDVKWQSLk(D)	1907.0425	114.0511	4.0	77516.1/8.85	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3
3	5.05	55.6	2	11/25	M262m K263k K270k	(R)SLLASGmkLNESVTkAK(N)	1776.9888	244.1049	11.9	93697.3/7.82	HUMAN	RQ9UJA3	REVERSE DNA replication licensing factor MCM8 OS=Homo sapiens GN=MCM8 PE=1 SV=2
4	4.50	50.7	2	12/25	M262m K263k K272k	(R)SLLASGmkLNESVTKAk(N)	1776.9888	244.1049	11.9	93697.3/7.82	HUMAN	RQ9UJA3	REVERSE DNA replication licensing factor MCM8 OS=Homo sapiens GN=MCM8 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.11	84.4	5	6/25	K83k	(R) A F|I/T N/I/P F D V k W Q/S L K (D)	1907.0425	114.0511	4.0	77516.1/8.85	HUMAN	P52272	293675	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3

Fragment-ion (m/z)	72.081	86.097	87.100	120.081	133.088	191.119	192.123	200.144	215.134	216.098	219.113	228.135
Frac. Inten.(% of TIC)	0.07	0.51	1.71	0.28	1.65	11.04	2.54	1.72	2.40	4.74	8.79	1.74
Rel. Inten.(% of BP)	0.40	2.79	9.43	1.55	9.10	60.92	14.02	9.49	13.23	26.16	48.49	9.63
Score	0.50	0.22	-0.09	1.00	-0.09	0.50	-0.14	0.50	0.75	0.75	0.50	0.75
Ion-type	V	LI		F		a_2		NI-28	IT	QS	b_2	NI
Delta ppm	4.5	2.0		1.0		0.1		16.7	-26.6	-2.7	-4.6	-1.6

Fragment-ion (m/z)	311.174	329.182	347.229	414.269	442.260	499.899^{+3}	501.235^{+2}	681.361^{+2}	737.907^{+2}	845.460^{+2}	901.989	902.495	1361.720
Frac. Inten.(% of TIC)	2.10	4.21	1.90	2.37	1.87	1.93	2.41	18.12	4.81	5.29	4.67	5.40	7.73
Rel. Inten.(% of BP)	11.60	23.23	10.50	13.07	10.33	10.66	13.33	100.00	26.55	29.22	25.75	29.77	42.67
Score	0.50	0.75	1.50	0.50	0.75	-0.11	-0.13	1.50	1.50	1.50	1.50	-0.30	1.50
Ion-type	QSL-H_2O	QSL	y_3	ITNI-28	ITNI			y_{10}^{+2}	y_{11}^{+2}	y_{13}^{+2}	y++$_{14}$		y_{10}
Delta ppm	3.9	-3.2	-0.9	-7.7	-16.5			-5.1	0.4	9.5	-5.2		-0.8



Result Summary

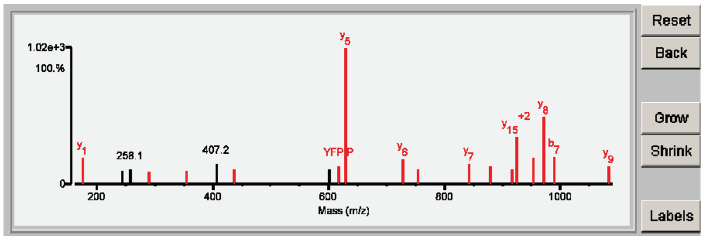
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.90	82.5	9	6/25	K463k	(K)EkPYFPIPEEYTFIQNVPLEDR(V)	2724.3556	114.0686	9.0	90513.8/5.76	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.90	82.5	9	6/25	K463k	(K) E k P Y F P I|P E E Y\T F|I/Q/N/V/P L E/D/R (V)	2724.3556	114.0686	9.0	90513.8/5.76	HUMAN	Q00839	293689	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=5

Fragment-ion (m/z)	70.065	86.096	120.079	175.120	243.155	258.149	290.145	354.171	407.215	437.240	602.254	618.344	629.326
Frac. Inten.(% of TIC)	0.00	0.07	0.14	4.24	2.17	2.32	2.03	2.20	3.37	2.45	2.31	3.02	22.49
Rel. Inten.(% of BP)	0.02	0.30	0.64	18.87	9.64	10.34	9.03	9.79	14.99	10.90	10.28	13.44	100.00
Score	0.20	0.22	1.00	1.50	-0.10	-0.10	1.50	0.25	-0.15	0.75	-0.10	0.75	1.50
Ion-type	PR	LI	F	y_1			y_2	b_2-H_2O		PIPE		YFPIP	y_5
Delta ppm	-3.2	-9.6	-19.0	4.3			-2.1	-19.7		-1.0		23.0	1.6

Fragment-ion (m/z)	728.384	754.369^{+2}	842.434	878.452^{+2}	916.943^{+2}	925.468^{+2}	953.491	970.487	989.517	1083.602	1094.593	1106.054^{+2}
Frac. Inten.(% of TIC)	4.09	2.35	3.35	3.07	2.43	7.86	4.32	10.98	4.52	2.91	3.37	3.91
Rel. Inten.(% of BP)	18.20	10.44	14.90	13.67	10.79	34.96	19.22	48.82	20.10	12.96	15.00	17.38
Score	1.50	0.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50	-0.15	-0.17
Ion-type	y_6	b_{11}^{+2}	y_7	b_{13}^{+2}	y_{15}-NH_3^{+2}	y_{15}^{+2}	y_8-NH_3	y_8	b_7	y_9		
Delta ppm	-13.9	13.0	-3.6	39.5	4.3	17.3	23.0	-8.2	7.0	20.8		



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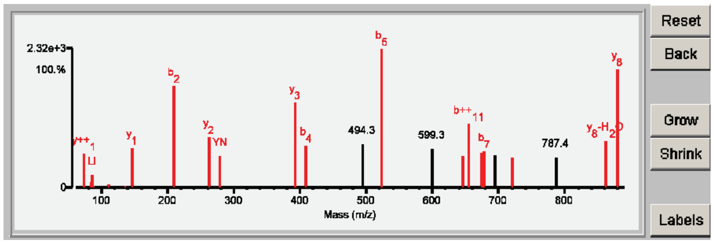
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.46	86.3	10	4/25	K523k	(K)HAAENPGkYNILGTNTIMDK(M)	2187.0863	114.0643	9.3	90513.8/5.76	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.46	86.3	10	4/25	K523k	(K) H A\A E\N\P G\k Y N I\L/G T/N T I/M/D/K (M)	2187.0863	114.0643	9.3	90513.8/5.76	HUMAN	Q00839	293689	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=5

Fragment-ion (m/z)	70.065	74.060	84.080	86.096	87.054	110.072	136.076	147.111	209.104	262.135	278.114	393.184	409.186	494.259	523.225	599.287	646.824^{+2}	655.328	674.327	677.308	694.325	721.363	787.403	861.414	879.433
Frac. Inten.(% of TIC)	0.01	3.21	0.52	1.22	0.15	0.27	0.15	3.76	9.60	4.78	2.94	8.07	3.99	4.13	13.19	3.69	2.98	6.02	3.37	3.46	3.05	2.90	2.86	4.50	11.19
Rel. Inten.(% of BP)	0.05	24.36	3.92	9.24	1.14	2.06	1.12	28.48	72.79	36.26	22.28	61.23	30.25	31.31	100.00	27.98	22.56	45.68	25.57	26.23	23.16	21.98	21.67	34.11	84.89
Score	0.20	1.50	0.50	0.22	0.33	1.00	1.00	1.50	0.50	1.50	0.75	1.50	0.50	-0.31	0.50	-0.28	0.25	0.50	0.75	0.50	-0.23	1.50	-0.22	0.50	1.50
Ion-type	PR	$y{+}{+}_1$	KQ	LI	NR	a_1	Y	y_1	b_2	y_2	YN	y_3	b_4		b_5		b_{11}-NH_3^{+2}	$b{+}{+}_{11}$	PGkYN	b_7		y_6		y_8-H_2O	y_8
Delta ppm	-1.8	-5.9	-5.7	-9.6	-14.8	-7.9	1.5	-12.9	-0.5	-17.3	-1.9	9.6	5.6		-3.1		28.8	14.7	0.4	10.4		11.8		0.0	10.5
						1.00																			
						H																			
						2.1																			



Result Summary

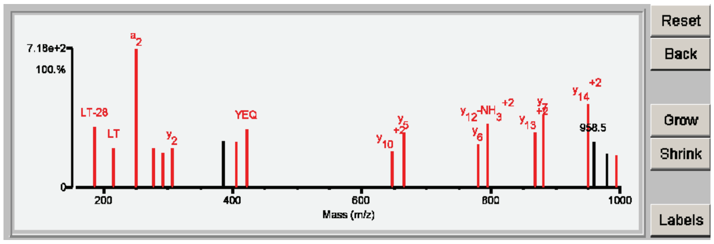
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.51	85.0	9	4/25	K46k	(R)NYYEQWGkLTDCVVMR(D)	2061.9521	114.0559	5.9	37429.9/8.97	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.51	85.0	9	4/25	K46k	(R) N Y|Y/E Q W/G k/L/T/D/C V/V/M R (D)	2061.9521	114.0559	5.9	37429.9/8.97	HUMAN	P22626	645677	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2

Fragment-ion (m/z)	84.042	84.079	86.095	129.105	136.074	187.144	215.138	250.118	278.111	293.110	306.158	385.154^{+2}	405.224
Frac. Inten.(% of TIC)	0.10	0.27	0.25	0.10	0.27	5.72	3.70	12.89	3.73	3.24	3.74	4.33	4.30
Rel. Inten.(% of BP)	0.77	2.08	1.92	0.77	2.10	44.36	28.72	100.00	28.93	25.11	28.98	33.57	33.36
Score	1.00	0.50	0.22	0.20	1.00	0.50	0.75	0.50	0.50	0.75	1.50	-0.34	1.50
Ion-type	E	KQ	LI	RKQ	Y	LT-28	LT	a_2	b_2	YE	y_2		y_3
Delta ppm	-30.8	-27.1	-21.2	18.3	-14.6	-3.7	-7.5	-5.3	-14.5	-13.3	-3.7		-9.3

Fragment-ion (m/z)	421.176	646.825^{+2}	664.321	779.347	795.382^{+2}	868.393^{+2}	880.406	949.963^{+2}	958.492	980.021^{+2}	993.498	1036.479^{+2}
Frac. Inten.(% of TIC)	5.48	3.40	5.13	4.01	5.90	5.17	6.81	7.81	4.20	3.12	3.05	3.31
Rel. Inten.(% of BP)	42.51	26.39	39.82	31.09	45.75	40.11	52.81	60.62	32.59	24.22	23.64	25.71
Score	0.75	1.50	1.50	1.50	0.50	1.50	1.50	1.50	-0.33	-0.24	1.50	-0.26
Ion-type	YEQ	y_{10}^{+2}	y_5	y_6	$y_{12}\text{-NH}_3^{+2}$	y_{13}^{+2}	y_7	y_{14}^{+2}			y_8	
Delta ppm	7.9	-2.3	-9.7	-8.7	0.3	-26.8	5.0	15.9			12.6	



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Result Summary

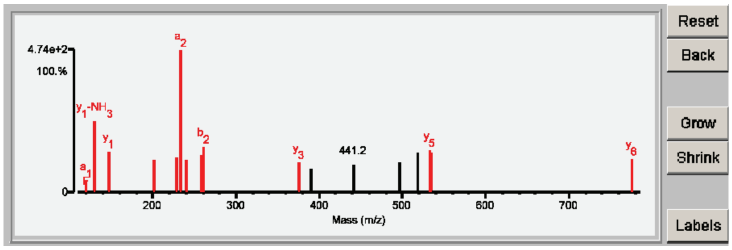
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.01	75.2	6	7/25	K15k	(K)FLVEYkSAVEK(K)	1312.7147	114.0516	6.1	49512.9/5.52	HUMAN	O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1
2	10.39	55.5	5	10/25	K20k	(K)FLVEYKSAVEk(K)	1312.7147	114.0516	6.1	49512.9/5.52	HUMAN	O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1
3	7.45	61.1	2	10/25	K405k	(K)EVASkYEVLFK(E)	1312.7147	114.0516	6.1	49512.9/5.51	HUMAN	RO14929	REVERSE Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1
4	6.91	59.0	1	10/25	None	(K)TMNLGFKVELFK(L)	1426.7763	-0.0099	-7.0	83756.1/8.41	HUMAN	RQ7Z388	REVERSE Protein dpy-19 homolog 4 OS=Homo sapiens GN=DPY19L4 PE=2 SV=1
5	6.37	56.3	3	13/25	None	(R)LSSQLFEK(F)	951.5146	-0.0012	-1.3	23718.4/6.18	HUMAN	RP05231	REVERSE Interleukin-6 OS=Homo sapiens GN=IL6 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.01	75.2	6	7/25	K15k	(K) F L\V/E Y/k/S A/V E/K (K)	1312.7147	114.0516	6.1	49512.9/5.52	HUMAN	O14929	273751	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1

Fragment-ion (m/z)	60.041	72.080	84.079	85.083	86.096	87.055	120.080	129.100	130.081	136.074	147.109
Frac. Inten.(% of TIC)	3.02	0.38	0.65	3.53	0.80	3.41	1.42	0.28	8.75	0.12	5.01
Rel. Inten.(% of BP)	17.21	2.16	3.69	20.10	4.58	19.45	8.09	1.61	49.90	0.66	28.56
Score	-0.17	0.50	0.50	-0.20	0.22	-0.19	1.00	0.20	0.50	1.00	1.50
Ion-type		V	KQ		LI		a_1	RKQ	y_1-NH$_3$	Y	y_1
Delta ppm		-5.2	-19.9		-9.6		-18.9	-19.7	-38.9	-16.1	-23.1
							1.00				
							F				
							-9.8				

Fragment-ion (m/z)	201.124	229.118	233.165	240.136	258.142	261.157	375.229	390.193	441.231	496.764^{+2}	517.781	533.290	534.268^{+2}	775.437
Frac. Inten.(% of TIC)	4.05	4.23	17.54	3.95	4.54	5.70	3.67	2.97	3.36	3.64	4.91	5.18	4.82	4.07
Rel. Inten.(% of BP)	23.10	24.14	100.00	22.51	25.87	32.47	20.95	16.95	19.13	20.76	27.96	29.53	27.50	23.21
Score	0.50	0.75	0.50	0.50	0.75	0.50	1.50	-0.17	-0.19	-0.21	-0.28	1.50	1.50	1.50
Ion-type	VE-28	VE	a_2	SAV-H_2O	y_2-H_2O	b_2	y_3					y_5	y_8^{+2}	y_6
Delta ppm	-3.3	-7.8	-4.0	3.9	-9.0	-14.4	13.8					-5.9	-8.3	7.7
					SAV									
					-13.3									



Result Summary

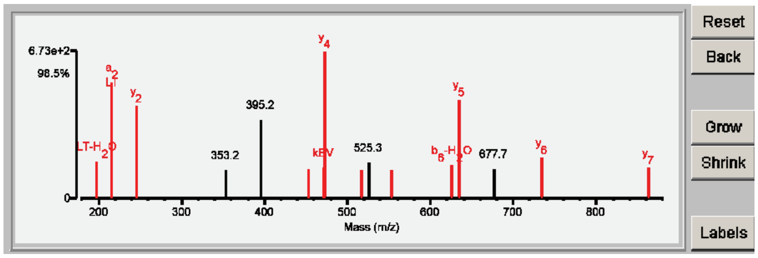
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.42	63.8	6	8/25	K74k	(K)ELTSLVkEVYPEAR(K)	1633.8796	114.0545	6.6	17561.2/9.38	HUMAN	O00422	Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.42	63.8	6	8/25	K74k	(K) E L T S L V/k/E/V/Y/P E/A R (K)	1633.8796	114.0545	6.6	17561.2/9.38	HUMAN	O00422	706743	Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	74.062	84.042	84.080	86.093	110.071	113.073	136.076	197.127	215.139	246.154
Frac. Inten.(% of TIC)	0.00	0.21	2.79	0.08	13.17	0.28	2.36	2.68	0.30	3.31	10.23	8.11
Rel. Inten.(% of BP)	0.02	1.59	21.18	0.62	100.00	2.12	17.92	20.33	2.29	25.15	77.74	61.64
Score	0.20	0.50	-0.21	1.00	-1.00	0.22	-0.18	-0.20	1.00	0.50	0.75	1.50
Ion-type	PR	V		E		LI			Y	LT-H_2O	a_2 LT	y_2
Delta ppm	3.9	-14.9		-32.0		-37.5			2.3	-15.0	-3.8 -3.8	-9.2

Fragment-ion (m/z)	353.155	395.192	453.256	471.272	472.249	516.302	525.298	553.289^{+2}	625.357	635.318	677.689	734.384	863.430
Frac. Inten.(% of TIC)	2.48	6.91	2.59	2.73	12.96	2.48	3.20	2.47	2.95	8.71	2.62	3.64	2.74
Rel. Inten.(% of BP)	18.82	52.52	19.64	20.73	98.48	18.85	24.31	18.76	22.42	66.14	19.89	27.62	20.78
Score	-0.19	-0.53	0.50	0.75	1.50	0.50	-0.24	1.50	0.25	1.50	-0.20	1.50	1.50
Ion-type			kEV-H_2O	kEV	y_4	a_5		y_8^{+2}	b_6-H_2O	y_5		y_6	y_7
Delta ppm			19.8	31.3	-4.7	-3.8		6.4	-0.1	5.3		1.4	5.0



Result Summary

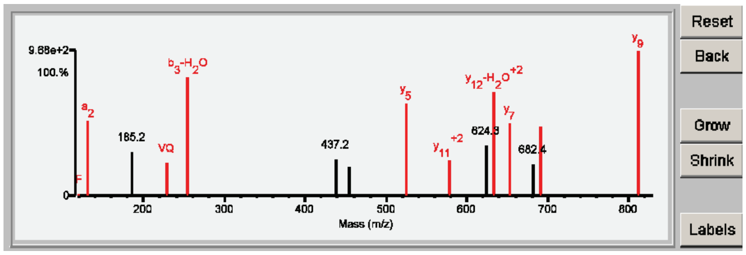
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.48	68.4	5	10/25	K100k	(K)GTLVQTkGTGASGSFK(L)	1538.8173	114.0494	3.9	21842.2/10.99	HUMAN	Q02539	Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3
1	9.48	68.4	5	10/25	K97k	(K)GTLVQTkGTGASGSFK(L)	1538.8173	114.0494	3.9	21364.9/10.94	HUMAN	P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	9.48	68.4	5	10/25	K98k	(K)GTLVQTkGTGASGSFK(L)	1538.8173	114.0494	3.9	22350.0/11.02	HUMAN	P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	9.48	68.4	5	10/25	K97k	(K)GTLVQTkGTGASGSFK(L)	1538.8173	114.0494	3.9	21865.4/11.03	HUMAN	P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2
1	9.48	68.4	5	10/25	K100k	(K)GTLVQTkGTGASGSFK(L)	1538.8173	114.0494	3.9	22580.3/10.91	HUMAN	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.48	68.4	5	10/25	K100k	(K) G T L/V Q/T k/G T/G A/S G S F K (L)	1538.8173	114.0494	3.9	21842.2/10.99	HUMAN	Q02539	271327	Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3
1	9.48	68.4	5	10/25	K97k	(K) G T L/V Q/T k/G T/G A/S G S F K (L)	1538.8173	114.0494	3.9	21364.9/10.94	HUMAN	P16403	271345	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	9.48	68.4	5	10/25	K98k	(K) G T L/V Q/T k/G T/G A/S G S F K (L)	1538.8173	114.0494	3.9	22350.0/11.02	HUMAN	P16402	271361	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	9.48	68.4	5	10/25	K97k	(K) G T L/V Q/T k/G T/G A/S G S F K (L)	1538.8173	114.0494	3.9	21865.4/11.03	HUMAN	P10412	271371	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2
1	9.48	68.4	5	10/25	K100k	(K) G T L/V Q/T k/G T/G A/S G S F K (L)	1538.8173	114.0494	3.9	22580.3/10.91	HUMAN	P16401	271381	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3

Fragment-ion (m/z)	72.080	84.042	84.080	86.058	86.096	96.041	101.069	113.067	117.100	120.078	129.101	131.078	185.163
Frac. Inten.(% of TIC)	0.19	3.07	0.39	2.59	0.87	2.54	0.13	3.43	2.91	0.15	0.09	6.73	3.92
Rel. Inten.(% of BP)	1.49	23.73	3.04	20.03	6.75	19.59	0.97	26.54	22.47	1.19	0.71	52.01	30.29
Score	0.50	-0.24	0.50	-0.20	0.22	-0.20		-0.27	-0.22	1.00	0.20	0.50	-0.30
Ion-type	V		KQ		LI		KQ			F	RKQ	a_2	
Delta ppm	-5.2		-5.7		-9.6					-24.8	-11.9	-33.6	

Fragment-ion (m/z)	228.132	254.151	437.204	454.252	525.267	577.794^{+2}	624.315^{+2}	632.817^{+2}	653.334	682.351	691.353^{+2}	811.393
Frac. Inten.(% of TIC)	2.94	10.57	3.22	2.59	8.28	3.19	4.47	9.29	6.52	2.82	6.13	12.94
Rel. Inten.(% of BP)	22.70	81.68	24.91	20.00	63.97	24.66	34.51	71.80	50.37	21.77	47.39	100.00
Score	0.75	0.25	-0.25	-0.20	1.50	1.50	-0.35	0.50	1.50	-0.22	1.50	1.50
Ion-type	VQ	b_3-H_2O			y_5	y_{11}^{+2}		y_{12}-H_2O^{+2}	y_7		y_{13}^{+2}	y_9
Delta ppm	-16.5	-1.6			0.7	0.4		-1.2	13.9		-6.1	-2.3



Result Summary

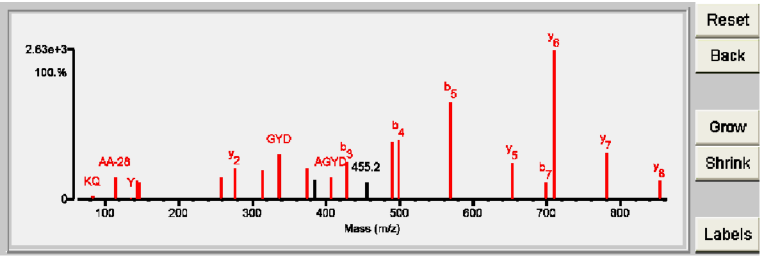
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.93	95.4	10	2/25	K67k	(K)kALAAAGYDVEK(N)	1235.6630	114.0588	11.8	21842.2/10.99	HUMAN	Q02539	Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3
1	19.93	95.4	10	2/25	K64k	(K)kALAAAGYDVEK(N)	1235.6630	114.0588	11.8	21364.9/10.94	HUMAN	P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	19.93	95.4	10	2/25	K65k	(K)kALAAAGYDVEK(N)	1235.6630	114.0588	11.8	22350.0/11.02	HUMAN	P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	19.93	95.4	10	2/25	K64k	(K)kALAAAGYDVEK(N)	1235.6630	114.0588	11.8	21865.4/11.03	HUMAN	P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2
1	19.93	95.4	10	2/25	K68k	(K)kALAAAGYDVEK(N)	1235.6630	114.0588	11.8	22019.1/11.71	HUMAN	P22492	Histone H1t OS=Homo sapiens GN=HIST1H1T PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.93	95.4	10	2/25	K67k	(K) k A\L\A|A|A/G|Y/D/V/E/K (N)	1235.6630	114.0588	11.8	21842.2/10.99	HUMAN	Q02539	271327	Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3
1	19.93	95.4	10	2/25	K64k	(K) k A\L\A|A|A/G|Y/D/V/E/K (N)	1235.6630	114.0588	11.8	21364.9/10.94	HUMAN	P16403	271345	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	19.93	95.4	10	2/25	K65k	(K) k A\L\A|A|A/G|Y/D/V/E/K (N)	1235.6630	114.0588	11.8	22350.0/11.02	HUMAN	P16402	271361	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	19.93	95.4	10	2/25	K64k	(K) k A\L\A|A|A/G|Y/D/V/E/K (N)	1235.6630	114.0588	11.8	21865.4/11.03	HUMAN	P10412	271371	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2
1	19.93	95.4	10	2/25	K68k	(K) k A\L\A|A|A/G|Y/D/V/E/K (N)	1235.6630	114.0588	11.8	22019.1/11.71	HUMAN	P22492	271477	Histone H1t OS=Homo sapiens GN=HIST1H1T PE=1 SV=4

Fragment-ion (m/z)	72.081	84.080	86.095	115.085	129.100	136.074	143.081	147.111	258.140	276.157	314.185	336.119	375.229
Frac. Inten.(% of TIC)	0.07	0.43	0.16	2.75	0.09	0.24	2.27	2.14	2.70	3.87	3.56	5.66	3.92
Rel. Inten.(% of BP)	0.38	2.30	0.84	14.84	0.50	1.30	12.26	11.56	14.55	20.84	19.18	30.51	21.11
Score	0.50	0.50	0.22	0.50	0.20	1.00	0.75	1.50	0.50	1.50	0.50	0.75	1.50
Ion-type	V	KQ	LI	AA-28	RKQ	Y	AA	y_1	y_2-H_2O	y_2	b_2	GYD	y_3
Delta ppm	5.9	-10.4	-14.2	-11.2	-16.6	-11.7	-2.8	-10.9	-20.7	6.9	9.3	-0.0	13.3

Fragment-ion (m/z)	384.183	407.172	427.259	455.203	490.246	498.308	569.341	653.315	697.387	710.336	781.371	852.426
Frac. Inten.(% of TIC)	2.49	2.84	4.62	2.08	7.17	7.45	12.19	4.49	2.20	18.55	5.82	2.24
Rel. Inten.(% of BP)	13.44	15.33	24.89	11.22	38.65	40.15	65.69	24.18	11.84	100.00	31.37	12.08
Score	-0.13	0.75	0.50	-0.11	1.50	0.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type		AGYD	b_3		y_4	b_4	b_5	y_5	b_7	y_6	y_7	y_8
Delta ppm		39.7	-16.5		-9.5	9.3	0.0	1.4	-17.0	0.4	-2.1	19.2



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Result Summary

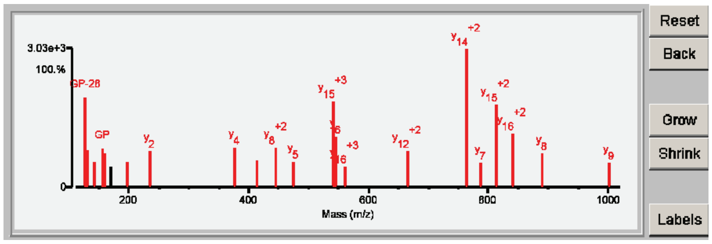
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	25.77	97.9	11	1/25	K46k	(K)ASGPPVSELITkAVAASK(E)	1725.9745	114.0436	0.4	21364.9/10.94	HUMAN	P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	25.77	97.9	11	1/25	K47k	(K)ASGPPVSELITkAVAASK(E)	1725.9745	114.0436	0.4	22350.0/11.02	HUMAN	P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	25.77	97.9	11	1/25	K46k	(K)ASGPPVSELITkAVAASK(E)	1725.9745	114.0436	0.4	21865.4/11.03	HUMAN	P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2
2	18.68	82.7	7	5/25	K52k	(K)ASGPPVSELITKAVAASk(E)	1725.9745	114.0436	0.4	21364.9/10.94	HUMAN	P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
2	18.68	82.7	7	5/25	K53k	(K)ASGPPVSELITKAVAASk(E)	1725.9745	114.0436	0.4	22350.0/11.02	HUMAN	P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	25.77	97.9	11	1/25	K46k	(K) A S|G/P/P V/S E L/I/T/k/A/V/A A/S K (E)	1725.9745	114.0436	0.4	21364.9/10.94	HUMAN	P16403	271345	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2
1	25.77	97.9	11	1/25	K47k	(K) A S|G/P/P V/S E L/I/T/k/A/V/A A/S K (E)	1725.9745	114.0436	0.4	22350.0/11.02	HUMAN	P16402	271361	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2
1	25.77	97.9	11	1/25	K46k	(K) A S|G/P/P V/S E L/I/T/k/A/V/A A/S K (E)	1725.9745	114.0436	0.4	21865.4/11.03	HUMAN	P10412	271371	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2

Fragment-ion (m/z)	70.064	84.080	86.094	127.085	131.080	141.065	155.080	159.074	169.127	198.083	234.144	376.218	413.196
Frac. Inten.(% of TIC)	0.01	0.15	0.26	8.99	3.74	2.57	3.87	3.44	2.15	2.62	3.64	4.00	2.72
Rel. Inten.(% of BP)	0.07	1.05	1.88	64.33	26.73	18.39	27.72	24.61	15.36	18.72	26.05	28.63	19.49
Score	0.20	0.50	0.22	0.50	0.50	0.50	0.75	0.75	-0.15	0.25	1.50	1.50	0.75
Ion-type	PR	KQ	LI	GP-28	a_2 AS-28	b_2-H_2O AS-H_2O	GP	b_2 AS		b_3-H_2O	y_2	y_4	PVSE
Delta ppm	-18.9	-12.8	-22.4	-22.7	-22.9 -22.9	-11.0 -11.0	-16.1	-22.7 -22.7		-27.3	-5.3	-3.3	-18.8

Fragment-ion (m/z)	445.261^{+2}	475.284	542.323^{+3}	546.320	561.317^{+3}	666.379^{+2}	764.438^{+2}	788.457	812.955^{+2}	841.478^{+2}	889.501	1002.585
Frac. Inten.(% of TIC)	4.05	2.52	8.61	5.04	2.06	3.63	13.98	2.41	8.30	5.46	3.37	2.40
Rel. Inten.(% of BP)	29.00	18.01	61.58	36.06	14.72	25.98	100.00	17.25	59.39	39.08	24.12	17.20
Score	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_8^{+2}	y_5	y_{15}^{+3}	y_6	y_{16}^{+3}	y_{12}^{+2}	y_{14}^{+2}	y_7	y_{15}^{+2}	y_{16}^{+2}	y_8	y_9
Delta ppm	4.9	-7.1	17.9	-8.9	-6.5	-1.8	-3.6	-7.2	-14.4	0.1	-10.6	-8.8



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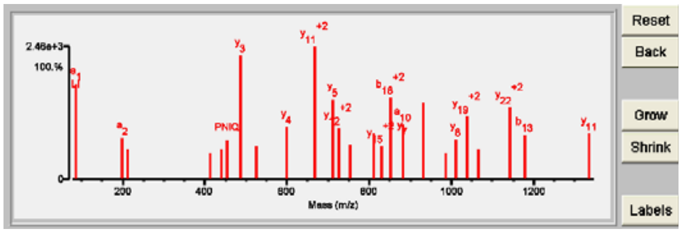
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	27.25	100.0	13	0/25	K119k	(K)LLGGVTIAQGGVLPNIQAVLLPkK(T)	2399.4748	114.0460	1.2	14233.6/10.86	HUMAN	Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3
1	27.25	100.0	13	0/25	K120k	(K)LLGGVTIAQGGVLPNIQAVLLPKk(T)	2399.4748	114.0460	1.2	14233.6/10.86	HUMAN	Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3
1	27.25	100.0	13	0/25	K119k	(K)LLGGVTIAQGGVLPNIQAVLLPkK(T)	2399.4748	114.0460	1.2	13995.4/10.88	HUMAN	Q8IUE6	Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3
1	27.25	100.0	13	0/25	K120k	(K)LLGGVTIAQGGVLPNIQAVLLPKk(T)	2399.4748	114.0460	1.2	13995.4/10.88	HUMAN	Q8IUE6	Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3
1	27.25	100.0	13	0/25	K119k	(K)LLGGVTIAQGGVLPNIQAVLLPkK(T)	2399.4748	114.0460	1.2	15144.6/10.74	HUMAN	P16104	Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2
1	27.25	100.0	13	0/25	K120k	(K)LLGGVTIAQGGVLPNIQAVLLPKk(T)	2399.4748	114.0460	1.2	15144.6/10.74	HUMAN	P16104	Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	27.25	100.0	13	0/25	K119k	(K) L L/G G V|T/I/A Q/G G V|L|P N I|Q/A|V/L/L/P k K (T)	2399.4748	114.0460	1.2	14233.6/10.86	HUMAN	Q96QV6	271549	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

Fragment-ion (m/z)	86.096	199.183	212.103	412.294	440.285	453.237	486.305	524.278	599.390	667.909^{+2}	712.473	724.461^{+2}	752.445^{+2}	811.539	831.023^{+2}	852.001^{+2}	882.568	930.556^{+2}	987.104^{+2}	1010.643	1037.618^{+2}	1066.628	1144.158^{+2}	1179.692	1334.806
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	6.92 72.40 0.50 a_1 -13.0 0.50 LI -0.3	2.95 30.91 0.50 a_2 9.1	2.13 22.33 0.75 PN -4.1	1.92 20.09 0.50 a_5 3.3	2.16 22.64 0.50 b_5 -6.5	2.81 29.40 0.75 PNIQ -20.5	8.93 93.46 1.50 y_3 3.6	2.41 25.21 0.75 PNIQA -11.5	3.80 39.81 1.50 y_4 4.8	9.55 100.00 1.50 y_{11}^{+2} -2.9	5.76 60.33 1.50 y_5 2.3	3.70 38.72 1.50 y_{12}^{+2} 10.1	2.53 26.44 0.50 b_{16}^{+2} -5.7	3.34 34.91 1.50 y_6 -1.4	2.41 25.28 1.50 y_{15}^{+2} 16.2	5.90 61.77 0.50 b_{18}^{+2} 5.5	3.96 41.49 1.50 a_{10} 29.1 y_7 -10.9	5.51 57.69 1.50 y_{17}^{+2} -0.7	1.95 20.45 1.50 y_{18}^{+2} 5.2	2.91 30.51 1.50 y_8 6.7	4.54 47.52 1.50 y_{19}^{+2} -4.4	2.18 22.83 0.50 b_{12} 0.9	5.17 54.09 1.50 y_{22}^{+2} -17.9	3.22 33.67 0.50 b_{13} -16.1	3.33 34.89 1.50 y_{11} -6.7



Result Summary

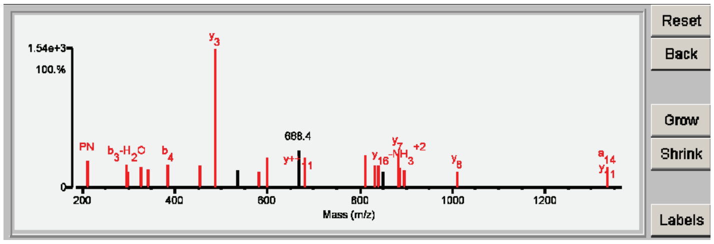
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.97	89.9	8	3/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14105.5/11.05	HUMAN	Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14107.5/10.90	HUMAN	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	13906.3/10.88	HUMAN	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	13936.3/10.88	HUMAN	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14091.5/10.90	HUMAN	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14095.6/10.90	HUMAN	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	19.97	89.9	8	3/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14121.5/11.05	HUMAN	Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0592	7.5	14019.5/10.90	HUMAN	Q9BTM1	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1
2	19.08	87.1	8	4/25	K120k	(R)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0592	7.5	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.97	89.9	8	3/25	K119k	(R) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14135.6/11.05	HUMAN	P04908	271551	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(R) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14105.5/11.05	HUMAN	Q93077	271553	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14107.5/10.90	HUMAN	P20671	271557	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	13906.3/10.88	HUMAN	Q96KK5	271565	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	13936.3/10.88	HUMAN	Q99878	271569	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14091.5/10.90	HUMAN	P0C0S8	271585	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14095.6/10.90	HUMAN	Q6FI13	271625	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	13988.4/10.90	HUMAN	Q16777	271635	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	19.97	89.9	8	3/25	K119k	(R) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14121.5/11.05	HUMAN	Q7L7L0	271685	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
1	19.97	89.9	8	3/25	K119k	(K) V T I A|Q/G G V L|P N I|Q/A|V L/L/P k K (T)	2059.2638	114.0592	7.5	14019.5/10.90	HUMAN	Q9BTM1	271761	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1

Fragment-ion (m/z)	72.079	86.094	212.103	296.192	297.199	325.184	340.201	385.244	453.240	486.303	536.208	582.326^{+2}	599.392
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.25 1.15 0.50 a_1 -38.5 0.50 V -23.2	0.28 1.29 0.22 LI -27.0	4.13 18.90 0.75 PN -3.6	3.59 16.43 0.25 b_3-H_2O -19.8	2.57 11.78 0.50 PNI-28 20.5	3.26 14.94 0.75 PNI -13.6	2.97 13.61 0.75 Pk 7.0	3.55 16.25 0.50 b_4 -4.0	3.47 15.87 0.75 PNIQ -15.7	21.85 100.00 1.50 y_3 0.1	2.63 12.02 -0.12	2.46 11.26 0.50 b_{12}^{+2} -29.8	4.72 21.60 1.50 y_4 7.3

Fragment-ion (m/z)	667.926	668.416^{+2}	681.908^{+2}	811.530	830.997^{+2}	839.499	850.503	882.576	886.527^{+2}	895.034^{+2}	1010.631	1334.822
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.39 10.96 1.50 $y{+}{+}_{11}$ 22.5	5.86 26.80 -0.27	4.71 21.56 0.50 b_{14}^{+2} 25.1	5.17 23.65 1.50 a_9 31.4 y_6 -12.1	3.49 15.97 1.50 y_{15}^{+2} -13.9	3.39 15.50 0.50 b_9 -0.6	2.49 11.39 -0.11	5.26 24.09 1.50 y_7 -1.7	3.07 14.05 0.50 y_{16}-NH_3^{+2} 2.2	2.62 11.98 1.50 y_{16}^{+2} -5.2	2.54 11.63 1.50 y_8 -4.5	3.27 14.97 1.50 a_{14} 31.0 y_{11} 4.5



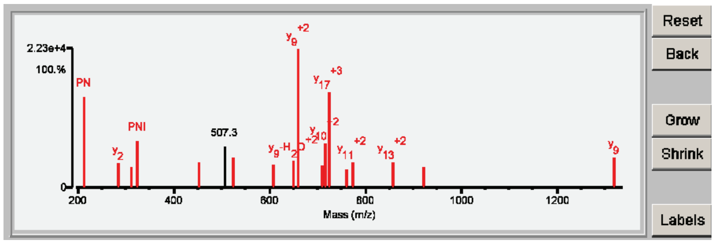
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.16	92.3	8	2/25	K119k K120k	(R)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(R)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14105.5/11.05	HUMAN	Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14107.5/10.90	HUMAN	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	13906.3/10.88	HUMAN	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHHK(T)	2778.5989	228.1125	8.9	13936.3/10.88	HUMAN	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14091.5/10.90	HUMAN	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14095.6/10.90	HUMAN	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(R)VTIAQGGVLPNIQAVLLPkkTESHHK(A)	2778.5989	228.1125	8.9	14121.5/11.05	HUMAN	Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
2	18.48	89.7	7	3/25	K120k K126k	(R)VTIAQGGVLPNIQAVLLPKkTESHHk(A)	2778.5989	228.1125	8.9	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.16	92.3	8	2/25	K119k K120k	(R) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14135.6/11.05	HUMAN	P04908	271551	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(R) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14105.5/11.05	HUMAN	Q93077	271553	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14107.5/10.90	HUMAN	P20671	271557	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(K) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	13906.3/10.88	HUMAN	Q96KK5	271565	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (T)	2778.5989	228.1125	8.9	13936.3/10.88	HUMAN	Q99878	271569	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(K) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14091.5/10.90	HUMAN	P0C0S8	271585	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	20.16	92.3	8	2/25	K119k K120k	(K) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14095.6/10.90	HUMAN	Q6FI13	271625	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	20.16	92.3	8	2/25	K119k K120k	(R) V T I A Q G G V/L/P N I/Q/A V/L/L/P k k T E S H/H K (A)	2778.5989	228.1125	8.9	14121.5/11.05	HUMAN	Q7L7L0	271685	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3

Fragment-ion (m/z)	70.065	72.081	84.081	86.096	87.099	101.071	110.071	212.102	284.181	313.188	325.186	453.251	507.259	524.282	609.336	651.346^{+2}	660.349^{+2}	708.411	716.887^{+2}	723.409^{+3}	761.109^{+3}	773.424^{+2}	858.485^{+2}	922.511^{+2}	1319.683
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.06 0.20 PR -4.6	0.50 2.88 0.50 a_1 -16.3 0.50 V -1.0	0.27 1.56 0.50 KQ -0.9	1.08 6.19 0.22 LI -0.3	3.76 21.61 -0.22	0.07 0.42 KQ	0.10 0.58 1.00 H -2.5	11.37 65.31 0.75 PN -7.9	3.01 17.30 1.50 y_2 31.6	2.60 14.95 0.75 IQA -2.0	5.95 34.17 0.75 PNI -5.9	3.23 18.58 0.75 PNIQ 8.6	5.20 29.86 -0.30	3.73 21.41 0.75 PNIQA -3.3	2.91 16.72 0.25 b_7-H_2O -1.5	3.29 18.91 0.50 y_9-H_2O^{+2} 10.8	17.41 100.00 1.50 y_9^{+2} 7.6	2.81 16.11 0.25 b_8-H_2O 8.2	5.64 32.43 1.50 y_{10}^{+2} 1.4	11.97 68.78 1.50 y_{17}^{+3} 9.3	2.34 13.44 1.50 y_{18}^{+3} 15.2	3.17 18.19 1.50 y_{11}^{+2} -5.1	3.26 18.74 1.50 y_{13}^{+2} 4.1	2.59 14.89 1.50 y_{14}^{+2} 0.9	3.72 21.37 1.50 y_9 1.1



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Result Summary

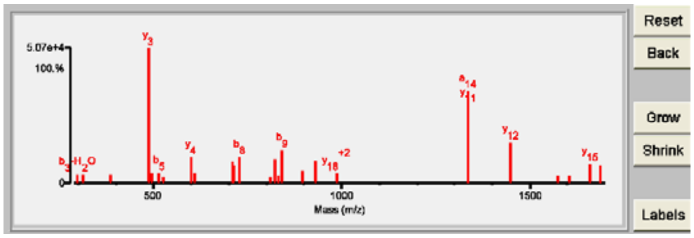
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.75	100.0	11	0/25	K120k	(R)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	23.75	100.0	11	0/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14135.6/11.05	HUMAN	P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
1	23.75	100.0	11	0/25	K120k	(R)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14105.5/11.05	HUMAN	Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	23.75	100.0	11	0/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14105.5/11.05	HUMAN	Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14107.5/10.90	HUMAN	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14107.5/10.90	HUMAN	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	13906.3/10.88	HUMAN	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	13906.3/10.88	HUMAN	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	13936.3/10.88	HUMAN	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	13936.3/10.88	HUMAN	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14091.5/10.90	HUMAN	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14091.5/10.90	HUMAN	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14095.6/10.90	HUMAN	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14095.6/10.90	HUMAN	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	23.75	100.0	11	0/25	K119k	(R)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14121.5/11.05	HUMAN	Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(R)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14121.5/11.05	HUMAN	Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
1	23.75	100.0	11	0/25	K120k	(K)VTIAQGGVLPNIQAVLLPKk(T)	2059.2638	114.0440	0.5	14019.5/10.90	HUMAN	Q9BTM1	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1
1	23.75	100.0	11	0/25	K119k	(K)VTIAQGGVLPNIQAVLLPkK(T)	2059.2638	114.0440	0.5	14019.5/10.90	HUMAN	Q9BTM1	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1
2	3.42	52.2	2	19/25	K869k	(K)kCKTKVFSKIPFLPPIR(Y)	2059.2249	114.0828	18.4	207721.9/5.30	HUMAN	RP38398	REVERSE Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.75	100.0	11	0/25	K120k	(R) V T/I/A|Q|G/G V|L|P N I Q A/V/L|L|P K k (T)	2059.2638	114.0440	0.5	14135.6/11.05	HUMAN	P04908	271551	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Fragment-ion (m/z)	296.197	313.188	385.244	486.303	495.295	513.302	526.298	599.386	609.336	708.403	712.470	726.413
Frac. Inten.(% of TIC)	1.54	1.38	1.51	23.03	1.58	1.69	1.15	4.35	1.59	3.62	3.08	4.38
Rel. Inten.(% of BP)	6.70	6.00	6.57	100.00	6.86	7.34	4.98	18.90	6.90	15.74	13.38	19.01
Score	0.25	0.75	0.50	1.50	0.25	0.50	0.75	1.50	0.25	0.25	1.50	0.50
Ion-type	b_3-H_2O	IQA	b_4	y_3	b_5-H_2O	b_5	NIQAV	y_4	b_7-H_2O	b_8-H_2O	y_5	b_8
Delta ppm	0.4	3.4	-1.2	-0.9	4.3	-1.4	-1.1	-2.9	0.3	-2.0	-1.7	-2.2

Fragment-ion (m/z)	811.523	821.485	831.006^{+2}	839.496	895.039^{+2}	930.555^{+2}	987.093^{+2}	1334.812	1447.893	1574.924	1603.988	1661.009	1688.004
Frac. Inten.(% of TIC)	1.16	3.96	1.31	5.58	2.07	3.82	1.75	15.66	7.01	1.27	1.22	3.15	3.13
Rel. Inten.(% of BP)	5.02	17.21	5.68	24.24	8.98	16.61	7.60	67.99	30.43	5.52	5.31	13.69	13.61
Score	1.50	0.25	1.50	0.50	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50	0.50
Ion-type	a_9 y_6	b_9-H_2O	y_{15}^{+2}	b_9	y_{16}^{+2}	y_{17}^{+2}	y_{18}^{+2}	a_{14} y_{11}	y_{12}	b_{16}	y_{14}	y_{15}	b_{17}
Delta ppm	23.9 -20.9	-3.7	-3.2	-2.9	1.1	-1.7	-5.5	24.9 -2.4	-4.6	-1.4	-0.8	-1.1	-4.2



Result Summary

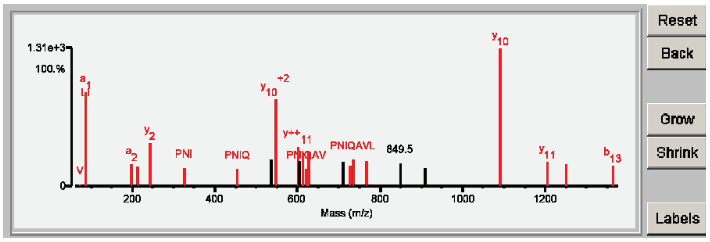
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	14107.5/10.90	HUMAN	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	13906.3/10.88	HUMAN	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	13936.3/10.88	HUMAN	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	14091.5/10.90	HUMAN	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	14095.6/10.90	HUMAN	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	16.35	85.6	5	5/25	K100k	(K)LLGkVTIAQGGVLPNIQAVLLPK(K)	2342.4534	114.0489	2.4	14019.5/10.90	HUMAN	Q9BTM1	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	14107.5/10.90	HUMAN	P20671	271557	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	13906.3/10.88	HUMAN	Q96KK5	271565	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	13936.3/10.88	HUMAN	Q99878	271569	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	14091.5/10.90	HUMAN	P0C0S8	271585	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	14095.6/10.90	HUMAN	Q6FI13	271625	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	13988.4/10.90	HUMAN	Q16777	271635	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	16.35	85.6	5	5/25	K100k	(K) L L G k V T\I A Q G G V|L|P N I/Q A V L L/P K (K)	2342.4534	114.0489	2.4	14019.5/10.90	HUMAN	Q9BTM1	271761	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=2 SV=1

Fragment-ion (m/z)	70.064	72.080	86.095	199.180	212.097	244.165	325.185	453.253	537.816^{+2}	546.847^{+2}	603.391	603.889
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.02 0.20 PR -18.9	0.23 1.39 0.50 V -13.5	11.44 68.06 0.50 a_1 -27.0 0.50 LI -14.2	2.69 15.99 0.50 a_2 -5.5	2.44 14.50 0.75 PN -33.8	5.23 31.10 1.50 y_2 -3.6	2.29 13.64 0.75 PNI -9.6	2.09 12.42 0.75 PNIQ 13.9	3.24 19.25 -0.19	10.52 62.59 1.50 y_{10}^{+2} 8.8	4.75 28.28 1.50 $y{++}_{11}$ 11.4	3.13 18.64 -0.19

Fragment-ion (m/z)	612.370^{+2}	623.347	626.384^{+2}	709.417	726.449	736.420	768.499	849.523	909.509	1092.675	1205.756	1251.734	1364.805
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	4.09 24.34 0.50 a_{12}^{+2} -13.2	2.06 12.25 0.75 PNIQAV -7.8	4.27 25.40 0.50 b_{12}^{+2} 14.1	3.01 17.89 -0.18	2.51 14.91 0.75 b_6 -4.6 LGkVTI -4.6	3.17 18.85 0.75 PNIQAVL -21.9	3.03 18.04 1.50 y_7 1.8	2.80 16.65 -0.17	2.19 13.04 -0.13	16.81 100.00 1.50 y_{10} -2.2	2.89 17.16 1.50 y_{11} -5.1	2.59 15.41 0.50 b_{12} -7.5	2.52 15.00 0.50 b_{13} -16.3



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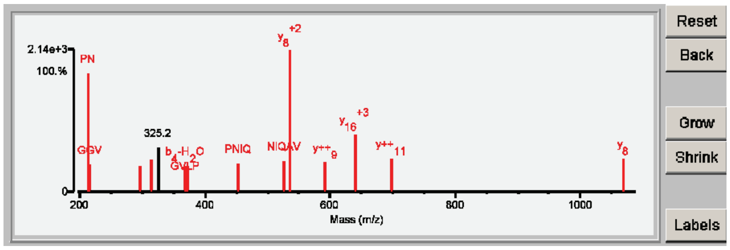
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.20	84.5	5	4/25	K119k	(K)VTIAQGGVLPNIQAVLLPkKTESHK(A)	2641.5399	114.0859	15.6	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	17.20	84.5	5	4/25	K120k	(K)VTIAQGGVLPNIQAVLLPKkTESHK(A)	2641.5399	114.0859	15.6	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
2	14.98	79.5	4	6/25	K125k	(K)VTIAQGGVLPNIQAVLLPKKTESHk(A)	2641.5399	114.0859	15.6	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.20	84.5	5	4/25	K119k	(K)VTIAQGGVL/PNIQA/VL/L/PkKTE/SHK(A)	2641.5399	114.0859	15.6	13988.4/10.90	HUMAN	Q16777	271635	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4

Fragment-ion (m/z)	70.065	72.081	84.045	86.096	87.100	101.070	110.070	120.080	129.101	130.085	167.082	212.102	214.120	296.195	313.187	325.171	367.224	371.213	453.244	526.288	534.797+2	591.331	639.692+3	697.421	1068.591
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.09 0.20 PR -4.6	0.89 5.26 0.50 a_1 -16.3 0.50 V -1.0	0.52 3.04 1.00 E 4.9	1.59 9.38 0.22 LI -6.1	5.17 30.50 -0.17	0.16 0.96 0.50 QK -7.3	0.19 1.13 1.00 H -8.8	5.67 33.44 -0.19	0.10 0.57 0.20 RKQ -9.6	3.41 20.11 0.50 y_1-NH_3 -12.0	3.83 22.60 -0.13	14.18 83.58 0.75 PN -10.2	3.30 19.45 0.75 GGV 2.3	3.07 18.12 0.25 b_3-H_2O -11.0	3.89 22.94 0.75 IQA -4.2	5.31 31.28 -0.18	3.08 18.16 0.75 b_4-H_2O -29.6 GVLP -29.6	3.07 18.09 1.50 y_3 24.9	3.45 20.35 0.75 PNIQ -5.8	3.70 21.83 0.75 NIQAV -22.2	16.96 100.00 1.50 y_8^{+2} 7.2	3.51 20.71 1.50 y^{++}_9 -7.1	6.94 40.90 1.50 y_{16}^{+3} -16.1	3.98 23.46 1.50 y^{++}_{11} 12.7	4.00 23.58 1.50 y_8 10.5



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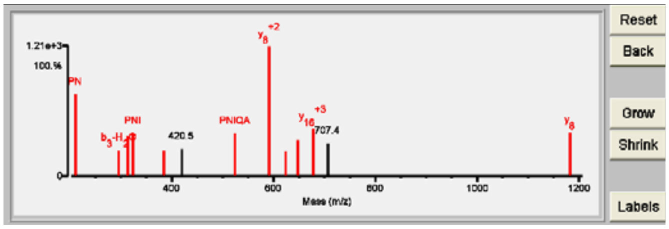
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.66	77.6	4	5/24	K120k K125k	(K)VTIAQGGVLPNIQAVLLPKkTESHk(A)	2641.5399	228.1024	5.8	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	13.66	77.6	4	5/24	K119k K125k	(K)VTIAQGGVLPNIQAVLLPkKTESHk(A)	2641.5399	228.1024	5.8	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
1	13.66	77.6	4	5/24	K119k K120k	(K)VTIAQGGVLPNIQAVLLPkkTESHK(A)	2641.5399	228.1024	5.8	13988.4/10.90	HUMAN	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4
2	7.91	69.7	1	9/24	M322m	(R)LKmSTFPTLFRYSVALAQARQRLR(E)	2853.6032	16.0392	15.4	104576.9/8.48	HUMAN	RQ86UX2	REVERSE Inter-alpha-trypsin inhibitor heavy chain H5 OS=Homo sapiens GN=ITIH5 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.66	77.6	4	5/24	K120k K125k	(K) V T I A\Q G G V L/P N I Q A V L/L/P K k T E S H k (A)	2641.5399	228.1024	5.8	13988.4/10.90	HUMAN	Q16777	271635	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4

Fragment-ion (m/z)	70.066	72.080	84.044	84.079	86.096	101.071	110.071	120.080	136.074	171.112	187.110	212.103	296.200	313.189	325.185	385.242	420.543^{+3}	524.287	591.822^{+2}	623.349	648.357^{+2}	677.719^{+3}	707.385	1182.614
Frac. Inten.(% of TIC)	0.01	0.84	0.27	0.25	1.82	0.14	0.16	3.92	10.15	3.31	7.18	9.76	3.06	4.80	5.14	3.15	3.31	5.09	15.50	3.01	4.36	5.62	3.89	5.27
Rel. Inten.(% of BP)	0.10	5.43	1.77	1.61	11.74	0.88	1.01	25.27	65.51	21.34	46.35	62.97	19.76	31.00	33.17	20.33	21.34	32.83	100.00	19.43	28.16	36.28	25.09	33.99
Score	0.20	0.50	1.00	0.50	0.22		1.00	-0.14	-0.36	0.75	-0.26	0.75	0.25	0.75	0.75	0.50	-0.12	0.75	1.50	0.75	1.50	1.50	-0.14	1.50
Ion-type	PR	a_1	E	KQ	LI	KQ	H			AV		PN	b_3-H$_2$O	IQA	PNI	b_4		PNIQA	y_8^{+2}	PNIQAV	y_9^{+2}	y_{16}^{+3}		y_8
Delta ppm	5.3	-26.0 0.50 V -10.8	0.1	-15.2	-3.8		-3.4			-12.9		-3.1	5.2	2.5	-8.7	-10.5		5.3	11.5	-5.5	0.7	4.5		-6.9



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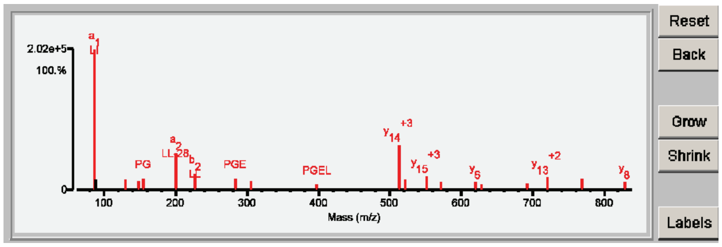
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	25.83	97.5	12	1/25	K110k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	14167.6/10.31	HUMAN	Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13950.3/10.31	HUMAN	P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13819.1/10.31	HUMAN	P62807	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13936.2/10.31	HUMAN	P58876	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13892.2/10.31	HUMAN	Q93079	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13904.2/10.31	HUMAN	P06899	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13890.2/10.31	HUMAN	O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13952.3/10.31	HUMAN	Q99880	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13989.3/10.31	HUMAN	Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13922.2/10.31	HUMAN	Q99877	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13906.2/10.31	HUMAN	P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13920.2/10.31	HUMAN	Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13920.2/10.31	HUMAN	Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13908.2/10.31	HUMAN	Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R)LLLPGELAkHAVSEGTK(A)	1763.0062	114.0532	5.5	13944.3/10.37	HUMAN	P57053	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2
2	15.89	82.1	6	8/25	K118k	(R)LLLPGELAKHAVSEGTk(A)	1763.0062	114.0532	5.5	14167.6/10.31	HUMAN	Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	25.83	97.5	12	1/25	K110k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	14167.6/10.31	HUMAN	Q96A08	272051	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13950.3/10.31	HUMAN	P33778	272057	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13819.1/10.31	HUMAN	P62807	272061	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13936.2/10.31	HUMAN	P58876	272065	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13892.2/10.31	HUMAN	Q93079	272069	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13904.2/10.31	HUMAN	P06899	272073	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13890.2/10.31	HUMAN	O60814	272077	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13952.3/10.31	HUMAN	Q99880	272083	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13989.3/10.31	HUMAN	Q99879	272085	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13922.2/10.31	HUMAN	Q99877	272091	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13906.2/10.31	HUMAN	P23527	272093	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13920.2/10.31	HUMAN	Q16778	272153	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13920.2/10.31	HUMAN	Q5QNW6	272159	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13908.2/10.31	HUMAN	Q8N257	272199	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3
1	25.83	97.5	12	1/25	K109k	(R) L L|L/P/G/E/L/A k/H/A/V/S E/G T/K (A)	1763.0062	114.0532	5.5	13944.3/10.37	HUMAN	P57053	272295	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2

Fragment-ion (m/z)	70.064	84.080	86.096	87.098	110.070	129.101	130.085	147.111	155.081	199.179	227.174	284.124	305.180	397.207	513.272^{+3}	521.257	550.966^{+3}	571.304^{+2}	620.324	627.845^{+2}	691.361	692.361^{+2}	720.876^{+2}	769.404^{+2}	828.421
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.04 0.20 PR -10.4	0.28 0.79 0.50 KQ -12.8	35.23 100.00 0.50 a_1 -23.5 0.50 LI -10.8	2.49 7.06 -0.07	0.07 0.19 1.00 H -11.6	0.10 0.29 0.20 RKQ -9.6	2.61 7.41 0.50 y_1-NH_3 -9.6	2.32 6.58 1.50 y_1 -10.9	2.99 8.50 0.75 PG -13.6	9.30 26.39 0.50 a_2 -11.5 LL-28 -11.5	3.98 11.30 0.75 b_2 -10.1 LL -10.1	2.90 8.23 0.75 PGE -5.3	2.27 6.45 1.50 y_3 -4.7	1.41 4.01 0.75 PGEL -5.9	11.41 32.39 1.50 y_{14}^{+3} 3.0	2.69 7.63 1.50 y_5 0.4	3.38 9.60 1.50 y_{15}^{+3} 1.1	1.92 5.45 1.50 y_{10}^{+2} 3.4	2.09 5.93 1.50 y_6 -0.8	1.47 4.18 1.50 y_{11}^{+2} 2.7	1.45 4.11 1.50 y_7 -1.9	1.55 4.41 1.50 y_{12}^{+2} -5.5	3.28 9.31 1.50 y_{13}^{+2} 1.0	2.79 7.92 1.50 y_{14}^{+2} 2.9	2.00 5.66 1.50 y_8 0.1



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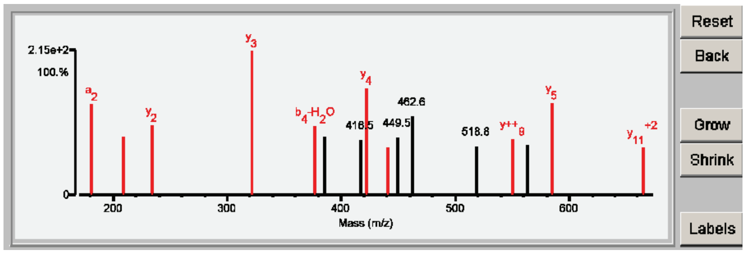
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.83	59.7	9	9/25	K122k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	14167.6/10.31	HUMAN	Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13950.3/10.31	HUMAN	P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13936.2/10.31	HUMAN	P58876	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13892.2/10.31	HUMAN	Q93079	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13952.3/10.31	HUMAN	Q99880	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13989.3/10.31	HUMAN	Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13922.2/10.31	HUMAN	Q99877	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13906.2/10.31	HUMAN	P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13920.2/10.31	HUMAN	Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13920.2/10.31	HUMAN	Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K)HAVSEGTKAVTkYTSSK(-)	1793.9392	114.0510	4.2	13908.2/10.31	HUMAN	Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3
2	9.11	52.6	7	11/25	K118k	(K)HAVSEGTkAVTKYTSSK(-)	1793.9392	114.0510	4.2	14167.6/10.31	HUMAN	Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.83	59.7	9	9/25	K122k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	14167.6/10.31	HUMAN	Q96A08	272051	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13950.3/10.31	HUMAN	P33778	272057	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13936.2/10.31	HUMAN	P58876	272065	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13892.2/10.31	HUMAN	Q93079	272069	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13952.3/10.31	HUMAN	Q99880	272083	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13989.3/10.31	HUMAN	Q99879	272085	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13922.2/10.31	HUMAN	Q99877	272091	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13906.2/10.31	HUMAN	P23527	272093	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13920.2/10.31	HUMAN	Q16778	272153	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13920.2/10.31	HUMAN	Q5QNW6	272159	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3
1	11.83	59.7	9	9/25	K121k	(K) H A\V S E G/T K/A\V T k/Y/T/S/S/K (-)	1793.9392	114.0510	4.2	13908.2/10.31	HUMAN	Q8N257	272199	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3

Fragment-ion (m/z)	60.044	72.082	74.061	84.081	85.085	102.058	110.068	129.100	136.070	181.112	209.100	234.139	321.177	377.200	385.710^{+2}	416.544	422.224	441.226	449.493^{+2}	462.582	518.787	549.794	562.805^{+2}	585.293	664.346^{+2}
Frac. Inten.(% of TIC)	3.38	0.14	4.57	0.66	5.63	0.12	0.51	0.48	7.74	6.18	3.98	4.75	9.79	4.67	3.95	3.71	7.26	3.26	3.88	5.33	3.28	3.80	3.43	6.29	3.20
Rel. Inten.(% of BP)	34.50	1.43	46.67	6.75	57.48	1.19	5.20	4.95	79.07	63.08	40.61	48.53	100.00	47.65	40.37	37.90	74.17	33.29	39.58	54.45	33.47	38.79	35.01	64.20	32.68
Score	-0.34	0.50	1.50	0.50	-0.57	1.00	1.00	0.20	-0.79	0.50	0.50	1.50	1.50	0.25	-0.40	-0.38	1.50	0.50	-0.40	-0.54	-0.33	1.50	-0.35	1.50	1.50
Ion-type		V	y++$_1$	KQ		E	a_1	RKQ		a_2	b_2	y_2	y_3	b_4-H_2O			y_4	b++$_9$				y++$_9$		y_5	y_{11}^{+2}
Delta ppm		22.5	17.0	-3.3		31.8	-38.8 1.00 H -28.8	-15.0		16.1	-23.4	-24.1	1.1	14.1			-0.8	-5.1				1.6		9.5	-28.2



Result Summary

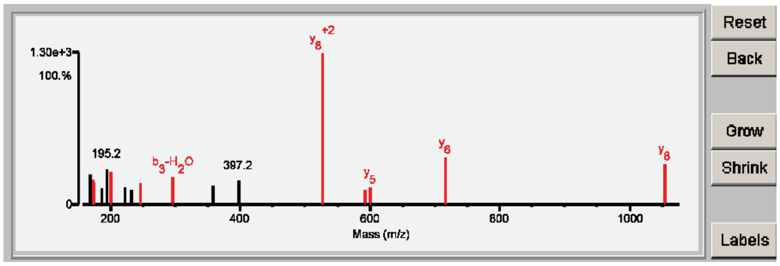
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.49	66.2	7	10/24	K123k	(R)VTIMPkDIQLAR(R)	1384.7981	114.0544	7.6	15508.3/11.13	HUMAN	Q16695	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	11.49	66.2	7	10/24	K123k	(R)VTIMPkDIQLAR(R)	1384.7981	114.0544	7.6	15404.2/11.13	HUMAN	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	11.49	66.2	7	10/24	K123k	(R)VTIMPkDIQLAR(R)	1384.7981	114.0544	7.6	15388.1/11.27	HUMAN	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	11.49	66.2	7	10/24	K123k	(R)VTIMPkDIQLAR(R)	1384.7981	114.0544	7.6	15328.0/11.27	HUMAN	P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2
1	11.49	66.2	7	10/24	K122k	(R)VTIMPkDIQLAR(R)	1384.7981	114.0544	7.6	15213.8/11.11	HUMAN	Q6NXT2	Histone H3-like OS=Homo sapiens PE=2 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.49	66.2	7	10/24	K123k	(R) V T\I/M/P k/D/I Q L/A/R (R)	1384.7981	114.0544	7.6	15508.3/11.13	HUMAN	Q16695	272455	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	11.49	66.2	7	10/24	K123k	(R) V T\I/M/P k/D/I Q L/A/R (R)	1384.7981	114.0544	7.6	15404.2/11.13	HUMAN	P68431	272467	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	11.49	66.2	7	10/24	K123k	(R) V T\I/M/P k/D/I Q L/A/R (R)	1384.7981	114.0544	7.6	15388.1/11.27	HUMAN	Q71DI3	272515	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	11.49	66.2	7	10/24	K123k	(R) V T\I/M/P k/D/I Q L/A/R (R)	1384.7981	114.0544	7.6	15328.0/11.27	HUMAN	P84243	272631	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2
1	11.49	66.2	7	10/24	K122k	(R) V T\I/M/P k/D/I Q L/A/R (R)	1384.7981	114.0544	7.6	15213.8/11.11	HUMAN	Q6NXT2	272715	Histone H3-like OS=Homo sapiens PE=2 SV=3

Fragment-ion (m/z)	70.064	72.080	84.080	86.096	104.051	128.106	138.088	169.133	173.127	175.117	187.137	195.188
Frac. Inten.(% of TIC)	0.01	0.42	0.34	0.22	2.38	7.83	4.57	4.56	3.73	3.40	2.42	5.30
Rel. Inten.(% of BP)	0.03	1.85	1.47	0.95	10.40	34.24	20.02	19.95	16.31	14.87	10.59	23.18
Score	0.20	0.50	0.50	0.22	-0.10	-0.34	-0.20	-0.20	0.50	1.50	-0.11	-0.23
Ion-type	PR	a_1	KQ	LI					a_2	y_1		
Delta ppm	-11.8	-26.0 0.50 V -10.8	-14.0	-9.6					-14.2	-13.4		

Fragment-ion (m/z)	201.120	223.176	232.138	246.155	296.197	357.192	397.217	527.805^{+2}	593.321^{+2}	600.399	715.418	1054.609
Frac. Inten.(% of TIC)	5.03	2.66	2.24	3.13	4.29	2.90	3.52	22.85	2.18	2.66	7.20	6.17
Rel. Inten.(% of BP)	22.02	11.62	9.78	13.71	18.78	12.70	15.41	100.00	9.54	11.63	31.50	27.00
Score	0.50	-0.12	-0.10	1.50	0.25	-0.13	-0.15	1.50	1.50	1.50	1.50	1.50
Ion-type	b_2			y_2	b_3-H_2O			y_8^{+2}	y_9^{+2}	y_5	y_6	y_8
Delta ppm	-24.2			-4.3	-4.6			1.9	-5.8	27.4	11.6	8.2



Result Summary

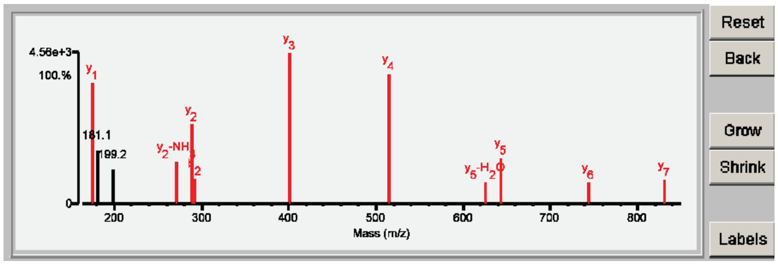
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.12	78.0	8	6/25	K57k	(R)YQkSTELLIR(K)	1250.7103	114.0514	6.2	15508.3/11.13	HUMAN	Q16695	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	15.12	78.0	8	6/25	K57k	(R)YQkSTELLIR(K)	1250.7103	114.0514	6.2	15404.2/11.13	HUMAN	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	15.12	78.0	8	6/25	K57k	(R)YQkSTELLIR(K)	1250.7103	114.0514	6.2	15388.1/11.27	HUMAN	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	15.12	78.0	8	6/25	K57k	(R)YQkSTELLIR(K)	1250.7103	114.0514	6.2	15328.0/11.27	HUMAN	P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2
1	15.12	78.0	8	6/25	K56k	(R)YQkSTELLIR(K)	1250.7103	114.0514	6.2	15213.8/11.11	HUMAN	Q6NXT2	Histone H3-like OS=Homo sapiens PE=2 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.12	78.0	8	6/25	K57k	(R) Y Q\k/S/T/E/L/L/I/R (K)	1250.7103	114.0514	6.2	15508.3/11.13	HUMAN	Q16695	272455	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	15.12	78.0	8	6/25	K57k	(R) Y Q\k/S/T/E/L/L/I/R (K)	1250.7103	114.0514	6.2	15404.2/11.13	HUMAN	P68431	272467	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	15.12	78.0	8	6/25	K57k	(R) Y Q\k/S/T/E/L/L/I/R (K)	1250.7103	114.0514	6.2	15388.1/11.27	HUMAN	Q71DI3	272515	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	15.12	78.0	8	6/25	K57k	(R) Y Q\k/S/T/E/L/L/I/R (K)	1250.7103	114.0514	6.2	15328.0/11.27	HUMAN	P84243	272631	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2
1	15.12	78.0	8	6/25	K56k	(R) Y Q\k/S/T/E/L/L/I/R (K)	1250.7103	114.0514	6.2	15213.8/11.11	HUMAN	Q6NXT2	272715	Histone H3-like OS=Homo sapiens PE=2 SV=3

Fragment-ion (m/z)	70.065	84.044	84.080	86.096	87.055	91.054	102.054	129.102	136.075	137.080	141.101	156.109
Frac. Inten.(% of TIC)	0.00	0.14	0.63	0.95	0.13	3.45	0.10	0.10	0.93	2.96	3.59	2.44
Rel. Inten.(% of BP)	0.01	0.82	3.82	5.76	0.80	20.90	0.64	0.62	5.64	17.93	21.75	14.75
Score	0.20	1.00	0.50	0.22	0.33	-0.21		0.20	1.00 1.00	-0.18	-0.22	-0.15
Ion-type	PR	E	KQ	LI	NR		E	RKQ	a_1 Y			
Delta ppm	-3.2	-9.4	-12.8	-8.4	-5.6			-5.0	-16.8 -8.7			

Fragment-ion (m/z)	158.091	175.119	181.096	199.180	271.176	288.202	292.132	401.287	514.372	625.409	643.414	744.466	831.499
Frac. Inten.(% of TIC)	2.76	13.19	5.81	3.79	4.58	8.65	2.78	16.53	14.21	2.29	4.99	2.32	2.67
Rel. Inten.(% of BP)	16.69	79.84	35.14	22.91	27.69	52.35	16.82	100.00	86.00	13.86	30.18	14.02	16.18
Score	0.50	1.50	-0.35	-0.23	0.50	1.50	0.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	y_1-NH_3	y_1			y_2-NH_3	y_2	b_2	y_3	y_4	y_5-H_2O	y_5	y_6	y_7
Delta ppm	-10.1	-1.4			-3.6	-2.5	4.9	-0.2	1.7	10.0	1.2	6.6	6.6



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Result Summary

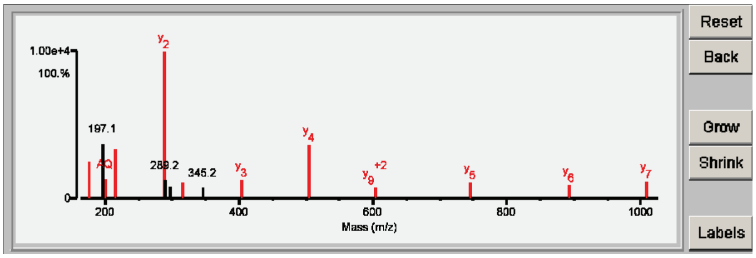
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.85	75.2	8	6/25	K80k	(R)EIAQDFkTDLR(F)	1335.6903	114.0521	6.4	15508.3/11.13	HUMAN	Q16695	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	16.85	75.2	8	6/25	K80k	(R)EIAQDFkTDLR(F)	1335.6903	114.0521	6.4	15404.2/11.13	HUMAN	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	16.85	75.2	8	6/25	K80k	(R)EIAQDFkTDLR(F)	1335.6903	114.0521	6.4	15388.1/11.27	HUMAN	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	16.85	75.2	8	6/25	K80k	(R)EIAQDFkTDLR(F)	1335.6903	114.0521	6.4	15328.0/11.27	HUMAN	P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2
2	8.49	51.8	4	12/25	None	(R)EEEIGKLFTDLR(S)	1449.7584	-0.0159	-11.0	133504.9/5.87	HUMAN	RQ66GS9	REVERSE Centrosomal protein of 135 kDa OS=Homo sapiens GN=CEP135 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.85	75.2	8	6/25	K80k	(R) E I/A Q/D/F/k/T/D/L/R (F)	1335.6903	114.0521	6.4	15508.3/11.13	HUMAN	Q16695	272455	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3
1	16.85	75.2	8	6/25	K80k	(R) E I/A Q/D/F/k/T/D/L/R (F)	1335.6903	114.0521	6.4	15404.2/11.13	HUMAN	P68431	272467	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2
1	16.85	75.2	8	6/25	K80k	(R) E I/A Q/D/F/k/T/D/L/R (F)	1335.6903	114.0521	6.4	15388.1/11.27	HUMAN	Q71DI3	272515	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3
1	16.85	75.2	8	6/25	K80k	(R) E I/A Q/D/F/k/T/D/L/R (F)	1335.6903	114.0521	6.4	15328.0/11.27	HUMAN	P84243	272631	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2

Fragment-ion (m/z)	84.043	84.080	86.096	87.055	89.070	102.054	120.079	129.065	129.099	141.101	175.118	197.129
Frac. Inten.(% of TIC)	0.20	0.57	0.42	0.06	4.96	0.06	0.15	0.19	0.08	2.16	6.77	10.06
Rel. Inten.(% of BP)	0.74	2.10	1.54	0.23	18.19	0.24	0.54	0.69	0.30	7.92	24.83	36.88
Score	1.00	0.50	0.22	0.33	-0.18	1.00	1.00	0.20		-0.08	1.50	-0.37
Ion-type	E	KQ	LI	NR		a_1	F	QKR	QKR		y_1	
Delta ppm	-13.0	-8.0	-7.3	-7.9		-21.1	-11.5	-9.7			-4.3	
						E						

Fragment-ion (m/z)	200.102	215.138	288.203	289.206	298.100	315.128	345.195^{+2}	403.227	504.279	604.314^{+2}	746.418	893.474	1008.516
Frac. Inten.(% of TIC)	3.71	9.21	27.28	3.37	2.16	2.81	2.07	3.41	9.81	2.05	2.83	2.36	3.24
Rel. Inten.(% of BP)	13.60	33.75	100.00	12.36	7.90	10.32	7.61	12.51	35.95	7.52	10.37	8.66	11.88
Score	0.75	0.50	1.50	-0.12	-0.08	0.75	-0.08	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	AQ	a_2	y_2			AQD		y_3	y_4	y_9^{+2}	y_5	y_6	y_7
Delta ppm	-8.8	-10.3	-0.7			-9.2		-6.3	2.7	12.0	3.3	-11.2	4.6



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Result Summary

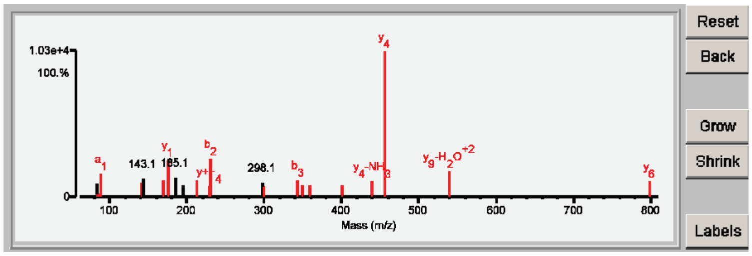
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.91	85.5	7	5/25	K32k	(R)DNIQGITkPAIR(R)	1325.7536	114.0625	13.6	11367.4/11.36	HUMAN	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
2	6.84	54.1	2	14/25	None	(R)EHYVVEVKLPAR(M)	1439.8005	0.0155	10.8	104738.6/5.87	HUMAN	O15327	Type II inositol-3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.91	85.5	7	5/25	K32k	(R) D N\I\Q G I/T/k/P/A I/R (R)	1325.7536	114.0625	13.6	11367.4/11.36	HUMAN	P62805	136470	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Fragment-ion (m/z)	70.065	84.043	84.081	86.096	88.038	141.100	143.116	169.098	175.120	185.057	195.041	212.066	213.051
Frac. Inten.(% of TIC)	0.01	2.43	0.71	0.62	4.48	2.71	3.40	3.18	7.10	3.76	2.28	2.28	3.39
Rel. Inten.(% of BP)	0.02	8.58	2.49	2.20	15.81	9.57	11.98	11.22	25.04	13.25	8.06	8.05	11.94
Score	0.20	-0.09	0.50	0.22	0.50	0.50	-0.12	0.75	1.50	-0.13	-0.08	0.25	0.25
Ion-type	PR		KQ	LI	a_1	PA-28		PA	y_1			b_2-H_2O	b_2-NH_3
Delta ppm	-0.4		0.3	-6.1	-23.9	-23.6		-2.7	8.3			-8.4	-2.8

Fragment-ion (m/z)	228.649	230.077	298.142	299.172	343.162	349.725^{+2}	359.240	400.250^{+2}	439.267	456.296	540.317^{+2}	799.489
Frac. Inten.(% of TIC)	2.18	7.39	2.67	2.15	3.19	2.19	2.32	2.23	3.07	28.35	4.87	3.05
Rel. Inten.(% of BP)	7.68	26.06	9.41	7.57	11.26	7.71	8.17	7.86	10.82	100.00	17.16	10.76
Score	1.50	0.50	-0.09	0.75	0.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type	$y{+}{+}_4$	b_2		QGI	b_3	y_5^{+2}	y_3	y_6^{+2}	y_4-NH_3	y_4	y_9-H_2O^{+2}	y_6
Delta ppm	-2.6	-5.4		-2.3	-1.2	16.5	0.8	18.8	0.6	6.4	-5.3	13.3



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Result Summary

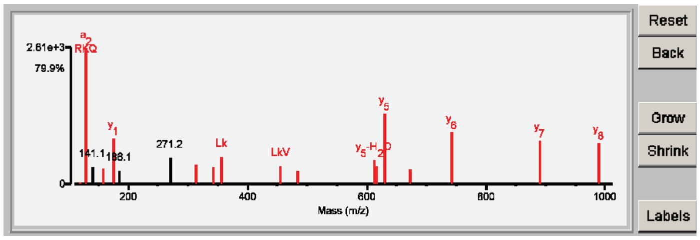
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.47	71.9	7	4/25	K60k	(R)GVLkVFLENVIR(D)	1386.8467	114.0550	8.0	11367.4/11.36	HUMAN	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
2	6.67	50.1	3	9/25	None	(K)RINVELSTKGQKK(G)	1500.8857	0.0161	10.7	69492.0/9.68	HUMAN	Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2
3	6.66	59.0	3	11/25	K571k	(R)KNLLKEMKkVR(S)	1386.8614	114.0404	-1.7	73675.4/9.73	HUMAN	A6PVS8	Leucine-rich repeat and IQ domain-containing protein 3 OS=Homo sapiens GN=LRRIQ3 PE=2 SV=1
4	6.11	58.2	2	11/25	K54k	(R)VkKMEKLLNKR(Y)	1386.8614	114.0404	-1.7	73675.4/9.73	HUMAN	RA6PVS8	REVERSE Leucine-rich repeat and IQ domain-containing protein 3 OS=Homo sapiens GN=LRRIQ3 PE=2 SV=1
5	3.67	51.4	3	11/25	K186k K188k	(K)QASKSKLkVkR(Q)	1272.8110	228.0907	3.2	25631.9/10.95	HUMAN	P60008	Spermatid-specific linker histone H1-like protein OS=Homo sapiens GN=HILS1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.47	71.9	7	4/25	K60k	(R) G V|L/k/V/F/L/E N V I/R (D)	1386.8467	114.0550	8.0	11367.4/11.36	HUMAN	P62805	272939	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Fragment-ion (m/z)	72.080	84.080	86.096	87.055	102.052	120.079	129.101	141.100	157.095	158.092	175.118	186.125
Frac. Inten.(% of TIC)	0.45	21.07	0.60	0.06	0.05	0.26	16.84	2.16	1.94	1.73	5.73	1.65
Rel. Inten.(% of BP)	2.15	100.00	2.84	0.28	0.26	1.24	79.92	10.23	9.20	8.21	27.18	7.83
Score	0.50	-1.00	0.22	0.33	1.00	1.00	0.50 0.50	-0.10	0.50	0.50	1.50	-0.08
Ion-type	V		LI	NR	E	F	a_2 RKQ		b_2	y_1-NH_3	y_1	
Delta ppm	-16.3		-8.4	-9.1	-29.9	-17.3	-15.0 -6.5		-18.2	-0.0	-5.4	

Fragment-ion (m/z)	271.155	314.220	342.214	356.229	455.299	484.284	612.354	616.353	630.357	672.896	743.442	890.510	989.572
Frac. Inten.(% of TIC)	3.27	2.34	2.04	3.44	2.20	1.71	2.92	2.19	8.68	1.75	6.45	5.38	5.10
Rel. Inten.(% of BP)	15.50	11.10	9.67	16.32	10.46	8.11	13.86	10.38	41.19	8.33	30.62	25.55	24.21
Score	-0.16	0.50	0.75	0.75	0.75	0.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type		kV-28	kV	Lk	LkV	y_4-NH_3	y_5-H_2O	y^{++}_9	y_5	y^{++}_{10}	y_6	y_7	y_8
Delta ppm		1.1	-1.1	-2.9	1.2	-8.9	12.1	-14.3	0.2	-11.5	0.7	0.3	-5.7



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Result Summary

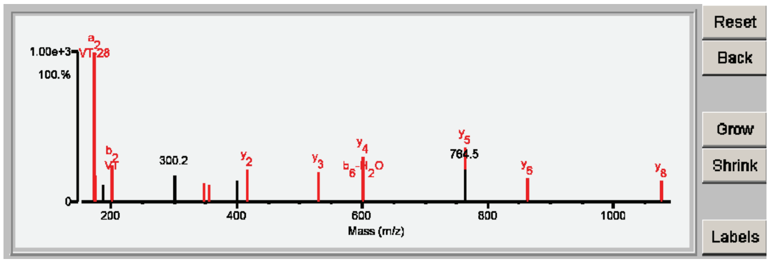
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.22	66.7	8	8/25	K92k	(K)TVTAMDVVYALkR(Q)	1466.8036	114.0569	8.8	11367.4/11.36	HUMAN	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.22	66.7	8	8/25	K92k	(K) T V\T A M/D V/V/Y/A/L/k/R (Q)	1466.8036	114.0569	8.8	11367.4/11.36	HUMAN	P62805	136470	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Fragment-ion (m/z)	70.065	72.079	74.060	84.081	86.096	101.068	104.052	120.080	136.075	173.128	175.115	187.139
Frac. Inten.(% of TIC)	0.00	0.50	2.67	6.12	0.39	6.18	2.96	5.36	0.32	19.58	3.47	2.32
Rel. Inten.(% of BP)	0.01	2.57	13.65	31.25	1.98	31.57	15.12	27.35	1.63	100.00	17.72	11.86
Score	0.20	0.50	0.50	-0.31	0.22	-0.32	-0.15	-0.27	1.00	0.50	1.50	-0.12
Ion-type	PR	V	a_1		LI				Y	a_2 VT-28	y_1	
Delta ppm	2.5	-17.7	-10.0		-7.3				-4.3	-9.0 -9.0	-24.9	

Fragment-ion (m/z)	201.126	300.199	348.186	356.234	400.212	417.241	530.338	601.278	601.385	764.443	764.547	863.511	1077.578
Frac. Inten.(% of TIC)	4.85	3.42	2.51	2.34	2.70	4.31	3.99	2.71	5.90	7.20	4.27	3.08	2.83
Rel. Inten.(% of BP)	24.78	17.48	12.81	11.93	13.80	22.02	20.37	13.85	30.14	36.77	21.81	15.70	14.43
Score	0.75	-0.17	0.75	0.75	-0.14	1.50	1.50	0.25	1.50	1.50	-0.22	1.50	1.50
Ion-type	b_2 VT		YAL	Lk		y_2	y_3	b_6-H_2O	y_4	y_5		y_6	y_8
Delta ppm	6.6 6.6		-20.6	10.6		-38.4	-6.0	19.6	12.1	1.9		1.4	-25.2



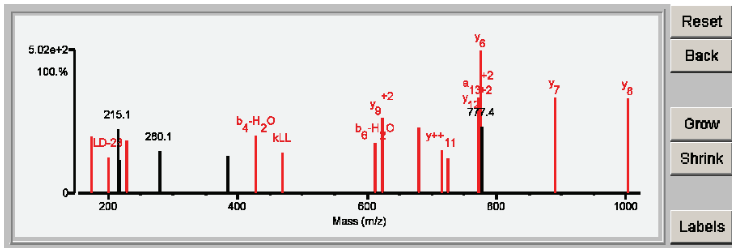
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.30	72.9	8	6/25	K199k	(R)ESVELALkLLDEDEIR(G)	1871.9961	114.0567	6.9	85853.2/4.29	HUMAN	O43719	HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.30	72.9	8	6/25	K199k	(R) E S V E/L/A/L/k/L/L/D E D E I/R (G)	1871.9961	114.0567	6.9	85853.2/4.29	HUMAN	O43719	151350	HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1

Fragment-ion (m/z)	72.081	84.083	86.097	102.057	129.100	175.117	201.123	215.147	217.074	229.117	280.128	384.216	427.181	427.271	469.313	611.308	622.825^{+2}	679.366^{+2}	714.904	724.375	771.434^{+2}	776.348	777.352^{+2}	889.438	1002.505
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.22 2.08 0.50 V 4.5	9.38 90.57 -0.91	0.54 5.21 0.22 LI 5.5	0.15 1.44 1.00 a_1 8.3 1.00 E 19.1	0.09 0.91 0.20 RKQ -18.9	4.14 40.01 1.50 y_1 -14.0	2.59 24.99 0.50 LD-28 -5.3	4.70 45.33 -0.45	2.46 23.79 -0.24	3.89 37.53 0.75 LD -11.3	3.08 29.72 -0.30	2.67 25.75 -0.26	4.22 40.77 0.25 b_4-H_2O -5.5	3.38 32.63 0.75 ALk 7.9	3.00 28.94 0.75 kLL -3.2	3.69 35.58 0.25 b_6-H_2O 6.4	5.44 52.55 1.50 y_9^{+2} -4.2	4.74 45.75 1.50 y_{10}^{+2} -5.3	3.11 29.98 1.50 $y{++}_{11}$ 22.4	2.54 24.53 0.25 b_7-H_2O -19.6	6.94 66.99 1.50 a_{13}^{+2} 34.6 y_{12}^{+2} 4.4	10.36 100.00 1.50 y_6 7.4	4.84 46.75 -0.47	6.94 67.03 1.50 y_7 13.4	6.89 66.47 1.50 y_8 -4.9



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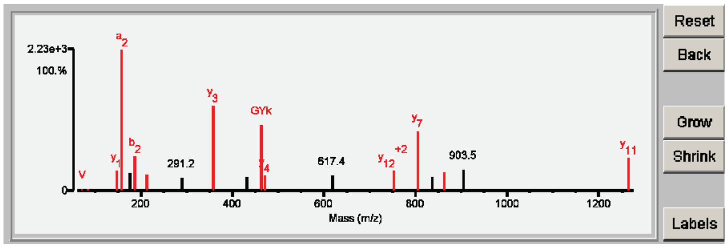
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.95	84.6	7	6/24	K175k	(R)SVGYkPDFVGFEIPDK(F)	1797.9058	114.0563	7.0	24579.5/6.21	HUMAN	P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2
2	5.33	60.0	1	13/24	M221m K232k K234k	(R)LmQETTLGSVDFkAk(Q)	1667.8673	244.0948	7.3	50199.9/5.29	HUMAN	RQ86TP1	REVERSE Protein prune homolog OS=Homo sapiens GN=PRUNE PE=1 SV=2
3	3.88	51.9	1	15/24	K140k K151k	(K)kSGCGWASVKYkGQK(L)	1683.8635	228.0985	6.6	50662.3/5.49	HUMAN	Q8N594	MPN domain-containing protein OS=Homo sapiens GN=MPND PE=1 SV=1
4	3.43	52.8	2	14/24	K994k	(K)QELEADVSHkETKRK(L)	1797.9454	114.0167	-13.7	207530.0/9.26	HUMAN	Q96QE3	ATPase family AAA domain-containing protein 5 OS=Homo sapiens GN=ATAD5 PE=1 SV=3
4	3.43	52.8	2	14/24	K997k	(K)QELEADVSHKETkRK(L)	1797.9454	114.0167	-13.7	207530.0/9.26	HUMAN	Q96QE3	ATPase family AAA domain-containing protein 5 OS=Homo sapiens GN=ATAD5 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.95	84.6	7	6/24	K175k	(R) S V|G Y/k/P D F V/G F E/I/P D/K (F)	1797.9058	114.0563	7.0	24579.5/6.21	HUMAN	P00492	295277	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2

Fragment-ion (m/z)	70.065	72.079	84.080	86.095	120.079	129.100	136.077	147.113	159.112	177.101	187.109	213.089	291.198	359.192	432.190	463.232	472.279	617.371	753.392^{+2}	805.410	836.424	863.432^{+2}	903.456	1263.624
Frac. Inten.(% of TIC)	0.00	0.31	0.29	0.17	0.16	0.08	0.06	3.35	23.05	2.89	5.70	2.64	2.13	13.96	2.30	10.77	2.49	2.44	3.25	9.75	2.24	3.09	3.43	5.42
Rel. Inten.(% of BP)	0.01	1.36	1.24	0.75	0.71	0.36	0.27	14.52	100.00	12.52	24.73	11.47	9.25	60.56	9.99	46.72	10.81	10.60	14.08	42.29	9.73	13.42	14.86	23.51
Score	0.20	0.50	0.50	0.22	1.00	0.20	1.00	1.50	0.50	-0.13	0.50	0.75	-0.09	1.50	-0.10	0.75	1.50	-0.11	1.50	1.50	-0.10	1.50	-0.15	1.50
Ion-type	PR	V	KQ	LI	F	RKQ	Y	y_1	a_2		b_2	PD		y_3		GYk	y_4		y_{12}^{+2}	y_7		y_{14}^{+2}		y_{11}
Delta ppm	-3.2	-21.9	-11.6	-13.1	-17.3	-15.8	12.6	4.1	-12.0		-1.2	5.3		-1.7		1.2	6.2		8.5	1.4		4.7		-1.4



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Result Summary

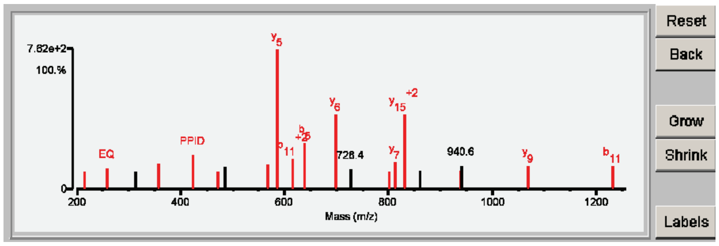
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.58	79.7	9	7/25	K240k	(R)NkNPAPPIDAVEQILPTLVR(L)	2185.2339	114.0608	7.8	57862.2/5.25	HUMAN	P52292	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.58	79.7	9	7/25	K240k	(R) N k\N\P A|P P I D A\V|E/Q/I|L/P T L V R (L)	2185.2339	114.0608	7.8	57862.2/5.25	HUMAN	P52292	318397	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.081	179.111	215.136	258.112	312.178	357.184	423.228	471.231	485.224	566.788^{+2}	585.372	616.320^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 **PR** -17.5	0.10 0.56 0.50 **KQ** 0.3	3.03 16.69 -0.17	2.24 12.35 0.75 **TL** -19.6	2.75 15.14 0.75 **EQ** 9.9	2.22 12.24 -0.12	3.30 18.19 0.75 **b$_2$** -15.4 **VEQ** 16.1	4.41 24.30 0.75 **PPID** 7.1	2.32 12.77 0.50 **b$_3$** -2.0	2.82 15.55 -0.16	3.11 17.15 0.50 **b$_{10}^{+2}$** -5.9	18.14 100.00 1.50 **y$_5$** 0.2	3.88 21.41 0.50 **b$_{11}^{+2}$** -9.7

Fragment-ion (m/z)	639.309	698.456	728.356	801.430^{+2}	811.538	830.991^{+2}	861.446	939.588	940.587^{+2}	1068.660	1231.626	1679.720
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	5.90 32.51 0.50 **b$_5$** -20.2	9.71 53.52 1.50 **y$_6$** -0.5	2.56 14.12 -0.14	2.23 12.28 0.50 **b$_{14}^{+2}$** 15.1	3.44 18.97 1.50 **y$_7$** -2.8	9.69 53.43 1.50 **y$_{15}^{+2}$** 6.8	2.43 13.38 -0.13	2.35 12.95 1.50 **y$_8$** -10.9	3.01 16.59 -0.17	3.01 16.57 1.50 **y$_9$** 17.3	3.07 16.94 0.50 **b$_{11}$** -15.1	4.27 23.55 -0.24



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Result Summary

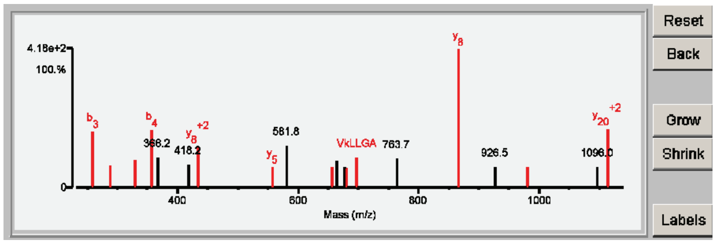
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.79	68.8	7	9/25	K300k	(K)TGVVPQLVkLLGASELPIVTPALR(A)	2471.4960	114.0576	5.7	57862.2/5.25	HUMAN	P52292	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.79	68.8	7	9/25	K300k	(K) T\G V\V|P Q L V k L L G A S E/L/P I/V/T P A L R (A)	2471.4960	114.0576	5.7	57862.2/5.25	HUMAN	P52292	318397	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Fragment-ion (m/z)	72.080	86.094	101.069	102.055	258.142	288.112	329.214	357.210	366.187	418.205	433.781^{+2}	557.328	581.810^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.08 0.43 0.50 V -5.2	0.14 0.76 0.22 LI -22.4	0.12 0.66 0.50 QK -17.2	0.09 0.49 1.00 b_1 -14.2 1.00 E -3.5	7.48 40.34 0.50 b_3 -16.0	2.87 15.48 0.75 ASE -29.5	3.69 19.91 0.50 a_4 -16.2	7.62 41.11 0.50 b_4 -12.7	4.00 21.56 -0.22	3.07 16.58 -0.17	5.48 29.54 1.50 y_8^{+2} 10.3	2.75 14.83 1.50 y_5 -23.1	5.63 30.38 -0.30

Fragment-ion (m/z)	656.412	663.379	677.009	680.410	696.427	763.709	764.381^{+3}	866.539	926.503	979.621	1095.999^{+2}	1115.160^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.80 15.09 1.50 y_6 5.0	3.62 19.53 -0.20	2.75 14.85 -0.15	2.60 14.02 0.75 PQLVk 0.3	3.99 21.51 0.75 VkLLGA -20.8	3.88 20.92 -0.21	2.59 13.99 -0.14	18.54 100.00 1.50 y_8 -7.4	2.84 15.33 -0.15	2.76 14.90 1.50 y_9 -9.5	2.76 14.88 -0.15	7.82 42.17 1.50 y_{20}^{+2} -8.9



Result Summary

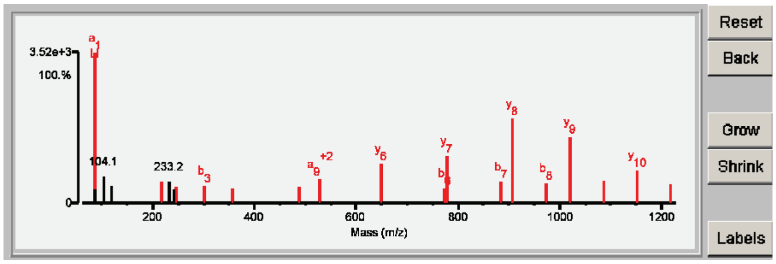
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.62	86.9	10	6/24	K459k	(K)LGETEkLSIMIEECGGLDK(I)	2122.0406	114.0501	3.2	57862.2/5.25	HUMAN	P52292	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.62	86.9	10	6/24	K459k	(K) L G E\T E k\L\S\I|M|I/E/E/C/G G L D K (I)	2122.0406	114.0501	3.2	57862.2/5.25	HUMAN	P52292	318397	Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1

Fragment-ion (m/z)	70.066	84.081	86.095	87.099	104.051	120.079	217.132	233.163	244.091	245.130	300.150	356.222
Frac. Inten.(% of TIC)	0.06	0.17	20.88	1.94	3.68	2.49	2.95	3.00	1.92	2.23	2.35	2.14
Rel. Inten.(% of BP)	0.28	0.79	100.00	9.29	17.65	11.94	14.12	14.38	9.20	10.70	11.24	10.23
Score	-0.00	0.50	0.50 0.50	-0.09	-0.18	-0.12	0.50	-0.14	-0.09	1.50	0.50	0.75
Ion-type		KQ	a_1 LI				MI-28			y^{++}_5 MI	b_3	kL
Delta ppm		-2.1	-24.7 -11.9				-28.1			-29.0 -12.3	-21.6	-23.9

Fragment-ion (m/z)	489.264	529.293^{+2}	649.301	772.383	778.335	885.464	907.386	972.504	1020.477	1085.588	1151.511	1216.637
Frac. Inten.(% of TIC)	2.26	3.37	5.37	2.02	6.46	2.96	11.77	2.69	9.22	3.05	4.48	2.52
Rel. Inten.(% of BP)	10.84	16.16	25.74	9.70	30.94	14.19	56.36	12.90	44.17	14.61	21.48	12.09
Score	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50
Ion-type	y_5	a_9^{+2}	y_6	b_6	y_7	b_7	y_8	b_8	y_9	b_9	y_{10}	b_{10}
Delta ppm	-5.8	-10.0	4.9	-2.0	-6.0	-5.2	3.8	3.5	10.5	2.8	3.4	9.4



Result Summary

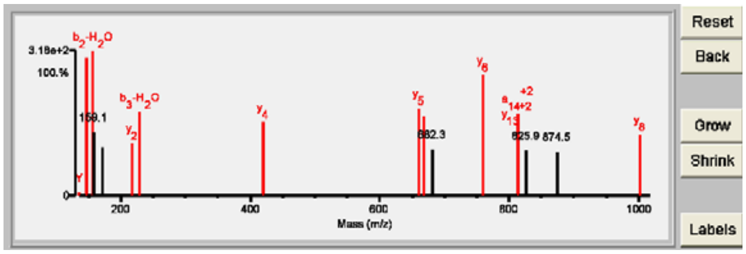
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.43	62.5	8	10/25	K537k	(R)SSAYESLMEIVkNSAK(D)	1756.8786	114.0594	8.8	97170.8/4.68	HUMAN	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2
2	7.66	55.6	6	12/25	K541k	(R)SSAYESLMEIVKNSAk(D)	1756.8786	114.0594	8.8	97170.8/4.68	HUMAN	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.43	62.5	8	10/25	K537k	(R) S S A/Y E/S L M/E I/V/k/N S/A/K (D)	1756.8786	114.0594	8.8	97170.8/4.68	HUMAN	Q14974	159221	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Fragment-ion (m/z)	70.063	84.077	86.096	87.052	102.054	104.052	120.080	129.088	136.073	147.076	147.109	157.061	159.086
Frac. Inten.(% of TIC)	0.16	7.72	0.52	0.16	0.13	6.38	4.33	3.30	0.20	8.64	3.60	9.07	4.04
Rel. Inten.(% of BP)	1.74	85.10	5.77	1.77	1.39	70.35	47.73	36.42	2.24	95.24	39.70	100.00	44.49
Score	-0.02	-0.85	0.22	0.33	1.00	-0.70	-0.48	-0.36	1.00	0.50	1.50	0.25	-0.44
Ion-type			LI	NR	E				Y	a_2	y_1	b_2-H_2O	
Delta ppm			-10.8	-37.8	-13.3				-21.2	-3.5	-24.5	3.4	

Fragment-ion (m/z)	171.110	218.151	228.099	419.227	661.365	667.360^{+2}	682.342	760.417	813.409^{+2}	825.923	874.501^{+2}	1002.539
Frac. Inten.(% of TIC)	3.06	3.32	5.28	4.59	5.44	5.02	2.89	7.61	5.16	2.82	2.75	3.81
Rel. Inten.(% of BP)	33.71	36.58	58.22	50.57	59.96	55.32	31.88	83.84	56.84	31.10	30.31	42.00
Score	-0.34	1.50	0.25	1.50	1.50	1.50	-0.32	1.50	1.50	-0.31	-0.30	1.50
Ion-type		y_2	b_3-H_2O	y_4	y_5	y_{11}^{+2}		y_6	a_{14}^{+2} 16.2 y_{13}^{+2}			y_8
Delta ppm		4.0	6.2	4.8	3.2	-1.9		-19.3	-6.2			-19.3



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Result Summary

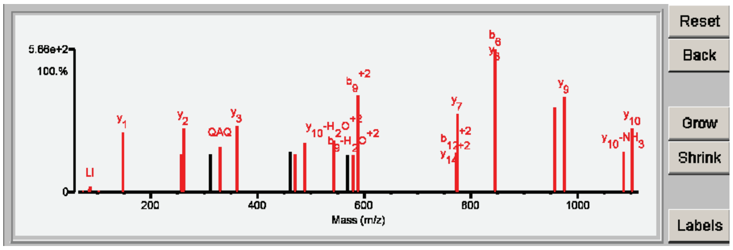
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.41	90.5	10	3/25	K730k	(K)kYLEVVLNTLQQASQAQVDK(S)	2275.2292	114.0652	9.3	97170.8/4.68	HUMAN	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.41	90.5	10	3/25	K730k	(K) k Y L E V V|L N T\L/Q/Q|A/S Q A/Q/V/D/K (S)	2275.2292	114.0652	9.3	97170.8/4.68	HUMAN	Q14974	318441	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Fragment-ion (m/z)	72.080	84.042	84.080	86.097	101.070	147.109	257.127	262.143	311.159	328.172	361.208	461.209	471.265
Frac. Inten.(% of TIC)	0.12	0.12	0.27	0.50	0.11	4.96	3.09	5.19	3.14	3.75	5.47	3.31	3.12
Rel. Inten.(% of BP)	1.03	1.03	2.33	4.25	0.96	42.54	26.52	44.47	26.91	32.15	46.84	28.38	26.72
Score	0.50	1.00	0.50	0.22		1.50	0.75	1.50	-0.27	0.75	1.50	-0.28	0.75
Ion-type	V	E	KQ	LI	KQ	y_1	QQ	y_2		QAQ	y_3		$y_4\text{-H}_2\text{O}$ TLQQ
Delta ppm	-16.3	-23.7	-8.0	0.9		-26.5	5.7	13.9		27.9	-0.4		18.7 16.4

Fragment-ion (m/z)	489.266	542.761^{+2}	567.301	578.829^{+2}	587.836^{+2}	772.411^{+2}	775.395	846.460	957.470	974.506	1085.550	1102.558
Frac. Inten.(% of TIC)	4.02	4.25	3.01	3.04	7.93	3.25	6.47	11.67	6.88	7.79	3.32	5.20
Rel. Inten.(% of BP)	34.47	36.47	25.82	26.06	68.00	27.83	55.49	100.00	59.01	66.74	28.46	44.61
Score	1.50	0.50	-0.26	0.25	0.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type	y_4	$y_{10}\text{-H}_2\text{O}^{+2}$		$b_9\text{-H}_2\text{O}^{+2}$	b_9^{+2}	b_{12}^{+2} y_{14}^{+2}	y_7	b_6 y_8	$y_9\text{-NH}_3$	y_9	$y_{10}\text{-NH}_3$	y_{10}
Delta ppm	-1.7	-21.1		11.7	14.1	-22.7 4.2	0.2	-15.2 33.8	6.8	15.9	25.4	8.5



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Result Summary

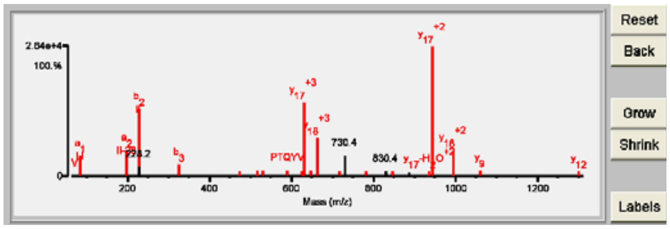
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.96	92.3	9	4/25	K213k	(R)LLVPTQYVGAIIGkEGATIR(N)	2099.2223	114.0498	3.1	63456.8/9.26	HUMAN	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=1
2	9.06	82.0	2	14/25	K164k K166k	(K)LLVKVDAkTkAQLDEWK(A)	1985.1430	228.1292	19.6	100186.0/6.06	HUMAN	P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3
2	9.06	82.0	2	14/25	K166k K173k	(K)LLVKVDAKTkAQLDEWk(A)	1985.1430	228.1292	19.6	100186.0/6.06	HUMAN	P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3
2	9.06	82.0	2	14/25	K164k K173k	(K)LLVKVDAkTKAQLDEWk(A)	1985.1430	228.1292	19.6	100186.0/6.06	HUMAN	P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3
3	8.24	80.2	2	15/25	K160k K173k	(K)LLVkVDAKTKAQLDEWk(A)	1985.1430	228.1292	19.6	100186.0/6.06	HUMAN	P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.96	92.3	9	4/25	K213k	(R) L L|V|P T/Q/Y V/G A I/I/G k/E/G A T I R (N)	2099.2223	114.0498	3.1	63456.8/9.26	HUMAN	Q9NZI8	309997	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=1

Fragment-ion (m/z)	72.082	86.097	199.182	227.177	228.178	326.244	473.265^{+2}	517.306	529.804^{+2}	589.297	624.025^{+3}
Frac. Inten.(% of TIC)	0.04	4.10	5.15	13.64	1.83	2.25	0.96	1.28	1.23	1.33	1.11
Rel. Inten.(% of BP)	0.15	15.67	19.67	52.12	7.00	8.61	3.66	4.89	4.70	5.09	4.26
Score	0.50	0.50	0.50	0.75	-0.07	0.50	1.50	1.50	1.50	0.75	0.50
Ion-type	V	a_1	a_2	b_2		b_3	y_8^{+2}	y_5	y_9^{+2}	PTQYV	$y_{17}\text{-}H_2O^{+3}$
Delta ppm	18.4	6.7	6.6	5.7		0.9	11.7	-6.7	5.5	-1.4	22.3
		0.50	II-28	II							
		LI	6.6	5.7							
		6.7									

Fragment-ion (m/z)	630.016^{+3}	646.348	663.036^{+3}	717.359	730.381^{+2}	781.441^{+2}	830.433	845.451^{+2}	887.490	935.508^{+2}	944.521^{+2}	994.055^{+2}	1058.598	1299.738
Frac. Inten.(% of TIC)	14.96	1.18	7.71	0.91	4.06	0.97	0.98	0.91	0.84	0.93	26.16	5.26	1.17	1.03
Rel. Inten.(% of BP)	57.19	4.50	29.48	3.48	15.51	3.70	3.74	3.49	3.22	3.55	100.00	20.10	4.48	3.94
Score	1.50	1.50	1.50	0.75	-0.16	1.50	-0.04	1.50	-0.03	0.50	1.50	1.50	1.50	1.50
Ion-type	y_{17}^{+3}	y_6	y_{18}^{+3}	PTQYVGA		y_{14}^{+2}		y_{15}^{+2}		$y_{17}\text{-}H_2O^{+2}$	y_{17}^{+2}	y_{18}^{+2}	y_9	y_{12}
Delta ppm	2.4	-6.6	-2.4	3.7		3.0		-19.5		-5.1	3.1	2.5	2.8	0.4



Result Summary

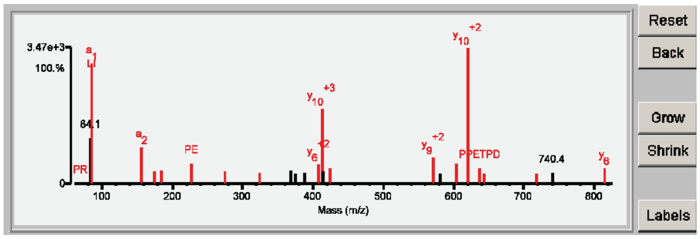
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.12	83.4	7	7/25	K450k	(K)IAPPETPDSkVR(M)	1309.7110	114.0412	-1.2	63456.8/9.26	HUMAN	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=1
2	6.18	67.5	3	15/25	None	(R)IASNFKPGSYPSR(Y)	1423.7328	0.0194	13.6	59379.9/10.10	HUMAN	RQ14498	REVERSE RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2
3	5.53	64.2	2	16/25	None	(K)LARTGNFFLTQR(A)	1423.7805	-0.0282	-19.8	42785.5/5.92	HUMAN	RQ8NFZ8	REVERSE Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1
4	5.02	56.5	2	16/25	None	(R)ALEELGEELHKR(E)	1423.7540	-0.0017	-1.2	150587.8/6.37	HUMAN	Q2M1P5	Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2
5	4.98	60.7	2	17/25	None	(R)LAAAEAPSGPEVRR(I)	1423.7652	-0.0130	-9.1	37413.9/7.91	HUMAN	RQ15599	REVERSE Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.12	83.4	7	7/25	K450k	(K) I A|P/P E T/P/D/S k/V/R (M)	1309.7110	114.0412	-1.2	63456.8/9.26	HUMAN	Q9NZI8	309997	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=1

Fragment-ion (m/z)	70.066	84.082	86.097	157.133	175.117	185.131	227.103	274.189	324.159	369.197	375.870	389.211^{+3}
Frac. Inten.(% of TIC)	0.01	6.84	17.75	5.31	1.72	1.93	2.96	1.77	1.57	1.99	1.42	1.59
Rel. Inten.(% of BP)	0.07	34.19	88.72	26.53	8.62	9.66	14.79	8.83	7.87	9.97	7.11	7.95
Score	0.20	-0.34	0.50	0.50	1.50	0.50	0.75	1.50	0.75	-0.10	-0.07	-0.08
Ion-type	PR		a_1	a_2	y_1	b_2	PE	y_2	PPE			
Delta ppm	6.8		-9.6	-9.8	-8.9	5.1	-4.1	6.0	6.8			
			0.50									
			LI									
			3.2									

Fragment-ion (m/z)	408.212^{+2}	413.877^{+3}	413.994	425.202	571.799^{+2}	580.982	603.361	620.319^{+2}	637.276	643.313	718.386	740.355	815.426
Frac. Inten.(% of TIC)	2.79	10.99	1.72	2.33	3.79	1.39	2.94	20.00	2.24	1.48	1.51	1.63	2.35
Rel. Inten.(% of BP)	13.93	54.93	8.57	11.66	18.94	6.93	14.68	100.00	11.19	7.38	7.53	8.15	11.73
Score	1.50	1.50	-0.09	0.75	1.50	-0.07	1.50	1.50	0.75	0.75	1.50	-0.08	1.50
Ion-type	y_6^{+2}	y_{10}^{+3}		PETP	y_9^{+2}		y_4	y_{10}^{+2}	PPETPD	TPDSk	y_5		y_6
Delta ppm	-23.6	-13.4		-5.1	9.7		5.3	-1.0	-12.4	12.2	2.5		-14.1



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Result Summary

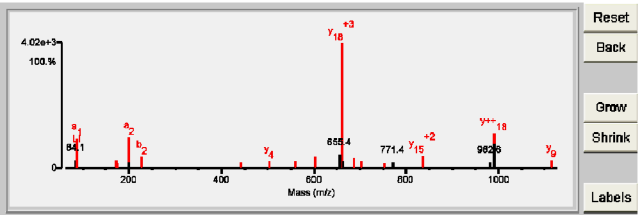
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.88	82.1	8	7/25	K141k	(K)ILPTLEAVAALGNkVVESLR(A)	2093.2329	114.0780	15.9	43290.6/5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2
2	7.15	66.3	2	15/25	K585k	(K)LLEkVPVDTGVVGLLIGKSR(T)	2093.2693	114.0416	-0.6	124153.0/5.53	HUMAN	RQ8IZS8	REVERSE Voltage-dependent calcium channel subunit alpha-2/delta-3 OS=Homo sapiens GN=CACNA2D3 PE=1 SV=1
2	7.15	66.3	2	15/25	K599k	(K)LLEKVPVDTGVVGLLIGkSR(T)	2093.2693	114.0416	-0.6	124153.0/5.53	HUMAN	RQ8IZS8	REVERSE Voltage-dependent calcium channel subunit alpha-2/delta-3 OS=Homo sapiens GN=CACNA2D3 PE=1 SV=1
3	6.63	64.7	3	16/25	K65k K67k	(K)LLLLTCGIWLLHIGkTk(E)	1979.1874	228.1234	17.0	13618.4/9.15	HUMAN	RQ9BZ99	REVERSE Putative transcript Y 11 protein OS=Homo sapiens GN=TTTY11 PE=5 SV=1
4	6.54	62.8	2	16/25	None	(R)LIKEALSYRGLQHLILALR(Q)	2207.3387	-0.0278	-12.6	95035.5/6.45	HUMAN	RQ86TV6	REVERSE Tetratricopeptide repeat protein 7B OS=Homo sapiens GN=TTC7B PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.88	82.1	8	7/25	K141k	(K) I L|P T L/E A V/A A L/G N k|V/V/E S L/R (A)	2093.2329	114.0780	15.9	43290.6/5.19	HUMAN	Q12905	315817	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2

Fragment-ion (m/z)	70.064	84.080	86.097	171.116	175.117	199.110	199.179	200.184	227.174	441.249	504.268	558.322^{+2}	603.356
Frac. Inten.(% of TIC)	0.00	2.07	7.40	1.90	1.30	2.20	7.69	1.35	2.82	1.43	1.77	1.66	2.82
Rel. Inten.(% of BP)	0.01	6.57	23.47	6.03	4.11	6.98	24.38	4.29	8.94	4.54	5.61	5.26	8.95
Score	0.20	-0.07	0.50 0.50	0.75	1.50	0.75	0.50	-0.04	0.50	0.75	1.50	1.50	1.50
Ion-type	PR		a_1 LI	LG PT-28	y_1	PT	a_2		b_2	PTLE	y_4	y_9^{+2}	y_5
Delta ppm	-13.2		5.5 5.5	19.8 19.8	-9.4	8.9	-5.0		-4.0	33.1	-19.9	18.3	17.3

Fragment-ion (m/z)	655.418^{+3}	661.053^{+3}	662.376^{+2}	685.887	702.418	753.428	771.436	835.467^{+2}	982.568	991.051	991.575	1115.634
Frac. Inten.(% of TIC)	3.49	31.55	1.78	2.49	1.88	1.31	1.56	3.20	1.47	8.79	6.14	1.90
Rel. Inten.(% of BP)	11.07	100.00	5.65	7.89	5.96	4.17	4.95	10.14	4.67	27.86	19.47	6.02
Score	-0.11	1.50	-0.06	1.50	1.50	0.50	-0.05	1.50	-0.05	1.50	-0.19	1.50
Ion-type		y_{18}^{+3}		y^{++}_{12}	y_6	b^{++}_{14}		y_{15}^{+2}		y^{++}_{18}		y_9
Delta ppm		19.0		-6.1	5.7	-12.9		2.5		-6.7		15.4



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Result Summary

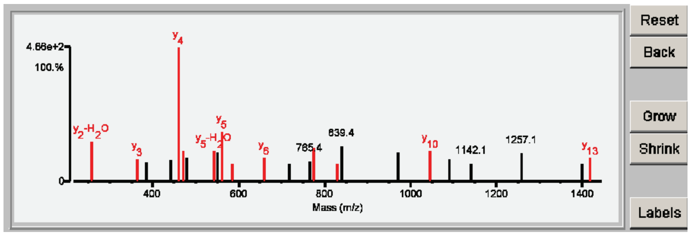
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.12	61.7	8	12/25	K328k	(R)kILGQEGDASYLASEISTWDGVIVTPSEK(A)	3093.5627	114.0640	6.6	43062.4/5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.12	61.7	8	12/25	K328k	(R) k I L\G Q E G D A S Y L A S E I/S T W/D G V/I/V/T/P/S E K (A)	3093.5627	114.0640	6.6	43062.4/5.19	HUMAN	Q12905	315817	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2

Fragment-ion (m/z)	86.094	258.140	363.173	385.189	441.141	460.230	469.329	478.749	543.264	549.336	561.285	585.311	660.342
Frac. Inten.(% of TIC)	0.13	5.43	3.02	2.58	2.87	18.21	4.06	3.14	4.20	3.90	6.78	2.41	3.23
Rel. Inten.(% of BP)	0.72	29.81	16.56	14.15	15.74	100.00	22.27	17.24	23.05	21.43	37.21	13.25	17.76
Score	0.22	0.50	1.50	-0.14	-0.16	1.50	0.50	-0.17	0.50	-0.21	1.50	0.75	1.50
Ion-type	LI	y_2-H$_2$O	y_3			y_4	b_3		y_5-H$_2$O		y_5	DGVIVT	y_6
Delta ppm	-22.4	-19.9	-40.0			-22.6	30.5		-24.7		-4.9	-24.3	-22.2

Fragment-ion (m/z)	717.864	765.368	773.426	829.921^{+2}	839.421	971.449^{+2}	1044.544	1089.550	1142.150	1257.097	1399.712	1418.706
Frac. Inten.(% of TIC)	2.42	2.69	4.58	2.48	4.82	4.04	4.09	3.08	2.40	3.86	2.45	3.13
Rel. Inten.(% of BP)	13.29	14.79	25.13	13.62	26.45	22.17	22.48	16.93	13.21	21.20	13.45	17.20
Score	-0.13	-0.15	1.50	0.25	-0.26	-0.22	1.50	-0.17	-0.13	-0.21	-0.13	1.50
Ion-type			y_7	b_{15}-H$_2$O^{+2}			y_{10}					y_{13}
Delta ppm			-18.2	18.8			-12.6					-7.3



Result Summary

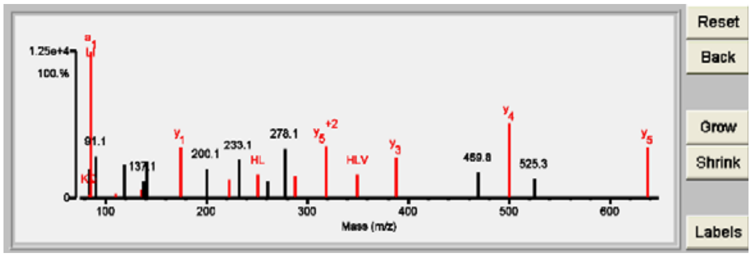
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.03	60.6	5	11/25	K804k	(R)IADLQGkTSYHLVLR(A)	1713.9646	114.0679	13.7	123743.8/5.50	HUMAN	P42702	Leukemia inhibitory factor receptor OS=Homo sapiens GN=LIFR PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.03	60.6	5	11/25	K804k	(R) I A D L Q G k T S Y/H/L/V/L/R (A)	1713.9646	114.0679	13.7	123743.8/5.50	HUMAN	P42702	360053	Leukemia inhibitory factor receptor OS=Homo sapiens GN=LIFR PE=1 SV=1

Fragment-ion (m/z)	84.044	84.080	86.096	87.054	91.053	110.071	119.048	136.075	137.078	141.101	175.119	200.139	223.155
Frac. Inten.(% of TIC)	3.48	0.50	17.10	0.08	4.90	0.49	3.80	0.96	1.95	4.38	5.87	3.46	2.10
Rel. Inten.(% of BP)	20.32	2.94	100.00	0.46	28.65	2.89	22.23	5.64	11.42	25.61	34.34	20.22	12.28
Score	-0.20	0.50	0.50	0.33	-0.29	1.00	-0.22	1.00	-0.11	-0.26	1.50	-0.20	0.50
Ion-type		KQ	a_1	NR		H		Y			y_1		HL-28
Delta ppm		-4.5	-22.3	-11.4		-6.1		-4.3			-0.9		-7.8
			0.50										
			LI										
			-9.6										

Fragment-ion (m/z)	233.092	251.150	261.087	278.114	288.204	319.212^{+2}	350.218	387.271	469.795^{+2}	500.358	525.310^{+2}	637.414
Frac. Inten.(% of TIC)	4.51	2.74	1.94	5.79	2.51	6.10	2.70	4.68	3.02	8.76	2.19	5.99
Rel. Inten.(% of BP)	26.40	16.01	11.35	33.86	14.65	35.65	15.78	27.37	17.64	51.20	12.82	35.02
Score	-0.26	0.75	-0.11	-0.34	1.50	1.50	0.75	1.50	-0.18	1.50	-0.13	1.50
Ion-type		HL			y_2	y_5^{+2}	HLV	y_3		y_4		y_5
Delta ppm		-4.2			2.7	2.7	-4.8	-0.6		4.4		-0.8



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Result Summary

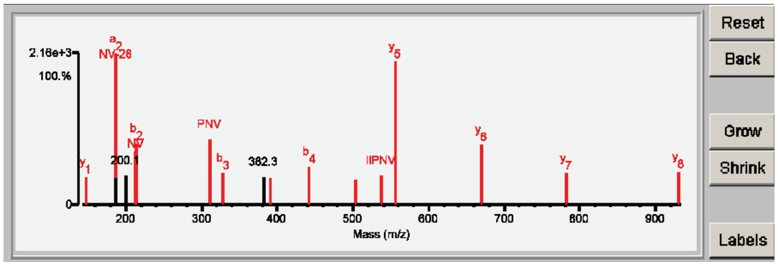
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.38	83.8	8	5/25	K118k	(R)NVNIFkFIIPNVVK(Y)	1644.9836	114.0589	9.1	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.38	83.8	8	5/25	K118k	(R) N V\N\I\F k/F/I/I/P N V V/K (Y)	1644.9836	114.0589	9.1	36688.9/8.44	HUMAN	P00338	351281	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Fragment-ion (m/z)	70.064	72.081	84.080	86.096	87.053	88.038	120.081	141.101	147.112	186.123	187.121	200.138
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.02 0.20 **PR** -16.1	0.20 1.28 0.50 **V** -3.8	0.32 2.04 0.50 **KQ** -14.0	0.38 2.43 0.22 **LI** -3.8	2.99 19.29 0.50 a_1 -42.3 0.50 **NR** -29.7	3.98 25.66 -0.26	0.14 0.90 1.00 **F** 1.0	3.59 23.18 -0.23	2.89 18.65 1.50 y_1 -4.8	15.51 100.00 0.50 a_2 -12.4 **NV**-28 -12.4	2.77 17.89 -0.18	3.04 19.62 -0.20

Fragment-ion (m/z)	212.103	214.120	311.169	328.159	382.255	390.219	441.249	503.292	537.321	556.344	669.425	782.517	929.601
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	5.45 35.14 0.75 **PN** -4.1	6.34 40.89 0.75 b_2 1.8 **NV** 1.8	6.75 43.51 0.75 **PNV** -9.9	3.22 20.77 0.50 b_3 -10.5	2.83 18.24 -0.18	2.72 17.54 0.75 **kF** 12.1	3.93 25.35 0.50 b_4 5.2	2.58 16.66 0.75 **kFI** -14.0	2.98 19.23 0.75 **IIPNV** -37.4	14.61 94.23 1.50 y_5 -3.1	6.12 39.46 1.50 y_6 -6.3	3.29 21.22 1.50 y_7 4.3	3.35 21.63 1.50 y_8 20.0



Result Summary

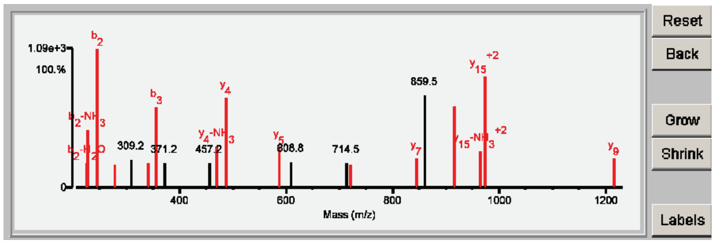
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.39	74.7	7	7/25	K14k	(K)DQLIYNLLkEEQTPQNK(I)	2074.0815	114.0590	7.4	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2
2	6.95	56.7	4	11/25	K22k	(K)DQLIYNLLKEEQTPQNk(I)	2074.0815	114.0590	7.4	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2
3	4.91	53.2	3	14/25	K462k K465k	(K)RSIGSKELDQSQkVEkK(T)	1960.0822	228.0584	-12.6	56564.2/7.32	HUMAN	RQ6Y288	REVERSE Beta-1,3-glucosyltransferase OS=Homo sapiens GN=B3GALTL PE=1 SV=2
3	4.91	53.2	4	14/25	K462k K466k	(K)RSIGSKELDQSQkVEKk(T)	1960.0822	228.0584	-12.6	56564.2/7.32	HUMAN	RQ6Y288	REVERSE Beta-1,3-glucosyltransferase OS=Homo sapiens GN=B3GALTL PE=1 SV=2
3	4.91	53.2	4	14/25	K465k K466k	(K)RSIGSKELDQSQKVEkk(T)	1960.0822	228.0584	-12.6	56564.2/7.32	HUMAN	RQ6Y288	REVERSE Beta-1,3-glucosyltransferase OS=Homo sapiens GN=B3GALTL PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.39	74.7	7	7/25	K14k	(K) D Q|L|I Y N/L L/k E/E Q/T/P Q N K (I)	2074.0815	114.0590	7.4	36688.9/8.44	HUMAN	P00338	351281	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Fragment-ion (m/z)	70.064	84.081	86.094	133.061	226.085	227.066	244.093	278.110	309.157	340.157	357.177	371.188	457.197
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.02 0.20 PR -20.3	0.18 1.48 0.50 KQ 0.3	0.16 1.27 0.22 LI -29.3	5.83 46.86 -0.47	2.21 17.72 0.25 b_2-H$_2$O 6.5	5.16 41.46 0.25 b_2-NH$_3$ -3.7	12.45 100.00 0.50 b_2 -2.8	2.05 16.51 0.75 YN -15.9	2.53 20.33 -0.20	2.22 17.86 0.75 b_3-NH$_3$ 17.0 PQN -16.0	7.15 57.41 0.50 b_3 -3.2	2.13 17.12 -0.17	2.13 17.14 -0.17

Fragment-ion (m/z)	469.224	486.263	587.309	608.799^{+2}	714.455	721.387^{+2}	844.436	859.512^{+2}	916.486^{+2}	964.532^{+2}	973.030^{+2}	1215.580
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.71 29.80 0.50 y_4-NH$_3$ -36.3	8.06 64.77 1.50 y_4 -7.6	3.60 28.96 1.50 y_5 -9.3	2.28 18.29 -0.18	2.21 17.72 -0.18	2.08 16.73 1.50 y_{11}^{+2} 1.5	2.57 20.66 1.50 y_7 23.5	8.22 66.05 -0.66	7.26 58.37 1.50 y_{14}^{+2} 5.7	3.23 25.97 0.50 y_{15}-NH$_3^{+2}$ 23.4	9.94 79.83 1.50 y_{15}^{+2} 6.8	2.64 21.20 1.50 y_9 -13.7



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Result Summary

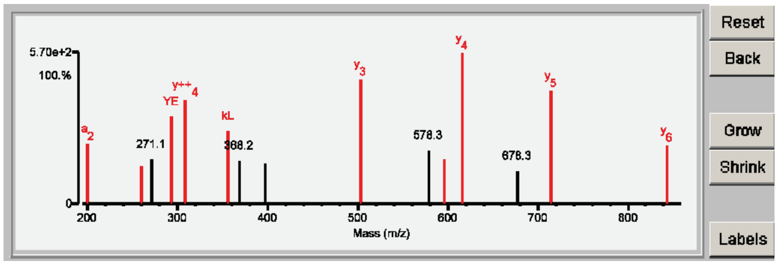
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.47	72.7	5	8/25	K243k	(K)QVVESAYEVIkLK(G)	1505.8574	114.0574	8.9	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2
2	9.49	63.6	4	10/25	K245k	(K)QVVESAYEVIKLk(G)	1505.8574	114.0574	8.9	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.47	72.7	5	8/25	K243k	(K) Q V V E S A Y/E/V/I/k/L K (G)	1505.8574	114.0574	8.9	36688.9/8.44	HUMAN	P00338	351281	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Fragment-ion (m/z)	70.064	72.081	84.045	84.081	86.097	91.051	102.054	129.101	136.074	183.116	200.139	260.195	271.141
Frac. Inten.(% of TIC)	0.20	0.77	0.20	0.40	0.27	2.74	0.20	0.22	0.68	6.95	4.93	3.08	3.61
Rel. Inten.(% of BP)	1.64	6.20	1.61	3.19	2.14	22.13	1.60	1.79	5.50	56.14	39.80	24.86	29.18
Score	-0.02	0.50	1.00	0.50	0.22	-0.22		0.20	1.00	-0.56	0.50	1.50	-0.29
Ion-type		V	E	KQ	LI		E	RKQ	Y		a_2	y_2	
Delta ppm		4.5	7.3	1.5	3.2			-8.8	-13.9		-8.7	-8.7	

Fragment-ion (m/z)	293.119	308.204	356.235	368.185	397.180	502.338	578.297	596.292	615.429	678.318	714.490	843.536
Frac. Inten.(% of TIC)	7.19	8.53	5.96	3.52	3.29	10.19	4.35	3.65	12.38	2.65	9.26	4.78
Rel. Inten.(% of BP)	58.07	68.89	48.16	28.42	26.61	82.33	35.15	29.46	100.00	21.43	74.81	38.59
Score	0.75	1.50	0.75	-0.28	-0.27	1.50	-0.35	0.25	1.50	-0.21	1.50	1.50
Ion-type	YE	$y{+}{+}_4$	kL			y_3		b_6-H_2O	y_4		y_5	y_6
Delta ppm	17.1	-28.4	12.0			6.9		-21.2	15.9		4.4	7.4



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Result Summary

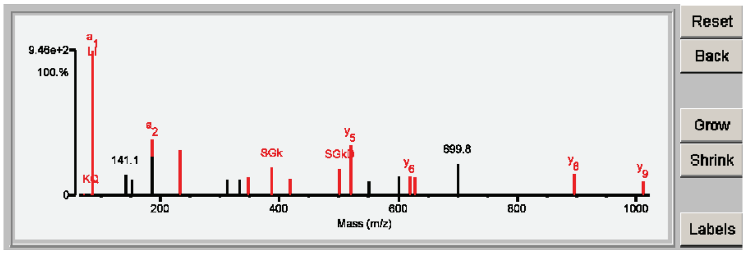
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.86	73.3	8	8/25	K81k	(K)IVSGkDYNVTANSK(L)	1495.7751	114.0488	3.7	36688.9/8.44	HUMAN	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.86	73.3	8	8/25	K81k	(K) I V S G/k/D/Y N/V/T/A/N/S K (L)	1495.7751	114.0488	3.7	36688.9/8.44	HUMAN	P00338	351281	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Fragment-ion (m/z)	72.080	84.080	86.096	87.055	129.099	136.073	141.098	153.105	185.165	186.167	234.143	312.674^{+2}	333.156
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.22 0.97 0.50 V -16.3	0.32 1.38 0.50 KQ -6.8	22.83 100.00 0.50 a_1 -15.4 0.50 LI -2.6	0.18 0.79 0.33 NR -4.5	0.18 0.80 0.20 RKQ -25.9	0.06 0.28 1.00 Y -16.8	3.31 14.50 -0.15	2.38 10.41 -0.10	8.97 39.29 0.50 a_2 -7.2	6.08 26.64 -0.27	7.12 31.18 1.50 y_2 -7.4	2.40 10.49 -0.10	2.38 10.41 -0.10

Fragment-ion (m/z)	348.187	387.198	419.228	502.228	520.275	551.791	600.324	619.345	627.289^{+2}	699.842^{+2}	896.425	1011.495
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.82 12.37 1.50 y_3 -3.6	4.31 18.86 0.75 SGk -5.3	2.59 11.36 1.50 y_4 7.9	4.19 18.35 0.75 SGkD 3.4	7.88 34.51 1.50 y_5 5.1	2.29 10.05 -0.10	2.99 13.11 -0.13	3.07 13.45 1.50 y_6 6.0	2.88 12.63 1.50 y_{10}^{+2} -32.5	4.90 21.45 -0.21	3.37 14.77 1.50 y_8 -24.8	2.27 9.93 1.50 y_9 20.6



Result Summary

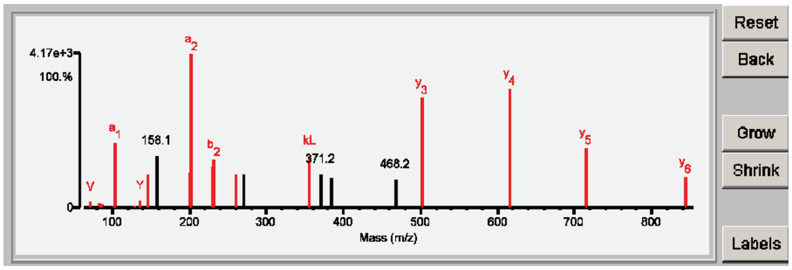
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.77	82.0	7	5/24	K244k	(K)MVVESAYEVIkLK(G)	1508.8393	114.0548	7.3	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
2	10.26	70.0	5	8/24	K246k	(K)MVVESAYEVIKLk(G)	1508.8393	114.0548	7.3	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.77	82.0	7	5/24	K244k	(K) M V\V E S A Y/E/V/I/k/L/K (G)	1508.8393	114.0548	7.3	36638.7/5.71	HUMAN	P07195	351361	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2

Fragment-ion (m/z)	72.080	84.044	84.081	86.096	102.055	104.052	129.101	136.075	147.111	158.099	201.124	203.121
Frac. Inten.(% of TIC)	0.64	0.18	0.49	0.36	0.19	6.61	0.17	0.68	3.37	5.29	3.55	15.66
Rel. Inten.(% of BP)	4.10	1.15	3.14	2.29	1.18	42.20	1.07	4.34	21.51	33.79	22.67	100.00
Score	0.50		0.50	0.22	1.00	0.50	0.20	1.00	1.50	-0.34	0.50	0.50
Ion-type	V	E	KQ	LI	E	a_1	RKQ	Y	y_1		EV-28	a_2
Delta ppm	-5.2		-2.1	-7.3	3.4	-15.8	-8.1	-4.3	-13.6		-4.3	-7.7

Fragment-ion (m/z)	229.117	231.116	260.198	271.142	356.227	371.178	384.225^{+2}	468.245	502.334	615.419	714.488	843.533
Frac. Inten.(% of TIC)	4.22	4.89	3.39	3.45	5.23	3.38	2.96	2.90	11.13	12.06	6.10	3.12
Rel. Inten.(% of BP)	26.93	31.26	21.64	22.03	33.39	21.62	18.88	18.53	71.06	77.06	38.95	19.95
Score	0.75	0.50	1.50	-0.22	0.75	-0.22	-0.19	-0.19	1.50	1.50	1.50	1.50
Ion-type	EV	b_2	y_2		kL				y_3	y_4	y_5	y_6
Delta ppm	-10.4	-4.2	4.0		-10.2				-0.5	-0.2	0.5	3.4



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Result Summary

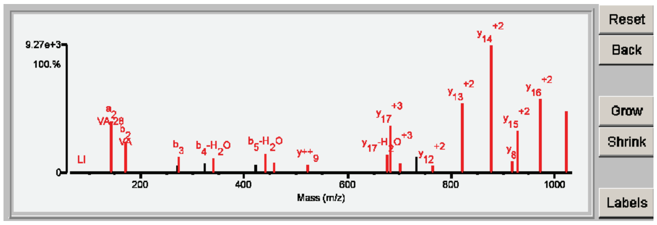
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.36	94.0	9	4/25	K308k	(R)GLTSVINQkLKDDEVAQLK(K)	2099.1707	114.0505	3.4	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
2	17.79	92.7	8	5/25	K310k	(R)GLTSVINQKLkDDEVAQLK(K)	2099.1707	114.0505	3.4	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
3	16.21	91.0	7	6/25	K318k	(R)GLTSVINQKLKDDEVAQLk(K)	2099.1707	114.0505	3.4	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
4	8.75	73.3	4	11/25	K159k	(R)GLLSSVVVLSGkSDTLSPLAR(S)	2099.2070	114.0141	-13.0	34288.6/9.76	HUMAN	RQ7Z5J1	REVERSE Hydroxysteroid 11-beta-dehydrogenase 1-like protein OS=Homo sapiens GN=HSD11B1L PE=2 SV=1
5	4.71	54.4	3	15/25	None	(R)LTSRLQRMTELGELPELAR(L)	2213.2071	0.0141	6.4	32868.8/9.65	HUMAN	RP29372	REVERSE DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.36	94.0	9	4/25	K308k	(R) G L|T|S/V|I/N/Q/k L/K/D D E V A Q L K (K)	2099.1707	114.0505	3.4	36638.7/5.71	HUMAN	P07195	351361	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2

Fragment-ion (m/z)	72.080	84.080	86.095	129.101	143.116	171.110	270.140	272.157	323.166	341.180	422.242
Frac. Inten.(% of TIC)	0.04	0.08	0.11	0.05	7.76	4.73	1.08	2.47	1.41	2.21	1.24
Rel. Inten.(% of BP)	0.23	0.40	0.59	0.28	40.25	24.50	5.59	12.80	7.31	11.43	6.41
Score	0.50	0.50	0.22	0.20	0.50	0.75	-0.06	0.50	-0.07	0.25	-0.06
Ion-type	V	KQ	LI	RKQ	a_2	b_2		b_3		b_4-H_2O	
Delta ppm	-10.8	-14.0	-20.0	-11.1	-23.7	-21.0		-15.7		-9.2	
					VA-28	VA					
					-23.7	-21.0					

Fragment-ion (m/z)	440.248	458.257	523.282	675.696^{+3}	681.702^{+3}	700.900^{+2}	732.405	764.914^{+2}	821.941^{+2}	878.479^{+2}	917.459	928.018^{+2}	971.530^{+2}	1022.056^{+2}
Frac. Inten.(% of TIC)	2.91	1.60	1.23	2.69	7.17	1.38	2.32	1.15	10.54	19.29	1.70	6.38	11.10	9.35
Rel. Inten.(% of BP)	15.07	8.30	6.38	13.94	37.17	7.18	12.04	5.96	54.65	100.00	8.80	33.06	57.55	48.46
Score	0.25	0.50	1.50	0.50	1.50	1.50	-0.12	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	b_5-H_2O	b_5	$y{+}{+}_9$	y_{17}-H_2O^{+3}	y_{17}^{+3}	y_{11}^{+2}		y_{12}^{+2}	y_{13}^{+2}	y_{14}^{+2}	y_8	y_{15}^{+2}	y_{16}^{+2}	y_{17}^{+2}
Delta ppm	-6.7	-10.7	3.4	-12.5	-7.8	13.8		-7.7	-0.7	-5.4	1.6	0.1	-4.1	-1.4



Result Summary

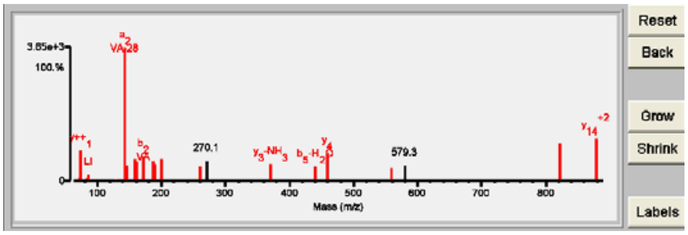
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.24	93.2	7	2/25	K308k	(R)GLTSVINQkLKDDEVAQLK(K)	2099.1707	114.0507	3.5	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
1	18.24	93.2	7	2/25	K310k	(R)GLTSVINQKLkDDEVAQLK(K)	2099.1707	114.0507	3.5	36638.7/5.71	HUMAN	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
2	10.83	68.7	3	10/25	None	(R)IQLLLEPTLTTSDVDGLSGLK(R)	2213.2275	-0.0061	-2.8	75127.6/6.22	HUMAN	RQ8WU76	REVERSE Sec1 family domain-containing protein 2 OS=Homo sapiens GN=SCFD2 PE=1 SV=2
3	9.85	64.0	4	9/25	M31m	(K)EKISYLPDVLKNHVLmLGK(F)	2197.2413	15.9800	-6.7	32668.7/6.44	HUMAN	RP46926	REVERSE Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1
4	9.80	64.1	3	8/25	K932k	(K)SQAkIVIGLDNVAGVSVTSLK(D)	2099.2070	114.0143	-12.9	118401.3/9.37	HUMAN	Q9UBC5	Myosin-Ia OS=Homo sapiens GN=MYO1A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.24	93.2	7	2/25	K308k	(R) G L\T S V/I/N Q k L K D D E/V/A Q/L/K (K)	2099.1707	114.0507	3.5	36638.7/5.71	HUMAN	P07195	351361	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2

Fragment-ion (m/z)	72.080	74.060	84.043	84.080	86.096	87.056	101.070	129.102	143.116	147.112	159.110	161.092
Frac. Inten.(% of TIC)	0.51	5.92	0.12	0.46	1.19	0.09	0.11	0.26	25.69	2.90	4.20	3.63
Rel. Inten.(% of BP)	1.98	23.04	0.48	1.79	4.64	0.37	0.44	1.00	100.00	11.27	16.33	14.13
Score	0.50	1.50	1.00	0.50	0.22	0.33		0.20	0.50	1.50	0.50	0.50
Ion-type	V	y++$_1$	E	KQ	LI	NR	KQ	RKQ	a$_2$ VA-28	y$_1$	SV-28	TS-28
Delta ppm	-14.9	-4.6	-14.2	-14.0	-4.9	3.6		-2.6	-19.5 -19.5	-8.2	-27.7	-10.3

Fragment-ion (m/z)	171.110	187.106	189.089	200.101	260.198	270.143	371.225	440.249	459.289	558.361	579.313^{+2}	821.944^{+2}	878.489^{+2}
Frac. Inten.(% of TIC)	4.65	3.75	3.16	4.26	2.67	3.78	3.21	2.65	5.39	2.60	3.06	7.46	8.29
Rel. Inten.(% of BP)	18.11	14.60	12.28	16.56	10.40	14.72	12.47	10.31	20.96	10.13	11.89	29.05	32.25
Score	0.75	0.75	0.75	0.75	1.50	-0.15	0.50	0.25	1.50	1.50	-0.12	1.50	1.50
Ion-type	b$_2$ VA	SV	TS	AQ	y$_2$		y$_3$-NH$_3$	b$_5$-H$_2$O	y$_4$	y$_5$		y$_{13}^{+2}$	y$_{14}^{+2}$
Delta ppm	-21.0 -21.0	-16.7	4.3	-12.8	2.8		-10.8	-5.6	-8.8	0.9		2.5	6.4



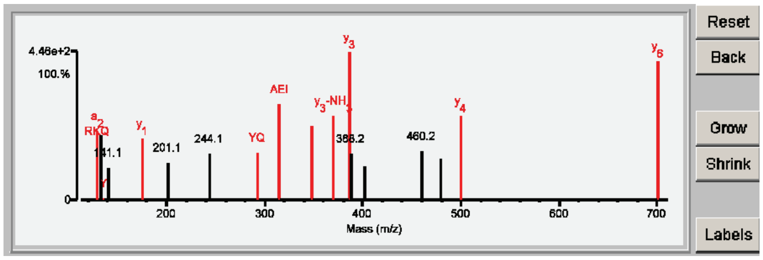
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pl (Da)	Species	Accession #	Protein Name
1	10.58	72.0	4	9/25	K152k	(R)VGCkYQAEIPDR(L)	1435.6998	114.0551	7.9	75023.5/9.70	HUMAN	O94776	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pl (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.58	72.0	4	9/25	K152k	(R) V G C k Y Q/A E/I/P D/R (L)	1435.6998	114.0551	7.9	75023.5/9.70	HUMAN	O94776	414541	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	75.052	84.043	84.079	86.096	102.052	129.103	133.039	136.076	141.068	175.116	201.107	244.131	292.130	314.160	347.662^{+2}	370.165	387.197	388.196^{+2}	402.227	460.178	479.235	500.281	700.362
Frac. Inten.(% of TIC)	0.00	0.46	3.29	0.14	0.41	0.33	0.12	5.69	5.33	0.15	2.61	5.05	3.03	3.85	3.95	7.92	6.15	6.95	12.18	3.80	2.79	4.05	3.42	6.92	11.39
Rel. Inten.(% of BP)	0.04	3.79	26.98	1.17	3.33	2.69	1.02	46.73	43.79	1.22	21.46	41.45	24.85	31.63	32.42	65.00	50.48	57.02	100.00	31.18	22.94	33.27	28.11	56.77	93.51
Score	0.20	0.50	-0.21	1.00	0.50	0.22		0.50	-0.35	1.00	-0.17	1.50	-0.20	-0.25	0.75	0.75	0.75	0.50	1.50	-0.25	-0.18	-0.26	-0.22	1.50	1.50
Ion-type	PR	a_1		E	KQ	LI	E	a_2		Y		y_1			YQ	AEI	a_5^{+2}	y_3-NH$_3$	y_3					y_4	y_6
Delta ppm	-1.8	-27.4		-20.1	-25.9	-10.8		-4.9		-1.4		-18.0			-1.0	-38.3	-26.9	-18.4	-5.6					-3.6	-0.8
		0.50						0.50																	
		V						RKQ									CkYQ^{+2}								
		-12.1						3.6									25.5								



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Result Summary

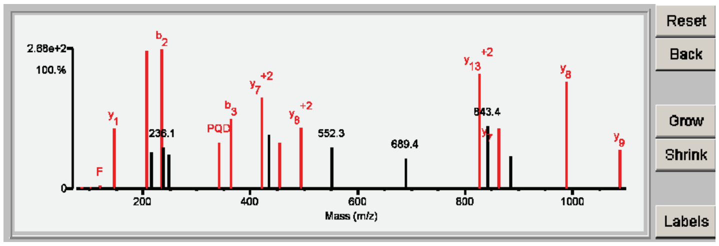
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.34	75.5	7	8/25	K241k	(K)SFEAPIkLVFPQDLLEK(G)	1974.0946	114.0541	5.4	41488.6/6.00	HUMAN	Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.34	75.5	7	8/25	K241k	(K) S F\E|A/P I k L/V/F/P Q D L L E/K (G)	1974.0946	114.0541	5.4	41488.6/6.00	HUMAN	Q8TCT9	292483	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1

Fragment-ion (m/z)	84.082	86.094	102.051	120.077	147.111	207.109	215.133	235.103	236.108	247.103	341.147	364.149	421.744^{+2}
Frac. Inten.(% of TIC)	0.10	0.17	0.18	0.25	4.42	10.18	2.67	10.26	3.05	2.46	3.42	5.13	6.71
Rel. Inten.(% of BP)	1.02	1.69	1.71	2.39	43.03	99.25	26.02	100.00	29.68	24.00	33.31	49.94	65.38
Score	0.50	0.22	1.00	1.00	1.50	0.50	-0.26	0.50	-0.30	-0.24	0.75	0.50	1.50
Ion-type	KQ	LI	E	F	y_1	a_2		b_2			PQD	b_3	y_7^{+2}
Delta ppm	18.1	-28.2	-34.8	-32.3	-11.6	-24.1		-23.9			1.6	-5.2	22.5

Fragment-ion (m/z)	435.180^{+2}	455.282	495.256^{+2}	552.342	689.386	827.483^{+2}	842.456	843.437^{+2}	862.986^{+2}	883.545	989.525	1088.630
Frac. Inten.(% of TIC)	4.02	3.37	4.56	3.00	2.26	8.46	3.20	4.57	4.41	2.45	7.89	2.83
Rel. Inten.(% of BP)	39.14	32.86	44.45	29.20	21.98	82.43	31.14	44.56	42.99	23.85	76.90	27.59
Score	-0.39	0.75	1.50	-0.29	-0.22	1.50	1.50	-0.45	1.50	-0.24	1.50	1.50
Ion-type		kLV	y_8^{+2}			y_{13}^{+2}	y_7		y_{14}^{+2}		y_8	y_9
Delta ppm		-36.1	-25.0			0.4	-6.7		-17.5		-5.2	28.8



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Result Summary

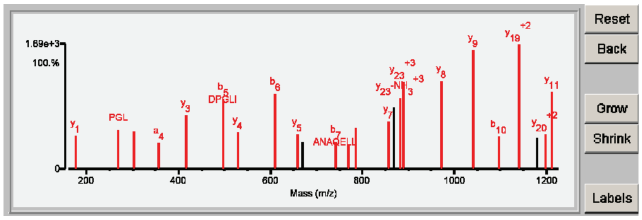
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.78	90.7	15	3/25	K27k	(K)LDPGLIMEQVkVQIAVANAQELLQR(M)	2776.5390	114.0651	7.7	10500.1/8.42	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.78	90.7	15	3/25	K27k	(K) L D/P G L|I|M\E Q V\k V Q I/A V/A/N/A/Q/E/L/L/Q/R (M)	2776.5390	114.0651	7.7	10500.1/8.42	HUMAN	Q9Y5L4	783265	Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1

Fragment-ion (m/z)	84.079	175.118	268.165	303.175	355.191	416.259	496.275	529.341	609.358	658.391	669.365^{+2}	740.411
Frac. Inten.(% of TIC)	0.06	2.58	2.95	2.92	1.97	4.13	5.38	2.83	5.76	2.67	2.12	2.07
Rel. Inten.(% of BP)	0.66	26.98	30.83	30.49	20.56	43.12	56.20	29.61	60.16	27.92	22.17	21.59
Score	0.50	1.50	0.75	1.50	0.50	1.50	0.75	1.50	0.50	1.50	-0.22	0.75
Ion-type	KQ	y_1	PGL	y_2	a_4	y_3	b_5 DPGLI	y_4	b_6	y_5		b_7 ANAQELL
Delta ppm	-15.2	-7.1	-5.8	-9.3	-20.8	-5.8	-6.2 -6.2	-9.6	-5.5	4.2		11.5 21.4

Fragment-ion (m/z)	769.403	786.447	857.484	868.462	882.502^{+3}	888.160^{+3}	971.540	1042.568	1096.568	1141.633^{+2}	1180.663	1198.171^{+2}	1212.676
Frac. Inten.(% of TIC)	1.91	3.13	3.64	4.74	5.45	6.66	6.79	9.16	2.52	9.57	2.40	2.65	5.93
Rel. Inten.(% of BP)	19.96	32.73	38.07	49.56	56.96	69.57	70.90	95.68	26.36	100.00	25.12	27.69	61.99
Score	0.50	1.50	1.50	-0.50	0.50	1.50	1.50	1.50	0.50	1.50	-0.25	1.50	1.50
Ion-type	$y_6\text{-NH}_3$	y_6	y_7		$y_{23}\text{-NH}_3^{+3}$	y_{23}^{+3}	y_8	y_9	b_{10}	y_{19}^{+2}		y_{20}^{+2}	y_{11}
Delta ppm	-22.2	0.9	0.4		17.6	-2.5	13.8	3.4	-3.8	12.9		9.2	5.4



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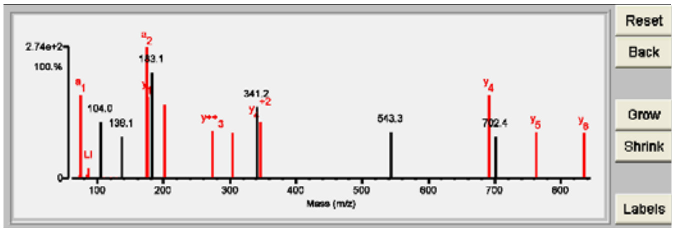
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.70	63.3	7	7/25	K312k	(R)TVLEHYALEDDPLAAFkQR(Q)	2216.1346	114.0760	14.2	39646.4/8.55	HUMAN	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.70	63.3	7	7/25	K312k	(R) T V\L E H Y A L E D D P L/A/A/F/k/Q/R (Q)	2216.1346	114.0760	14.2	39646.4/8.55	HUMAN	Q3ZCQ8	783499	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2

Fragment-ion (m/z)	70.064	72.080	74.061	84.046	84.082	86.096	104.049	110.071	120.079	129.105	136.070	173.128	175.114	183.144	201.122	273.157	303.169	341.108	341.221	346.697^{+2}	543.329^{+3}	692.381	702.398	763.400	834.454
Frac. Inten.(% of TIC)	0.01	0.28	7.36	0.23	0.35	0.94	4.95	0.12	0.12	0.18	3.72	11.56	7.14	9.38	6.45	4.21	3.98	4.51	6.26	5.01	4.10	7.32	3.75	4.06	4.01
Rel. Inten.(% of BP)	0.08	2.39	63.63	1.99	3.00	8.10	42.84	1.08	1.05	1.52	32.16	100.00	61.77	81.14	55.77	36.40	34.43	39.00	54.13	43.31	35.49	63.34	32.46	35.12	34.72
Score	0.20	0.50	0.50	1.00 1.00	0.50	0.22	-0.43	1.00	1.00	0.20	-0.32	0.50	1.50	-0.81	0.50	1.50	1.50	-0.39	-0.54	1.50	-0.35	1.50	-0.32	1.50	1.50
Ion-type	PR	V	a_1	b_1-H_2O E	KQ	LI		H	F	RKQ		a_2	y_1		b_2	$y{+}{+}_3$	y_2			y_4^{+2}		y_4		y_5	y_6
Delta ppm	-18.9	-5.2	-3.2	3.7 16.8	9.8	-6.1		-7.0	-18.1	18.3		-9.5	-29.4		-10.8	-14.5	-27.8			5.6		-3.8		-27.4	-5.0



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Result Summary

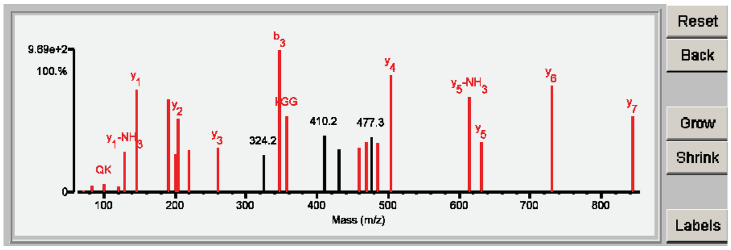
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.64	86.7	8	4/25	K80k	(R)FAQIVQkGGQ(-)	1075.5895	114.0457	2.3	9343.6/5.02	HUMAN	Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B OS=Homo sapiens GN=TIMM8B PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.64	86.7	8	4/25	K80k	(R) F A\Q|I|V/Q/k/G/G/Q (-)	1075.5895	114.0457	2.3	9343.6/5.02	HUMAN	Q9Y5J9	783559	Mitochondrial import inner membrane translocase subunit Tim8 B OS=Homo sapiens GN=TIMM8B PE=1 SV=1

Fragment-ion (m/z)	72.082	84.081	101.072	120.079	130.045	147.076	191.116	200.099	204.094	219.112	261.117	324.197
Frac. Inten.(% of TIC)	0.11	0.47	0.51	0.42	2.76	7.06	6.42	2.62	5.07	2.88	3.07	2.57
Rel. Inten.(% of BP)	1.17	4.80	5.21	4.25	28.26	72.21	65.71	26.78	51.84	29.45	31.42	26.30
Score	0.50		0.50	1.00 1.00	0.50	1.50	0.50	0.75	1.50	0.50	1.50	-0.26
Ion-type	V	QK	QK	a_1 F	y_1-NH_3	y_1	a_2	AQ	y_2	b_2	y_3	
Delta ppm	19.8		9.5	-26.4 -17.3	-38.2	-5.6	-14.1	-23.8	-21.0	-11.0	-8.2	

Fragment-ion (m/z)	347.170	357.179	410.223	430.231	460.266	470.278	477.265^{+2}	485.244	503.251	614.287	631.312	730.384	843.477
Frac. Inten.(% of TIC)	9.77	5.18	3.90	2.99	3.04	3.51	3.83	3.34	8.07	6.52	3.44	7.29	5.18
Rel. Inten.(% of BP)	100.00	53.01	39.95	30.60	31.10	35.88	39.18	34.23	82.56	66.68	35.25	74.58	53.00
Score	0.50	0.75	-0.40	-0.31	0.50	0.75	-0.39	0.75	1.50	0.50	1.50	1.50	1.50
Ion-type	b_3	kGG			b_4	VQk		QkGG	y_4	y_5-NH_3	y_5	y_6	y_7
Delta ppm	-7.4	-27.4			19.7	10.9		-7.4	-12.8	-3.5	-6.4	-0.6	10.6



Result Summary

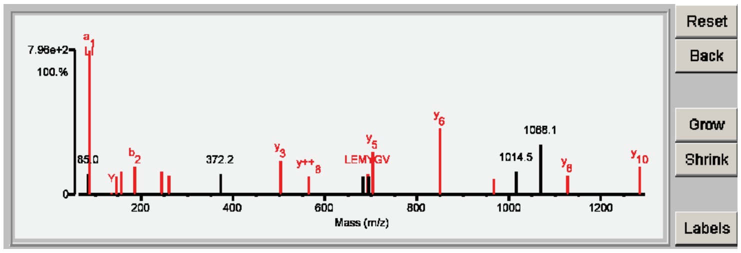
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.66	77.0	9	6/25	K209k	(K)IAQDLEMYGVNYFSIkNK(K)	2133.0685	114.0583	6.9	67820.4/6.07	HUMAN	P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3
2	17.04	74.3	8	7/25	K211k	(K)IAQDLEMYGVNYFSIKNk(K)	2133.0685	114.0583	6.9	67820.4/6.07	HUMAN	P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.66	77.0	9	6/25	K209k	(K) I A\Q/D L E M Y/G V/N Y/F/S I/k/N/K (K)	2133.0685	114.0583	6.9	67820.4/6.07	HUMAN	P26038	405757	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3

Fragment-ion (m/z)	72.078	84.078	85.047	86.094	120.078	129.099	136.077	147.117	157.132	185.124	244.089	261.153
Frac. Inten.(% of TIC)	0.14	0.11	3.11	22.08	0.12	0.08	0.34	2.65	3.50	4.30	3.42	3.00
Rel. Inten.(% of BP)	0.63	0.49	14.08	100.00	0.52	0.38	1.53	11.98	15.83	19.47	15.49	13.58
Score	0.50	0.50	-0.14	0.50 0.50	1.00	0.20	1.00	1.50	0.50	0.50	0.75	1.50
Ion-type	V	KQ		a_1 LI	F	RKQ	Y	y_1	a_2	b_2	QD	y_2
Delta ppm	-35.7	-30.6		-36.3 -23.5	-27.3	-22.8	6.0	28.5	-14.9	-31.1	-18.4	-11.6

Fragment-ion (m/z)	372.229	503.302	564.311	683.027	693.336	695.624	703.405	850.470	967.967	1014.542	1068.053^{+2}	1127.582	1283.666
Frac. Inten.(% of TIC)	3.17	5.19	2.74	2.80	3.06	2.70	6.60	10.06	2.39	3.58	7.67	2.97	4.24
Rel. Inten.(% of BP)	14.34	23.52	12.42	12.68	13.85	12.22	29.88	45.55	10.80	16.23	34.75	13.47	19.22
Score	-0.14	1.50	1.50	-0.13	0.75	-0.12	1.50	1.50	1.50	-0.16	-0.35	1.50	1.50
Ion-type		y_3	$y{++}_8$		LEMYGV		y_5	y_6	$y{++}_{15}$			y_8	y_{10}
Delta ppm		15.9	26.0		10.8		-6.3	-10.1	-2.0			-1.8	-6.4



Result Summary

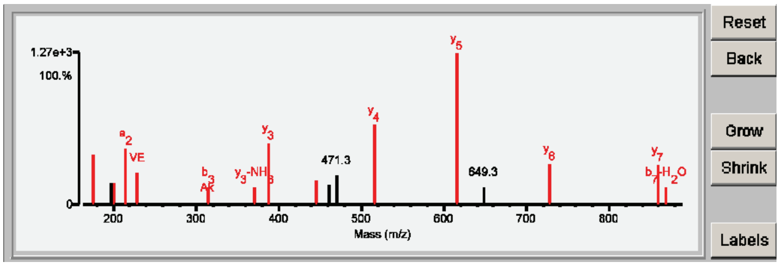
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.43	69.9	7	8/24	K109k	(K)EIAkMAEMLVELVR(R)	1631.8859	114.0681	14.4	14649.7/4.69	HUMAN	Q9Y605	MORF4 family-associated protein 1 OS=Homo sapiens GN=MRFAP1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.43	69.9	7	8/24	K109k	(K) E I A\k M A E/M/L/V/E/L V/R (R)	1631.8859	114.0681	14.4	14649.7/4.69	HUMAN	Q9Y605	405769	MORF4 family-associated protein 1 OS=Homo sapiens GN=MRFAP1 PE=1 SV=1

Fragment-ion (m/z)	72.079	84.079	86.096	104.053	115.034	129.101	142.096	175.117	197.120	201.082	215.138	229.116
Frac. Inten.(% of TIC)	0.13	10.62	0.46	5.70	1.90	0.08	1.96	5.72	2.45	2.40	6.43	3.58
Rel. Inten.(% of BP)	0.78	61.54	2.68	33.02	11.03	0.47	11.35	33.13	14.19	13.90	37.29	20.73
Score	0.50	-0.62	0.22	-0.33	-0.11	0.20	-0.11	1.50	-0.14	0.75	0.50	0.75
Ion-type	V		LI			RKQ		y_1		AE	a_2	VE
Delta ppm	-17.7		-2.6			-12.7		-10.6		-32.2	-8.4	-14.8

Fragment-ion (m/z)	314.181	370.239	387.265	445.229	461.188	471.267^{+2}	516.312	615.388	649.319	728.478	859.480	869.422
Frac. Inten.(% of TIC)	1.93	2.03	6.97	2.68	2.21	3.32	9.03	17.26	1.94	4.68	4.51	2.01
Rel. Inten.(% of BP)	11.19	11.78	40.39	15.51	12.83	19.24	52.32	100.00	11.23	27.15	26.14	11.66
Score	0.75	0.50	1.50	0.75	-0.13	-0.19	1.50	1.50	-0.11	1.50	1.50	0.25
Ion-type	b_3 Ak	y_3-NH_3	y_3	AEML			y_4	y_5		y_6	y_7	b_7-H_2O
Delta ppm	29.5 -6.3	-16.2	-15.6	37.9			-4.1	8.9		16.1	-31.3	2.5



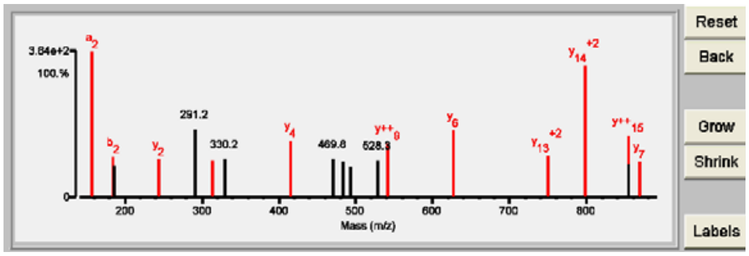
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.70	62.2	9	11/25	K107k	(R)ALGQNPTNAEVLkVLGNPK(S)	1963.0971	114.0557	6.2	22764.1/5.56	HUMAN	P14649	Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1
1	11.70	62.2	9	11/25	K50k	(R)ALGQNPTNAEVLkVLGNPK(S)	1963.0971	114.0557	6.2	16930.2/4.56	HUMAN	P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.70	62.2	9	11/25	K107k	(R) A L\G Q/N/P/T N A E/V L/k/V L/G N/P K (S)	1963.0971	114.0557	6.2	22764.1/5.56	HUMAN	P14649	429221	Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1
1	11.70	62.2	9	11/25	K50k	(R) A L\G Q/N/P/T N A E/V L/k/V L/G N/P K (S)	1963.0971	114.0557	6.2	16930.2/4.56	HUMAN	P60660	429229	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2

Fragment-ion (m/z)	73.080	75.055	84.080	86.097	129.066	157.133	185.126	186.096	244.157	291.196	313.153	330.180	415.233	469.778^{+2}	483.272	492.300	528.342	541.332	627.385	748.922^{+2}	797.456^{+2}	854.482	854.990	869.504	948.009
Frac. Inten.(% of TIC)	2.59	5.51	0.14	0.11	0.08	12.73	3.50	2.81	3.31	5.99	3.17	3.35	4.98	3.37	3.11	2.63	3.23	4.74	5.79	3.65	11.47	5.40	2.88	3.14	2.34
Rel. Inten.(% of BP)	20.34	43.31	1.06	0.85	0.60	100.00	27.51	22.09	26.02	47.02	24.87	26.33	39.16	26.44	24.46	20.64	25.36	37.26	45.45	28.66	90.11	42.40	22.59	24.65	18.41
Score	-0.20	-0.43	0.50	0.22	0.20	0.50	0.50	-0.22	1.50	-0.47	0.75	-0.26	1.50	-0.26	-0.24	-0.21	-0.25	1.50	1.50	1.50	1.50	1.50	-0.23	1.50	-0.18
Ion-type			KQ	LI	QKR	a_2	b_2		y_2		PTN		y_4					y^{++}_{9}	y_6	y_{13}^{+2}	y_{14}^{+2}	y^{++}_{15}		y_7	
Delta ppm			-9.2	5.5	1.1	-1.5	-12.2		-36.7		6.6		7.8					-14.7	3.4	-4.1	5.3	10.7		-18.3	



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Result Summary

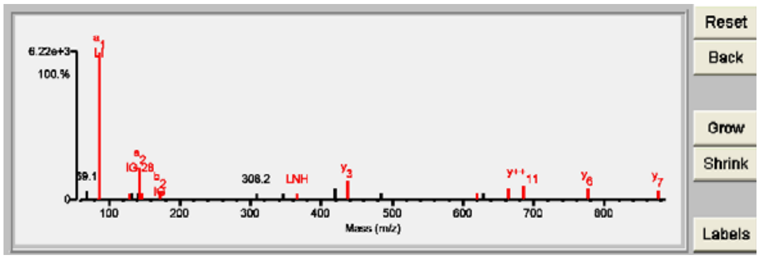
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.64	82.8	8	8/25	K91k	(R)LGIGTkMLNHVLNICEK(D)	1940.0456	114.0578	7.2	19398.5/8.96	HUMAN	Q9GZZ1	N-acetyltransferase 13 OS=Homo sapiens GN=NAT13 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.64	82.8	8	8/25	K91k	(R) L G\I G T k/M/L N H/V/L/N I/C E/K (D)	1940.0456	114.0578	7.2	19398.5/8.96	HUMAN	Q9GZZ1	435007	N-acetyltransferase 13 OS=Homo sapiens GN=NAT13 PE=1 SV=1

Fragment-ion (m/z)	69.071	72.081	84.080	86.096	87.055	110.070	129.100	130.085	133.041	141.102	143.115	147.113	171.111
Frac. Inten.(% of TIC)	2.35	0.11	0.42	44.02	0.06	0.21	0.10	1.77	1.90	1.91	9.50	2.12	2.27
Rel. Inten.(% of BP)	5.34	0.26	0.95	100.00	0.13	0.48	0.24	4.03	4.31	4.35	21.58	4.82	5.17
Score	-0.05	0.50	0.50	0.50	0.33	1.00	0.20	0.50	-0.04	-0.04	0.50	1.50	0.75
Ion-type		V	KQ	a_1	NR	H	RKQ	y_1-NH$_3$			a_2	y_1	b_2
Delta ppm		0.3	-8.0	-10.8	0.1	-14.3	-18.9	-12.0			-17.4	4.1	-12.9
				0.50							IG-28		IG
				LI							-17.4		-12.9
				-10.8									

Fragment-ion (m/z)	308.170	346.191	365.188	418.197	436.185	485.224	620.328^{+2}	629.342^{+3}	663.327	685.855	776.399	875.467
Frac. Inten.(% of TIC)	1.86	1.81	1.76	3.32	5.49	2.11	1.94	1.97	3.06	3.97	3.03	2.94
Rel. Inten.(% of BP)	4.22	4.12	3.99	7.55	12.47	4.79	4.40	4.47	6.94	9.03	6.88	6.67
Score	-0.04	-0.04	0.75	-0.08	1.50	-0.05	1.50	-0.04	1.50	1.50	1.50	1.50
Ion-type			LNH		y_3		y_{10}^{+2}		y_5	y^{++}_{11}	y_6	y_7
Delta ppm			-14.7		-2.6		-1.7		21.5	8.3	2.1	2.3



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Result Summary

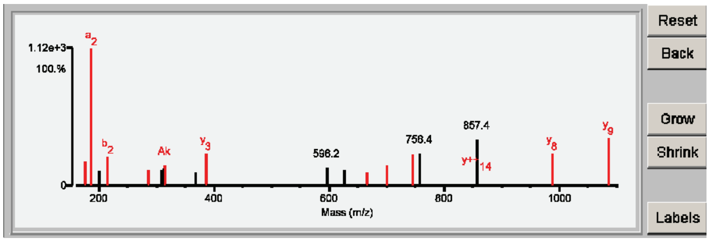
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.99	68.1	9	9/25	K126k	(R)TLAEIAkVELDNMPLR(G)	1812.9888	114.0564	7.0	54231.9/9.01	HUMAN	Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4
2	5.67	50.1	2	14/25	M507m	(K)ELVSVmVTLALHISVGSR(I)	1911.0732	15.9720	-11.9	446704.2/6.12	HUMAN	RQ8TCZ9	REVERSE Fibrocystin OS=Homo sapiens GN=PKHD1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.99	68.1	9	9/25	K126k	(R) T L|A\E I/A/k/V/E L/D N M/P L/R (G)	1812.9888	114.0564	7.0	54231.9/9.01	HUMAN	Q15233	447819	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4

Fragment-ion (m/z)	70.064	72.083	84.043	84.081	86.096	175.116	187.144	201.111	215.138	286.169	308.149	312.184
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -16.1	0.09 0.40 0.50 V 30.9	0.11 0.50 1.00 b_1-H_2O -33.2 1.00 E -20.1	3.92 17.68 -0.18	0.49 2.22 0.22 LI -10.8	3.91 17.60 1.50 y_1 -19.1	22.19 100.00 0.50 a_2 -4.8	2.31 10.40 -0.10	4.64 20.92 0.50 b_2 -8.0	2.57 11.59 0.50 b_3 -27.4 EIA-28 -27.4	2.47 11.12 -0.11	2.77 12.46 -0.12

Fragment-ion (m/z)	314.171	368.252	385.257	596.239	627.314	664.851	700.372^{+2}	745.348	756.395^{+2}	856.986	857.444	987.500	1086.574
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.38 15.25 0.75 Ak -40.0	2.13 9.60 -0.10	5.21 23.49 1.50 y_3 4.2	2.97 13.38 -0.13	2.63 11.83 -0.12	2.17 9.79 1.50 y^{++}_{10} -3.4	3.39 15.29 1.50 y_{11}^{+2} -0.2	4.96 22.37 1.50 y_6 -24.1	5.19 23.37 -0.23	2.06 9.26 1.50 y^{++}_{14} 37.7	7.49 33.77 -0.34	5.30 23.90 1.50 y_8 7.7	7.63 34.39 1.50 y_9 12.0



Result Summary

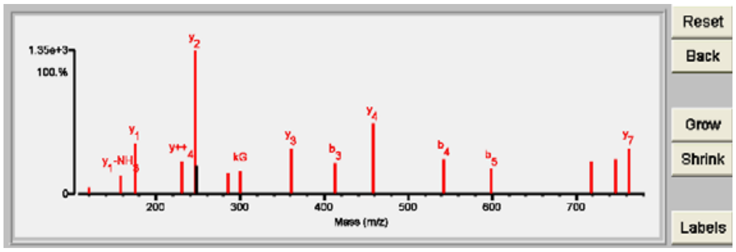
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.49	79.5	10	4/24	K371k	(R)RQQEGFkGTFPDAR(E)	1636.8190	114.0583	8.8	54231.9/9.01	HUMAN	Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4
2	6.24	50.9	3	10/24	K99k	(R)kTNMLWQVFDQAR(R)	1636.8264	114.0509	4.6	20909.3/5.85	HUMAN	RP01275	REVERSE Glucagon OS=Homo sapiens GN=GCG PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.49	79.5	10	4/24	K371k	(R) R Q\Q\E\G\F\k/G T F/P/D/A/R (E)	1636.8190	114.0583	8.8	54231.9/9.01	HUMAN	Q15233	447819	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4

Fragment-ion (m/z)	70.066	72.078	84.045	84.081	86.096	87.053	90.095	112.085	120.081	158.091	175.119	229.624
Frac. Inten.(% of TIC)	0.00	2.45	0.15	0.71	6.14	0.08	8.22	0.08	0.78	2.44	6.46	4.11
Rel. Inten.(% of BP)	0.00	13.45	0.82	3.89	33.64	0.45	45.04	0.45	4.30	13.39	35.38	22.50
Score	0.20	-0.13	1.00	0.50	-0.34	0.33	-0.45	0.33	1.00	0.50	1.50	1.50
Ion-type	PR		E	KQ		NR		R	F	y_1-NH$_3$	y_1	$y{+}{+}_4$
Delta ppm	8.2		6.1	-2.1		-30.9		-16.3	0.2	-8.2	2.6	11.2

Fragment-ion (m/z)	246.158	247.159	285.162	300.166	361.180	413.228	458.234	542.265	599.295	718.362	746.358	763.393
Frac. Inten.(% of TIC)	18.24	3.74	2.72	2.90	5.86	3.92	8.91	4.38	3.26	4.16	4.48	5.79
Rel. Inten.(% of BP)	100.00	20.51	14.88	15.92	32.12	21.48	48.84	24.03	17.88	22.81	24.57	31.74
Score	1.50	-0.21	0.50	0.75	1.50	0.50	1.50	0.50	0.50	0.50	0.50	1.50
Ion-type	y_2		b_2	kG	y_3	b_3	y_4	b_4	b_5	a_6	b_6	y_7
Delta ppm	6.6		-21.6	-6.8	-7.8	2.3	-3.7	-7.3	7.7	-2.6	-1.1	25.5
											y_7-NH$_3$	
											15.4	



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Result Summary

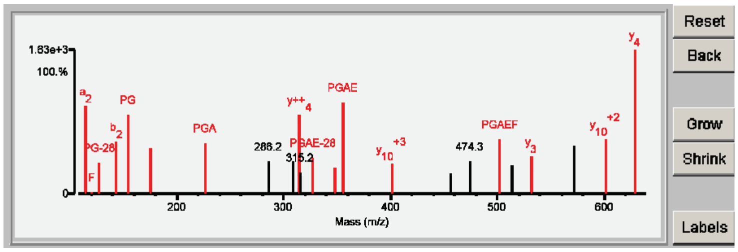
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.23	78.5	4	8/25	K467k	(R)AAPGAEFAPNkR(R)	1228.6433	114.0484	4.0	54231.9/9.01	HUMAN	Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.23	78.5	4	8/25	K467k	(R) A A|P G A E F A/P/N k/R (R)	1228.6433	114.0484	4.0	54231.9/9.01	HUMAN	Q15233	447819	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4

Fragment-ion (m/z)	70.065	84.082	115.086	120.079	127.087	143.080	155.080	175.117	226.116	286.169	309.155	314.678	315.188
Frac. Inten.(% of TIC)	0.00	2.75	7.62	0.18	2.71	4.54	6.88	3.97	4.41	2.83	2.79	6.86	1.82
Rel. Inten.(% of BP)	0.00	21.98	60.92	1.46	21.62	36.28	54.99	31.74	35.23	22.60	22.26	54.78	14.58
Score	0.20	-0.22	0.50	1.00	0.50	0.50	0.75	1.50	0.75	-0.23	-0.22	1.50	-0.15
Ion-type	**PR**		a$_2$	**F**	**PG**-28	b$_2$	**PG**	y$_1$	**PGA**			y++$_4$	
Delta ppm	-6.1		-15.5	-15.6	-5.4	-18.2	-17.4	-11.1	-15.5			-5.7	

Fragment-ion (m/z)	327.165	348.157	355.160	400.861^{+3}	456.201	474.274	502.230	513.273	531.294	571.319	600.802^{+2}	628.353
Frac. Inten.(% of TIC)	3.20	2.27	7.94	2.61	1.74	2.81	4.76	2.53	3.29	4.19	4.80	12.51
Rel. Inten.(% of BP)	25.58	18.12	63.41	20.85	13.88	22.48	38.05	20.22	26.26	33.52	38.34	100.00
Score	0.50	0.75	0.75	1.50	-0.14	-0.22	0.75	-0.20	1.50	-0.34	1.50	1.50
Ion-type	**PGAE**-28	**EFA**	**PGAE**	y$_{10}^{+3}$			**PGAEF**		y$_3$		y$_{10}^{+2}$	y$_4$
Delta ppm	-7.0	1.2	-6.8	-36.5			-1.2		-11.0		-13.6	1.1



Result Summary

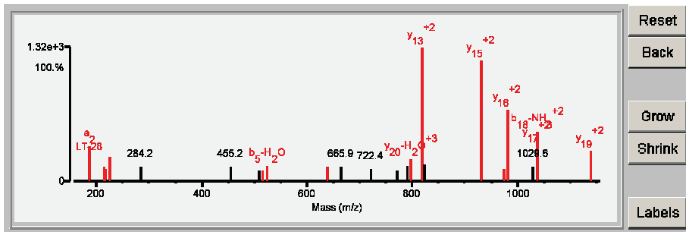
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.04	82.0	7	9/25	K1548k	(R)TLQSLLTPQPPLLkALYTYESK(M)	2504.4011	114.0523	3.6	227921.8/5.83	HUMAN	Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=2
2	11.45	80.3	6	10/25	K1556k	(R)TLQSLLTPQPPLLKALYTYESk(M)	2504.4011	114.0523	3.6	227921.8/5.83	HUMAN	Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.04	82.0	7	9/25	K1548k	(R) T L\Q/S L/L/T/P Q/P P L L k/A L Y T Y E S K (M)	2504.4011	114.0523	3.6	227921.8/5.83	HUMAN	Q92621	456475	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=2

Fragment-ion (m/z)	86.095	101.067	187.141	215.138	216.106	226.120	284.161	455.247	508.281	515.330	525.298	638.363	665.851^{+2}
Frac. Inten.(% of TIC)	0.09	0.10	5.12	2.13	1.69	3.49	2.10	2.14	1.49	1.54	2.15	2.04	2.14
Rel. Inten.(% of BP)	0.47	0.51	26.49	11.00	8.76	18.04	10.86	11.07	7.70	7.97	11.13	10.57	11.05
Score	0.22	0.50	0.50	0.75	0.75	0.75	-0.11	-0.11	-0.08	0.50	0.25	0.25	-0.11
Ion-type	LI	QK	a_2 LT-28	b_2 LT	QS	QP				a_5	b_5-H_2O	b_6-H_2O	
Delta ppm	-17.7	-37.0	-20.8 -20.8	-9.4 -9.4	33.4	3.5				19.3	-12.4	-39.1	

Fragment-ion (m/z)	722.414	770.366	790.372^{+3}	796.095^{+3}	818.946^{+2}	822.534	931.503^{+2}	974.480	982.034^{+2}	1029.612^{+2}	1038.566^{+2}	1138.633^{+2}
Frac. Inten.(% of TIC)	1.78	1.58	2.20	3.24	19.33	2.47	17.46	1.73	10.30	2.08	7.14	4.45
Rel. Inten.(% of BP)	9.21	8.19	11.40	16.78	100.00	12.78	90.31	8.93	53.28	10.76	36.95	23.03
Score	-0.09	-0.08	-0.11	0.50	1.50	-0.13	1.50	1.50	1.50	-0.11	1.50	1.50
Ion-type				y_{20}-H_2O^{+3}	y_{13}^{+2}		y_{15}^{+2}	y_8	y_{16}^{+2}		b_{18}-NH_3^{+2} y_{17}^{+2}	y_{19}^{+2}
Delta ppm				-12.7	-5.6		-3.6	-3.2	3.3		-24.2 -6.2	1.9



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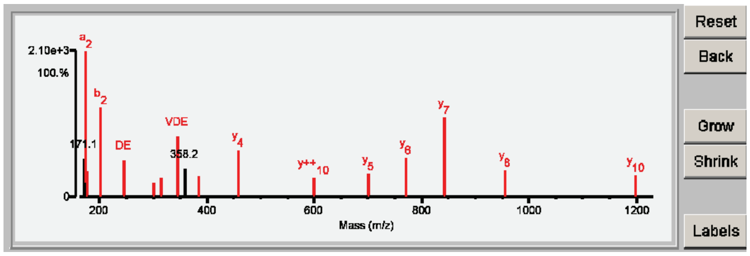
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.97	78.8	9	6/25	K302k	(K)AEVVDEIAAkLGLR(K)	1483.8479	114.0526	6.0	68120.6/5.95	HUMAN	Q8TAT6	Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.97	78.8	9	6/25	K302k	(K) A E\V\V/D E/I/A/A/k/L G L/R (K)	1483.8479	114.0526	6.0	68120.6/5.95	HUMAN	Q8TAT6	449479	Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3

Fragment-ion (m/z)	72.081	84.045	84.078	86.095	102.054	110.062	155.083	171.147	173.090	174.096	175.119	201.086	245.076	300.152	314.175	344.147	358.161^{+2}	385.218	458.308	600.343	700.440	771.485	842.520	955.604	1199.678
Frac. Inten.(% of TIC)	0.31	0.10	5.25	0.20	0.21	2.37	4.10	4.44	16.98	1.73	3.04	10.41	4.34	1.69	2.27	7.10	3.30	2.36	5.38	2.27	2.63	4.63	9.19	3.13	2.57
Rel. Inten.(% of BP)	1.81	0.61	30.90	1.16	1.24	13.96	24.13	26.17	100.00	10.21	17.92	61.32	25.55	9.95	13.37	41.79	19.43	13.90	31.66	13.35	15.46	27.26	54.11	18.41	15.15
Score	0.50		-0.31	0.22	1.00	-0.14	-0.24	-0.26	0.50	-0.10	1.50	0.50	0.75	0.50	0.75	0.75	-0.19	0.75	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	V	E		LI	E				a_2		y_1	b_2	DE	b_3	Ak	VDE		AAk	y_4	y^{++}_{10}	y_5	y_6	y_7	y_8	y_{10}
Delta ppm	-2.4			-13.1	-7.4				-17.7		-2.6	-10.3	-9.4	-15.6	-26.0	2.3		-6.2	-1.6	4.2	-8.8	2.4	-0.3	-0.4	3.3



Result Summary

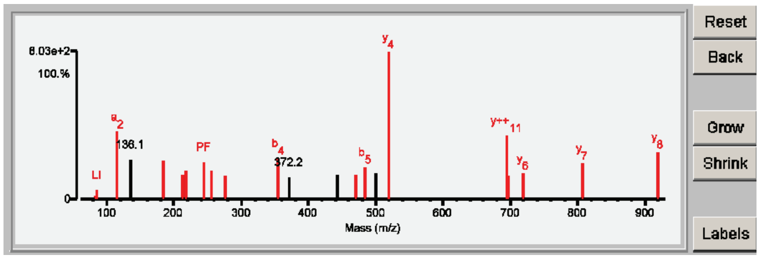
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.36	86.2	8	4/25	K55k	(K)AAIVEkLSSLPFQK(I)	1530.8890	114.0541	6.8	14478.6/5.10	HUMAN	P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.36	86.2	8	4/25	K55k	(K) A A I|V\E\k/L/S/S L/P F/Q K (I)	1530.8890	114.0541	6.8	14478.6/5.10	HUMAN	P61970	454919	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.080	86.096	115.089	120.080	129.103	136.074	185.161	213.158	217.135	245.125	256.167
Frac. Inten.(% of TIC)	0.01	0.46	1.18	8.19	0.10	0.12	4.89	4.73	3.05	3.53	4.53	3.43
Rel. Inten.(% of BP)	0.05	2.56	6.54	45.32	0.57	0.68	27.05	26.19	16.90	19.55	25.05	18.96
Score	0.20	0.50	0.22	0.50	1.00	0.20	-0.27	0.50	0.75	0.50	0.75	0.50
Ion-type	PR	KQ	LI	a_2	F	RKQ		IV-28	IV	PF-28	PF	b_3
Delta ppm	-1.8	-12.8	-10.8	7.9	-10.6	5.9		-25.6	-12.9	-0.6	-17.3	1.3

Fragment-ion (m/z)	275.171	355.232	372.185^{+2}	442.297	471.260	484.262	500.255	519.294	695.393	697.418	719.421	806.441	919.513
Frac. Inten.(% of TIC)	2.86	4.97	2.71	3.02	3.00	3.89	3.22	18.07	7.84	2.82	3.14	4.37	5.87
Rel. Inten.(% of BP)	15.82	27.49	15.01	16.74	16.60	21.55	17.80	100.00	43.42	15.59	17.37	24.16	32.48
Score	1.50	0.50	-0.15	-0.17	0.75	0.50	-0.18	1.50	1.50	0.75	1.50	1.50	1.50
Ion-type	y_2	b_4			VEk	b_5		y_4	$y{++}_{11}$	IVEkL	y_6	y_7	y_8
Delta ppm	-0.3	-9.2			6.0	-31.7		2.8	3.2	-10.0	16.6	0.4	-12.9



Result Summary

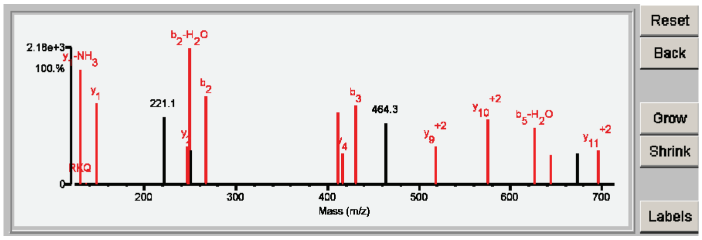
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.95	82.1	9	4/25	K56k	(K)EHYVDLkDRPFFAGLVK(Y)	2034.0807	114.0410	-0.9	17148.8/5.83	HUMAN	P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1
2	7.86	67.7	1	9/25	K97k	(K)VLGAFFPRDkLDVYHEK(L)	2034.0807	114.0410	-0.9	17148.8/5.83	HUMAN	RP15531	REVERSE Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1
3	5.53	57.6	1	12/25	M1063m	(K)LLmRHEYKEKIMGVQEK(D)	2132.1355	15.9863	-4.0	142737.8/5.46	HUMAN	RQ5TCY1	REVERSE Tau-tubulin kinase 1 OS=Homo sapiens GN=TTBK1 PE=1 SV=2
3	5.53	57.6	1	12/25	M1072m	(K)LLMRHEYKEKImGVQEK(D)	2132.1355	15.9863	-4.0	142737.8/5.46	HUMAN	RQ5TCY1	REVERSE Tau-tubulin kinase 1 OS=Homo sapiens GN=TTBK1 PE=1 SV=2
4	5.18	59.0	2	11/25	M254m	(R)VKLVRQmYEHLICVESK(G)	2132.1355	15.9863	-4.0	86045.6/5.68	HUMAN	RQ8WYQ5	REVERSE Protein DGCR8 OS=Homo sapiens GN=DGCR8 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.95	82.1	9	4/25	K56k	(K) E H\Y\V D\L/k/D/R P F F A/G L/V/K (Y)	2034.0807	114.0410	-0.9	17148.8/5.83	HUMAN	P15531	438491	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.079	84.080	86.095	110.068	120.078	129.100	130.084	136.073	147.111	221.099	246.177	249.096
Frac. Inten.(% of TIC)	0.00	0.44	0.72	0.56	0.24	0.28	0.24	10.57	0.12	7.43	6.13	3.54	12.57
Rel. Inten.(% of BP)	0.03	3.50	5.72	4.49	1.94	2.19	1.91	84.11	0.97	59.07	48.74	28.19	100.00
Score	0.20	0.50	0.50	0.22	1.00	1.00	0.20	0.50	1.00	1.50	-0.49	1.50	0.25
Ion-type	PR	V	KQ	LI	H	F	RKQ	y_1-NH_3	Y	y_1		y_2	b_2-H_2O
Delta ppm	-11.8	-19.1	-14.0	-18.9	-29.7	-19.8	-17.3	-13.5	-20.5	-11.6		-15.5	-14.9

Fragment-ion (m/z)	250.095	267.105	412.157	416.288	430.170	464.284^{+3}	517.800^{+2}	575.330^{+2}	626.252	644.262	672.697^{+3}	696.394^{+2}
Frac. Inten.(% of TIC)	3.22	8.11	6.64	2.85	7.27	5.64	3.54	5.92	5.21	2.70	2.90	3.14
Rel. Inten.(% of BP)	25.62	64.49	52.83	22.66	57.85	44.82	28.12	47.09	41.46	21.46	23.07	24.99
Score	-0.26	0.50	0.25	1.50	0.50	-0.45	1.50	1.50	0.25	0.50	-0.23	1.50
Ion-type		b_2	b_3-H_2O	y_4	b_3		y_9^{+2}	y_{10}^{+2}	b_5-H_2O	b_5		y_{11}^{+2}
Delta ppm		-17.1	-14.4	4.0	-7.5		-20.5	9.4	-9.6	-10.5		0.5



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Result Summary

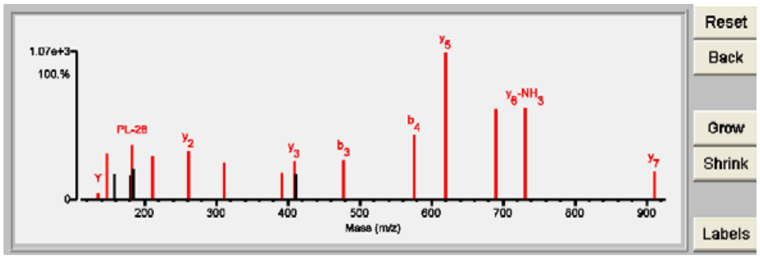
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.26	85.3	7	5/25	K105k	(R)kYAVLYQPLFDK(R)	1484.8148	114.0499	4.3	45374.4/4.36	HUMAN	P55209	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.26	85.3	7	5/25	K105k	(R) k Y A\V\L|Y Q/P L/F/D/K (R)	1484.8148	114.0499	4.3	45374.4/4.36	HUMAN	P55209	448905	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.080	85.085	86.096	101.069	120.079	136.075	147.112	159.106	181.093	183.148
Frac. Inten.(% of TIC)	0.01	0.17	0.90	2.93	0.38	0.21	0.13	0.70	5.02	2.84	2.63	5.95
Rel. Inten.(% of BP)	0.04	1.07	5.55	18.13	2.38	1.29	0.78	4.33	31.08	17.55	16.29	36.87
Score	0.20	0.50	0.50	-0.18	0.22		1.00	1.00	1.50	-0.18	-0.16	0.50
Ion-type	PR	V	KQ		LI	KQ	F	Y	y_1			PL-28
Delta ppm	-3.2	-5.2	-12.8		-10.8		-14.0	-5.8	-4.8			-10.8

Fragment-ion (m/z)	184.142	211.144	262.137	310.175^{+2}	391.195	409.209	410.216^{+2}	477.237	576.308	619.343	689.394	730.389	910.466
Frac. Inten.(% of TIC)	3.44	4.79	5.38	4.01	2.95	4.19	2.88	4.28	7.05	16.15	9.89	10.06	3.05
Rel. Inten.(% of BP)	21.29	29.65	33.30	24.80	18.27	25.95	17.86	26.52	43.64	100.00	61.25	62.31	18.89
Score	-0.21	0.75	1.50	1.50	0.50	1.50	-0.18	0.50	0.50	1.50	0.50	0.50	1.50
Ion-type		PL	y_2	y_5^{+2}	y_3-H_2O	y_3		b_3	b_4	y_5	b_5	y_6-NH_3	y_7
Delta ppm		-6.2	-10.1	-4.0	-5.6	3.0		-20.8	-12.4	-2.4	-8.2	16.0	-1.0



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Result Summary

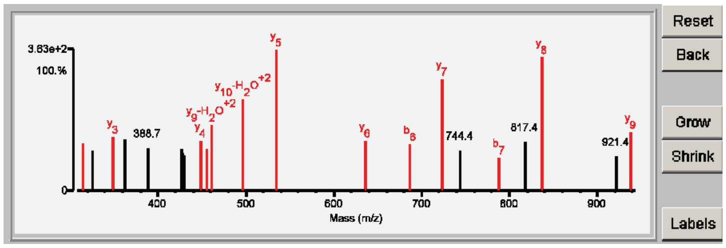
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.96	62.9	10	11/25	K24k	(R)kVLGSSTSATNSTSVSSR(K)	1768.9035	114.0509	4.2	11986.6/9.85	HUMAN	Q15004	PCNA-associated factor OS=Homo sapiens GN=PAF PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.96	62.9	10	11/25	K24k	(R) k V L\G S S\T\S A/T/N/S/T/S/V/S S R (K)	1768.9035	114.0509	4.2	11986.6/9.85	HUMAN	Q15004	478119	PCNA-associated factor OS=Homo sapiens GN=PAF PE=1 SV=1

Fragment-ion (m/z)	84.080	87.055	303.652^{+2}	314.214	326.195	349.182	362.705	388.697^{+2}	426.280^{+2}	428.732	429.243	448.252
Frac. Inten.(% of TIC)	8.23	0.07	3.46	3.23	2.71	3.62	3.45	2.94	2.86	2.62	2.42	3.39
Rel. Inten.(% of BP)	85.81	0.73	36.04	33.65	28.22	37.78	36.02	30.61	29.87	27.34	25.27	35.33
Score	-0.86	0.33	-0.36	0.50	-0.28	1.50	-0.36	-0.31	-0.30	-0.27	-0.25	1.50
Ion-type		NR		a_2		y_3						y_4
Delta ppm		0.1		-16.8		-2.6						0.4

Fragment-ion (m/z)	455.302	460.710^{+2}	496.239^{+2}	535.286	636.353	686.381	723.365	744.360	787.432	817.423	837.412	921.383	938.457
Frac. Inten.(% of TIC)	2.85	4.46	6.18	9.59	3.44	3.18	7.57	2.78	2.29	3.32	9.02	2.33	4.01
Rel. Inten.(% of BP)	29.76	46.49	64.48	100.00	35.88	33.15	78.97	29.02	23.84	34.58	94.08	24.30	41.77
Score	0.50	0.50	0.50	1.50	1.50	0.50	1.50	-0.29	0.50	-0.35	1.50	-0.24	1.50
Ion-type	b_3	y_9-H_2O^{+2}	y_{10}-H_2O^{+2}	y_5	y_6	b_6	y_7		b_7		y_8		y_9
Delta ppm	6.5	-32.9	-9.5	4.2	34.2	-5.3	3.0		-0.6		6.9		3.3



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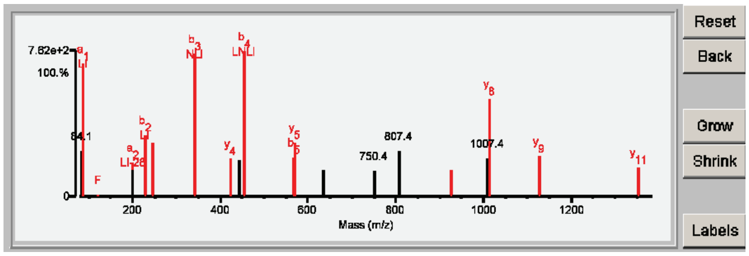
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.33	76.6	7	9/25	K48k	(K)LLNLISkLFCSGT(-)	1465.8083	114.0442	0.8	6030.1/10.30	HUMAN	Q13794	Phorbol-12-myristate-13-acetate-induced protein 1 OS=Homo sapiens GN=PMAIP1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.33	76.6	7	9/25	K48k	(K) L L|N\L|I|S/k L/F/C S G T (-)	1465.8083	114.0442	0.8	6030.1/10.30	HUMAN	Q13794	27551	Phorbol-12-myristate-13-acetate-induced protein 1 OS=Homo sapiens GN=PMAIP1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.082	84.079	86.095	87.055	120.080	199.187	200.150	227.177	228.134	246.111	341.214	424.146	443.270^{+2}	454.304	567.372	571.213	636.366	750.361	807.392	926.434	1007.448	1013.467	1126.562	1353.668
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.07 0.57 -0.01	3.61 30.86 -0.31	3.64 31.19 -0.31	10.60 90.75 0.50 a_1 -25.8 0.50 LI -13.1	0.07 0.64 0.33 NR -5.6	0.11 0.94 1.00 F -9.8	2.74 23.47 0.50 a_2 26.2 LI-28 26.2	2.19 18.77 -0.19	4.96 42.47 0.75 b_2 0.4 LI 0.4	4.43 37.88 0.75 NL -4.2	4.33 37.10 0.50 y_3-H$_2$O 9.6	11.48 98.28 0.75 b_3 -15.3 NLI -15.3	3.07 26.28 1.50 y_4 -7.7	2.97 25.41 -0.25	11.68 100.00 0.75 b_4 0.2 LNLI 0.2	3.18 27.22 0.50 b_5 -27.9	4.39 37.53 1.50 y_5 -9.1	2.18 18.69 -0.19	2.02 17.31 -0.17	3.65 31.25 -0.31	2.15 18.40 1.50 y_7 -6.9	3.02 25.82 -0.26	7.82 66.92 1.50 y_8 -4.6	3.28 28.05 1.50 y_9 5.3	2.34 20.03 1.50 y_{11} -11.4



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Result Summary

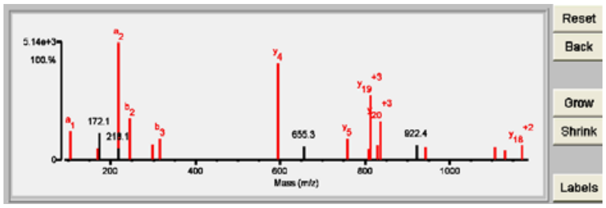
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.02	87.5	9	5/25	K86k	(R)MIAPEGSLVFHEkAWNAYPYCR(T)	2639.2534	114.0576	5.3	31540.2/6.41	HUMAN	P48739	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2
2	4.54	50.9	2	15/25	M204m M209m	(K)TFHEVSQKNAPFLEmLRNDmSVK(R)	2721.3487	31.9623	-10.0	31941.9/5.64	HUMAN	RP0C7T9	REVERSE Putative basic leucine zipper and W2 domain-containing protein 1-like 1 OS=Homo sapiens GN=BZW1L1 PE=2 SV=1
2	4.54	50.9	2	15/25	M204m M209m	(K)TFHEVSQKNAPFLEmLRNDmSVK(R)	2721.3487	31.9623	-10.0	48043.5/5.75	HUMAN	RQ7L1Q6	REVERSE Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1
3	3.30	55.7	1	15/25	M429m	(K)MLDFFQGHIDGCVTIPADVEImTK(E)	2737.3034	16.0076	4.6	57073.6/6.78	HUMAN	RP48454	REVERSE Serine/threonine-protein phosphatase 2B catalytic subunit gamma isoform OS=Homo sapiens GN=PPP3CC PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.02	87.5	9	5/25	K86k	(R) M I|A|P/E/G S L V F H E k A/W/N/A/Y/P Y C R (T)	2639.2534	114.0576	5.3	31540.2/6.41	HUMAN	P48739	501601	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2

Fragment-ion (m/z)	70.064	84.081	86.096	104.052	136.073	159.092	169.095	172.115	217.136	218.140	245.132	298.142
Frac. Inten.(% of TIC)	0.01	1.68	0.09	4.71	0.10	0.05	1.86	4.39	19.23	1.86	6.89	2.60
Rel. Inten.(% of BP)	0.03	8.75	0.46	24.52	0.51	0.24	9.67	22.84	100.00	9.70	35.83	13.53
Score	0.20	-0.09	0.22	0.50	1.00	2.00	0.75	-0.23	0.50	-0.10	0.50	1.50
Ion-type	PR		LI	a_1	Y	W	AP		a_2		b_2	y^{++}_4 APE
Delta ppm	-18.9		-9.6	-12.9	-19.0	3.3	-13.3		-6.5		0.3	19.5 8.6

Fragment-ion (m/z)	316.168	595.268	655.341^{+2}	758.335	807.385^{+3}	813.390^{+3}	829.365	837.085^{+3}	922.440^{+2}	943.405	1106.530	1129.484	1171.053^{+2}
Frac. Inten.(% of TIC)	3.52	15.85	2.14	3.59	1.78	10.57	2.36	6.39	2.46	2.02	1.99	1.55	2.31
Rel. Inten.(% of BP)	18.30	82.43	11.11	18.65	9.27	54.97	12.28	33.22	12.77	10.50	10.36	8.05	12.02
Score	0.50	1.50	-0.11	1.50	0.50	1.50	1.50	1.50	-0.13	1.50	1.50	1.50	1.50
Ion-type	b_3	y_4		y_5	$y_{19}\text{-}H_2O^{+3}$	y_{19}^{+3}	y_6	y_{20}^{+3}		y_7	y^{++}_{17}	y_8	y_{18}^{+2}
Delta ppm	-1.7	3.2		7.9	6.5	9.0	-1.4	26.9		-4.4	5.6	-4.2	6.9



Result Summary

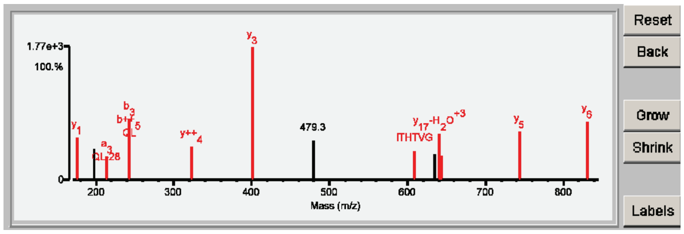
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.89	72.4	6	7/25	K103k	(K)GAIQLGITHTVGSLSTkPER(D)	2065.1400	114.0689	11.9	62633.7/8.41	HUMAN	Q99755	Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha OS=Homo sapiens GN=PIP5K1A PE=1 SV=1
2	5.91	68.3	1	11/25	K935k K937k	(K)IDKRNYQIGkTkVFLK(E)	1951.1487	228.0602	-11.8	243559.3/8.88	HUMAN	Q13459	Myosin-IXb OS=Homo sapiens GN=MYO9B PE=1 SV=2
3	5.24	50.3	2	10/25	None	(K)NVQALFQRNPQLFESIFK(D)	2179.1658	0.0431	19.8	121165.8/8.74	HUMAN	RQ9Y6K5	REVERSE 2'-5'-oligoadenylate synthetase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.89	72.4	6	7/25	K103k	(K) G A I\Q L\G I T H T V G S L/S/T/k/P E/R (D)	2065.1400	114.0689	11.9	62633.7/8.41	HUMAN	Q99755	500231	Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha OS=Homo sapiens GN=PIP5K1A PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.043	84.080	86.096	87.100	101.071	110.070	120.080	129.101	143.117	157.129
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.04 0.20 PR 3.9	0.21 1.17 0.50 V -10.8	0.16 0.90 1.00 E -13.0	0.47 2.71 0.50 KQ -4.5	2.36 13.47 0.22 LI -6.1	3.66 20.92 -0.21	0.31 1.77 0.50 a_2 -13.2 KQ	0.26 1.47 1.00 H -11.6	6.97 39.81 -0.40	0.15 0.88 0.20 RKQ -8.1	3.42 19.56 -0.20	3.78 21.58 -0.22

Fragment-ion (m/z)	175.118	197.131	214.154	242.149	322.168	401.217	479.265	609.334	634.677^{+3}	640.677^{+3}	643.348	744.407	831.434
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	5.63 32.17 1.50 y_1 -3.7	4.04 23.09 -0.23	3.12 17.85 0.50 a_3 -10.7 QL-28 -10.7	8.03 45.87 0.75 b_3 -7.1 b++$_5$ -4.8 QL -7.1	4.41 25.21 1.50 y++$_4$ -37.7	17.51 100.00 1.50 y_3 8.0	5.18 29.60 -0.30	3.77 21.54 0.75 ITHTVG -4.4	3.30 18.85 -0.19	5.99 34.24 0.50 y_{17}-H$_2$O^{+3} -7.4	3.25 18.55 1.50 y_4 -7.1	6.37 36.40 1.50 y_5 9.3	7.63 43.61 1.50 y_6 2.6



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Result Summary

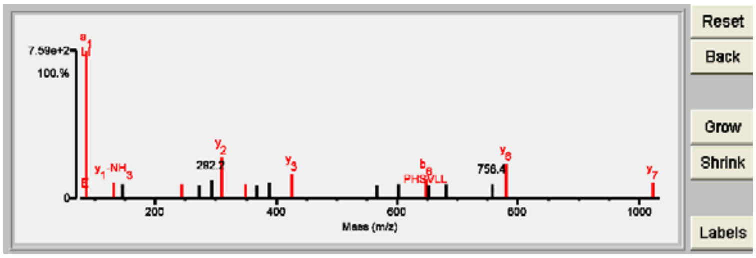
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.72	69.7	6	10/25	K27k	(K)LPHSVLLEIQkELLDYK(G)	2038.1583	114.0587	7.3	40422.9/7.56	HUMAN	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.72	69.7	6	10/25	K27k	(K) L P H\S V L\L E I Q/k/E L L/D/Y K (G)	2038.1583	114.0587	7.3	40422.9/7.56	HUMAN	Q9Y617	716561	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Fragment-ion (m/z)	84.042	84.081	86.096	101.070	102.053	129.101	130.088	136.076	146.125	243.130
Frac. Inten.(% of TIC)	0.22	0.21	30.80	0.09	0.16	0.13	3.39	0.16	2.98	3.13
Rel. Inten.(% of BP)	0.71	0.68	100.00	0.29	0.51	0.41	11.01	0.53	9.68	10.15
Score	1.00	0.50	0.50			0.20	0.50	1.00	-0.10	0.75
Ion-type	E	KQ	a_1	KQ	E	RKQ	y_1-NH_3	Y		EL
Delta ppm	-27.2	1.5	-14.2			-10.4	10.3	4.5		-19.0
			0.50							
			LI							
			-1.5							

Fragment-ion (m/z)	272.141	292.184	310.182	348.192	368.164	388.720	425.206	567.299	601.389	647.397	652.313	680.370	758.390	780.406	1022.553
Frac. Inten.(% of TIC)	2.71	3.88	8.43	3.13	2.71	3.33	5.20	2.81	2.91	4.13	2.79	3.07	3.11	7.20	3.34
Rel. Inten.(% of BP)	8.80	12.61	27.38	10.15	8.80	10.83	16.88	9.11	9.44	13.40	9.05	9.97	10.11	23.38	10.84
Score	-0.09	-0.13	1.50	0.50	-0.09	-0.11	1.50	-0.09	-0.09	0.75	-0.09	-0.10	-0.10	1.50	1.50
Ion-type			y_2	b_3			y_3			b_6				y_6	y_7
Delta ppm			18.3	-34.2			7.8			12.8				-10.0	0.9
										PHSVLL					
										12.8					



Result Summary

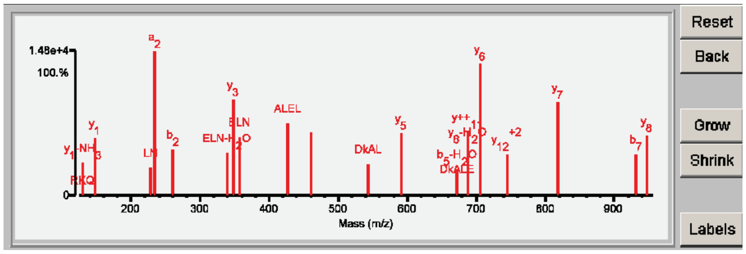
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.94	97.4	9	1/25	K323k	(R)FLDkALELNMLSLK(G)	1634.9186	114.0688	14.8	40422.9/7.56	HUMAN	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2
2	8.53	52.4	4	11/25	K333k	(R)FLDKALELNMLSLk(G)	1634.9186	114.0688	14.8	40422.9/7.56	HUMAN	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.94	97.4	9	1/25	K323k	(R) F L|D/k A L/E|L/N/M/L/S L/K (G)	1634.9186	114.0688	14.8	40422.9/7.56	HUMAN	Q9Y617	716561	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Fragment-ion (m/z)	84.081	86.097	102.055	120.081	121.085	129.102	130.087	147.113	228.136	233.166	261.163	339.172
Frac. Inten.(% of TIC)	0.48	0.94	0.09	0.83	2.64	0.09	2.63	4.54	2.21	11.49	3.73	3.42
Rel. Inten.(% of BP)	4.19	8.16	0.81	7.26	22.99	0.74	22.90	39.52	19.25	100.00	32.44	29.74
Score	0.50	0.22	1.00	1.00	-0.23	0.20	0.50	1.50	0.75	0.50	0.50	0.50
Ion-type	KQ	LI	E	a_1		RKQ	y_1-NH_3	y_1	LN	a_2	b_2	ELN-H_2O
Delta ppm	3.9	0.9	0.4	-9.8 1.00 F -0.6		-1.1	7.3	2.0	0.6	1.1	6.7	14.8

Fragment-ion (m/z)	347.232	357.182	427.261	460.317	542.298	591.359	671.347	687.402	705.405	744.918^{+2}	818.486	931.503	947.532
Frac. Inten.(% of TIC)	7.65	4.65	5.73	5.06	2.46	4.98	2.15	5.06	10.43	3.29	7.42	3.24	4.77
Rel. Inten.(% of BP)	66.62	40.52	49.91	44.08	21.46	43.36	18.72	44.08	90.83	28.66	64.56	28.22	41.56
Score	1.50	0.75	0.75	1.50	0.75	1.50	0.75	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type	y_3	ELN	ALEL	y_4	DkAL	y_5	b_5-H_2O	$y{+}{+}_{11}$	y_6	y_{12}^{+2}	y_7	b_7	y_8
Delta ppm	9.2	10.8	11.7	8.8	5.9	9.4	-7.8 DkALE 14.9	10.6 y_6-H_2O 23.6	12.5	13.5	7.4	14.6	9.4



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Result Summary

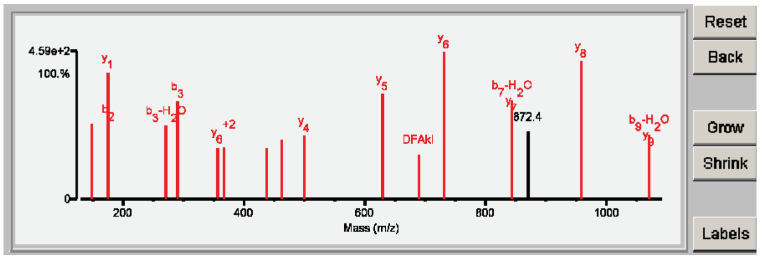
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.26	88.5	11	2/25	K51k	(R)SSDFAkIINNTENLVR(E)	1820.9501	114.0540	5.7	40422.9/7.56	HUMAN	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.26	88.5	11	2/25	K51k	(R) S/S\D\F\A k I/I/N/N/T/E/N L V/R (E)	1820.9501	114.0540	5.7	40422.9/7.56	HUMAN	Q9Y617	716561	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2

Fragment-ion (m/z)	60.044	70.064	84.044	84.082	86.094	87.054	102.054	120.082	147.075	175.067	175.116	272.085
Frac. Inten.(% of TIC)	4.82	0.00	0.08	7.29	0.60	0.10	0.08	0.31	4.64	4.68	7.89	4.56
Rel. Inten.(% of BP)	52.53	0.03	0.93	79.38	6.50	1.06	0.91	3.36	50.54	50.92	85.94	49.69
Score	0.50	0.20	1.00	-0.79	0.22	0.33		1.00	0.50	0.50	1.50	0.25
Ion-type	a_1	PR	E		LI	NR	E	F	a_2	b_2	y_1	b_3-H_2O
Delta ppm	-16.4	-20.3	-5.8		-24.7	-16.0		6.0	-19.1	-31.0	-15.1	-14.4

Fragment-ion (m/z)	290.098	356.226	366.213^{+2}	437.171	462.741^{+2}	501.314	630.359	689.351	731.402	845.447	872.443	959.485	1072.563
Frac. Inten.(% of TIC)	6.11	3.17	3.28	3.15	3.73	4.00	6.57	2.77	9.18	6.14	4.16	8.63	4.04
Rel. Inten.(% of BP)	66.50	34.55	35.75	34.29	40.58	43.53	71.56	30.19	100.00	66.89	45.34	94.03	44.05
Score	0.50	0.75	1.50	0.50	1.50	1.50	1.50	0.75	1.50	1.50	-0.45	1.50	1.50
Ion-type	b_3	kI	y_6^{+2}	b_4	$y{+}{+}_{15}^{+2}$	y_4	y_5	DFAkI	y_6	b_7-H_2O y_7		y_8	b_9-H_2O y_9
Delta ppm	-6.5	-11.0	19.5	8.5	-9.8	-0.7	3.9	-16.5	-3.7	36.4 -0.5		-5.7	18.2 -11.0



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Result Summary

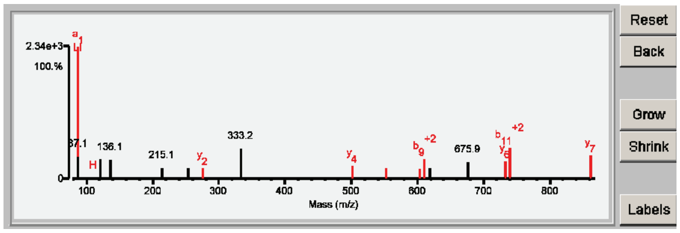
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.16	62.4	8	9/24	K207k	(K)ICkPLHELIMQLLEETPEEK(Q)	2450.2669	114.0420	-0.4	25569.4/5.57	HUMAN	P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.16	62.4	8	9/24	K207k	(K) I C k P L H E L\I\M Q\L L/E/E/T/P E/E K (Q)	2450.2669	114.0420	-0.4	25569.4/5.57	HUMAN	P68402	476703	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.080	84.043	86.096	87.100	101.072	102.054	110.070	120.079	129.101	136.073	215.137
Frac. Inten.(% of TIC)	0.01	6.17	0.14	30.22	4.99	0.11	0.07	0.18	4.65	0.09	4.15	2.45
Rel. Inten.(% of BP)	0.02	20.41	0.45	100.00	16.52	0.38	0.23	0.59	15.38	0.30	13.73	8.10
Score	0.20	-0.20	1.00	0.50	-0.17	0.50		1.00	-0.15	0.20	-0.14	-0.08
Ion-type	PR		E	a_1		QK	E	H		RKQ		
Delta ppm	-6.1		-13.0	-18.9 0.50 LI -6.1		5.5		-7.9		-7.3		

Fragment-ion (m/z)	253.134	276.159	333.168	502.249	553.298^{+2}	603.300	609.841^{+2}	618.356^{+2}	675.859^{+2}	732.338	739.375^{+2}	861.397
Frac. Inten.(% of TIC)	2.45	2.55	6.78	2.88	2.55	2.30	4.65	2.34	3.63	4.07	7.18	5.41
Rel. Inten.(% of BP)	8.12	8.45	22.43	9.53	8.43	7.61	15.38	7.74	12.00	13.46	23.76	17.90
Score	-0.08	1.50	-0.22	1.50	0.50	1.50	0.50	-0.08	-0.12	1.50	0.50	1.50
Ion-type		y_2		y_4	b_8^{+2}	y_5	b_9^{+2}			y_6	b_{11}^{+2}	y_7
Delta ppm		13.0		-2.7	4.1	2.4	6.0			-4.4	-16.0	15.1



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Result Summary

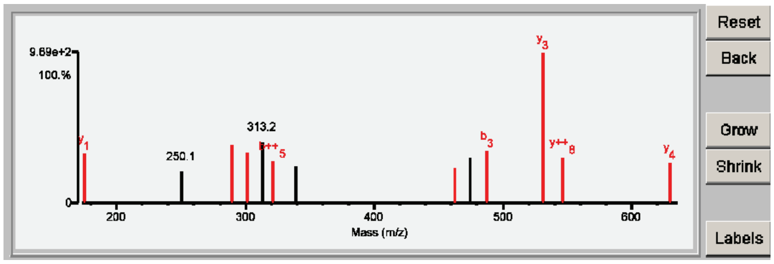
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.81	55.3	6	8/25	K165k	(R)WYHPGCFVkNR(E)	1463.7001	114.0508	5.0	113084.4/8.99	HUMAN	P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.81	55.3	6	8/25	K165k	(R) W Y H|P G\C F/V/k/N/R (E)	1463.7001	114.0508	5.0	113084.4/8.99	HUMAN	P09874	482543	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.081	84.081	86.096	87.054	110.073	120.078	129.105	132.081	136.076	159.091	170.059	175.113
Frac. Inten.(% of TIC)	0.01	0.47	9.41	4.60	0.09	0.44	0.47	0.14	5.81	0.15	0.19	7.09	5.01
Rel. Inten.(% of BP)	0.07	3.09	61.56	30.12	0.58	2.89	3.07	0.92	38.01	0.96	1.25	46.39	32.81
Score	0.20	0.50	-0.62	-0.30	0.33	1.00	1.00	0.20	-0.38	1.00	2.00 2.00	-0.46	1.50
Ion-type	PR	V			NR	H	F	RKQ		Y	a_1 W		y_1
Delta ppm	-0.4	-1.0			-12.5	13.0	-23.9	18.3		0.1	-10.5 -3.6		-35.7

Fragment-ion (m/z)	250.095	289.163	301.128	313.178	321.136	339.212	462.193	474.276	487.204	531.299	546.260	630.367
Frac. Inten.(% of TIC)	3.17	6.01	5.18	6.23	4.29	3.76	3.57	4.62	5.32	15.28	4.64	4.07
Rel. Inten.(% of BP)	20.72	39.34	33.89	40.77	28.09	24.62	23.35	30.24	34.80	100.00	30.34	26.63
Score	-0.21	1.50	0.75	-0.41	0.50	-0.25	0.75	-0.30	0.50	1.50	1.50	1.50
Ion-type		y_2	YH		$b{++}_5$		PGCF		b_3	y_3	$y{++}_8$	y_4
Delta ppm		2.8	-7.7		-30.6		24.7		-13.2	-2.2	-26.1	-1.4



Result Summary

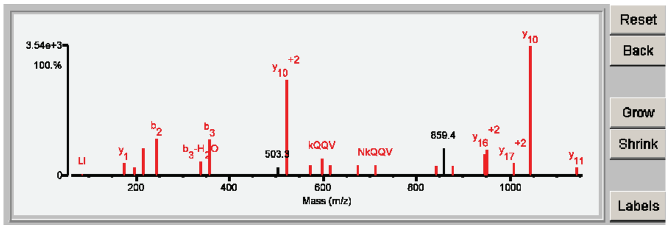
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.65	93.4	9	2/25	K269k	(K)ELLIFNkQQVPSGESAILDR(V)	2257.2187	114.0494	2.7	113084.4/8.99	HUMAN	P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4
2	9.20	66.0	4	12/25	K1201k	(R)TLEAEKQSKQLAELEQQkR(T)	2257.2147	114.0534	4.4	237348.2/5.85	HUMAN	RQ9HD67	REVERSE Myosin-X OS=Homo sapiens GN=MYO10 PE=1 SV=3
3	8.90	63.9	3	13/25	K539k K544k	(K)AIVICPTDEDLkDRTIkR(T)	2143.1540	228.1141	11.9	95739.0/6.49	HUMAN	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2
4	8.67	52.5	3	14/25	K82k	(R)GAYGVVEKMRHVPSGQIMAVk(R)	2257.1944	114.0737	13.0	37492.6/7.01	HUMAN	P52564	Dual specificity mitogen-activated protein kinase kinase 6 OS=Homo sapiens GN=MAP2K6 PE=1 SV=1
5	7.48	73.6	2	12/25	M108m K105k K107k	(K)LLEVLSGEMLPKPTkGkmR(I)	2127.2028	244.0652	-6.6	246469.3/5.15	HUMAN	P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.65	93.4	9	2/25	K269k	(K) E L\L|I/F/N k Q Q|V/P/S G E/S A I L D/R (V)	2257.2187	114.0494	2.7	113084.4/8.99	HUMAN	P09874	482543	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.080	84.042	86.095	175.116	197.127	215.137	243.131	338.205	356.217	503.279	522.767^{+2}
Frac. Inten.(% of TIC)	0.00	0.07	0.05	0.31	2.36	1.62	4.91	6.71	2.62	6.60	1.56	17.46
Rel. Inten.(% of BP)	0.01	0.31	0.20	1.31	9.94	6.81	20.70	28.27	11.02	27.79	6.58	73.56
Score	0.20	0.50	1.00	0.22	1.50	0.75	0.50	0.50	0.25	0.50	-0.07	1.50
Ion-type	PR	V	E	LI	y_1	VP	a_2	b_2	b_3-H_2O	b_3		y_{10}^{+2}
Delta ppm	3.9	-13.5	-26.1	-18.9	-15.7	-13.5	-13.6	-18.2	-9.8	-5.9		-5.3

Fragment-ion (m/z)	572.310^{+2}	598.333	614.839^{+2}	674.387	712.374	842.412	859.429	878.459^{+2}	947.481	951.985^{+2}	1008.535^{+2}	1044.528	1143.584
Frac. Inten.(% of TIC)	1.88	3.24	1.92	1.88	2.01	1.74	5.00	1.81	3.86	4.83	2.25	23.74	1.57
Rel. Inten.(% of BP)	7.91	13.66	8.11	7.92	8.45	7.35	21.07	7.64	16.24	20.33	9.46	100.00	6.63
Score	1.50	0.75	0.50	1.50	0.75	0.50	-0.21	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_{11}^{+2}	kQQV	b_9^{+2}	y_6	NkQQV	y_8-H_2O		y_{15}^{+2}	y_9	y_{16}^{+2}	y_{17}^{+2}	y_{10}	y_{11}
Delta ppm	10.6	2.5	1.4	5.2	-1.1	-29.6		6.9	1.3	-2.2	5.7	-3.9	-14.1



Result Summary

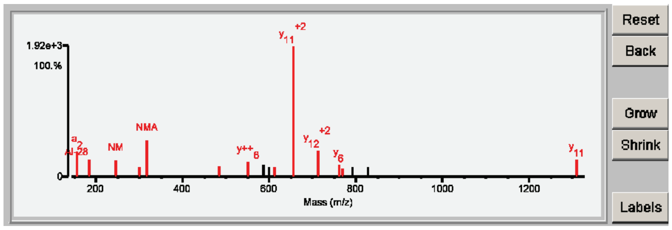
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.68	78.9	9	7/25	K278k	(K)ALNMAIPGGPkFEPLVR(D)	1810.0044	114.0546	6.0	273601.9/8.95	HUMAN	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2
2	7.29	50.8	3	14/25	K487k	(K)EIkELEELAAAPNVKR(L)	1810.0069	114.0521	4.7	87978.3/7.75	HUMAN	RQ9BVJ6	REVERSE U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1
3	5.12	58.1	1	15/25	None	(K)ICALRQVNPGWRRGLK(H)	1924.0810	-0.0221	-11.5	138735.2/9.46	HUMAN	RQ92833	REVERSE Protein Jumonji OS=Homo sapiens GN=JARID2 PE=2 SV=2
4	5.12	56.3	2	13/25	K4033k K4034k	(K)KEEPLPkkEQLASAK(D)	1695.9640	228.0950	4.7	566659.8/6.12	HUMAN	RQ9Y6V0	REVERSE Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=3
5	4.55	54.3	2	14/25	K4033k K4041k	(K)KEEPLPkKEQLASAk(D)	1695.9640	228.0950	4.7	566659.8/6.12	HUMAN	RQ9Y6V0	REVERSE Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.68	78.9	9	7/25	K278k	(K) A L\N\M A/I/P G G/P k/F/E/P\L V R (D)	1810.0044	114.0546	6.0	273601.9/8.95	HUMAN	Q6P2Q9	520433	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2

Fragment-ion (m/z)	70.067	72.079	84.080	86.095	87.051	120.078	129.102	136.069	157.133	185.134	246.093	299.181	317.128
Frac. Inten.(% of TIC)	0.00	0.23	7.15	0.40	2.39	0.16	0.08	2.13	5.99	4.07	3.85	2.13	8.48
Rel. Inten.(% of BP)	0.01	0.74	23.41	1.32	7.82	0.53	0.28	6.99	19.62	13.32	12.60	6.97	27.75
Score	0.20	0.50	-0.23	0.22	-0.08	1.00	0.20	-0.07	0.50	0.75	0.75	0.50	0.75
Ion-type	PR	V		LI		F	RKQ		a_2 AI-28	b_2 AI	NM	b_3	NMA
Delta ppm	23.9	-20.5		-13.1		-21.4	-0.3		-11.7 -11.7	23.5 23.5	4.1	29.2	-3.2

Fragment-ion (m/z)	484.318	550.313	587.339	599.332	613.369	655.870^{+2}	712.408^{+2}	760.444	769.422	791.382	827.419	1310.715
Frac. Inten.(% of TIC)	2.56	3.45	2.67	2.15	2.21	30.55	6.04	2.66	2.01	2.31	2.25	4.06
Rel. Inten.(% of BP)	8.40	11.29	8.75	7.03	7.25	100.00	19.78	8.72	6.57	7.55	7.37	13.29
Score	1.50	1.50	-0.09	-0.07	1.50	1.50	1.50	1.50	0.50	-0.08	-0.07	1.50
Ion-type	y_4	$y{+}{+}_8$			y_5	y_{11}^{+2}	y_{12}^{+2}	y_6	$b{+}{+}_{14}$			y_{11}
Delta ppm	-13.0	-6.8			3.6	8.8	2.0	11.3	34.5			-5.0



Result Summary

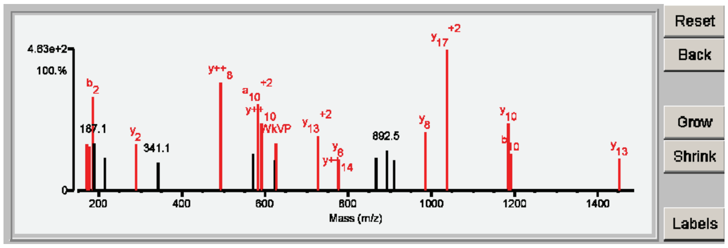
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.85	74.2	8	9/25	K727k	(K)ANIPWkVPGLPTPIENMILR(Y)	2259.2682	114.0569	5.9	273601.9/8.95	HUMAN	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.85	74.2	8	9/25	K727k	(K) A N\I/P W k/V/P G L|P T/P I/E N M I/L/R (Y)	2259.2682	114.0569	5.9	273601.9/8.95	HUMAN	Q6P2Q9	520433	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2

Fragment-ion (m/z)	84.081	86.097	171.109	175.112	186.084	187.088	215.138	288.197	341.087	493.279	571.221	581.844^{+2}
Frac. Inten.(% of TIC)	3.98	0.18	3.57	3.36	7.21	3.72	2.59	3.58	2.22	8.30	2.85	6.63
Rel. Inten.(% of BP)	36.58	1.62	32.77	30.91	66.19	34.22	23.82	32.90	20.42	76.29	26.15	60.87
Score	-0.37	0.22	0.75	1.50	0.50	-0.34	-0.24	1.50	-0.20	1.50	-0.26	0.50
Ion-type		LI	GL	y_1	b_2			y_2		y^{++}_8		a_{10}^{+2}
Delta ppm		0.9	-29.2	-38.0	-25.9			-19.1		0.0		6.1

Fragment-ion (m/z)	592.324	623.868	625.344	725.926^{+2}	775.417	866.511	892.483	910.280	985.544	1038.081^{+2}	1183.653	1190.640	1450.766
Frac. Inten.(% of TIC)	5.21	2.42	3.67	4.28	2.35	2.59	3.11	2.35	4.49	10.89	5.15	2.84	2.46
Rel. Inten.(% of BP)	47.85	22.19	33.74	39.33	21.63	23.75	28.53	21.61	41.25	100.00	47.33	26.09	22.63
Score	1.50	-0.22	0.75	1.50	1.50	-0.24	-0.29	-0.22	1.50	1.50	1.50	0.50	1.50
Ion-type	y^{++}_{10}		WkVP	y_{13}^{+2}	y_6 4.5 y^{++}_{14}				y_8	y_{17}^{+2}	y_{10}	b_{10}	y_{13}
Delta ppm	-7.8		-4.4	25.1	-33.0				-5.8	3.2	2.2	-24.8	-29.6



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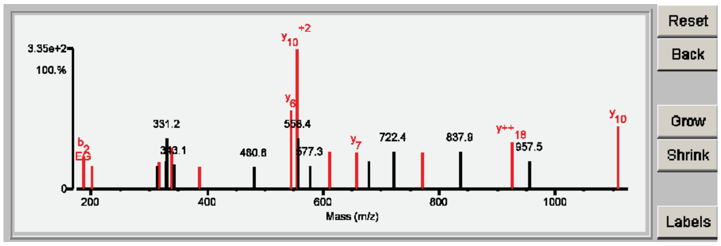
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.96	58.1	9	13/25	K24k	(K)DAEAEGLSGTTLLPkLIPSGAGR(E)	2253.2085	114.0725	12.5	20648.1/6.83	HUMAN	Q9UI14	Prenylated Rab acceptor protein 1 OS=Homo sapiens GN=RABAC1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.96	58.1	9	13/25	K24k	(K) D A\E\A\E/G L S G T T L/L/P k/L/I/P S G A G R (E)	2253.2085	114.0725	12.5	20648.1/6.83	HUMAN	Q9UI14	515311	Prenylated Rab acceptor protein 1 OS=Homo sapiens GN=RABAC1 PE=1 SV=1

Fragment-ion (m/z)	84.077	123.083	187.070	201.128	313.992	316.126	328.123	331.197	340.201	343.128	387.136	480.754^{+2}	544.293	555.322^{+2}	558.386	577.322	611.873	657.364	677.853	722.382	770.462	837.876^{+2}	926.526	957.452	1109.649
Frac. Inten.(% of TIC)	4.47	2.32	3.30	2.36	2.31	2.63	2.77	5.06	4.13	2.44	2.23	2.24	7.77	13.80	4.99	2.28	3.75	3.64	2.82	3.74	3.58	3.72	4.67	2.73	6.23
Rel. Inten.(% of BP)	32.38	16.82	23.94	17.12	16.76	19.09	20.05	36.68	29.92	17.71	16.19	16.22	56.31	100.00	36.15	16.55	27.20	26.39	20.47	27.14	25.94	26.99	33.84	19.78	45.18
Score	-0.32	-0.17	0.75	0.75	-0.17	0.50	-0.20	-0.37	0.75	-0.18	0.75	-0.16	1.50	1.50	-0.36	-0.17	1.50	1.50	-0.20	-0.27	1.50	-0.27	1.50	-0.20	1.50
Ion-type			b_2 EG	LS		b_3			Pk		b_4 EAEG		y_6	y_{10}^{+2}			y^{++}_{11}	y_7			y_8		y^{++}_{18}		y_{10}
Delta ppm			-13.0 -13.0	17.6		33.8			6.7		-40.9 -40.9		16.9	-5.8			9.6	-6.0			13.0		-10.9		6.1



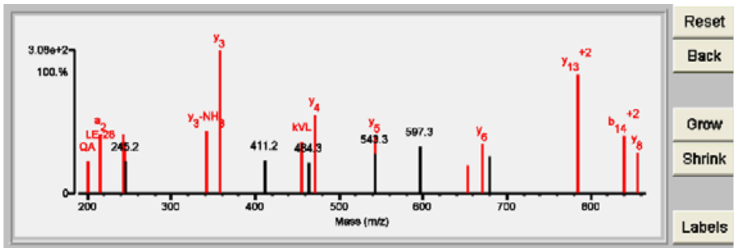
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.92	75.6	8	8/25	K456k	(R)ELIkVLEEANQAINPK(L)	1809.0116	114.0516	4.5	72371.8/8.82	HUMAN	Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.92	75.6	8	8/25	K456k	(R) E L\I/k V L E E/A N/Q/A/I/N|P K (L)	1809.0116	114.0516	4.5	72371.8/8.82	HUMAN	Q92841	154101	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1

Fragment-ion (m/z)	84.079	85.081	86.095	102.057	132.077	200.103	215.138	243.130	244.164	245.168	341.182	358.213	411.211	455.308	464.257	471.291	542.330	543.321^{+2}	597.298	653.359	670.385	679.360	784.424^{+2}	840.454^{+2}	855.451
Frac. Inten.(% of TIC)	0.36	2.45	0.40	0.22	3.45	2.72	4.98	4.96	4.32	2.73	5.23	11.91	2.76	4.31	2.58	6.59	4.83	3.36	3.97	2.38	4.13	3.14	9.98	4.86	3.38
Rel. Inten.(% of BP)	3.00	20.58	3.37	1.89	28.93	22.82	41.78	41.61	36.22	22.92	43.92	100.00	23.18	36.18	21.65	55.30	40.51	28.19	33.36	19.96	34.69	26.37	83.75	40.80	28.35
Score	0.50	-0.21	0.22	1.00 1.00	-0.29	0.75	0.50	0.75	1.50	-0.23	0.50	1.50	-0.23	0.75	-0.22	1.50	1.50	-0.28	-0.33	0.50	1.50	-0.26	1.50	0.50	1.50
Ion-type	KQ		LI	a_1 E		QA	a_2 LE-28	b_2 LE	y_2		y_3-NH_3	y_3		kVL		y_4	y_5			y_6-NH_3	y_6		y_{13}^{+2}	b_{14}^{+2}	y_8
Delta ppm	-16.4		-17.7	6.3 17.1		-6.3	-8.4 -8.4	-21.1 -21.1	-5.2		-1.0	11.5		20.3		-3.1	0.6			-4.6	-4.6		-1.7	2.4	-20.3



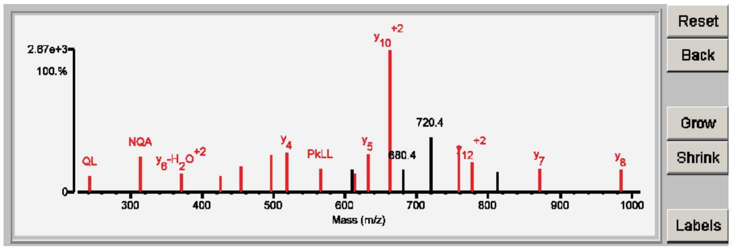
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.76	81.1	8	5/25	K470k	(R)EANQAINPkLLQLVEDR(G)	1951.0607	114.0444	0.7	69148.5/9.06	HUMAN	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.76	81.1	8	5/25	K470k	(R) E A N Q A/I/N/P k/L/L/Q/L/V E D R (G)	1951.0607	114.0444	0.7	69148.5/9.06	HUMAN	P17844	154367	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1

Fragment-ion (m/z)	72.083	84.081	86.096	101.071	136.074	242.149	314.144	371.202^{+2}	425.181	453.273	496.219	518.261	566.379	609.297^{+2}	613.336	631.343	662.885^{+2}	680.390^{+2}	719.908	720.403	759.395	776.455^{+2}	812.477	872.477	985.558
Frac. Inten.(% of TIC)	0.09	0.08	0.31	0.08	2.39	2.20	4.90	2.57	2.22	3.67	5.14	5.45	3.24	3.13	2.52	5.23	19.60	3.03	6.76	7.55	6.41	4.17	2.76	3.30	3.18
Rel. Inten.(% of BP)	0.46	0.43	1.60	0.41	12.22	11.23	25.01	13.12	11.31	18.73	26.23	27.83	16.51	15.96	12.86	26.68	100.00	15.46	34.47	38.52	32.71	21.28	14.06	16.86	16.22
Score	0.50	0.50	0.22		-0.12	0.75	0.75	0.50	0.25	0.75	0.25	1.50	0.75	-0.16	0.50	1.50	1.50	-0.15	1.50	-0.39	1.50	1.50	-0.14	1.50	1.50
Ion-type	V	KQ	LI	KQ		QL	NQA	y_6-H_2O^{+2}	b_4-H_2O	PkL	b_5-H_2O	y_4	PkLL		y_5-H_2O	y_5	y_{10}^{+2}		$y{++}_{11}$		y_6	y_{12}^{+2}		y_7	y_8
Delta ppm	28.1	-0.9	-9.6			-10.0	-8.6	9.6	5.6	-21.4	5.4	8.9	20.2		9.3	3.1	3.2		5.0		-6.5	11.2		-7.9	-9.5



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Result Summary

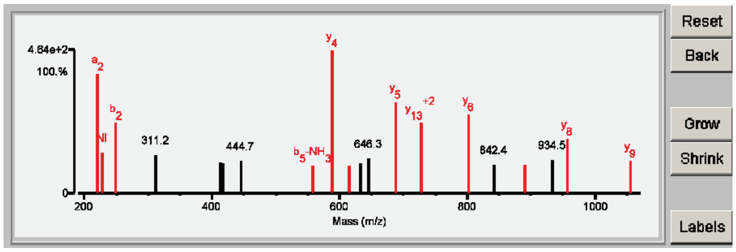
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.50	69.5	7	10/25	K54k	(K)TFVNITPAEVGVLVGkDR(S)	1915.0647	114.0398	-1.5	15054.3/8.44	HUMAN	P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.50	69.5	7	10/25	K54k	(K) T F|V N I/T P A E/V/G V|L/V/G k D R (S)	1915.0647	114.0398	-1.5	15054.3/8.44	HUMAN	P07737	519509	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2

Fragment-ion (m/z)	70.066	72.080	84.079	86.096	221.126	228.124	249.120	311.187	413.200	417.225	444.748^{+2}	558.289	589.303
Frac. Inten.(% of TIC)	0.00	0.35	5.24	0.12	10.53	3.61	6.15	3.40	2.77	2.59	2.90	2.44	12.58
Rel. Inten.(% of BP)	0.02	2.78	41.61	0.97	83.68	28.70	48.84	27.04	21.98	20.58	23.06	19.37	100.00
Score	0.20	0.50	-0.42	0.22	0.50	0.75	0.50	-0.27	-0.22	-0.21	-0.23	0.25	1.50
Ion-type	PR	V		LI	a_2	NI	b_2					b_5-NH$_3$	y_4
Delta ppm	15.3	-16.3		-7.3	-15.2	-48.1	-19.1					-6.8	-3.8

Fragment-ion (m/z)	614.850	632.317	646.329^{+2}	688.381	727.890^{+2}	801.455	842.426^{+2}	890.989	934.462	957.580	1056.602	1130.575
Frac. Inten.(% of TIC)	2.47	2.67	3.04	7.99	6.25	6.93	2.51	2.48	2.98	4.79	2.81	2.40
Rel. Inten.(% of BP)	19.65	21.18	24.16	63.53	49.67	55.04	19.93	19.74	23.69	38.05	22.33	19.05
Score	0.50	-0.21	-0.24	1.50	1.50	1.50	-0.20	1.50	-0.24	1.50	1.50	-0.19
Ion-type	b++$_{12}$			y_5	y_{13}^{+2}	y_6		y++$_{16}$		y_8	y_9	
Delta ppm	28.0			11.2	-16.0	-3.4		-11.9		33.7	-13.2	



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Result Summary

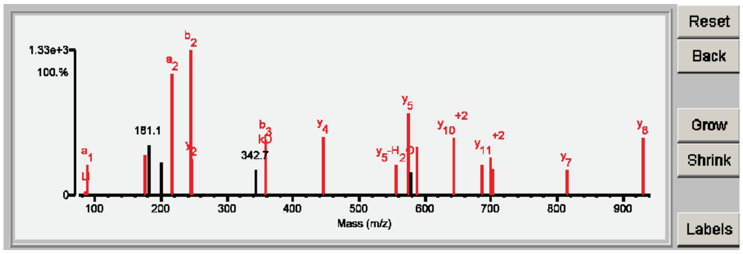
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.32	87.2	10	4/25	K707k	(R)DELLkDLQQSIAR(E)	1528.8329	114.0576	8.9	96023.6/6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.32	87.2	10	4/25	K707k	(R) D E|L|L/k/D/L/Q/Q/S I/A/R (E)	1528.8329	114.0576	8.9	96023.6/6.13	HUMAN	Q8WUM4	486463	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1

Fragment-ion (m/z)	84.044	84.080	86.097	88.039	101.071	102.054	175.115	181.058	199.072	217.082	245.077	246.152	342.695
Frac. Inten.(% of TIC)	0.19	0.30	0.48	2.94	0.07	0.08	3.92	4.82	3.21	11.88	14.10	3.61	2.46
Rel. Inten.(% of BP)	1.38	2.13	3.40	20.87	0.49	0.54	27.82	34.20	22.77	84.28	100.00	25.58	17.46
Score	1.00	0.50	0.22	0.50			1.50	-0.34	-0.23	0.50	0.50	1.50	-0.17
Ion-type	E	KQ	LI	a_1	KQ	E	y_1			a_2	b_2	y_2	
Delta ppm	-1.1	-9.2	3.2	-17.1			-23.7			-6.4	-2.9	-18.1	

Fragment-ion (m/z)	358.165	446.274	556.333	574.331	578.314	586.830^{+2}	643.374^{+2}	685.376	699.909^{+2}	702.391	815.473	930.502
Frac. Inten.(% of TIC)	5.48	5.70	2.93	8.05	2.27	4.74	5.61	2.92	3.62	2.53	2.46	5.62
Rel. Inten.(% of BP)	38.90	40.46	20.80	57.12	16.09	33.65	39.83	20.70	25.65	17.97	17.47	39.87
Score	0.75	1.50	0.50	1.50	-0.16	1.50	1.50	0.75	1.50	1.50	1.50	1.50
Ion-type	b_3 8.4 kD	y_4	y_5-H_2O	y_5		y_9^{+2}	y_{10}^{+2}	a_5 -19.4 y_6-NH_3 18.9 DLQQSI	y_{11}^{+2}	y_6	y_7	y_8
Delta ppm	-22.9	3.7	22.7	1.0		11.9	15.0	33.7	2.4	2.8	-0.5	1.9



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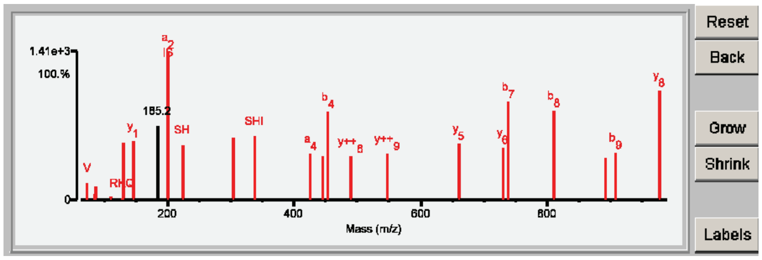
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.68	94.4	11	1/24	K164k	(R)DLSHIGDAVVISCAkDGVK(F)	1984.0168	114.0726	14.1	28769.0/4.57	HUMAN	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1
2	15.97	80.9	9	4/24	K168k	(R)DLSHIGDAVVISCAKDGVk(F)	1984.0168	114.0726	14.1	28769.0/4.57	HUMAN	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.68	94.4	11	1/24	K164k	(R) D L S H\I G D\A\V\V/I/S/C/A/k D/G V/K (F)	1984.0168	114.0726	14.1	28769.0/4.57	HUMAN	P12004	485421	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1

Fragment-ion (m/z)	72.080	84.079	86.095	110.070	129.100	130.084	147.112	185.165	201.123	225.099	303.209	338.183	425.212	446.223	453.208	489.729	546.270	660.377	731.402	738.347	809.383	891.436	908.446	978.471
Frac. Inten.(% of TIC)	1.26	0.42	1.03	0.23	0.14	4.40	4.45	5.56	11.19	4.14	4.69	4.83	3.46	3.32	6.68	3.32	3.49	4.29	3.95	7.39	6.70	3.24	3.55	8.29
Rel. Inten.(% of BP)	11.28	3.72	9.19	2.08	1.22	39.31	39.75	49.65	100.00	36.98	41.94	43.16	30.95	29.63	59.68	29.66	31.15	38.30	35.31	66.03	59.87	28.92	31.69	74.07
Score	0.50	0.50	0.22	1.00	0.20	0.50	1.50	-0.50	0.75	0.75	1.50	0.75	0.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	0.50	1.50	0.50	1.50
Ion-type	**V**	**KQ**	**LI**	**H**	**RKQ**	y_1-NH_3	y_1		a_2 **IS**	**SH**	y_3	**SHI**	a_4	$y{+}{+}_7$	b_4	$y{+}{+}_8$	$y{+}{+}_9$	y_5	y_6	b_7	b_8	y_7	b_9	y_8
Delta ppm	-5.2	-19.9	-11.9	-14.3	-15.0	-17.3	-4.1		-7.3 -7.3	-0.5	19.2	-2.6	-9.2	4.1	-6.0	-15.9	-16.9	14.4	-4.1	5.4	3.5	0.9	-2.6	4.1



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Result Summary

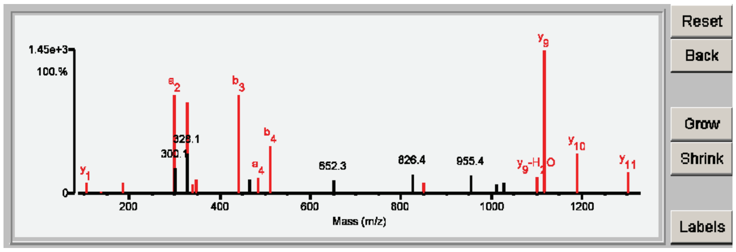
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.36	79.8	5	9/25	K254k	(K)YYLAPkIEDEEGS(-)	1513.7057	114.0508	4.9	28769.0/4.57	HUMAN	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.36	79.8	5	9/25	K254k	(K) Y Y|L|A|P k\I E D E E G/S (-)	1513.7057	114.0508	4.9	28769.0/4.57	HUMAN	P12004	242711	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1

Fragment-ion (m/z)	84.083	86.096	106.053	136.076	185.131	299.138	300.142	327.132	328.134^{+2}	340.200	348.192	440.218
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.47 8.06 -0.08	0.05 0.30 0.22 LI -2.6	1.37 7.53 1.50 y_1 31.4	0.22 1.22 1.00 a_1 -7.3 1.00 Y 0.8	1.30 7.14 0.75 LA 10.0	12.59 69.18 0.50 a_2 -6.4	3.14 17.27 -0.17	11.56 63.50 0.50 b_2 -8.0	5.01 27.51 -0.28	1.18 6.47 0.75 Pk 2.9	1.74 9.55 0.75 YLA -3.1	12.60 69.19 0.50 b_3 -1.8

Fragment-ion (m/z)	466.237	483.262	511.258	652.296	826.400	850.416	955.443	1012.460	1026.485	1099.496	1117.504	1188.546	1301.629
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.76 9.64 -0.10	1.99 10.95 0.50 a_4 2.1	5.95 32.67 0.50 b_4 3.9	1.70 9.31 -0.09	2.35 12.89 -0.13	1.27 6.95 0.50 b_6 -36.4	2.24 12.33 -0.12	1.17 6.42 -0.06	1.38 7.56 -0.08	2.04 11.22 0.50 y_9-H_2O 5.4	18.21 100.00 1.50 y_9 3.0	5.08 27.88 1.50 y_{10} 6.7	2.65 14.55 1.50 y_{11} 5.4



Result Summary

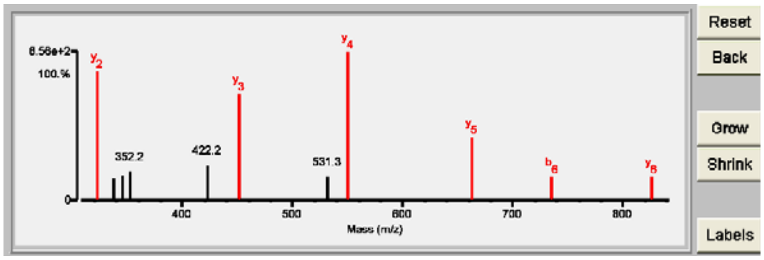
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.97	60.6	7	10/25	K21k	(R)GASNkYLVEFR(A)	1283.6743	114.0479	3.5	42153.5/4.96	HUMAN	Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2
2	6.85	51.5	4	12/25	None	(K)QRYRMIDFLR(F)	1397.7470	-0.0249	-17.8	33301.0/11.29	HUMAN	Q5T653	39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.97	60.6	7	10/25	K21k	(R) G A\S N k/Y|L/V/E/F/R (A)	1283.6743	114.0479	3.5	42153.5/4.96	HUMAN	Q16186	7886	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2

Fragment-ion (m/z)	60.054	70.066	72.083	84.080	86.098	101.069	110.070	120.083	129.062	136.075	158.090	175.118
Frac. Inten.(% of TIC)	2.07	0.00	0.11	12.51	0.46	6.12	6.67	0.10	2.95	0.22	3.09	3.19
Rel. Inten.(% of BP)	15.48	0.02	0.83	93.73	3.45	45.81	49.92	0.78	22.08	1.61	23.15	23.91
Score	-0.15	0.20	0.50	-0.94	0.22	0.50	-0.50	1.00	0.50 0.50	1.00	0.50	1.50
Ion-type		PR	V		LI	a_2		F	b_2 QKR	Y	y_1-NH_3	y_1
Delta ppm		6.8	29.5		13.6	-22.2		16.9	-29.1 -29.1	-4.3	-17.1	-4.9

Fragment-ion (m/z)	190.097	222.141	322.184	337.642	345.178^{+2}	352.175	422.233	451.231	531.295	550.297	663.380	735.348	826.457
Frac. Inten.(% of TIC)	3.50	2.48	11.62	2.04	2.22	2.62	3.19	9.52	2.15	13.35	5.66	2.06	2.11
Rel. Inten.(% of BP)	26.20	18.59	87.04	15.28	16.59	19.60	23.92	71.27	16.13	100.00	42.36	15.41	15.81
Score	-0.26	-0.19	1.50	-0.15	-0.17	-0.20	-0.24	1.50	-0.16	1.50	1.50	0.50	1.50
Ion-type			y_2					y_3		y_4	y_5	b_6	y_6
Delta ppm			-11.7					2.1		-2.7	-3.5	8.0	13.4



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Result Summary

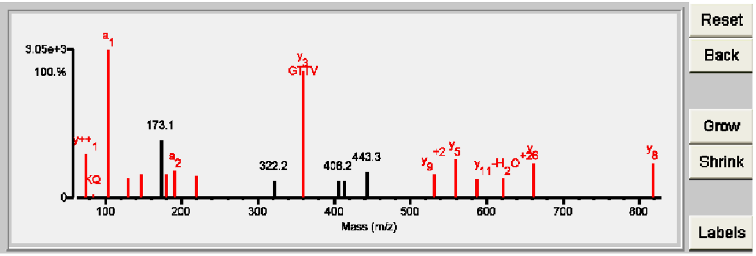
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.38	79.9	7	6/24	K34k	(K)MSLkGTTVTPDK(R)	1277.6770	114.0530	7.2	42438.8/4.96	HUMAN	Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2
2	5.39	55.8	3	12/24	K42k	(K)MSLKGTTVTPDk(R)	1277.6770	114.0530	7.2	42438.8/4.96	HUMAN	Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.38	79.9	7	6/24	K34k	(K) M S|L/k/G T/T/V T/P D/K (R)	1277.6770	114.0530	7.2	42438.8/4.96	HUMAN	Q16186	7886	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2

Fragment-ion (m/z)	72.080	74.058	84.080	86.095	104.052	129.101	130.084	147.113	173.126	180.095	191.084	219.073
Frac. Inten.(% of TIC)	0.17	5.79	0.35	0.14	19.38	0.07	2.49	3.08	7.62	3.02	3.51	2.83
Rel. Inten.(% of BP)	0.89	29.89	1.78	0.72	100.00	0.38	12.84	15.88	39.32	15.56	18.12	14.61
Score	0.50	1.50	0.50	0.22	0.50	0.20	0.50	1.50	-0.39	1.50	0.50	0.50
Ion-type	V	$y{++}_1$	KQ	LI	a_1	RKQ	y_1-NH_3	y_1		$y{++}_3$	a_2	b_2
Delta ppm	-6.6	-22.1	-9.2	-21.2	-11.0	-11.1	-15.8	-2.1		-27.7	-6.7	-30.5

Fragment-ion (m/z)	322.185	359.191	406.224	414.235	443.260^{+2}	444.265^{+2}	530.791^{+2}	559.304	587.316^{+2}	621.852^{+2}	660.354	818.431
Frac. Inten.(% of TIC)	2.28	16.60	2.23	2.22	3.32	2.48	3.13	5.06	2.41	2.63	4.58	4.61
Rel. Inten.(% of BP)	11.75	85.64	11.49	11.45	17.12	12.78	16.13	26.13	12.44	13.58	23.63	23.80
Score	-0.12	1.50	-0.11	-0.11	-0.17	-0.13	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type		y_3 GTTV					y_9^{+2}	y_5	y_{10}^{+2}	y_{11}-H_2O^{+2}	y_6	y_8
Delta ppm		-3.4 -3.4					10.0	-8.6	-20.0	23.1	-3.2	6.4



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Result Summary

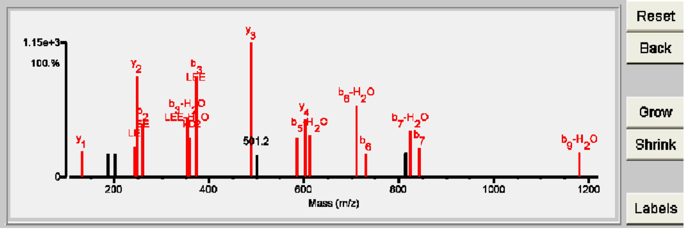
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.17	83.6	6	6/25	K239k	(K)EELEEVIkDI(-)	1216.6307	114.0540	8.3	26582.3/4.74	HUMAN	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3
2	7.13	65.9	2	10/25	K2030k	(R)LDEkLEEVNK(F)	1216.6420	114.0428	-0.1	295591.4/7.89	HUMAN	RQ86UK0	REVERSE ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=2
3	5.57	54.6	2	11/25	None	(K)RQVSIEEGERK(A)	1330.7074	-0.0226	-17.0	23707.0/5.42	HUMAN	P20340	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3
4	5.56	62.2	4	12/25	K51k	(K)LEDIIEEIDk(A)	1216.6307	114.0540	8.3	27677.0/8.25	HUMAN	RP19404	REVERSE NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2
5	4.54	59.8	3	12/25	None	(K)LSFHQTQVSQR(L)	1330.6862	-0.0015	-1.1	71194.8/6.98	HUMAN	Q969Z0	Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.17	83.6	6	6/25	K239k	(K) E E\L\E E V|I|k/D/I (-)	1216.6307	114.0540	8.3	26582.3/4.74	HUMAN	P28066	521763	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3

Fragment-ion (m/z)	72.080	84.079	86.096	102.055	132.106	187.098	201.124	243.131	247.130	259.092	354.162
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.10 0.81 0.50 V -5.2	5.28 41.75 -0.42	0.36 2.83 0.22 LI -9.6	0.08 0.60 1.00 a_1 -1.5 1.00 E -1.5	2.42 19.09 1.50 y_1 33.3	2.24 17.71 -0.18	2.24 17.72 -0.18	2.91 22.96 0.75 LE -12.9	9.54 75.41 1.50 y_2 5.1	4.98 39.34 0.75 b_2 -2.2 EE -2.2	5.65 44.64 0.50 b_3-H_2O -10.1 LEE-H_2O -10.1

Fragment-ion (m/z)	358.171	372.175	489.262	501.199	584.349	602.338	612.250	711.306	729.338	812.413	814.930	824.420	842.418	1181.540
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.76 29.68 0.75 kD -3.4	9.49 74.96 0.75 b_3 -4.4 LEE -4.4	12.66 100.00 1.50 y_3 -9.9	2.14 16.92 -0.17	3.78 29.87 0.75 y_4-H_2O 15.7 EVIk 15.7	5.46 43.12 1.50 y_4 -21.1	3.90 30.80 0.25 b_5-H_2O -2.2	6.80 53.73 0.25 b_6-H_2O -19.2	2.19 17.28 0.50 b_6 11.5	2.22 17.57 -0.18	2.30 18.14 -0.18	4.40 34.78 0.25 b_7-H_2O 19.4	2.80 22.13 0.50 b_7 4.9	2.33 18.37 0.25 b_9-H_2O -24.3



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Result Summary

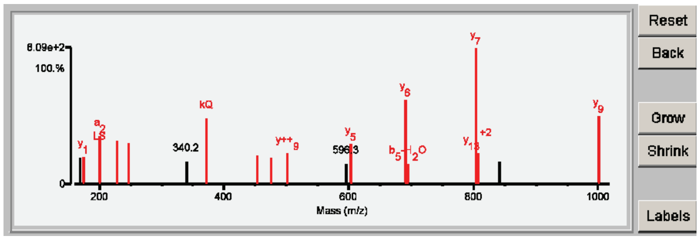
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.83	85.9	9	5/25	K201k	(R)EVLEkQPVLSQTEAR(D)	1726.9334	114.0610	9.8	29204.4/5.72	HUMAN	P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4
2	7.76	51.7	4	12/25	None	(K)MRSQKIGEVIQEMQR(L)	1840.9611	0.0332	18.0	73198.0/8.23	HUMAN	RQ567U6	REVERSE Coiled-coil domain-containing protein 93 OS=Homo sapiens GN=CCDC93 PE=1 SV=2
3	3.71	56.1	2	13/25	M37m K28k	(R)LDVRkPSSPAVPVmSK(L)	1710.9571	130.0372	-0.3	57652.9/9.26	HUMAN	RP0C6C1	REVERSE Ankyrin repeat domain-containing protein 34C OS=Homo sapiens GN=ANKRD34C PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.83	85.9	9	5/25	K201k	(R) E V|L E k Q/P/V/L/S/Q/T E/A/R (D)	1726.9334	114.0610	9.8	29204.4/5.72	HUMAN	P28070	524003	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.079	84.042	84.080	86.095	101.067	104.051	169.132	175.116	201.125	229.122
Frac. Inten.(% of TIC)	0.00	0.14	0.08	0.29	0.34	0.09	2.76	3.27	3.34	5.86	5.32
Rel. Inten.(% of BP)	0.00	0.83	0.46	1.76	2.06	0.56	16.52	19.59	19.98	35.08	31.84
Score	0.20	0.50	1.00	0.50	0.22		-0.17	-0.20	1.50	0.75	0.50
Ion-type	PR	V	E	KQ	LI	KQ			y_1	a_2	b_2
Delta ppm	2.5	-17.7	-27.2	-14.0	-18.9				-16.9	0.2	9.2
										LS	y_2-NH_3
										0.2	-35.0

Fragment-ion (m/z)	246.159	340.151	371.204	452.250	476.238	500.774	596.312^{+3}	604.317	691.334	695.369	804.426	806.934^{+2}	840.364	1000.543
Frac. Inten.(% of TIC)	5.15	2.80	8.12	3.51	3.15	3.76	2.52	4.96	10.36	2.49	16.71	3.76	2.80	8.40
Rel. Inten.(% of BP)	30.80	16.73	48.59	21.00	18.86	22.52	15.10	29.67	62.01	14.92	100.00	22.52	16.73	50.25
Score	1.50	-0.17	0.75	1.50	1.50	1.50	-0.15	1.50	1.50	0.25	1.50	1.50	-0.17	1.50
Ion-type	y_2		kQ	$y{+}{+}_8$	y_4	$y{+}{+}_9$		y_5	y_6	b_5-H_2O	y_7	y_{13}^{+2}		y_9
Delta ppm	13.5		-2.5	4.1	-17.3	-1.7		20.2	-4.4	-5.8	6.2	-2.7		0.5



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.29	67.4	5	6/24	K377k	(R)WENHNkSLQLEAQTYQR(I)	2145.0472	114.0850	18.6	57819.3/5.40	HUMAN	O95376	Protein ariadne-2 homolog OS=Homo sapiens GN=ARIH2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.29	67.4	5	6/24	K377k	(R)WENHNkSLQLE|A/QT/Y/Q/R(I)	2145.0472	114.0850	18.6	57819.3/5.40	HUMAN	O95376	34041	Protein ariadne-2 homolog OS=Homo sapiens GN=ARIH2 PE=1 SV=1

Fragment-ion (m/z)	70.065	74.060	84.044	84.080	86.097	101.071	102.057	110.073	129.101	132.083	136.076	159.090	175.121	303.178	339.190^{+2}	366.179	466.246	521.231	551.268	568.287	678.328	695.357	747.365	766.392
Frac. Inten.(% of TIC)	0.01	4.36	0.71	0.82	0.96	0.33	0.19	0.12	0.24	6.55	0.36	0.40	5.95	5.43	4.03	5.35	10.99	3.84	5.78	6.53	11.85	6.36	6.21	12.63
Rel. Inten.(% of BP)	0.08	34.52	5.66	6.50	7.57	2.59	1.54	0.93	1.89	51.88	2.84	3.20	47.11	42.99	31.90	42.40	87.06	30.42	45.76	51.70	93.87	50.41	49.14	100.00
Score	0.20	-0.35	1.00	0.50	0.22			1.00	0.20	-0.52	1.00	2.00	1.50	1.50	-0.32	-0.42	1.50	0.75	-0.46	-0.52	0.50	1.50	0.50	1.50
Ion-type	PR		E	KQ	LI	KQ	E	H	RKQ		Y	a_1	y_1	y_2			y_3	QTYQ			y_5-NH_3	y_5	b++11	y_6
Delta ppm	-7.5		-1.1	-5.7	2.0			13.9	-7.3		0.1	-14.3	12.3	2.9			11.5	-9.9			10.5	14.9	5.1	10.4
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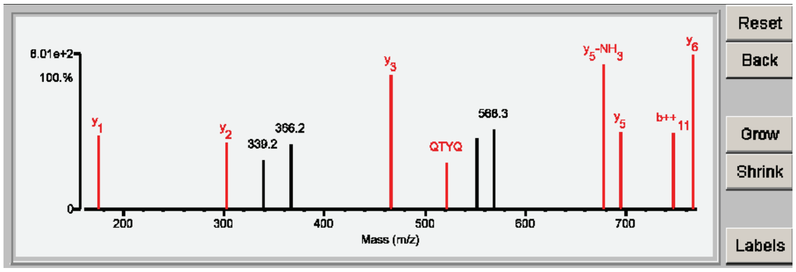


Result Summary

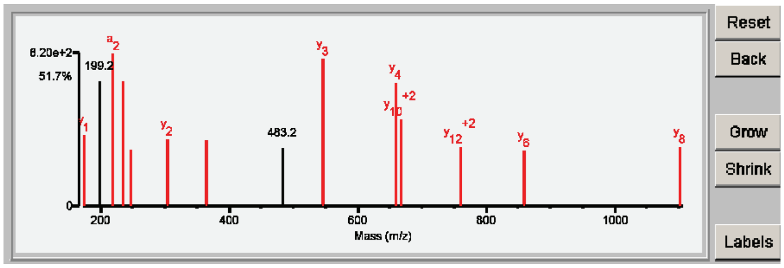
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.66	53.2	9	9/24	K153k	(R)DMLLANPHELSLLkER(N)	1879.0106	114.0636	10.4	44522.8/4.95	HUMAN	Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.66	53.2	9	9/24	K153k	(R) D M\L L/A N/P H/E L/S L/L/k/E/R (N)	1879.0106	114.0636	10.4	44522.8/4.95	HUMAN	Q5TDH0	152905	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.079	84.080	86.096	87.097	110.069	112.110	120.080	153.063	171.075	175.119	199.178
Frac. Inten.(% of TIC)	0.00	2.85	8.13	1.12	2.74	0.09	3.77	3.53	2.56	14.35	3.44	6.09
Rel. Inten.(% of BP)	0.03	19.85	56.63	7.79	19.08	0.60	26.28	24.61	17.83	100.00	23.99	42.40
Score	0.20	-0.20	-0.57	0.22	-0.19	1.00	-0.26	-0.25	-0.18	-1.00	1.50	-0.42
Ion-type	PR			LI		H					y_1	
Delta ppm	-11.8			-10.8		-23.4					3.1	

Fragment-ion (m/z)	219.079	235.116	247.073	304.161	364.166	483.248	546.293	659.379	668.354^{+2}	760.916^{+2}	859.500	1101.613
Frac. Inten.(% of TIC)	7.42	6.04	2.74	3.28	3.24	2.82	7.13	5.99	4.20	2.89	2.67	2.91
Rel. Inten.(% of BP)	51.73	42.11	19.07	22.89	22.55	19.63	49.68	41.71	29.26	20.16	18.60	20.24
Score	0.50	0.75	0.50	1.50	0.75	-0.20	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	a_2	PH	b_2	y_2	PHE		y_3	y_4	y_{10}^{+2}	y_{12}^{+2}	y_6	y_8
Delta ppm	-7.7	-15.5	-9.7	-3.1	8.7		-12.1	-6.5	-27.9	4.0	0.4	-11.8



Result Summary

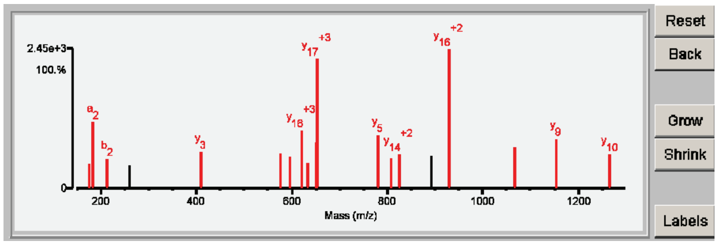
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.92	83.3	10	4/25	K170k	(R)NPPLAEALLSGDLEkFSR(V)	1957.0389	114.0731	14.6	44522.8/4.95	HUMAN	Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1
2	5.43	51.6	2	13/25	None	(K)NPVNNLIRKDYLEEPEK(T)	2071.0818	0.0302	14.6	61002.8/5.80	HUMAN	Q9NQS3	Poliovirus receptor-related protein 3 OS=Homo sapiens GN=PVRL3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.92	83.3	10	4/25	K170k	(R) N/P|P L/A E A L|L/S/G D L/E/k/F S/R (V)	1957.0389	114.0731	14.6	44522.8/4.95	HUMAN	Q5TDH0	152905	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.081	84.044	84.080	86.096	102.055	175.120	184.109	212.106	260.099	409.218	576.784^{+2}	595.345
Frac. Inten.(% of TIC)	0.01	4.62	0.09	6.63	0.73	0.13	2.30	6.32	2.83	2.26	3.44	3.38	3.00
Rel. Inten.(% of BP)	0.11	34.72	0.67	49.87	5.45	0.96	17.27	47.50	21.25	17.03	25.89	25.44	22.58
Score	0.20	-0.35		-0.50	0.22	1.00	1.50	0.50	0.50	-0.17	1.50	1.50	0.75
Ion-type	PR		E		LI	E	y_1	a_2	b_2		y_3	y_9^{+2}	PLAEAL
Delta ppm	-4.6				-0.3	-2.5	4.8	-3.0	9.1		-2.4	-2.8	-2.2

Fragment-ion (m/z)	620.671^{+3}	633.321^{+2}	651.363	653.031^{+3}	780.409	806.464	825.443^{+2}	892.501	930.506^{+2}	1065.545	1152.579	1265.660
Frac. Inten.(% of TIC)	5.46	2.43	4.42	12.33	5.07	2.91	3.27	3.17	13.30	3.93	4.76	3.23
Rel. Inten.(% of BP)	41.07	18.25	33.23	92.75	38.11	21.88	24.57	23.86	100.00	29.54	35.82	24.30
Score	1.50	1.50	1.50	1.50	1.50	0.50	1.50	-0.24	1.50	1.50	1.50	1.50
Ion-type	y_{16}^{+3}	y_{10}^{+2}	y_4	y_{17}^{+3}	y_5	b_8	y_{14}^{+2}		y_{16}^{+2}	y_8	y_9	y_{10}
Delta ppm	6.1	-10.5	9.2	20.0	11.4	27.4	17.7		10.0	12.1	12.6	9.1



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Result Summary

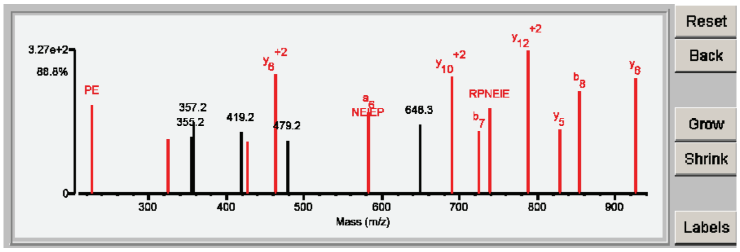
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.29	66.3	5	8/25	K325k	(R)GGRPNEIEPPPPEMPPWQkR(Q)	2312.1604	114.0737	12.7	55401.0/9.15	HUMAN	Q8NCA5	Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.29	66.3	5	8/25	K325k	(R) G G R P N E I\E|P P/P P E M/P/P W Q k R (Q)	2312.1604	114.0737	12.7	55401.0/9.15	HUMAN	Q8NCA5	205169	Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1

Fragment-ion (m/z)	70.066	72.082	84.044	86.096	87.053	102.051	104.054	159.102	227.104	324.150	355.161
Frac. Inten.(% of TIC)	0.00	9.26	0.10	0.53	3.35	0.14	3.21	3.20	5.10	3.10	3.29
Rel. Inten.(% of BP)	0.01	100.00	1.07	5.69	36.17	1.55	34.70	34.62	55.11	33.45	35.60
Score	0.20	-1.00		0.22	0.50 0.50	1.00	-0.35	-0.35	0.75	0.75	-0.36
Ion-type	PR		E	LI	a_2 NR	E			PE	PPE	
Delta ppm	13.9			-3.8	-36.6 -24.0	-39.7			2.9	-21.3	

Fragment-ion (m/z)	357.199^{+2}	419.234	427.200	463.257^{+2}	479.230	583.293	648.277	690.361^{+2}	724.359	739.389	787.409^{+2}	828.448	853.438	925.504
Frac. Inten.(% of TIC)	4.11	3.56	2.96	6.82	3.03	4.64	3.99	6.75	3.63	4.86	8.20	3.67	5.85	6.66
Rel. Inten.(% of BP)	44.38	38.51	31.93	73.70	32.72	50.14	43.07	72.91	39.27	52.50	88.64	39.62	63.15	71.90
Score	-0.44	-0.39	0.50	1.50	-0.33	0.75	-0.43	1.50	0.50	0.75	1.50	1.50	0.50	1.50
Ion-type			$b{+}{+}_8$	y_6^{+2}		a_6 NEIEP		y_{10}^{+2}	b_7	RPNEIE	y_{12}^{+2}	y_5	b_8	y_6
Delta ppm			-29.5	6.6		-5.6 32.9		19.5	-21.2	19.6	10.8	0.2	24.7	3.5



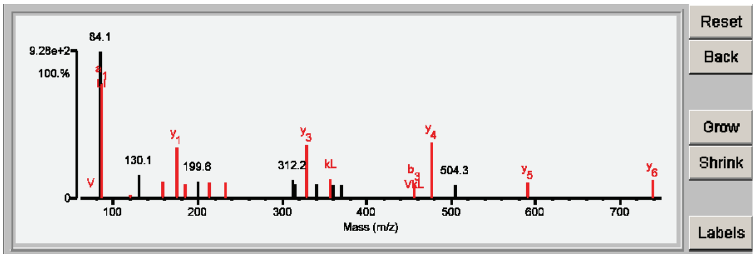
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.54	60.0	8	9/25	K377k	(R)LVkLFDFPGR(G)	1191.6885	114.0528	7.6	56084.8/9.02	HUMAN	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.54	60.0	8	9/25	K377k	(R) L V\k\L/F/D/F/P/G/R (G)	1191.6885	114.0528	7.6	56084.8/9.02	HUMAN	Q9P258	562483	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2

Fragment-ion (m/z)	70.065	72.081	84.079	86.095	120.080	129.099	130.079	158.089	175.118	185.165	199.646	213.158	232.134	312.164^{+2}	315.724^{+2}	329.192	340.180	356.219	359.132	370.207	455.305	476.259	504.259	591.283	738.354
Frac. Inten.(% of TIC)	0.01	0.08	21.46	16.89	0.46	0.06	3.38	2.41	7.41	2.18	2.41	2.34	2.36	2.70	2.15	7.75	2.06	2.80	1.97	1.93	2.08	8.13	1.91	2.38	2.67
Rel. Inten.(% of BP)	0.05	0.39	100.00	78.70	2.16	0.29	15.75	11.22	34.51	10.14	11.22	10.88	11.01	12.60	10.03	36.12	9.61	13.04	9.18	8.98	9.71	37.90	8.92	11.11	12.45
Score	0.20	0.50	-1.00	0.50	1.00	0.20	-0.16	0.50	1.50	0.50	-0.11	0.50	1.50	-0.13	-0.10	1.50	-0.10	0.75	-0.09	-0.09	0.75	1.50	-0.09	1.50	1.50
Ion-type	PR	V		a_1	F	RKQ		y_1-NH_3	y_1	a_2		b_2	y_2			y_3		kL			b_3	y_4		y_5	y_6
Delta ppm	2.5	7.3		-29.3 0.50 LI -16.6	-7.3	-29.0		-22.8	-7.1	-6.7		-12.9	-25.9			-3.0		-32.4			12.9 VkL 12.9	-4.6		-10.2	-4.3



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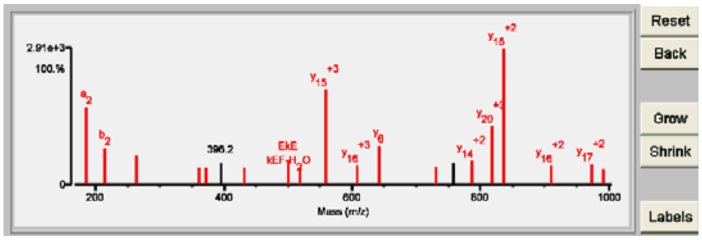
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.86	94.7	10	2/25	K37k	(R)VLMEkEFPGFLENQKDPLAVDK(I)	2547.3163	114.0670	9.1	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
2	11.95	75.2	6	10/25	K47k	(R)VLMEKEFPGFLENQkDPLAVDK(I)	2547.3163	114.0670	9.1	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
3	6.08	64.7	2	13/25	K54k	(R)VLMEKEFPGFLENQKDPLAVDk(I)	2547.3163	114.0670	9.1	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
4	5.81	58.8	3	15/25	K3601k K3604k	(K)VLHPDMAKVPPASPkTAkMMQR(S)	2433.2927	228.0906	1.8	566659.8/6.12	HUMAN	Q9Y6V0	Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=3
5	5.54	55.7	1	14/25	M383m	(R)TNmQRTRSKKSPNIVHCEAFLK(E)	2645.3763	16.0071	4.6	64118.2/4.96	HUMAN	RQ9Y4X5	REVERSE Protein ariadne-1 homolog OS=Homo sapiens GN=ARIH1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.86	94.7	10	2/25	K37k	(R) V L|M E/k/E/F|P/G F L E N Q K D/P L/A/V/D K (I)	2547.3163	114.0670	9.1	11203.2/6.82	HUMAN	P60903	704043	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

Fragment-ion (m/z)	70.066	72.080	84.081	86.096	120.080	185.165	213.158	262.142	361.209	372.195	396.204	432.249	501.244	519.258	557.633^{+3}	606.663^{+3}	642.382	730.399^{+3}	758.410^{+2}	787.424^{+2}	817.090^{+3}	835.948^{+2}	909.485^{+2}	974.002^{+2}	991.477
Frac. Inten.(% of TIC)	0.00	0.32	0.24	0.31	0.24	10.58	4.99	4.07	2.36	2.34	2.96	2.23	3.35	2.30	12.92	2.64	5.29	2.51	2.89	3.19	7.98	18.60	2.67	2.81	2.21
Rel. Inten.(% of BP)	0.02	1.72	1.29	1.64	1.29	56.87	26.82	21.90	12.68	12.59	15.94	11.99	17.99	12.36	69.49	14.22	28.46	13.52	15.52	17.17	42.92	100.00	14.36	15.11	11.87
Score	0.20	0.50 0.50	0.50	0.22	1.00	0.50	0.50	1.50	1.50	0.75	-0.16	1.50	0.75	0.75	1.50	1.50	1.50	1.50	-0.16	1.50	1.50	1.50	1.50	1.50	0.50
Ion-type	PR	a_1 V	KQ	LI	F	a_2	b_2	y_2	y_3	QKD		y_4	EkE kEF-H_2O	kEF	y_{15}^{+3}	y_{16}^{+3}	y_6	y_{18}^{+3}		y_{14}^{+2}	y_{20}^{+3}	y_{15}^{+2}	y_{16}^{+2}	y_{17}^{+2}	b_7
Delta ppm	6.8	-12.1 -12.1	-3.3	-2.6	-8.1	-0.2	-6.4	9.7	1.5	19.5		9.5	27.0 -3.4	3.5	5.2	17.5	-0.3	27.4		11.5	19.7	7.8	10.8	5.2	-14.4



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Result Summary

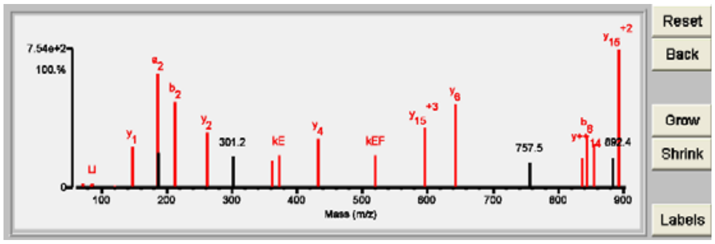
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.39	87.1	10	5/25	K37k K47k	(R)VLMEkEFPGFLENQkDPLAVDK(I)	2547.3163	228.1078	7.9	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
2	8.48	63.2	4	11/25	K37k K54k	(R)VLMEkEFPGFLENQKDPLAVDk(I)	2547.3163	228.1078	7.9	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
3	5.33	51.9	2	14/25	M383m K390k	(R)TNmQRTRSKkSPNIVHCEAFLK(E)	2645.3763	130.0479	3.6	64118.2/4.96	HUMAN	RQ9Y4X5	REVERSE Protein ariadne-1 homolog OS=Homo sapiens GN=ARIH1 PE=1 SV=2
3	5.33	51.9	2	14/25	M383m K389k	(R)TNmQRTRSkKSPNIVHCEAFLK(E)	2645.3763	130.0479	3.6	64118.2/4.96	HUMAN	RQ9Y4X5	REVERSE Protein ariadne-1 homolog OS=Homo sapiens GN=ARIH1 PE=1 SV=2
4	5.32	55.1	3	12/25	K740k	(K)EkDFLVGANALTDEHNRQLPHEK(S)	2661.3380	114.0862	15.6	141417.9/6.88	HUMAN	RO15090	REVERSE Zinc finger protein 536 OS=Homo sapiens GN=ZNF536 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.39	87.1	10	5/25	K37k K47k	(R) V L|M E k E\F/P/G F L E N Q k/D/P L/A/V/D/K (I)	2547.3163	228.1078	7.9	11203.2/6.82	HUMAN	P60903	704043	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

Fragment-ion (m/z)	70.067	72.083	84.079	86.095	120.079	147.111	185.165	187.143	213.159	262.139	301.161	361.211	372.188
Frac. Inten.(% of TIC)	0.00	0.43	0.25	0.46	0.13	4.00	11.04	3.33	8.35	5.35	3.01	2.58	3.16
Rel. Inten.(% of BP)	0.02	3.19	1.84	3.41	1.01	29.84	82.46	24.89	62.32	39.92	22.46	19.29	23.58
Score	0.20	0.50 0.50	0.50	0.22	1.00	1.50	0.50	-0.23	0.50	1.50	-0.21	1.50	0.75
Ion-type	PR	a_1 V	KQ	LI	F	y_1	a_2		b_2	y_2		y_3	kE
Delta ppm	23.9	11.5 26.7	-18.7	-11.9	-13.1	-11.6	-2.9		-11.0	-4.0		8.4	-1.2

Fragment-ion (m/z)	432.247	519.258	595.643^{+3}	642.382	757.411	757.509	835.951^{+2}	844.426	855.094^{+3}	883.446	892.447^{+3}	892.970^{+2}
Frac. Inten.(% of TIC)	4.79	3.15	5.77	8.11	2.43	2.51	2.78	4.96	4.22	2.79	3.00	13.39
Rel. Inten.(% of BP)	35.77	23.52	43.11	60.53	18.18	18.73	20.75	37.06	31.54	20.82	22.41	100.00
Score	1.50	0.75	1.50	1.50	1.50	-0.18	0.50	1.50	1.50	-0.20	-0.21	1.50
Ion-type	y_4	kEF	y_{15}^{+3}	y_6	y_7		$y_{14}\text{-NH}_3^{+2}$	b_6 y^{++}_{14}	y_{20}^{+3}			y_{15}^{+2}
Delta ppm	4.0	2.0	-2.2	0.3	2.3		33.8	1.4 -12.5	6.9			7.8



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Result Summary

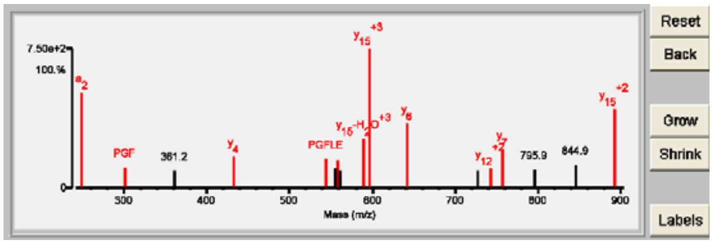
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.11	77.1	5	9/25	K47k	(K)EFPGFLENQkDPLAVDK(I)	1946.9858	114.0579	7.3	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
2	7.02	58.1	2	13/25	K54k	(K)EFPGFLENQKDPLAVDk(I)	1946.9858	114.0579	7.3	11203.2/6.82	HUMAN	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2
3	6.42	56.2	2	14/25	None	(R)EFTGLEPIVSDVIRGICR(D)	2061.0797	-0.0360	-17.5	59483.3/8.17	HUMAN	O43405	Cochlin OS=Homo sapiens GN=COCH PE=1 SV=1
4	6.15	51.6	3	15/25	K643k	(K)EFNEYQAHAGPITkVSR(A)	1946.9719	114.0718	14.0	78164.8/6.48	HUMAN	Q96MR6	WD repeat-containing protein 65 OS=Homo sapiens GN=WDR65 PE=2 SV=2
5	4.94	52.7	2	16/25	M2149m K2143k K2145k	(K)EFGILAkTkYFQmLK(M)	1817.0030	244.0408	-19.4	250750.0/5.67	HUMAN	P50748	Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.11	77.1	5	9/25	K47k	(K) E F/P G F/L E N Q k/D/P L/A V D K (I)	1946.9858	114.0579	7.3	11203.2/6.82	HUMAN	P60903	704043	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

Fragment-ion (m/z)	70.066	72.081	84.041	86.096	120.079	130.084	186.088	231.108	249.120	302.139	361.226	432.244	544.269
Frac. Inten.(% of TIC)	0.01	0.07	2.14	0.15	0.10	2.09	3.64	2.86	11.99	2.59	2.12	3.88	3.58
Rel. Inten.(% of BP)	0.04	0.41	12.24	0.88	0.60	12.00	20.83	16.39	68.71	14.81	12.16	22.24	20.52
Score	0.20	0.50	-0.12	0.22	1.00	0.50	-0.21	-0.16	0.50	0.75	-0.12	1.50	0.75
Ion-type	PR	V		LI	F	y_1-NH_3			a_2	PGF		y_4	PGFLE
Delta ppm	18.2	-2.4		-2.6	-14.8	-17.3			-17.9	-40.4		-2.3	-15.0

Fragment-ion (m/z)	555.232^{+2}	557.624^{+3}	561.244	589.647^{+3}	595.642^{+3}	642.393	727.356^{+2}	742.382^{+2}	757.404	795.893	844.928	892.969^{+2}
Frac. Inten.(% of TIC)	2.50	3.54	2.19	6.18	17.46	8.12	2.22	2.51	4.86	2.38	2.84	9.96
Rel. Inten.(% of BP)	14.35	20.25	12.57	35.41	100.00	46.49	12.73	14.36	27.87	13.63	16.29	57.07
Score	-0.14	0.50	-0.13	0.50	1.50	1.50	-0.13	1.50	1.50	-0.14	-0.16	1.50
Ion-type		y_{14}-NH_3^{+3}		y_{15}-H_2O^{+3}	y_{15}^{+3}	y_6		y_{12}^{+2}	y_7			y_{15}^{+2}
Delta ppm		11.6		10.2	-3.5	16.5		-12.1	-7.2			7.3



Result Summary

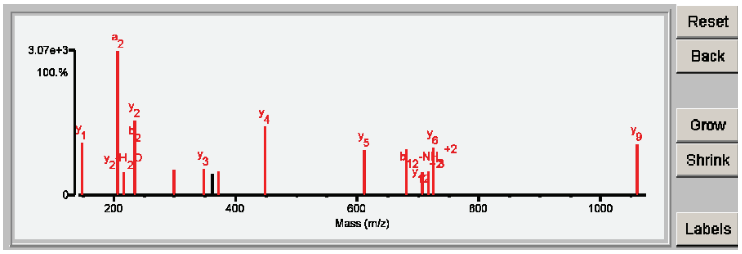
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.55	84.9	10	4/25	K27k	(K)YAGkDGYNYTLSK(T)	1479.7114	114.0466	2.3	11740.5/6.56	HUMAN	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.55	84.9	10	4/25	K27k	(K) Y/A|G k/D G\Y/N/Y/T/L/S/K (T)	1479.7114	114.0466	2.3	11740.5/6.56	HUMAN	P31949	704059	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2

Fragment-ion (m/z)	84.081	86.096	87.053	91.054	119.050	129.102	130.091	136.075	137.078	147.112	207.112	216.131	234.143
Frac. Inten.(% of TIC)	0.61	0.11	0.10	3.54	3.30	0.23	2.71	1.82	5.84	5.68	15.79	2.50	8.20
Rel. Inten.(% of BP)	3.86	0.68	0.65	22.43	20.93	1.47	17.16	11.53	37.02	35.98	100.00	15.81	51.95
Score	0.50	0.22	0.33	-0.22	-0.21	0.20	0.50	1.00 1.00	-0.37	1.50	0.50	0.50	1.50
Ion-type	KQ	LI	NR			RKQ	y_1-NH_3	a_1 Y		y_1	a_2	y_2-H_2O	y_2
Delta ppm	0.3	-1.5	-30.9			-5.0	34.9	-16.1 -8.0		-7.5	-7.2	-14.2	-8.7

Fragment-ion (m/z)	235.108	300.165	347.227	361.176	371.204	448.280	611.342	680.340^{+2}	706.313	715.842^{+2}	725.384	1060.495
Frac. Inten.(% of TIC)	5.46	2.72	2.92	2.41	2.60	7.44	4.94	5.07	2.51	2.64	5.21	5.65
Rel. Inten.(% of BP)	34.55	17.21	18.48	15.25	16.46	47.10	31.30	32.08	15.89	16.75	33.02	35.79
Score	0.50	0.75	1.50	-0.15	0.75	1.50	1.50	1.50	0.75	1.50	1.50	1.50
Ion-type	b_2	Gk	y_3		AGk	y_4	y_5	y_{11}^{+2}	b_6 AGkDGY	b_{12}-NH_3^{+2} y_{12}^{+2}	y_6	y_9
Delta ppm	-3.0	-10.1	-5.7		-2.3	7.4	4.1	13.8	-4.8 -4.8	37.6 -9.7	1.9	-0.1



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Result Summary

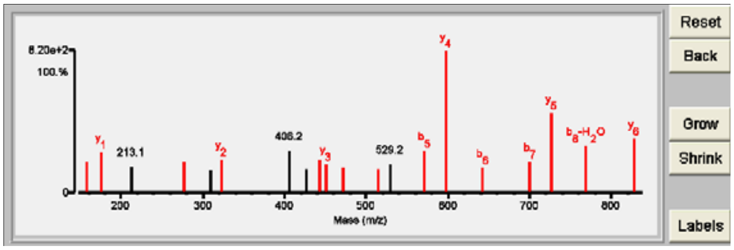
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.12	74.4	11	7/25	K150k	(K)kAEAGAGSATEFQFR(G)	1569.7656	114.0561	7.8	20120.4/10.13	HUMAN	Q9NQ39	Putative 40S ribosomal protein S10-like protein OS=Homo sapiens GN=RPS10P5 PE=5 SV=1
1	14.12	74.4	11	7/25	K139k	(K)kAEAGAGSATEFQFR(G)	1569.7656	114.0561	7.8	18897.9/10.15	HUMAN	P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.12	74.4	11	7/25	K150k	(K) k A E\A\G\A\G\S A/T/E/F/Q/F/R (G)	1569.7656	114.0561	7.8	20120.4/10.13	HUMAN	Q9NQ39	663053	Putative 40S ribosomal protein S10-like protein OS=Homo sapiens GN=RPS10P5 PE=5 SV=1
1	14.12	74.4	11	7/25	K139k	(K) k A E\A\G\A\G\S A/T/E/F/Q/F/R (G)	1569.7656	114.0561	7.8	18897.9/10.15	HUMAN	P46783	663631	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1

Fragment-ion (m/z)	60.044	74.061	84.080	102.053	120.081	158.088	175.118	213.084	276.128	309.129	322.192	406.210	426.213
Frac. Inten.(% of TIC)	5.94	3.91	0.41	0.08	0.12	3.47	4.44	2.85	3.41	2.52	3.72	4.61	2.63
Rel. Inten.(% of BP)	37.80	24.90	2.59	0.48	0.74	22.06	28.22	18.13	21.72	16.02	23.63	29.32	16.70
Score	-0.38	-0.25	0.50	1.00	1.00	0.50	1.50	-0.18	0.75	-0.16	1.50	-0.29	-0.17
Ion-type			KQ	E	F	y_1-NH_3	y_1		QF		y_2		
Delta ppm			-5.7	-21.1	-1.5	-27.2	-6.0		-28.5		13.8		

Fragment-ion (m/z)	443.228	450.236	470.743^{+2}	514.271	529.222	571.271	597.318	642.310	699.333	726.362	768.361	827.408
Frac. Inten.(% of TIC)	3.70	3.17	2.79	2.60	3.11	4.67	15.72	2.80	3.45	8.75	5.15	6.00
Rel. Inten.(% of BP)	23.55	20.18	17.75	16.51	19.80	29.72	100.00	17.80	21.93	55.67	32.75	38.14
Score	0.50	1.50	0.25	0.50	-0.20	0.50	1.50	0.50	0.50	1.50	0.25	1.50
Ion-type	b_3	y_3	b_{10}-H_2O^{+2}	b_4		b_5	y_4	b_6	b_7	y_5	b_8-H_2O	y_6
Delta ppm	4.8	-21.2	30.1	14.6		-23.7	5.8	-18.0	-13.8	7.5	-4.3	3.6



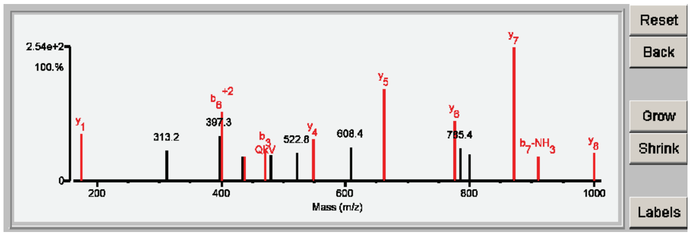
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.40	68.8	7	11/25	K12k	(K)VQkVMVQPINLIFR(Y)	1684.9931	114.0478	2.7	10678.4/7.86	HUMAN	Q5VYJ4	Putative small nuclear ribonucleoprotein polypeptide E-like protein 1 OS=Homo sapiens GN=SNRPEL1 PE=5 SV=1
1	11.40	68.8	7	11/25	K12k	(K)VQkVMVQPINLIFR(Y)	1684.9931	114.0478	2.7	10803.7/9.46	HUMAN	P62304	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.40	68.8	7	11/25	K12k	(K) V Q k\V M V|Q/P/I/N/L I F/R (Y)	1684.9931	114.0478	2.7	10678.4/7.86	HUMAN	Q5VYJ4	698231	Putative small nuclear ribonucleoprotein polypeptide E-like protein 1 OS=Homo sapiens GN=SNRPEL1 PE=5 SV=1
1	11.40	68.8	7	11/25	K12k	(K) V Q k\V M V|Q/P/I/N/L I F/R (Y)	1684.9931	114.0478	2.7	10803.7/9.46	HUMAN	P62304	703613	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1

Fragment-ion (m/z)	70.063	72.081	84.080	101.070	106.047	133.078	134.086	175.117	313.182	397.252	400.222^{+2}	434.745^{+2}	436.783	470.284	480.109	522.804	548.343	608.351	662.397	775.467	785.379	799.967^{+2}	872.526	910.507	1000.604
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.05 0.20 PR -34.6	0.63 4.22 0.50 a_1 -14.9 0.50 V 0.3	0.18 1.18 QK	0.19 1.27 0.50 QK -13.3	2.69 18.16 -0.13	3.91 26.41 -0.19	3.38 22.78 -0.16	5.28 35.61 1.50 y_1 -10.0	3.42 23.10 -0.16	5.05 34.07 -0.24	7.69 51.91 0.50 b_6^{+2} -17.8	2.70 18.24 -0.13	2.70 18.24 1.50 $y{+}{+}_7$ 26.6	3.51 23.69 0.75 b_3 23.5 QkV 23.5	2.92 19.70 -0.14	3.16 21.32 -0.15	4.60 31.07 1.50 y_4 -23.3	3.69 24.91 -0.18	10.24 69.09 1.50 y_5 -2.7	6.68 45.05 1.50 y_6 -20.1	3.66 24.71 -0.18	2.95 19.90 -0.14	14.82 100.00 1.50 y_7 -11.1	2.77 18.67 0.25 b_7-NH$_3$ 26.6	3.17 21.40 1.50 y_8 10.6



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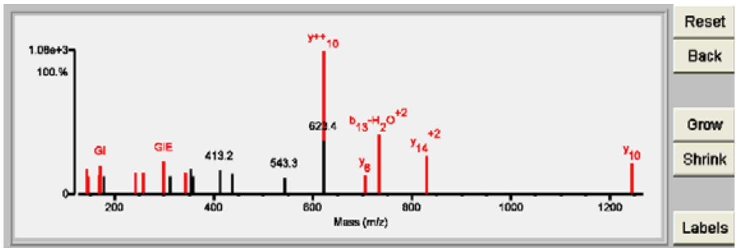
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.63	71.8	5	8/25	K305k	(R)GDLGIEIPAEkVFLAQK(M)	1828.0215	114.0642	10.9	57937.2/7.95	HUMAN	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4
1	13.63	71.8	5	8/25	K348k	(R)GDLGIEIPAEkVFLAQK(M)	1828.0215	114.0642	10.9	61830.5/7.65	HUMAN	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2
2	10.62	66.4	3	10/25	K311k	(R)GDLGIEIPAEKVFLAQk(M)	1828.0215	114.0642	10.9	57937.2/7.95	HUMAN	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4
2	10.62	66.4	3	10/25	K354k	(R)GDLGIEIPAEKVFLAQk(M)	1828.0215	114.0642	10.9	61830.5/7.65	HUMAN	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.63	71.8	5	8/25	K305k	(R) G D L/G\I E I/P A E k/V F L A Q/K (M)	1828.0215	114.0642	10.9	57937.2/7.95	HUMAN	P14618	344051	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4
1	13.63	71.8	5	8/25	K348k	(R) G D L/G\I E I/P A E k/V F L A Q/K (M)	1828.0215	114.0642	10.9	61830.5/7.65	HUMAN	P30613	344063	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2

Fragment-ion (m/z)	84.043	84.081	86.095	120.081	143.115	147.108	169.094	171.113	177.108	243.135	258.139	300.150	311.160	343.156	353.129	357.165	413.238^{+2}	438.215	543.283	622.852	623.351	705.412	733.400^{+2}	828.961^{+2}	1244.690
Frac. Inten.(% of TIC)	0.09	0.29	0.96	0.13	3.73	2.57	2.81	4.20	2.63	3.17	3.07	4.83	2.57	3.19	3.64	2.57	3.49	3.02	2.51	21.00	7.74	2.83	8.64	5.70	4.63
Rel. Inten.(% of BP)	0.42	1.40	4.57	0.61	17.74	12.25	13.38	20.02	12.51	15.10	14.64	22.98	12.24	15.19	17.31	12.23	16.61	14.37	11.94	100.00	36.86	13.50	41.13	27.15	22.04
Score	1.00	0.50	0.22	1.00	0.50	1.50	0.75	0.75	-0.13	0.75	0.50	0.75	-0.12	0.50	-0.17	-0.12	-0.17	-0.14	-0.12	1.50	-0.37	1.50	0.25	1.50	1.50
Ion-type	E	KQ	LI	F	GI-28	y_1	PA	GI		EI	a_3 y_2-NH_3	GIE		b_4						y^{++}_{10}		y_6	b_{13}-H_2O^{+2}	y_{14}^{+2}	y_{10}
Delta ppm	-21.3	-3.3	-13.1	4.4	-18.8	-32.0	-18.7	3.5		4.0	-24.1 -24.1	-17.3		-15.8						-2.6		-24.8	16.2	-10.4	-8.1



Result Summary

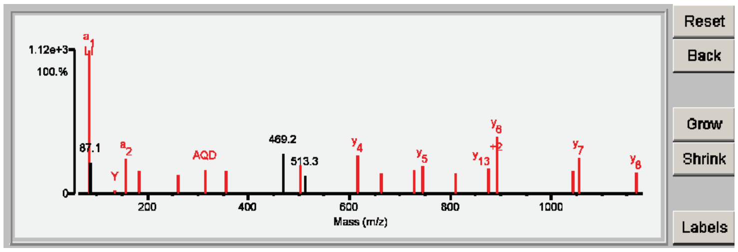
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.58	87.1	11	3/25	K209k	(K)IAQDLEMYGVNYFEIkNK(K)	2175.0791	114.0574	6.3	68564.2/6.03	HUMAN	P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1
1	21.58	87.1	11	3/25	K211k	(K)IAQDLEMYGVNYFEIKNk(K)	2175.0791	114.0574	6.3	68564.2/6.03	HUMAN	P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.58	87.1	11	3/25	K209k	(K) I A\Q D L/E/M Y/G V/N/Y/F/E/I/k/N K (K)	2175.0791	114.0574	6.3	68564.2/6.03	HUMAN	P35241	278256	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1

Fragment-ion (m/z)	72.080	84.080	86.097	87.100	120.080	129.102	136.074	157.133	185.130	261.159	315.126
Frac. Inten.(% of TIC)	0.11	0.14	20.99	4.49	0.11	0.13	0.38	5.20	3.32	2.82	3.53
Rel. Inten.(% of BP)	0.53	0.69	100.00	21.40	0.51	0.63	1.82	24.76	15.79	13.45	16.80
Score	0.50	0.50	0.50	-0.21	1.00	0.20	1.00	0.50	0.50	1.50	0.75
Ion-type	**V**	**KQ**	a_1		**F**	**RKQ**	**Y**	a_2	b_2	y_2	**AQD**
Delta ppm	-16.3	-14.0	-7.2		-4.0	-2.6	-12.4	-10.4	3.0	14.0	-15.9
			0.50								
			LI								
			5.5								

Fragment-ion (m/z)	357.183	469.217	503.291	513.283	616.376	663.329	728.386	745.407	810.376^{+2}	874.911^{+2}	892.482	1043.969^{+2}	1055.541	1169.601
Frac. Inten.(% of TIC)	3.26	5.92	4.16	2.53	5.70	2.94	3.51	4.00	2.91	3.68	8.42	3.36	5.28	3.09
Rel. Inten.(% of BP)	15.51	28.21	19.84	12.07	27.16	14.02	16.72	19.07	13.87	17.53	40.10	16.01	25.13	14.70
Score	0.75	-0.28	1.50	-0.12	1.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	**kN**		y_3		y_4	y^{++}_{10}	$y_5\text{-NH}_3$	y_5	y_{12}^{+2}	y_{13}^{+2}	y_6	$y_{16}\text{-H}_2\text{O}^{+2}$	y_7	y_8
Delta ppm	-18.5		-5.8		-2.7	-25.7	-10.6	-18.1	-26.5	-9.1	-7.8	-28.8	-10.8	5.3



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Result Summary

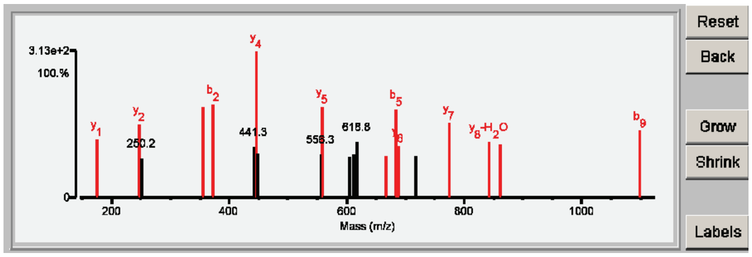
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.38	67.2	9	10/25	K526k	(K)kQLQALSSELAQAR(D)	1542.8598	114.0512	5.0	68564.2/6.03	HUMAN	P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.38	67.2	9	10/25	K526k	(K) k Q\L Q A\L/S/S/E|L/A Q/A/R (D)	1542.8598	114.0512	5.0	68564.2/6.03	HUMAN	P35241	556511	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1

Fragment-ion (m/z)	70.061	72.079	84.080	86.095	175.114	246.154	250.197	354.189	371.202	441.301	445.252	447.772^{+2}
Frac. Inten.(% of TIC)	2.83	5.79	0.31	0.58	3.91	4.95	2.67	6.13	6.26	3.42	9.82	3.01
Rel. Inten.(% of BP)	28.82	58.93	3.17	5.91	39.83	50.38	27.22	62.44	63.76	34.80	100.00	30.68
Score	-0.29	-0.59	0.50	0.22	1.50	1.50	-0.27	0.25	0.50	-0.35	1.50	-0.31
Ion-type			KQ	LI	y_1	y_2		b_2-NH_3	b_2		y_4	
Delta ppm			-5.7	-15.4	-30.0	-7.2		29.1	-8.7		0.3	

Fragment-ion (m/z)	556.323	558.327	604.384	611.282	618.788^{+2}	666.361	683.386	687.377	717.328	774.392	843.443	861.458	1099.559
Frac. Inten.(% of TIC)	2.89	6.13	2.73	2.92	3.74	2.80	5.94	3.52	2.83	5.04	3.70	3.56	4.51
Rel. Inten.(% of BP)	29.40	62.38	27.77	29.78	38.13	28.53	60.46	35.86	28.85	51.31	37.68	36.24	45.91
Score	-0.29	1.50	-0.28	-0.30	-0.38	0.25	0.50	1.50	-0.29	1.50	0.50	1.50	0.50
Ion-type		y_5				b_5-NH_3	b_5	y_6		y_7	y_8-H_2O	y_8	b_9
Delta ppm		-16.0				4.9	2.3	-2.1		-23.8	12.7	17.7	-15.0



Result Summary

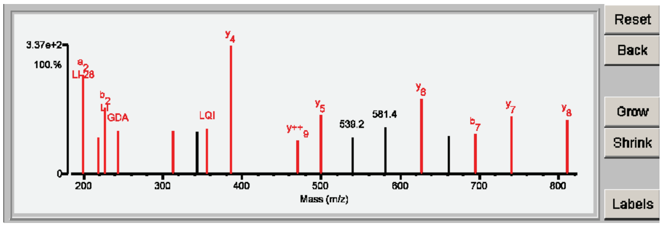
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.57	62.8	9	10/25	K556k	(R)ILAIGLINEALDEGDAQkTLQALQIPAAK(L)	3017.6881	114.0592	5.2	189252.9/6.08	HUMAN	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.57	62.8	9	10/25	K556k	(R) I L\A I G L I\N E A L D E G D A Q k T L/Q/A/L/Q/I/P A/A K (L)	3017.6881	114.0592	5.2	189252.9/6.08	HUMAN	P46940	321931	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1

Fragment-ion (m/z)	70.062	84.081	86.093	129.094	170.089	199.181	218.146	227.176	244.093	313.177	343.161	355.239
Frac. Inten.(% of TIC)	3.75	0.14	0.61	2.77	5.20	7.90	2.88	5.29	3.44	3.48	3.37	3.60
Rel. Inten.(% of BP)	36.81	1.35	5.97	27.21	51.06	77.61	28.28	52.01	33.84	34.23	33.10	35.41
Score	-0.37	0.50	0.22	-0.27	-0.51	0.50	1.50	0.75	0.75	0.75	-0.33	0.75
Ion-type		KQ	LI			a_2 LI-28	y_2	b_2 LI	GDA	ALQ		LQI
Delta ppm		7.4	-36.3			-4.5 -4.5	-17.5	-3.5 -3.5	-2.0	-35.5		11.3

Fragment-ion (m/z)	386.241	470.286	499.321	539.232	581.379	627.373	661.302	694.465	740.471	811.499	923.806^{+3}	927.474	1031.560
Frac. Inten.(% of TIC)	10.18	2.63	4.66	2.94	3.69	6.00	3.01	3.14	4.54	4.35	6.57	3.03	2.83
Rel. Inten.(% of BP)	100.00	25.84	45.76	28.90	36.22	58.99	29.62	30.90	44.57	42.70	64.56	29.79	27.80
Score	1.50	1.50	1.50	-0.29	-0.36	1.50	-0.30	0.50	1.50	1.50	-0.65	-0.30	-0.28
Ion-type	y_4	y^{++}_9	y_5			y_6		b_7	y_7	y_8			
Delta ppm	4.2	3.3	-4.9			-15.0		-32.8	5.9	-6.3			



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Result Summary

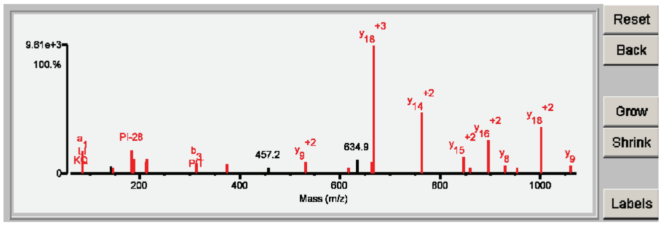
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.24	94.3	11	3/25	K147k	(K)LTPITYPQGLAMAkEIGAVK(Y)	2101.1726	114.0643	9.6	21450.2/8.77	HUMAN	P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1
2	19.57	89.9	8	6/25	K153k	(K)LTPITYPQGLAMAKEIGAVk(Y)	2101.1726	114.0643	9.6	21450.2/8.77	HUMAN	P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1
3	9.55	63.0	3	11/25	M1630m	(R)ITRLPIWVTGVmTDWILGK(N)	2199.2358	16.0010	2.7	192999.0/5.21	HUMAN	RQ9UPW8	REVERSE Protein unc-13 homolog A OS=Homo sapiens GN=UNC13A PE=2 SV=3
4	8.24	53.6	4	15/25	K28k	(K)LTVAAGMLGQVLAEGTSkVQK(A)	2101.1686	114.0683	11.5	35509.2/5.61	HUMAN	RO75208	REVERSE Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens GN=COQ9 PE=1 SV=1
5	7.15	57.9	2	13/25	None	(R)TIPGLNLVRSQDIVSGSRFR(T)	2215.2306	0.0063	2.8	69761.4/5.05	HUMAN	RP07911	REVERSE Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.24	94.3	11	3/25	K147k	(K) L T|P|I/T/Y/P Q G L A/M/A/k/E I/G A V/K (Y)	2101.1726	114.0643	9.6	21450.2/8.77	HUMAN	P63000	555171	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.079	86.096	142.120	147.112	183.149	187.143	211.145	215.136	312.190	374.237	457.247	530.788^{+2}
Frac. Inten.(% of TIC)	0.00	0.06	4.53	1.54	1.34	4.83	3.16	2.26	3.15	2.13	1.89	1.33	2.44
Rel. Inten.(% of BP)	0.02	0.24	17.15	5.81	5.09	18.28	11.95	8.56	11.91	8.05	7.16	5.05	9.22
Score	0.20	0.50	0.50 0.50	-0.06	1.50	0.50	0.50	0.75	0.75	0.75	1.50	-0.05	1.50
Ion-type	PR	KQ	a_1 LI		y_1	PI-28	a_2 IT-28	PI	b_2 IT	b_3 PIT	y_4		y_9^{+2}
Delta ppm	-6.1	-15.2	-17.7 -4.9		-8.2	-4.3	-14.4 -14.4	-1.0	-18.7 -18.7	-9.5 -9.5	-8.5		-13.4

Fragment-ion (m/z)	616.372	634.876^{+2}	661.690^{+3}	667.703^{+3}	763.919^{+2}	845.445^{+2}	858.496	895.981^{+2}	929.544	952.519	1001.046^{+2}	1060.586
Frac. Inten.(% of TIC)	1.19	2.80	2.40	26.43	12.61	3.51	1.20	6.95	1.74	1.34	9.50	1.67
Rel. Inten.(% of BP)	4.50	10.58	9.09	100.00	47.73	13.29	4.54	26.30	6.57	5.06	35.95	6.31
Score	1.50	-0.11	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_6		$y_{18}\text{-}H_2O^{+3}$	y_{18}^{+3}	y_{14}^{+2}	y_{15}^{+2}	y_7	y_{16}^{+2}	y_8	y^{++}_{17}	y_{18}^{+2}	y_9
Delta ppm	8.4		-8.8	5.2	-3.8	-9.3	-9.5	4.5	3.0	0.3	0.6	4.0



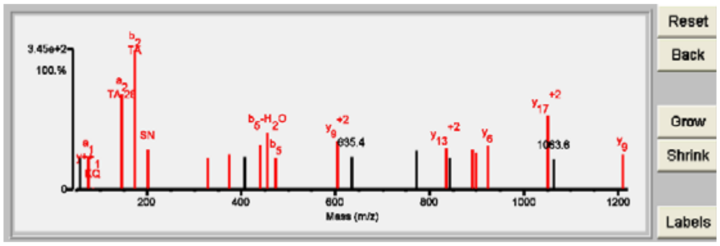
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^{+} Calculated (Da)	MH^{+} Error (Da)	MH^{+} Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.80	80.8	8	6/24	K165k	(K)TASNVEEAFINTAkEIYEK(I)	2157.0710	114.0630	8.9	23545.7/6.08	HUMAN	P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1
2	12.98	76.4	6	7/24	K170k	(K)TASNVEEAFINTAKEIYEk(I)	2157.0710	114.0630	8.9	23545.7/6.08	HUMAN	P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1
3	4.82	50.5	2	13/24	K62k	(K)EYIEKATNIFAEEVNSATk(A)	2157.0710	114.0630	8.9	23545.7/6.10	HUMAN	RP61019	REVERSE Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>15.80</td><td>80.8</td><td>8</td><td>6/24</td><td>K165k</td><td>(K) T A|S N\V|E/E A F I/N T A/k E I/Y E/K (I)</td><td>2157.0710</td><td>114.0630</td><td>8.9</td><td>23545.7/6.08</td><td>HUMAN</td><td>P61019</td><td>554681</td><td>Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1</td></tr>
</table>

Fragment-ion (m/z)	58.063	74.062	84.081	86.094	145.095	173.092	202.082	329.176	374.168	407.197	439.223	455.236	473.238	605.314^{+2}	635.396	771.418^{+2}	835.426^{+2}	842.894^{+2}	890.927^{+2}	899.947^{+2}	923.483	1050.003^{+2}	1063.577	1209.563
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.08 22.69 -0.23	3.19 23.53 1.50 a$_1$ 11.6 y++$_1$ 26.5	0.21 1.58 0.50 KQ 1.5	0.15 1.07 0.22 LI -32.8	9.28 68.45 0.50 a$_2$ -21.0 TA-28 -21.0	13.56 100.00 0.75 b$_2$ -6.7 TA -6.7	3.93 28.99 0.75 SN -6.6	3.14 23.13 0.75 INT -22.3	3.47 25.62 0.50 b$_4$ -0.1	3.18 23.47 -0.23	4.37 32.25 1.50 y$_3$ 10.6	5.53 40.79 0.25 b$_5$-H$_2$O 20.9	3.03 22.31 0.50 b$_5$ 3.9	4.72 34.81 1.50 y$_9^{+2}$ 8.5	3.17 23.39 -0.23	3.75 27.69 -0.28	3.99 29.40 1.50 y$_{13}^{+2}$ 1.3	3.04 22.40 -0.22	3.86 28.50 0.50 y$_{14}$-H$_2$O^{+2} -16.1	3.58 26.38 1.50 y$_{14}^{+2}$ 0.4	4.19 30.91 1.50 y$_6$ 0.0	7.11 52.44 1.50 y$_{17}^{+2}$ -14.9	3.00 22.11 -0.22	3.46 25.54 1.50 y$_9$ -39.4



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Result Summary

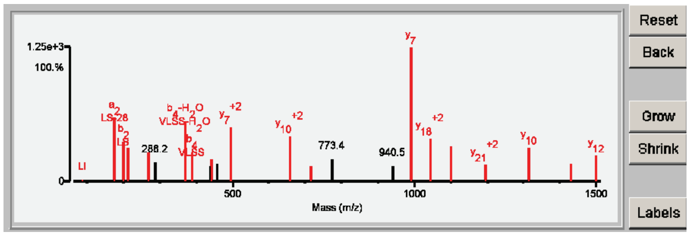
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.33	88.6	7	5/25	K410k	(R)SLSVLSSSTIIANPDIPEAYkLR(G)	2474.3501	114.0580	5.8	68138.6/6.91	HUMAN	P27694	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.33	88.6	7	5/25	K410k	(R) S L|S V|L/S S S T I I/A/N/P D I/P E A Y k L R (G)	2474.3501	114.0580	5.8	68138.6/6.91	HUMAN	P27694	286352	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2

Fragment-ion (m/z)	70.065	86.093	87.054	173.126	201.123	213.085	270.148	288.190	369.211	387.221	438.250	440.208	458.219
Frac. Inten.(% of TIC)	0.00	0.23	0.08	8.00	4.97	4.21	3.69	2.40	7.59	3.69	1.95	2.80	2.24
Rel. Inten.(% of BP)	0.01	1.35	0.49	47.30	29.37	24.91	21.79	14.20	44.87	21.82	11.50	16.54	13.23
Score	0.20	0.22	0.33	0.50	0.75	0.75	0.25	-0.14	0.50	0.75	-0.11	0.75	-0.13
Ion-type	**PR**	**LI**	**NR**	a_2	b_2	**PD**	b_3-H_2O		b_4-H_2O	b_4		**NPDI**	
Delta ppm	2.5	-39.8	-11.4	-18.2	-7.3	-16.3	8.4		-8.0	-8.8		-15.2	
				LS-28	**LS**				**VLSS**-H_2O	**VLSS**			
				-18.2	-7.3				-8.0	-8.8			

Fragment-ion (m/z)	495.765^{+2}	658.347^{+2}	715.377^{+2}	773.430	940.520^{+2}	990.534	1045.055^{+2}	1101.592	1194.629^{+2}	1315.689	1429.744	1500.778
Frac. Inten.(% of TIC)	6.86	5.78	2.01	2.80	2.00	16.92	5.47	4.45	2.03	4.23	2.28	3.31
Rel. Inten.(% of BP)	40.55	34.13	11.86	16.53	11.85	100.00	32.31	26.31	12.01	24.97	13.50	19.55
Score	1.50	1.50	1.50	-0.17	-0.12	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_7^{+2}	y_{10}^{+2}	y_{11}^{+2}			y_7	y_{18}^{+2}	y^{++}_{19}	y_{21}^{+2}	y_{10}	y_{11}	y_{12}
Delta ppm	-13.3	-10.9	2.9			-3.0	4.6	0.2	-10.6	-8.6	0.6	-1.5



Result Summary

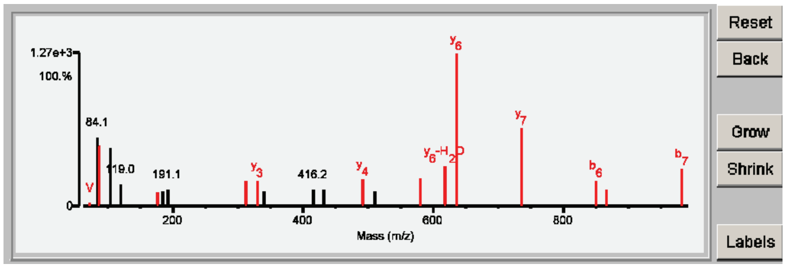
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.12	69.0	7	9/24	K141k	(K)IDkTDYMVGSYGPR(A)	1601.7628	114.0508	4.6	23207.2/5.02	HUMAN	P52565	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.12	69.0	7	9/24	K141k	(K) I D k T D Y|M|V/G/S/Y/G P/R (A)	1601.7628	114.0508	4.6	23207.2/5.02	HUMAN	P52565	242757	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3

Fragment-ion (m/z)	70.064	72.081	84.081	86.096	104.053	119.045	136.073	175.118	183.118	191.122	312.164
Frac. Inten.(% of TIC)	0.00	0.43	8.84	7.88	7.49	2.78	0.14	1.81	1.90	2.07	3.30
Rel. Inten.(% of BP)	0.02	2.20	44.91	40.04	38.08	14.14	0.70	9.20	9.66	10.51	16.74
Score	0.20	0.50	-0.45	0.50 0.50	-0.38	-0.14	1.00	1.50	-0.10	-0.11	0.50
Ion-type	PR	V		a_1 LI			Y	y_1			y_3-NH_3
Delta ppm	-18.9	-1.0		-21.2 -8.4			-19.8	-7.7			-7.5

Fragment-ion (m/z)	329.190	339.169	416.203^{+2}	430.717	492.259	509.279	579.282	618.293	636.309	735.386	850.391	866.407	981.440
Frac. Inten.(% of TIC)	3.32	1.93	2.06	2.05	3.47	1.90	3.65	5.13	19.68	9.97	3.30	2.12	4.76
Rel. Inten.(% of BP)	16.87	9.81	10.48	10.40	17.64	9.67	18.53	26.07	100.00	50.67	16.74	10.77	24.20
Score	1.50	-0.10	-0.10	-0.10	1.50	-0.10	1.50	0.50	1.50	1.50	0.50	1.50	0.50
Ion-type	y_3				y_4		y_5	y_6-H_2O	y_6	y_7	b_6	y_8	b_7
Delta ppm	-8.1				5.1		-11.8	-10.1	-0.9	9.9	-5.2	-13.3	4.1



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Result Summary

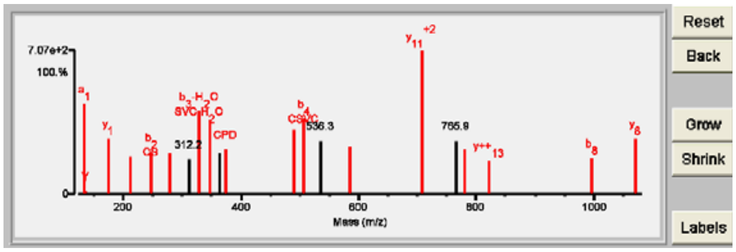
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.83	78.7	10	5/25	K157k	(K)CSVCPDYDLCSVCEGkGLHR(G)	2412.0199	114.0638	8.3	47687.5/5.10	HUMAN	Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.83	78.7	10	5/25	K157k	(K) C S\V\C\P D Y/D\L/C S/V/C E/G k G L H/R (G)	2412.0199	114.0638	8.3	47687.5/5.10	HUMAN	Q13501	731137	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1

Fragment-ion (m/z)	70.065	72.081	84.079	86.096	133.042	136.076	175.118	213.087	248.067	279.094	312.170^{+2}
Frac. Inten.(% of TIC)	0.01	0.17	6.61	0.38	7.27	0.30	4.50	3.02	3.35	3.29	2.81
Rel. Inten.(% of BP)	0.05	1.52	57.40	3.32	63.11	2.56	39.09	26.24	29.09	28.58	24.36
Score	0.20	0.50	-0.57	0.22	0.50	1.00	1.50	0.75	0.75	0.75	-0.24
Ion-type	PR	V		LI	a_1	Y	y_1	PD	b_2 CS	YD	
Delta ppm	1.1	0.3		-3.8	-12.1	-1.4	-3.7	-5.5	-17.9 -17.9	-16.6	

Fragment-ion (m/z)	329.123	347.142	364.159	373.125	491.174	507.157	536.255	585.290	708.831^{+2}	765.859^{+2}	781.425	822.872	997.341	1070.514
Frac. Inten.(% of TIC)	6.69	5.91	3.25	3.58	5.21	6.02	4.32	3.80	11.52	4.27	3.58	2.76	2.93	4.44
Rel. Inten.(% of BP)	58.05	51.32	28.25	31.04	45.27	52.23	37.54	32.95	100.00	37.06	31.11	23.92	25.41	38.54
Score	0.50	0.75	-0.28	0.75	0.75	0.75	-0.38	1.50	1.50	-0.37	1.50	1.50	0.50	1.50
Ion-type	b_3-H_2O SVC-H_2O	b_3 SVC		CPD	PDYD	b_4 CSVC		$y{+}{+}_9$	y_{11}^{+2}		y_6	$y{+}{+}_{13}$	b_8	y_8
Delta ppm	-17.0 -17.0	8.2 8.2		18.1	-9.1	-25.3 -25.3		-10.0	5.5		-22.5	-12.5	0.5	-1.9



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Result Summary

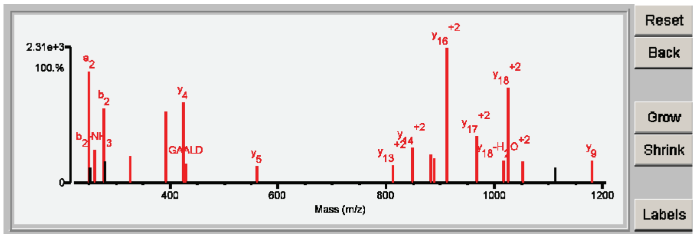
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.12	91.7	12	4/25	K435k	(K)NYDIGAALDTIQYSkHPPPL(-)	2213.1237	114.0680	10.8	47687.5/5.10	HUMAN	Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.12	91.7	12	4/25	K435k	(K) N Y|D|I/G/A/A/L D T I/Q/Y/S k/H/P/P P L (-)	2213.1237	114.0680	10.8	47687.5/5.10	HUMAN	Q13501	731137	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1

Fragment-ion (m/z)	86.095	87.055	88.038	136.075	250.118	251.121	261.088	278.114	279.112	326.206	393.145
Frac. Inten.(% of TIC)	0.11	1.28	2.96	0.16	11.41	1.63	3.41	7.62	2.13	2.76	7.20
Rel. Inten.(% of BP)	0.83	9.30	21.45	1.18	82.79	11.86	24.74	55.32	15.47	20.00	52.22
Score	0.22	0.50	-0.21	1.00	0.50	-0.12	0.25	0.50	-0.15	1.50	0.50
Ion-type	LI	a_1		Y	a_2		b_2-NH_3	b_2		y_3	b_3
Delta ppm	-11.9	-12.5		-5.8	-5.7		0.1	-2.3		-5.0	9.5
		0.50									
		NR									
		0.1									

Fragment-ion (m/z)	423.259	428.215	560.319	811.928^{+2}	847.454^{+2}	882.986^{+2}	889.507	911.478^{+2}	968.040^{+2}	1016.499^{+2}	1025.553^{+2}	1052.549	1112.055^{+2}	1180.615
Frac. Inten.(% of TIC)	8.22	1.99	1.69	1.81	3.55	2.88	2.52	13.78	4.80	2.26	9.71	2.14	1.62	2.35
Rel. Inten.(% of BP)	59.69	14.41	12.28	13.16	25.79	20.94	18.29	100.00	34.84	16.41	70.51	15.53	11.72	17.06
Score	1.50	0.75	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50	-0.12	1.50
Ion-type	y_4	GAALD	y_5	y_{13}^{+2}	y_{14}^{+2}	y_{15}^{+2}	y_7	y_{16}^{+2}	y_{17}^{+2}	y_{18}-H_2O^{+2}	y_{18}^{+2}	y_8		y_9
Delta ppm	-3.8	-0.4	-0.7	-2.6	6.3	20.6	20.1	-0.1	20.4	-29.6	18.5	-2.8		3.4



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Result Summary

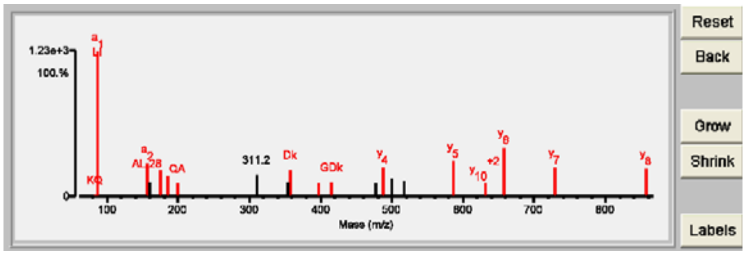
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.54	83.3	8	6/25	K456k	(R)LAGDkYQAAVQALR(E)	1503.8278	114.0517	5.4	53082.9/7.61	HUMAN	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.54	83.3	8	6/25	K456k	(R) L A\G D/k Y/Q/A/A/V/Q A L/R (E)	1503.8278	114.0517	5.4	53082.9/7.61	HUMAN	P34896	256085	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1

Fragment-ion (m/z)	70.064	72.079	84.079	86.095	101.070	136.075	157.133	159.084	175.115	185.127	200.101	311.181
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -18.9	0.13 0.51 0.50 V -17.7	0.42 1.67 0.50 KQ -15.2	25.10 100.00 0.50 a_1 -30.5 0.50 LI -17.7	0.16 0.63 KQ	0.13 0.53 1.00 Y -2.1	5.73 22.82 0.50 a_2 -8.5 AL-28 -8.5	2.39 9.54 -0.10	4.67 18.62 1.50 y_1 -20.9	3.54 14.12 0.75 b_2 -14.3 AL -14.3	2.24 8.94 0.75 QA -17.8	3.69 14.71 -0.15

Fragment-ion (m/z)	353.183	358.180	397.179	415.183	477.205	487.301	499.222^{+2}	517.275	586.372	631.331^{+2}	657.407	728.448	856.495
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.49 9.93 -0.10	4.70 18.74 0.75 Dk 18.4	2.15 8.57 0.50 GDk-H_2O -12.4	2.51 9.99 0.75 GDk -27.4	2.23 8.90 -0.09	5.08 20.25 1.50 y_4 4.1	3.14 12.49 -0.12	2.72 10.85 -0.11	6.05 24.09 1.50 y_5 8.7	2.31 9.22 1.50 y_{10}^{+2} -36.6	8.49 33.82 1.50 y_6 3.7	5.07 20.19 1.50 y_7 9.4	4.84 19.27 1.50 y_8 -5.8



Result Summary

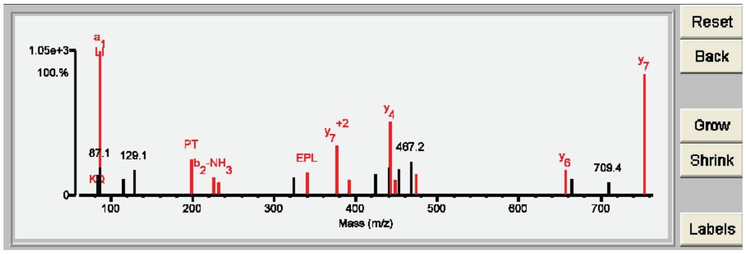
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.48	69.2	4	11/25	K237k	(R)IQTkEPLPTLPLGR(S)	1562.9265	114.0351	-4.7	48841.1/10.07	HUMAN	O43464	Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.48	69.2	4	11/25	K237k	(R) I Q T k E P L/P/T L/P L/G R (S)	1562.9265	114.0351	-4.7	48841.1/10.07	HUMAN	O43464	302643	Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2

Fragment-ion (m/z)	70.063	84.078	84.105	86.096	87.097	115.082	129.096	199.102	225.120	232.134	324.159	340.183	377.227^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.08 0.20 **PR** -33.2	0.25 1.38 0.50 **KQ** -31.8	2.51 14.03 -0.14	17.91 100.00 0.50 a_1 -20.0 0.50 **LI** -7.3	3.45 19.27 -0.19	2.08 11.64 -0.12	3.16 17.66 -0.18	4.48 25.03 0.75 **PT** -32.2	2.28 12.75 0.25 b_2-NH_3 -19.0	1.64 9.16 1.50 y_2 -28.5	2.19 12.23 -0.12	2.78 15.50 0.75 **EPL** -13.2	6.18 34.52 1.50 y_7^{+2} -19.9

Fragment-ion (m/z)	392.217^{+2}	423.218	439.743^{+2}	442.272	448.756^{+2}	452.200	467.241	473.233	656.399	664.358	709.443	753.447
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.90 10.59 0.50 a_6^{+2} -13.4	2.68 14.95 -0.15	3.49 19.51 -0.20	9.09 50.79 1.50 y_4 -12.3	1.86 10.41 0.50 a_7^{+2} -18.3	3.23 18.06 -0.18	4.26 23.80 -0.24	2.67 14.91 0.75 **TkE** -6.6	3.09 17.25 1.50 y_6 -15.1	2.09 11.65 -0.12	1.65 9.21 -0.09	15.06 84.14 1.50 y_7 -19.4



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Result Summary

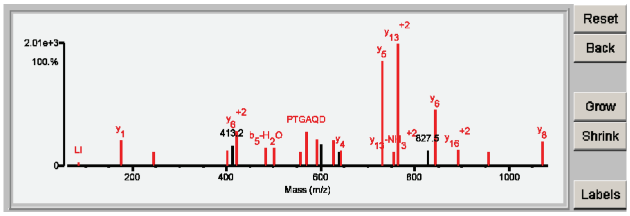
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.59	89.6	10	4/25	K306k	(K)FPASVPTGAQDLISkLLR(H)	1913.0855	114.0418	-0.6	39280.7/9.36	HUMAN	Q96GD4	Serine/threonine-protein kinase 12 OS=Homo sapiens GN=AURKB PE=1 SV=2
2	5.66	55.0	3	16/25	None	(K)KLDVVSAEGRELQKVLSR(L)	2027.1608	-0.0335	-16.5	80760.8/8.88	HUMAN	RQ14123	REVERSE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C OS=Homo sapiens GN=PDE1C PE=2 SV=1
3	4.42	50.7	3	15/25	None	(K)FYEKMLPYVIAVALDVR(D)	2027.1034	0.0238	11.7	96820.3/5.45	HUMAN	RQ9UBB9	REVERSE Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.59	89.6	10	4/25	K306k	(K) F/P|A S V|P T G A Q/D|L/I/S/k/L L/R (H)	1913.0855	114.0418	-0.6	39280.7/9.36	HUMAN	Q96GD4	62693	Serine/threonine-protein kinase 12 OS=Homo sapiens GN=AURKB PE=1 SV=2

Fragment-ion (m/z)	70.065	86.098	175.118	245.132	401.287	413.217	422.273^{+2}	484.259	502.267	556.330	570.257	591.351^{+2}
Frac. Inten.(% of TIC)	0.00	0.52	3.73	2.13	2.16	3.03	5.07	2.64	2.60	2.05	5.03	3.91
Rel. Inten.(% of BP)	0.02	2.88	20.81	11.89	12.07	16.90	28.31	14.75	14.54	11.43	28.09	21.82
Score	0.20	0.22	1.50	0.50	1.50	-0.17	1.50	0.25	0.50	0.75	0.75	0.50
Ion-type	PR	LI	y_1	b_2	y_3		y_6^{+2}	b_5-H_2O	b_5	SkLL	PTGAQD	$y_9-H_2O^{+2}$
Delta ppm	2.5	16.0	-7.7	9.2	-0.2		-3.2	4.9	0.4	-29.5	7.3	-4.9

Fragment-ion (m/z)	601.444	627.361^{+3}	638.712^{+3}	643.426	730.454	754.941^{+2}	763.437^{+2}	827.465	843.533	891.993^{+2}	956.626	1071.527	1071.653
Frac. Inten.(% of TIC)	3.09	3.68	2.11	2.18	15.43	2.01	17.91	2.17	8.22	2.42	2.01	2.27	3.64
Rel. Inten.(% of BP)	17.27	20.56	11.77	12.16	86.18	11.24	100.00	12.11	45.89	13.53	11.21	12.70	20.32
Score	-0.17	1.50	-0.12	1.50	1.50	0.50	1.50	-0.12	1.50	1.50	1.50	0.50	1.50
Ion-type		y_{17}^{+3}		y_4	y_5	$y_{13}-NH_3^{+2}$	y_{13}^{+2}		y_6	y_{16}^{+2}	y_7	b_{11}	y_8
Delta ppm		5.0		1.3	-4.5	21.2	-2.5		-9.4	-16.1	0.5	14.0	1.1



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Result Summary

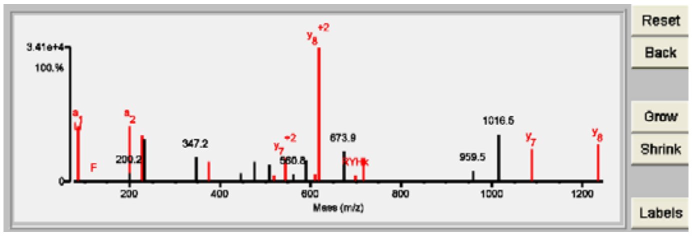
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.47	65.3	3	11/25	K533k	(K)LLFLRYHkEK(E)	1346.7943	114.0240	-13.0	410263.6/6.05	HUMAN	Q96Q15	Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=1 SV=2
2	10.67	64.4	3	12/25	K535k	(K)LLFLRYHKEk(E)	1346.7943	114.0240	-13.0	410263.6/6.05	HUMAN	Q96Q15	Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=1 SV=2
3	8.45	55.9	3	14/25	K1886k	(R)LLGGILFSDNAVk(K)	1346.7678	114.0505	5.2	229892.3/7.65	HUMAN	RP53804	REVERSE Tetratricopeptide repeat protein 3 OS=Homo sapiens GN=TTC3 PE=2 SV=1
4	7.88	59.9	2	14/25	M1462m K1467k	(K)IImEEVVkLEK(D)	1330.7651	130.0533	10.6	231619.2/6.56	HUMAN	Q92817	Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=2
5	7.63	59.9	2	14/25	M1462m K1470k	(K)IImEEVVKLEk(D)	1330.7651	130.0533	10.6	231619.2/6.56	HUMAN	Q92817	Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.47	65.3	3	11/25	K533k	(K) L L | F | L R Y H / k E K (E)	1346.7943	114.0240	-13.0	410263.6/6.05	HUMAN	Q96Q15	722689	Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=1 SV=2

Fragment-ion (m/z)	84.082	86.097	120.082	199.183	200.186	227.179	232.144	347.173	374.249	445.290	476.217	508.770^{+2}
Frac. Inten.(% of TIC)	0.06	8.03	0.08	8.06	1.26	6.78	6.17	3.54	2.89	1.19	2.96	2.34
Rel. Inten.(% of BP)	0.28	41.26	0.42	41.43	6.50	34.81	31.68	18.16	14.86	6.10	15.21	12.03
Score	0.50	0.50 0.50	1.00	0.50	-0.06	0.50	-0.32	-0.18	0.75	-0.06	-0.15	-0.12
Ion-type	**KQ**	a_1 **LI**	**F**	a_2		b_2			b_3 **LFL**			
Delta ppm	19.3	-3.8 9.0	10.2	9.1		11.4			10.6 10.6			

Fragment-ion (m/z)	518.278	544.289^{+2}	560.801^{+2}	589.307	608.815^{+2}	617.824^{+2}	673.889^{+2}	699.352	717.363	959.507	1016.530	1087.565	1234.633
Frac. Inten.(% of TIC)	0.92	3.49	1.12	3.16	1.07	19.47	4.48	0.90	3.45	1.59	6.89	4.76	5.36
Rel. Inten.(% of BP)	4.72	17.91	5.74	16.24	5.48	100.00	23.01	4.63	17.73	8.15	35.37	24.45	27.54
Score	1.50	1.50	-0.06	-0.16	0.50	1.50	-0.23	0.75	0.75	-0.08	-0.35	1.50	1.50
Ion-type	y_3	y_7^{+2}			y_8-H_2O^{+2}	y_8^{+2}		**RYHk**	**FLRYH**			y_7	y_8
Delta ppm	-29.5	-28.1			-29.0	-22.5		-25.0	-29.4			-32.9	-29.6



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.07	80.6	11	6/25	K374k	(K)DNTIEHLLPLFLAQLkDECPEVR(L)	2750.4182	114.0632	7.1	65309.0/5.00	HUMAN	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4

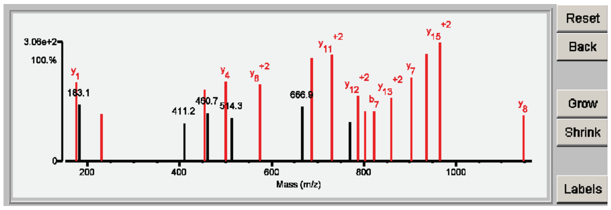
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.07	80.6	11	6/25	K374k	(K) D N\T I E H L\L|P L/F/L/A Q\L/k/D E C/P E V/R (L)	2750.4182	114.0632	7.1	65309.0/5.00	HUMAN	P30153	479	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4

Fragment-ion (m/z)	70.066	84.081	86.097	120.079	175.117	183.147	230.074	411.215	454.741^{+2}
Frac. Inten.(% of TIC)	0.01	0.16	0.34	0.24	5.47	3.90	3.30	2.67	5.00
Rel. Inten.(% of BP)	0.09	1.90	4.08	2.96	66.32	47.19	39.93	32.34	60.63
Score	0.20	0.50	0.22	1.00	1.50	-0.47	0.50	-0.32	0.50
Ion-type	PR	KQ	LI	F	y_1		b_2		a_8^{+2}
Delta ppm	18.2	-2.1	9.0	-14.8	-12.9		-18.4		-11.6

Fragment-ion (m/z)	460.733	500.280	514.326	573.760^{+2}	666.852^{+2}	685.818^{+2}	729.845^{+2}	770.418	786.381^{+2}
Frac. Inten.(% of TIC)	3.39	5.58	2.99	5.32	3.75	7.16	7.37	2.69	4.54
Rel. Inten.(% of BP)	41.04	67.56	36.17	64.42	45.45	86.72	89.24	32.64	55.00
Score	-0.41	1.50	-0.36	1.50	-0.45	0.50	1.50	-0.33	1.50
Ion-type		y_4		y_8^{+2}		y_{10}-NH_3^{+2}	y_{11}^{+2}		y_{12}^{+2}
Delta ppm		-4.6		-6.3		-5.8	-11.9		-18.8

Fragment-ion (m/z)	803.427	823.377	859.936^{+2}	904.387	936.484	964.980^{+2}	1146.534
Frac. Inten.(% of TIC)	3.47	3.48	4.43	5.85	7.42	8.25	3.24
Rel. Inten.(% of BP)	42.02	42.22	53.63	70.86	89.86	100.00	39.21
Score	0.50	0.50	1.50	1.50	0.50	1.50	1.50
Ion-type	$b{+}{+}_{14}$	b_7	y_{13}^{+2}	y_7	b_8	y_{15}^{+2}	y_8
Delta ppm	-10.6	-22.0	6.2	5.0	4.9	-19.8	11.8



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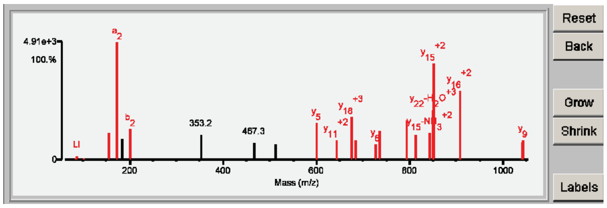
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.01	89.8	12	4/25	K546k	(K)SLQkIGPILDNSTLQSEVKPILEK(L)	2650.5026	114.0708	10.1	65309.0/5.00	HUMAN	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4
2	5.51	51.3	5	12/25	K561k	(K)SLQKIGPILDNSTLQSEVkPILEK(L)	2650.5026	114.0708	10.1	65309.0/5.00	HUMAN	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4
3	4.51	51.3	4	12/25	K566k	(K)SLQKIGPILDNSTLQSEVKPILEk(L)	2650.5026	114.0708	10.1	65309.0/5.00	HUMAN	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.01	89.8	12	4/25	K546k	(K) S L\Q/k I|G/P I/L/D/N/S T/L Q/S E V/K/P I L E K (L)	2650.5026	114.0708	10.1	65309.0/5.00	HUMAN	P30153	957	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4

Fragment-ion (m/z)	70.064	84.080	86.096	101.070	155.081	173.127	183.148	201.121	353.245	467.257	511.294	599.371	642.389^{+2}	675.381^{+3}	684.397	727.466	736.434^{+2}	793.451^{+2}	812.797^{+3}	842.443^{+2}	849.495^{+3}	850.963^{+2}	907.501^{+2}	1041.093^{+2}	1042.613
Frac. Inten.(% of TIC)	0.00	0.16	0.40	0.15	3.43	15.41	2.67	3.95	3.28	2.17	2.07	4.81	2.61	5.64	2.51	2.11	3.80	5.14	3.17	3.55	6.52	12.53	8.99	2.25	2.63
Rel. Inten.(% of BP)	0.03	1.07	2.59	0.99	22.27	100.00	17.32	25.66	21.31	14.11	13.46	31.22	16.91	36.61	16.32	13.67	24.69	33.37	20.59	23.03	42.34	81.33	58.35	14.61	17.09
Score	0.20	0.50	0.22		0.75	0.50	-0.17	0.50	-0.21	-0.14	-0.13	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50	1.50
Ion-type	PR	KQ	LI	KQ	GP	a_2		b_2				y_5	y_{11}^{+2}	y_{18}^{+3}	b_5	y_6	y_{13}^{+2}	y_{14}^{+2}	y_{21}^{+3}	y_{15}-NH_3^{+2}	y_{22}-H_2O^{+3}	y_{15}^{+2}	y_{16}^{+2}	y_{19}^{+2}	y_9
Delta ppm	-14.6	-6.8	-10.8		-12.3	-13.0		-18.2				-8.8	10.3	0.7	-11.7	-7.4	16.4	9.4	2.4	-0.5	20.5	6.8	1.8	14.8	-1.2



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Result Summary

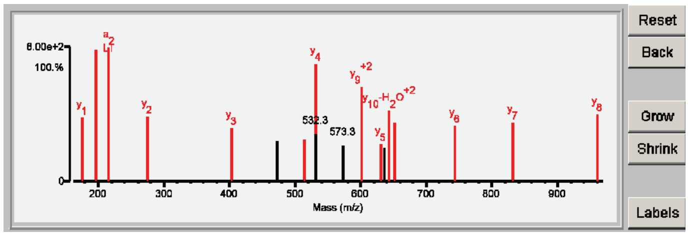
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.58	84.8	10	5/25	K41k	(K)EILTkESNVQEVR(C)	1544.8279	114.0506	4.6	35594.4/5.30	HUMAN	P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1
1	18.58	84.8	10	5/25	K41k	(K)EILTkESNVQEVR(C)	1544.8279	114.0506	4.6	35575.3/5.21	HUMAN	P62714	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.58	84.8	10	5/25	K41k	(K) E I L/T/k/E/S/N/V/Q/E/V/R (C)	1544.8279	114.0506	4.6	35594.4/5.30	HUMAN	P67775	255402	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1
1	18.58	84.8	10	5/25	K41k	(K) E I L/T/k/E/S/N/V/Q/E/V/R (C)	1544.8279	114.0506	4.6	35575.3/5.21	HUMAN	P62714	255409	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1

Fragment-ion (m/z)	60.054	72.082	84.044	84.079	86.096	87.054	129.065	175.117	197.128	215.137	274.183	403.234	472.228
Frac. Inten.(% of TIC)	2.55	0.30	0.22	0.31	0.40	0.09	0.12	5.11	10.42	10.67	5.14	4.27	3.26
Rel. Inten.(% of BP)	23.95	2.78	2.08	2.95	3.74	0.84	1.13	47.89	97.74	100.00	48.19	40.03	30.54
Score	-0.24	0.50	1.00	0.50	0.22	0.33	0.20	1.50	0.50	0.75	1.50	1.50	-0.31
Ion-type		V	E	KQ	LI	NR	QKR	y_1	LT-H_2O	a_2 LT	y_2	y_3	
Delta ppm		11.4	-9.4	-15.2	-9.6	-17.1	-10.5	-10.0	-10.4	-14.0 -14.0	-14.8	9.0	

Fragment-ion (m/z)	514.264	531.296	532.309^{+2}	573.278^{+2}	601.805^{+2}	630.354	635.308	643.311^{+2}	652.333^{+2}	744.385	831.422	960.459
Frac. Inten.(% of TIC)	3.31	9.32	3.76	2.89	7.49	2.97	2.70	5.57	4.72	4.40	4.68	5.34
Rel. Inten.(% of BP)	30.99	87.38	35.22	27.05	70.21	27.84	25.33	52.26	44.28	41.25	43.85	50.04
Score	0.50	1.50	-0.35	-0.27	1.50	1.50	-0.25	0.50	1.50	1.50	1.50	1.50
Ion-type	y_4-NH_3	y_4			y_9^{+2}	y_5		y_{10}-H_2O^{+2}	y_{10}^{+2}	y_6	y_7	y_8
Delta ppm	3.3	14.4			-7.7	-4.4		-26.9	-0.3	-20.1	-12.0	-15.9



Result Summary

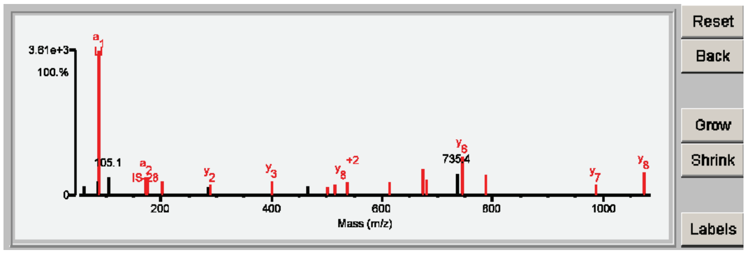
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.65	83.4	12	6/25	K391k	(K)ISQGNISkACLILR(S)	1572.8890	114.0490	3.6	74606.6/9.31	HUMAN	O76094	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.65	83.4	12	6/25	K391k	(K) I/S\Q/G N\I|S/k/A/C/L/I/L/R (S)	1572.8890	114.0490	3.6	74606.6/9.31	HUMAN	O76094	732129	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72 PE=1 SV=3

Fragment-ion (m/z)	60.050	70.064	84.044	84.079	86.095	101.069	105.064	173.127	175.119	201.122	283.101	288.201
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.01 6.72 -0.07	0.00 0.01 0.20 PR -20.3	2.91 9.70 -0.10	0.24 0.80 0.50 KQ -18.7	30.00 100.00 0.50 a$_1$ -29.3 0.50 LI -16.6	0.07 0.23 KQ	3.60 12.00 -0.12	3.76 12.54 0.50 a$_2$ -13.0 IS-28 -13.0	3.69 12.30 1.50 y$_1$ 2.6	3.04 10.15 0.75 b$_2$ -13.3 IS -13.3	1.64 5.48 -0.05	2.24 7.47 1.50 y$_2$ -6.6

Fragment-ion (m/z)	401.283	466.194	500.260	514.374	537.809^{+2}	613.311	674.394	679.877^{+2}	735.387	745.436	787.421^{+2}	987.566	1074.604
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.00 10.01 1.50 y$_3$ -9.2	1.88 6.28 -0.06	1.74 5.80 0.75 b$_5$ 25.3 QGNIS 25.3	2.27 7.57 1.50 y$_4$ 5.2	2.62 8.74 1.50 y$_8{}^{+2}$ 1.4	2.73 9.10 0.50 b$_6$ -33.4	5.41 18.04 1.50 y$_5$ -11.9	3.17 10.55 1.50 y$_{11}{}^{+2}$ -8.1	4.51 15.02 -0.15	7.97 26.58 1.50 y$_6$ -3.8	4.36 14.53 1.50 y$_{13}{}^{+2}$ -8.9	2.27 7.56 1.50 y$_7$ -11.0	4.84 16.15 1.50 y$_8$ -4.8



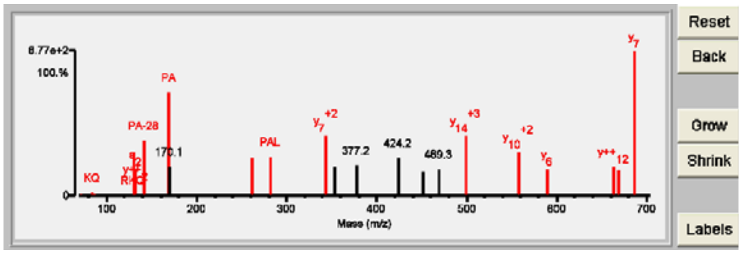
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.16	76.9	6	7/25	K162k	(K)ASPALVAkDPGTVANK(K)	1538.8537	114.0440	0.6	59179.9/4.70	HUMAN	Q92783	Signal transducing adapter molecule 1 OS=Homo sapiens GN=STAM PE=1 SV=3
2	6.49	55.7	2	13/25	K450k K454k	(K)LAPPkAGSkNLSNK(K)	1424.8220	228.0757	-6.2	255619.3/8.92	HUMAN	Q8IVL0	Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.16	76.9	6	7/25	K162k	(K) A S/P A/L V/A k D/P/G T V A/N K (K)	1538.8537	114.0440	0.6	59179.9/4.70	HUMAN	Q92783	736311	Signal transducing adapter molecule 1 OS=Homo sapiens GN=STAM PE=1 SV=3

Fragment-ion (m/z)	70.065	72.081	84.080	86.097	129.098	130.086	131.079	141.103	169.099	170.098	261.147	282.184	343.692^{+2}	353.131	377.214^{+2}	424.231	451.242	469.326	498.928^{+3}	557.796^{+2}	589.321	663.851	668.373	686.379	809.462
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.02 0.10 0.20 PR -4.6	0.20 1.25 0.50 V 0.3	0.32 2.04 0.50 KQ -12.8	0.19 1.23 0.22 LI 3.2	0.09 0.59 0.20 RKQ -35.9	4.80 30.38 0.50 y_1-NH_3 -4.3	2.91 18.43 1.50 a_2 -29.0 y^{++}_2 -20.6	6.06 38.33 0.50 PA-28 -1.7	11.26 71.27 0.75 PA 1.5	3.14 19.89 -0.20	4.19 26.50 1.50 y_2 -34.2	4.31 27.30 0.75 PAL 6.3	6.57 41.57 1.50 y_7^{+2} -10.0	3.14 19.89 -0.20	3.32 21.02 -0.21	4.17 26.41 -0.26	2.69 17.05 -0.17	2.85 18.03 -0.18	6.51 41.22 1.50 y_{14}^{+3} -38.4	4.79 30.29 1.50 y_{10}^{+2} -0.9	2.95 18.67 1.50 y_6 -15.8	3.19 20.17 1.50 y^{++}_{12} -31.7	2.72 17.23 0.50 y_7-H_2O -0.0	15.80 100.00 1.50 y_7 -6.2	3.80 24.06 -0.24



Result Summary

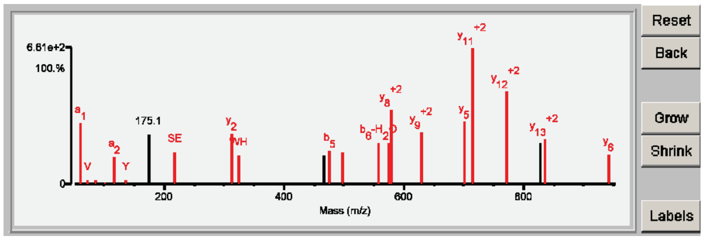
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.59	87.7	11	3/25	K81k	(R)SGDSEVYQLGDVSQkTTWHR(I)	2293.0844	114.0630	8.3	17259.8/9.59	HUMAN	Q04837	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.59	87.7	11	3/25	K81k	(R) S G D S E\V\Y/Q/L/G D/V/S Q/k/T T/W/H R (I)	2293.0844	114.0630	8.3	17259.8/9.59	HUMAN	Q04837	732779	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1

Fragment-ion (m/z)	60.045	72.081	84.045	84.079	86.096	101.068	117.063	136.075	175.111	217.080	312.176	324.138
Frac. Inten.(% of TIC)	6.27	0.47	0.09	0.12	0.46	0.16	2.85	0.40	5.07	3.23	5.23	2.88
Rel. Inten.(% of BP)	45.03	3.39	0.64	0.83	3.34	1.13	20.47	2.90	36.39	23.17	37.53	20.65
Score	0.50	0.50	1.00		0.22	0.50	0.50	1.00	-0.36	0.75	1.50	0.75
Ion-type	a_1	V	E	QK	LI	QK	a_2	Y		SE	y_2	WH
Delta ppm	-8.1	-1.0	4.9		-1.5	-25.1	-30.3	-2.1		-15.2	-5.7	-26.2

Fragment-ion (m/z)	467.234^{+2}	476.160	498.255	557.218	575.238	579.298^{+2}	628.819^{+2}	700.356	714.856^{+2}	771.423^{+2}	827.398^{+2}	835.422^{+2}	942.490
Frac. Inten.(% of TIC)	2.93	3.39	3.28	4.27	4.24	7.60	5.28	6.43	13.93	9.46	4.26	4.62	3.09
Rel. Inten.(% of BP)	21.03	24.36	23.59	30.64	30.46	54.58	37.90	46.14	100.00	67.94	30.60	33.18	22.22
Score	-0.21	0.50	1.50	0.25	0.50	1.50	1.50	1.50	1.50	1.50	-0.31	1.50	1.50
Ion-type		b_5	y_3	b_6-H_2O	b_6	y_8^{+2}	y_9^{+2}	y_5	y_{11}^{+2}	y_{12}^{+2}		y_{13}^{+2}	y_6
Delta ppm		-6.6	-4.0	-6.1	10.4	7.5	-15.1	5.4	5.2	36.6		-1.8	-0.9



Result Summary

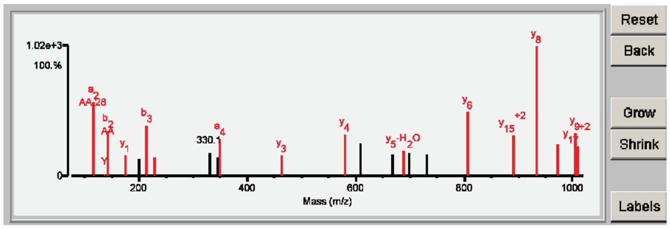
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.50	80.9	9	7/25	K137k	(R)AAAYSkLGNYAGAVQDCER(A)	2043.9553	114.0491	2.9	34063.3/4.81	HUMAN	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.50	80.9	9	7/25	K137k	(R) A A|A|Y/S k L G N Y/A/G A/V Q/D/C E/R (A)	2043.9553	114.0491	2.9	34063.3/4.81	HUMAN	O43765	718827	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Fragment-ion (m/z)	84.081	86.095	115.085	136.074	143.078	175.117	200.121	214.118	228.135	330.091	345.123^{+2}	349.176
Frac. Inten.(% of TIC)	0.08	0.09	8.83	0.20	5.41	2.46	2.14	6.09	2.22	2.69	2.23	4.53
Rel. Inten.(% of BP)	0.49	0.58	56.52	1.29	34.63	15.73	13.69	38.94	14.22	17.23	14.24	29.01
Score	0.50	0.22	0.50	1.00	0.75	1.50	-0.14	0.50	0.75	-0.17	-0.14	0.50
Ion-type	KQ	LI	a_2 AA-28	Y	b_2 AA	y_1		b_3	VQ			a_4
Delta ppm	-2.1	-13.1	-27.7 -27.7	-9.5	-30.1 -30.1	-14.0		-8.0	-2.5			-34.2

Fragment-ion (m/z)	464.192	579.217	608.809^{+2}	668.326	689.285	699.348	730.889	806.344	891.415^{+2}	934.411	972.962^{+2}	1005.442	1008.472^{+2}
Frac. Inten.(% of TIC)	2.43	5.00	3.95	2.66	2.97	2.80	2.59	7.64	4.87	15.63	3.83	5.11	3.54
Rel. Inten.(% of BP)	15.57	32.01	25.28	17.00	19.01	17.91	16.57	48.92	31.20	100.00	24.50	32.73	22.67
Score	1.50	1.50	-0.25	-0.17	0.50	-0.18	-0.17	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_3	y_4			y_5-H_2O			y_6	y_{15}^{+2}	y_8	y_{16}^{+2}	y_9	y_{17}^{+2}
Delta ppm	-0.2	-3.9			26.3			-2.1	-0.3	7.1	15.7	0.3	6.1



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Result Summary

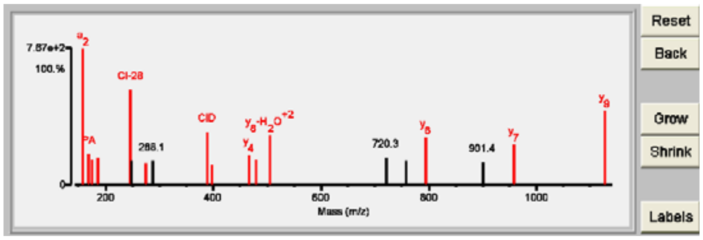
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.16	68.9	6	8/25	K160k	(R)AICIDPAYSkAYGR(M)	1584.7839	114.0483	3.1	34063.3/4.81	HUMAN	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.16	68.9	6	8/25	K160k	(R) A I\C I D/P A/Y/S k/A Y G/R (M)	1584.7839	114.0483	3.1	34063.3/4.81	HUMAN	O43765	718827	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Fragment-ion (m/z)	70.062	84.079	86.096	133.041	136.073	141.097	157.133	169.094	175.114	185.125	246.129	248.126
Frac. Inten.(% of TIC)	5.20	5.81	0.32	8.09	0.08	2.05	13.43	3.06	2.51	2.69	9.36	2.31
Rel. Inten.(% of BP)	38.74	43.26	2.36	60.23	0.62	15.30	100.00	22.80	18.66	20.06	69.70	17.20
Score	-0.39	-0.43	0.22	-0.60	1.00	0.50	0.50	0.75	1.50	0.50	0.50	-0.17
Ion-type			LI		Y	PA-28	a_2	PA	y_1	b_2	CI-28	
Delta ppm			-3.8		-19.0	-34.3	-3.4	-20.4	-30.0	-21.4	6.6	

Fragment-ion (m/z)	274.116	288.115	389.151	398.199	466.245	479.734^{+2}	506.237^{+2}	720.265	758.356^{+2}	795.416	901.429	958.490	1126.554
Frac. Inten.(% of TIC)	2.14	2.39	5.21	2.03	2.87	2.42	4.83	2.73	2.35	4.67	2.22	3.95	7.27
Rel. Inten.(% of BP)	15.94	17.76	38.78	15.10	21.40	18.05	35.99	20.36	17.48	34.79	16.54	29.45	54.15
Score	0.75	-0.18	0.75	1.50	1.50	1.50	0.50	-0.20	-0.17	1.50	-0.17	1.50	1.50
Ion-type	CI		CID	y^{++}_6	y_4	y_7^{+2}	y_8-H_2O^{+2}			y_6		y_7	y_9
Delta ppm	-20.4		5.6	-26.4	9.1	-13.5	-34.1			7.1		16.4	-9.3



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Result Summary

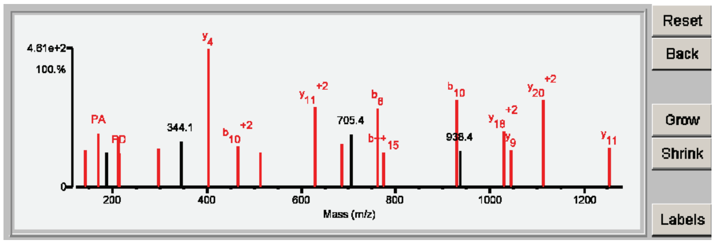
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.55	81.3	8	5/25	K419k	(K)ASKPLPPAPAPDEYLVSPITGEkIPASK(M)	2873.5659	114.0587	5.3	88886.6/5.15	HUMAN	Q15459	Splicing factor 3 subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1
2	13.05	69.7	7	6/25	K424k	(K)ASKPLPPAPAPDEYLVSPITGEKIPASk(M)	2873.5659	114.0587	5.3	88886.6/5.15	HUMAN	Q15459	Splicing factor 3 subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.55	81.3	8	5/25	K419k	(K) A S K P L P\P A|P A|P\D E Y L\V S/P I/T G E k I/P A S K (M)	2873.5659	114.0587	5.3	88886.6/5.15	HUMAN	Q15459	717209	Splicing factor 3 subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1

Fragment-ion (m/z)	70.067	71.068	84.078	86.096	141.103	169.094	187.145	211.140	213.082	297.685	344.141	402.235
Frac. Inten.(% of TIC)	0.01	4.74	0.09	0.14	3.07	4.47	2.87	4.19	2.84	3.21	3.77	11.56
Rel. Inten.(% of BP)	0.11	40.99	0.82	1.21	26.54	38.65	24.83	36.20	24.54	27.80	32.62	100.00
Score	0.20	-0.41	0.50	0.22	0.50	0.75	-0.25	0.75	0.75	0.50	-0.33	1.50
Ion-type	PR		KQ	LI	PA-28	PA		IP	PD	b++$_6$		y_4
Delta ppm	19.6		-39.0	-7.3	-5.2	-26.9		-22.7	-27.6	0.4		0.5

Fragment-ion (m/z)	465.761^{+2}	514.286	627.858^{+2}	686.706^{+3}	705.421^{+2}	762.460	774.391	930.548	938.447	1029.533^{+2}	1044.551	1113.607^{+2}	1254.703
Frac. Inten.(% of TIC)	3.36	2.95	6.72	3.63	4.38	6.54	2.93	7.23	2.98	4.69	3.10	7.25	3.27
Rel. Inten.(% of BP)	29.10	25.52	58.09	31.40	37.87	56.55	25.35	62.54	25.74	40.58	26.80	62.74	28.30
Score	0.50	0.50	1.50	1.50	-0.38	0.50	0.50	0.50	-0.26	1.50	1.50	1.50	1.50
Ion-type	b_{10}^{+2}	b++$_{11}$	y_{11}^{+2}	y_{18}^{+3}		b_8	b++$_{15}$	b_{10}		y_{18}^{+2}	y_9	y_{20}^{+2}	y_{11}
Delta ppm	-29.8	-28.6	3.3	13.8		10.2	-23.4	7.1		-8.4	-16.8	18.4	-1.7



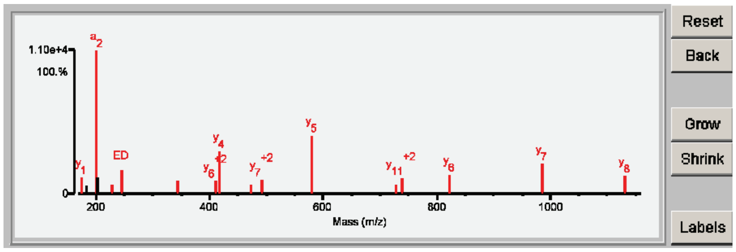
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.56	82.5	8	5/25	K38k	(K)DIEDVFYkYGAIR(D)	1588.8006	114.0552	7.2	27744.7/10.37	HUMAN	Q07955	Splicing factor, arginine/serine-rich 1 OS=Homo sapiens GN=SFRS1 PE=1 SV=2
2	7.83	51.1	4	13/25	None	(R)EVDIMLDEVENQLR(Q)	1702.8316	0.0241	14.2	223146.6/5.58	HUMAN	RP12882	REVERSE Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3
2	7.83	51.1	4	13/25	None	(R)EVDIMLDEVENQLR(Q)	1702.8316	0.0241	14.2	223072.6/5.65	HUMAN	RQ9Y623	REVERSE Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2
2	7.83	51.1	4	13/25	None	(R)EVDLMLDEVENQLR(Q)	1702.8316	0.0241	14.2	223045.6/5.64	HUMAN	RQ9UKX2	REVERSE Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1
2	7.83	51.1	4	13/25	None	(R)EVDLMLDEVENQLR(Q)	1702.8316	0.0241	14.2	222763.6/5.58	HUMAN	RP13535	REVERSE Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.56	82.5	8	5/25	K38k	(K) D I|E D\V/F/Y/k/Y/G A I/R (D)	1588.8006	114.0552	7.2	27744.7/10.37	HUMAN	Q07955	717611	Splicing factor, arginine/serine-rich 1 OS=Homo sapiens GN=SFRS1 PE=1 SV=2

Fragment-ion (m/z)	72.080	84.080	86.096	88.038	120.080	136.075	141.102	156.102	175.118	183.113	201.122	202.127	229.118	245.075	344.146	411.234^{+2}	416.262	473.197	492.768^{+2}	579.324	728.884^{+2}	737.870^{+2}	821.468	984.534	1131.594
Frac. Inten.(% of TIC)	0.14	6.82	0.21	1.48	0.18	0.12	2.98	3.19	3.04	1.54	26.62	2.97	1.74	4.48	2.28	2.47	7.78	1.68	2.57	10.88	1.69	2.77	3.61	5.46	3.31
Rel. Inten.(% of BP)	0.51	25.63	0.79	5.55	0.68	0.44	11.20	11.97	11.43	5.80	100.00	11.17	6.52	16.82	8.56	9.26	29.21	6.30	9.64	40.87	6.33	10.39	13.58	20.52	12.44
Score	0.50	-0.26	0.22	0.50	1.00	1.00	-0.11	-0.12	1.50	-0.06	0.50	-0.11	0.50	0.75	0.75	1.50	1.50	0.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	V		LI	a_1	F	Y			y_1		a_2		b_2	ED	EDV	y_6^{+2}	y_4	b_4	y_7^{+2}	y_5	y_{11}-H_2O^{+2}	y_{11}^{+2}	y_6	y_7	y_8
Delta ppm	-5.2		-10.8	-22.7	-10.6	-6.5			-7.7		-14.3		-6.0	-13.5	-0.1	-3.3	1.9	16.7	2.4	-1.8	26.6	-0.1	5.9	8.4	-0.1



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Result Summary

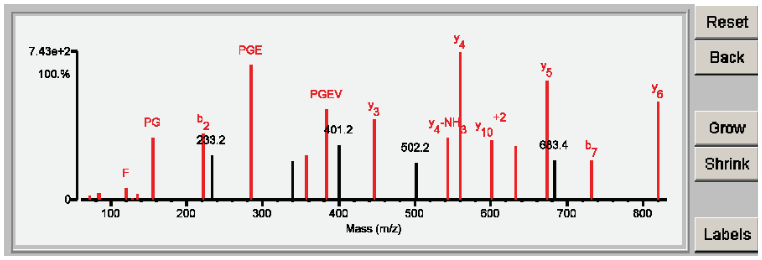
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.16	83.5	7	5/25	K330k	(K)YGEPGEVFINkGK(G)	1437.7373	114.0568	8.9	76149.8/9.45	HUMAN	P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2
2	14.11	80.2	7	6/25	K332k	(K)YGEPGEVFINKGk(G)	1437.7373	114.0568	8.9	76149.8/9.45	HUMAN	P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.16	83.5	7	5/25	K330k	(K) Y G\E/P G E\V|F/I/N/k G K (G)	1437.7373	114.0568	8.9	76149.8/9.45	HUMAN	P23246	717515	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2

Fragment-ion (m/z)	70.065	72.081	84.080	86.097	120.080	129.101	136.075	155.082	221.094	233.164	284.124
Frac. Inten.(% of TIC)	0.00	0.36	0.53	0.51	0.87	0.17	0.48	4.80	5.00	3.45	10.25
Rel. Inten.(% of BP)	0.00	3.21	4.67	4.57	7.75	1.49	4.24	42.76	44.54	30.67	91.24
Score	0.20	0.50	0.50	0.22	1.00	0.20	1.00	0.75	0.50	-0.31	0.75
Ion-type	PR	V	KQ	LI	F	RKQ	a_1	PG	b_2		PGE
Delta ppm	2.5	-2.4	-11.6	2.0	-4.8	-6.5	-10.9 1.00 Y -2.9	-5.2	2.9		-5.6

Fragment-ion (m/z)	339.183	357.188	383.193	401.181	446.272	502.249	543.283	560.319	601.819^{+2}	633.255	673.401	683.362	732.327	820.467
Frac. Inten.(% of TIC)	2.89	3.38	6.89	4.22	6.14	2.86	4.72	11.23	4.61	4.10	9.08	3.04	2.98	7.44
Rel. Inten.(% of BP)	25.76	30.12	61.31	37.53	54.61	25.42	42.02	100.00	41.06	36.47	80.87	27.10	26.54	66.23
Score	-0.26	0.75	0.75	-0.38	1.50	-0.25	0.50	1.50	1.50	0.50	1.50	-0.27	0.50	1.50
Ion-type		Nk	PGEV		y_3		y_4-NH_3	y_4	y_{10}^{+2}	b_6	y_5		b_7	y_6
Delta ppm		-4.5	-2.4		0.1		-10.0	6.8	-17.7	3.5	3.3		7.5	-0.7



Result Summary

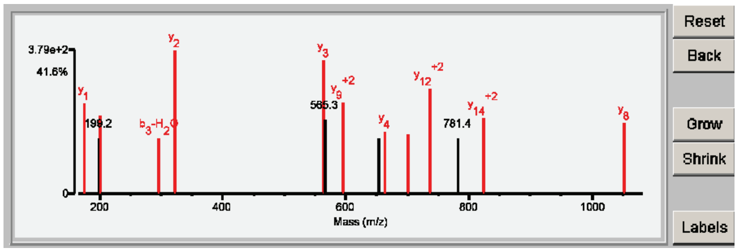
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.06	60.4	10	6/25	K154k	(R)EALLSSAVDHGSDEVkFR(Q)	1959.9770	114.0659	11.1	57488.5/6.01	HUMAN	P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.06	60.4	10	6/25	K154k	(R) E A\L L/S S/A/V D/H/G S D E/V/k/F/R (Q)	1959.9770	114.0659	11.1	57488.5/6.01	HUMAN	P78371	772107	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.081	84.043	84.080	86.095	87.055	102.054	110.071	120.082	157.129	175.115	199.179
Frac. Inten.(% of TIC)	0.00	0.46	0.28	20.31	1.93	0.16	0.19	0.32	0.12	5.03	5.34	3.31
Rel. Inten.(% of BP)	0.02	2.26	1.36	100.00	9.52	0.80	0.93	1.55	0.58	24.75	26.29	16.27
Score	0.20	0.50	1.00	-1.00	0.22	0.33	1.00	1.00	1.00	-0.25	1.50	-0.16
Ion-type	PR	V	E		LI	NR	a_1	H	F		y_1	
Delta ppm	-1.8	-2.4	-11.8		-13.1	-3.3	-16.2	-2.5	11.9		-24.9	
							E					

Fragment-ion (m/z)	201.088	296.160	322.190	564.323	565.326^{+2}	594.801^{+2}	652.805^{+2}	663.394	701.843	737.368^{+2}	781.398	824.393^{+2}	1051.521
Frac. Inten.(% of TIC)	4.60	3.31	8.45	7.86	4.40	5.42	3.26	3.65	3.48	6.22	3.29	4.48	4.14
Rel. Inten.(% of BP)	22.66	16.29	41.60	38.67	21.66	26.70	16.07	17.96	17.13	30.60	16.18	22.07	20.38
Score	0.50	0.25	1.50	1.50	-0.22	1.50	-0.16	1.50	1.50	1.50	-0.16	1.50	1.50
Ion-type	b_2	b_3-H_2O	y_2	y_3		y_9^{+2}		y_4	y++$_{11}$	y_{12}^{+2}		y_{14}^{+2}	y_8
Delta ppm	-1.9	-6.0	8.8	-3.8		16.6		0.8	6.0	13.9		3.8	3.6



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Result Summary

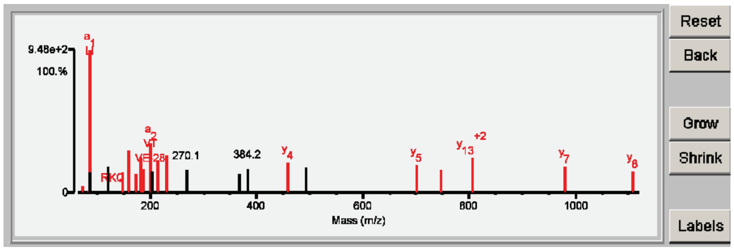
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.58	78.2	7	7/25	K275k	(K)LDVTSVEDYkALQK(Y)	1608.8479	114.0664	13.6	59671.4/5.45	HUMAN	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1
2	12.23	71.2	5	9/25	K279k	(K)LDVTSVEDYKALQk(Y)	1608.8479	114.0664	13.6	59671.4/5.45	HUMAN	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1
3	3.28	52.4	1	11/25	K797k	(R)kFIVDGVEVSVTTSK(I)	1608.8843	114.0300	-7.5	142695.6/5.09	HUMAN	Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.58	78.2	7	7/25	K275k	(K) L/D|V T S V/E/D Y/k/A L Q/K (Y)	1608.8479	114.0664	13.6	59671.4/5.45	HUMAN	P48643	772167	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1

Fragment-ion (m/z)	72.081	84.081	86.097	87.099	120.083	129.103	147.108	159.113	173.130	183.114	187.104	201.121
Frac. Inten.(% of TIC)	0.85	0.20	19.51	2.77	3.62	0.08	2.82	5.83	2.52	4.70	3.30	6.84
Rel. Inten.(% of BP)	4.34	1.03	100.00	14.22	18.58	0.41	14.47	29.91	12.93	24.08	16.93	35.04
Score	0.50	0.50	0.50 0.50	-0.14	-0.19	0.20	1.50	0.50	0.50	0.50	0.75	0.75
Ion-type	V	KQ	a_1 LI			RKQ	y_1	SV-28	VT-28	VT-H_2O	SV DV-28	a_2 VT VE-28
Delta ppm	-1.0	5.0	-9.6 3.2			5.1	-30.6	-4.4	4.9	-0.6	-26.3 -26.3	-19.2 -19.2 -19.2

Fragment-ion (m/z)	202.123	215.105	229.119	270.146	367.168^{+2}	384.233	459.301	492.771^{+2}	701.437	747.919^{+2}	805.410^{+2}	979.519	1108.565
Frac. Inten.(% of TIC)	3.00	4.41	5.09	3.15	2.58	3.32	4.15	3.34	3.70	3.06	4.79	3.52	2.85
Rel. Inten.(% of BP)	15.37	22.62	26.09	16.13	13.23	17.02	21.29	17.11	18.97	15.66	24.56	18.03	14.60
Score	-0.15	0.75	0.75	-0.16	-0.13	-0.17	1.50	-0.17	1.50	1.50	1.50	1.50	1.50
Ion-type		DV	b_2 VE				y_4		y_5	y_{12}^{+2}	y_{13}^{+2}	y_7	y_8
Delta ppm		5.4	0.5 0.5				18.2		9.5	34.3	4.3	-1.5	2.0



Result Summary

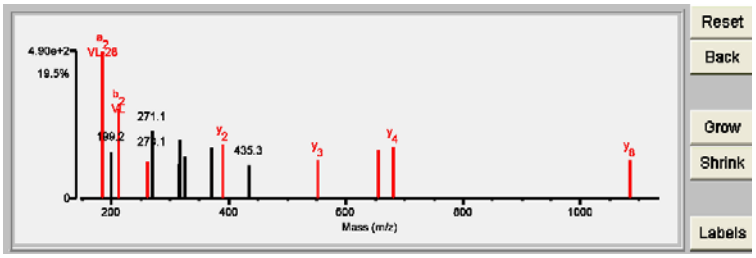
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.32	72.9	6	11/25	K249k	(R)IVLLDSSLEYKk(G)	1407.8094	114.0573	9.4	60534.3/6.10	HUMAN	P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4
2	10.77	70.8	5	12/25	K248k	(R)IVLLDSSLEYkK(G)	1407.8094	114.0573	9.4	60534.3/6.10	HUMAN	P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.32	72.9	6	11/25	K249k	(R) I V|L L/D S S L/E/Y/K/k (G)	1407.8094	114.0573	9.4	60534.3/6.10	HUMAN	P49368	386098	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4

Fragment-ion (m/z)	70.065	72.081	84.080	86.096	101.068	120.081	129.101	136.076	185.161	199.180	213.158	261.153
Frac. Inten.(% of TIC)	0.14	0.20	0.34	43.13	0.08	3.28	0.10	0.06	8.44	2.67	5.15	2.14
Rel. Inten.(% of BP)	0.32	0.46	0.79	100.00	0.19	7.59	0.23	0.14	19.56	6.19	11.93	4.96
Score	-0.00	0.50	0.50	0.50 0.50		-0.08	0.20	1.00	0.50	-0.06	0.75	1.50
Ion-type		V	KQ	a_1 LI	KQ		RKQ	Y	a_2 VL-28		b_2 VL	y_1
Delta ppm		3.1	-8.0	-4.9 -4.9			-6.5	2.3	-19.7 -19.7		-9.6 -9.6	-11.6

Fragment-ion (m/z)	270.146	271.134	314.212	316.131	326.225	370.166	389.252	435.271	552.326	655.355^{+2}	681.363	1083.548	1560.702
Frac. Inten.(% of TIC)	2.43	3.83	2.01	3.36	2.40	2.95	3.10	1.91	2.22	2.74	3.02	2.17	2.13
Rel. Inten.(% of BP)	5.64	8.87	4.66	7.80	5.57	6.84	7.19	4.42	5.15	6.36	6.99	5.04	4.95
Score	-0.06	-0.09	-0.05	-0.08	-0.06	-0.07	1.50	-0.04	1.50	1.50	1.50	1.50	-0.05
Ion-type							y_2		y_3	y_{10}^{+2}	y_4	y_8	
Delta ppm							3.6		21.3	1.9	8.8	14.8	



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Result Summary

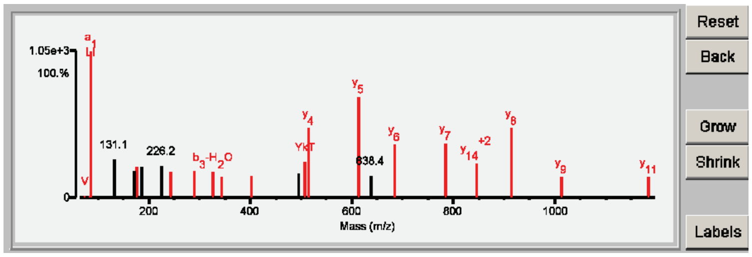
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.07	82.0	12	6/25	K507k	(K)LQTYkTAVETAVLLLR(I)	1819.0688	114.0526	5.0	60534.3/6.10	HUMAN	P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.07	82.0	12	6/25	K507k	(K) L Q|T\Y k/T A/V/E/T/A/V/L/L/L/R (I)	1819.0688	114.0526	5.0	60534.3/6.10	HUMAN	P49368	772195	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4

Fragment-ion (m/z)	72.080	84.078	86.094	131.113	171.106	175.113	185.161	225.128	226.182	242.147	288.197	325.177
Frac. Inten.(% of TIC)	0.21	0.17	15.33	4.03	2.77	3.22	3.17	2.48	3.30	2.63	2.86	2.71
Rel. Inten.(% of BP)	1.36	1.13	100.00	26.27	18.08	21.00	20.68	16.16	21.51	17.15	18.67	17.68
Score	0.50	0.50	0.50	-0.26	-0.18	1.50	-0.21	0.25	-0.22	0.50	1.50	0.25
Ion-type	V	KQ	a_1			y_1		b_2-NH_3		b_2	y_2	b_3-H_2O
Delta ppm	-5.2	-35.4	-43.2 0.50 LI -30.5			-32.8		16.1		-18.6	-22.6	-34.2

Fragment-ion (m/z)	343.201	401.294	496.301	507.273	514.370	613.438	638.397	684.468	785.512	846.522^{+2}	914.559	1013.642	1185.686
Frac. Inten.(% of TIC)	2.17	2.23	2.50	3.67	7.25	10.58	2.26	5.53	5.69	3.62	7.27	2.21	2.13
Rel. Inten.(% of BP)	14.19	14.54	16.30	23.96	47.33	69.03	14.77	36.06	37.13	23.63	47.47	14.44	13.93
Score	0.50	1.50	-0.16	0.75	1.50	1.50	-0.15	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	b_3	y_3		YkT	y_4	y_5		y_6	y_7	y_{14}^{+2}	y_8	y_9	y_{11}
Delta ppm	7.0	17.5		30.6	-2.6	-2.1		-13.1	-16.2	39.8	-8.4	6.4	-29.0



Result Summary

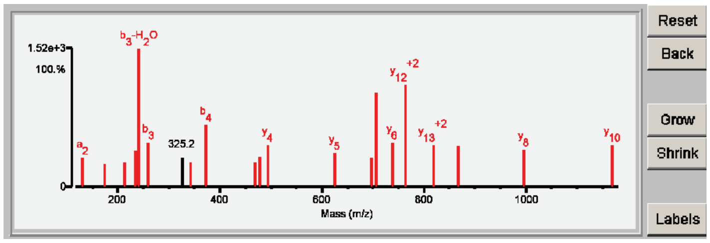
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.34	94.7	10	2/25	K260k	(K)GTVLIkTAEELMNFSK(G)	1780.9513	114.0592	8.6	59620.9/5.42	HUMAN	P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4
2	9.96	69.0	4	9/25	K270k	(K)GTVLIKTAEELMNFSk(G)	1780.9513	114.0592	8.6	59620.9/5.42	HUMAN	P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4
3	6.79	57.4	4	12/25	M779m K787k	(R)TGVIIImLCVFHFSk(V)	1764.9539	130.0566	9.9	91890.3/6.83	HUMAN	RQ9Y2C9	REVERSE Toll-like receptor 6 OS=Homo sapiens GN=TLR6 PE=2 SV=1
4	5.57	56.7	3	13/25	None	(K)KELLVGSEDFDIRVFK(E)	1895.0273	-0.0167	-8.8	79871.0/5.74	HUMAN	Q9BXC9	Bardet-Biedl syndrome 2 protein OS=Homo sapiens GN=BBS2 PE=1 SV=1
5	4.38	51.0	3	14/25	None	(K)IKERQEAASGGGNIHLSK(K)	1895.0093	0.0012	0.6	112135.9/6.52	HUMAN	RO94804	REVERSE Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.34	94.7	10	2/25	K260k	(K) G T V|L|I/k/T A/E/E/L/M/N F/S K (G)	1780.9513	114.0592	8.6	59620.9/5.42	HUMAN	P50990	772267	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4

Fragment-ion (m/z)	72.081	84.080	86.060	86.095	131.078	173.089	213.156	234.139	240.133	258.141	325.232	343.227	371.226
Frac. Inten.(% of TIC)	0.61	0.33	2.46	0.29	2.89	2.34	2.40	3.52	13.72	4.37	2.84	2.36	6.13
Rel. Inten.(% of BP)	4.43	2.39	17.92	2.09	21.07	17.08	17.49	25.67	100.00	31.89	20.69	17.19	44.72
Score	0.50	0.50	-0.18	0.22	0.50	0.75	0.75	1.50	0.25	0.50	-0.21	0.50	0.50
Ion-type	V	KQ		LI	a_2	TA	VL	y_2	b_3-H_2O	b_3		a_4	b_4
Delta ppm	-3.8	-8.0		-21.2	-36.6	-22.9	-23.7	-23.2	-9.4	-17.5		-23.8	-11.8

Fragment-ion (m/z)	469.310	478.225	495.260	626.288	697.338^{+2}	706.357^{+2}	739.387	762.889^{+2}	819.432^{+2}	868.425	997.476	1169.547
Frac. Inten.(% of TIC)	2.45	2.96	4.18	3.31	2.86	9.37	4.43	10.16	4.12	4.04	3.70	4.17
Rel. Inten.(% of BP)	17.83	21.56	30.48	24.13	20.86	68.32	32.25	74.03	30.00	29.41	26.99	30.40
Score	0.75	0.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	LIk	y_4-NH_3	y_4	y_5	y_{11}-H_2O^{+2}	y_{11}^{+2}	y_6	y_{12}^{+2}	y_{13}^{+2}	y_7	y_8	y_{10}
Delta ppm	-10.2	-9.3	6.9	-13.5	-7.2	13.3	7.9	-1.3	0.0	1.6	10.5	-2.7



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Result Summary

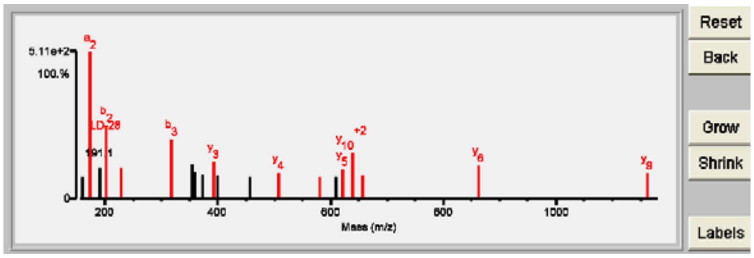
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.15	68.2	8	10/25	K341k	(R)SLDLLGLEkLDCGR(F)	1588.8363	114.0668	14.0	40929.8/5.02	HUMAN	O95551	TRAF and TNF receptor-associated protein OS=Homo sapiens GN=TTRAP PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.15	68.2	8	10/25	K341k	(R) S L\D\L/L/G L E/k/L/D/C G R (F)	1588.8363	114.0668	14.0	40929.8/5.02	HUMAN	O95551	806781	TRAF and TNF receptor-associated protein OS=Homo sapiens GN=TTRAP PE=1 SV=1

Fragment-ion (m/z)	70.064	84.077	86.097	102.054	143.116	159.036	173.127	191.104	201.122	229.115	316.148	354.167	358.177
Frac. Inten.(% of TIC)	0.00	3.75	0.69	0.11	2.87	2.71	17.90	3.77	8.98	3.76	7.26	4.25	3.27
Rel. Inten.(% of BP)	0.03	20.98	3.83	0.64	16.02	15.14	100.00	21.04	50.21	21.00	40.59	23.72	18.28
Score	0.20	-0.21	0.22	1.00	-0.16	-0.15	0.50	-0.21	0.50	0.75	0.50	-0.24	-0.18
Ion-type	**PR**		**LI**	**E**			a_2		b_2 **LD**-28	**LD**	b_3		
Delta ppm	-11.8		4.3	-8.4			-15.9		-12.3 -12.3	-19.6	-10.5		

Fragment-ion (m/z)	373.190	392.171	398.241	456.254	507.190	581.302	609.297	620.288	637.813^{+2}	655.373	862.412	1161.576
Frac. Inten.(% of TIC)	2.94	4.45	2.80	2.73	3.14	2.70	2.67	3.59	5.60	2.86	4.11	3.07
Rel. Inten.(% of BP)	16.45	24.88	15.67	15.28	17.53	15.10	14.91	20.08	31.30	15.98	22.96	17.16
Score	-0.16	1.50	-0.16	-0.15	1.50	1.50	-0.15	1.50	1.50	0.75	1.50	1.50
Ion-type		y_3			y_4	$y{+}{+}_9$		y_5	y_{10}^{+2}	**GLEkL**	y_6	y_9
Delta ppm		0.3			-16.6	24.6		9.9	-25.8	-8.6	-9.6	7.0



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Result Summary

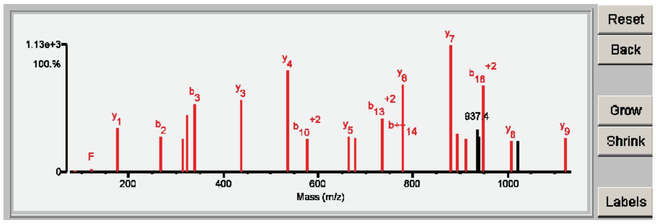
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.36	90.5	17	3/25	K43k	(R)EHALTSGTIkAMLSGPGQFAENETNEVNFR(E)	3248.5641	114.0845	12.4	12473.2/4.74	HUMAN	Q15369	Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.36	90.5	17	3/25	K43k	(R) E H\A\L T S G T I\k\A M\L\S\G P G Q\F A E/N/E/T/N/E/V/N/F/R (E)	3248.5641	114.0845	12.4	12473.2/4.74	HUMAN	Q15369	189451	Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1

Fragment-ion (m/z)	84.082	86.096	120.081	175.117	267.108	314.179	322.191	338.147	436.232	535.300	576.816^{+2}	664.336	677.840^{+2}	734.383^{+2}
Frac. Inten.(% of TIC)	0.13	0.17	0.20	3.83	3.05	2.88	4.95	5.87	6.25	8.80	2.82	3.10	2.93	4.66
Rel. Inten.(% of BP)	1.22	1.56	1.80	34.88	27.82	26.19	45.12	53.49	56.89	80.18	25.68	28.20	26.67	42.41
Score	0.50	0.22	1.00	1.50	0.50	0.75	1.50	0.50	1.50	1.50	0.50	1.50	0.50	0.50
Ion-type	KQ	LI	F	y_1	b_2	kA	y_2 HAL	b_3	y_3	y_4	b_{10}^{+2}	y_5	b_{12}^{+2}	b_{13}^{+2}
Delta ppm	8.6	-8.4	-1.5	-13.4	-8.5	-12.7	11.3 7.9	-0.6	4.8	3.0	20.2	-8.1	-4.8	-3.3

Fragment-ion (m/z)	777.910	778.387	879.440	892.464	910.468	937.447	938.970	947.476^{+2}	1008.478	1022.022^{+2}	1122.524
Frac. Inten.(% of TIC)	2.92	7.57	10.98	3.36	2.91	3.74	3.06	7.46	2.70	2.68	2.98
Rel. Inten.(% of BP)	26.61	68.98	100.00	30.65	26.47	34.03	27.90	67.99	24.61	24.39	27.15
Score	0.50	1.50	1.50	0.25	0.50	-0.34	-0.28	0.50	1.50	-0.24	1.50
Ion-type	b++14	y_6	y_7	b_9-H_2O	b_9			b_{18}^{+2}	y_8		y_9
Delta ppm	10.8	3.3	8.9	12.0	4.5			-2.9	3.6		5.8



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Result Summary

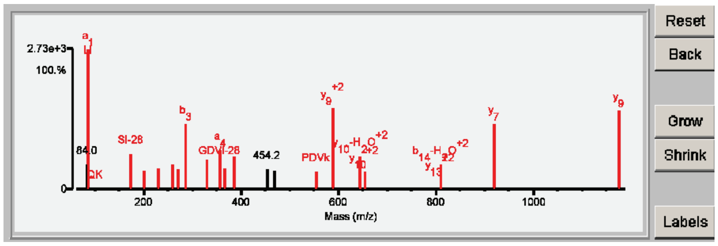
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.25	92.4	6	3/25	K109k	(R)LGDVISIQPCPDVkYGK(R)	1888.9837	114.0466	1.9	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
2	15.37	90.2	5	4/25	K112k	(R)LGDVISIQPCPDVKYGk(R)	1888.9837	114.0466	1.9	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
3	5.30	61.1	2	10/25	None	(K)TPSALEPLSSSTLQDSLEK(V)	2003.0179	0.0124	6.2	162423.8/10.71	HUMAN	Q5SNV9	Uncharacterized protein C1orf167 OS=Homo sapiens GN=C1orf167 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.25	92.4	6	3/25	K109k	(R) L G D\V|I S I/Q/P C/P D V k/Y G K (R)	1888.9837	114.0466	1.9	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.066	72.082	84.046	84.078	86.096	101.070	173.127	201.120	230.098	258.094	272.124	286.141	329.181
Frac. Inten.(% of TIC)	0.00	0.09	2.99	0.09	16.82	0.13	4.28	2.22	2.55	2.96	2.44	7.87	3.59
Rel. Inten.(% of BP)	0.01	0.54	17.80	0.52	100.00	0.77	25.46	13.20	15.18	17.58	14.52	46.79	21.33
Score	0.20	0.50	-0.18		0.50	0.50	0.50	0.75	0.50	0.75	0.75	0.50	0.75
Ion-type	**PR**	**V**		**QK**	**a**$_1$	**QK**	**SI**-28	**SI**	**CP**-28	**CP**	**GDV**	**b**$_3$	**SIQ**
Delta ppm	18.2	19.8			-13.0	-8.3	-12.4	-23.2	6.6	8.6	-5.5	0.2	-6.8
					0.50								
					LI								
					-0.3								

Fragment-ion (m/z)	357.213	367.199	385.210	454.233	468.240	554.293	589.284^{+2}	644.308^{+2}	653.312^{+2}	809.928^{+2}	920.480	1177.568
Frac. Inten.(% of TIC)	4.71	2.54	4.02	2.39	2.26	2.12	9.65	3.99	2.07	2.95	7.91	9.36
Rel. Inten.(% of BP)	27.99	15.08	23.90	14.21	13.41	12.58	57.39	23.70	12.33	17.55	47.02	55.65
Score	0.50	1.50	0.75	-0.14	-0.13	0.75	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	**a**$_4$	**b**$_4$-H$_2$O	**b**$_4$			**PDVk**	**y**$_9^{+2}$	**y**$_{10}$-H$_2$O^{+2}	**y**$_{10}^{+2}$	**b**$_{14}$-H$_2$O^{+2}	**y**$_7$	**y**$_9$
Delta ppm	-2.9	0.6	2.2			-2.7	-4.7	-4.7	-6.2	13.5	-3.6	0.5
	GDVI-28	**y**$_3$	**GDVI**							**y**$_{13}^{+2}$		
	-2.9	3.6	2.2							14.2		
		GDVI-H$_2$O										
		0.6										



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Result Summary

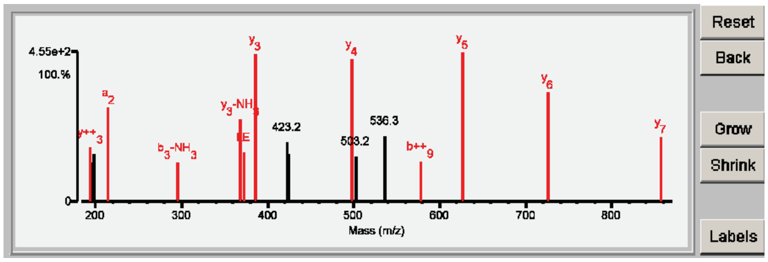
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.61	72.4	5	8/24	K217k	(K)QLAQIkEMVELPLR(H)	1667.9513	114.0568	7.8	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.61	72.4	5	8/24	K217k	(K) Q L A Q I k E/M/V|E/L/P L R (H)	1667.9513	114.0568	7.8	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	72.081	84.081	86.096	101.069	102.051	155.116	193.127	197.130	198.122	214.150	296.170	368.240
Frac. Inten.(% of TIC)	0.13	0.16	0.13	0.10	0.10	2.92	3.95	2.87	3.47	6.84	2.87	5.98
Rel. Inten.(% of BP)	1.22	1.44	1.18	0.90	0.91	26.80	36.31	26.36	31.91	62.79	26.36	54.95
Score	0.50	0.50	0.22	0.50	1.00	-0.27	1.50	-0.26	-0.32	0.50	0.25	0.50
Ion-type	V	KQ	LI	a_1 KQ	E		y^{++}_3			a_2	b_3-NH_3	y_3-NH_3
Delta ppm	4.5	5.0	-2.6	-31.0	-39.7		-25.0			-26.2	29.1	28.7

Fragment-ion (m/z)	372.188	385.261	423.237	424.210^{+2}	498.351	503.240^{+2}	536.327	578.308	627.384	726.453	857.517	986.577
Frac. Inten.(% of TIC)	3.56	10.80	4.36	3.52	10.38	3.29	4.79	2.95	10.89	7.98	4.72	3.23
Rel. Inten.(% of BP)	32.70	99.21	40.05	32.37	95.36	30.24	43.97	27.13	100.00	73.31	43.38	29.71
Score	0.75	1.50	-0.40	-0.32	1.50	-0.30	-0.44	0.50	1.50	1.50	1.50	-0.30
Ion-type	kE	y_3			y_4			b^{++}_9	y_5	y_6	y_7	
Delta ppm	-2.6	13.8			23.4			-9.7	1.7	2.4	29.9	



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Result Summary

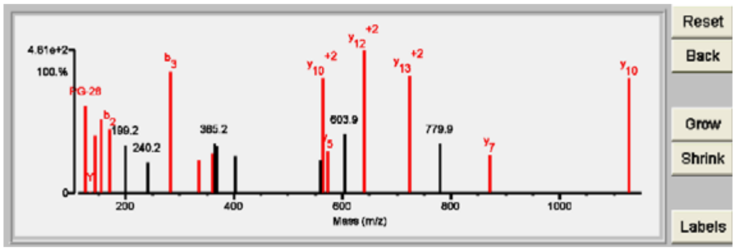
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.42	71.2	8	9/25	K251k	(R)GILLYGPPGTGkTLIAR(A)	1727.0214	114.0500	3.9	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.42	71.2	8	9/25	K251k	(R) G I\L\L/Y/G P/P G T/G k/T L/I A R (A)	1727.0214	114.0500	3.9	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.066	86.097	87.100	127.087	136.079	143.119	155.081	171.110	199.173	240.177	284.197	334.175	359.236
Frac. Inten.(% of TIC)	0.01	0.65	4.94	5.83	0.08	3.89	4.99	4.31	3.25	2.12	8.14	2.22	2.65
Rel. Inten.(% of BP)	0.07	6.75	51.48	60.82	0.88	40.58	52.08	44.93	33.92	22.07	84.92	23.17	27.62
Score	0.20	0.22	-0.51	0.50	1.00	0.50	0.75	0.50	-0.34	-0.22	0.50	0.75	1.50
Ion-type	PR	LI		PG-28	Y	a_2	PG	b_2			b_3	LYG	y_3
Delta ppm	13.9	11.3		-9.3	24.3	0.1	-10.3	-25.1			-4.5	-7.3	-10.9

Fragment-ion (m/z)	365.219	368.182	401.255	560.285	564.320^{+2}	573.377	603.866	641.376^{+2}	722.899^{+2}	779.928^{+2}	872.528	1127.646
Frac. Inten.(% of TIC)	3.35	3.13	2.49	2.25	7.77	2.82	3.99	9.59	7.91	3.32	2.56	7.74
Rel. Inten.(% of BP)	34.90	32.67	25.96	23.44	80.97	29.43	41.56	100.00	82.45	34.63	26.73	80.70
Score	-0.35	-0.33	-0.26	-0.23	1.50	1.50	-0.42	1.50	1.50	-0.35	1.50	1.50
Ion-type					y_{10}^{+2}	y_5		y_{12}^{+2}	y_{13}^{+2}		y_7	y_{10}
Delta ppm					-18.6	9.6		14.0	0.6		-3.4	-6.2



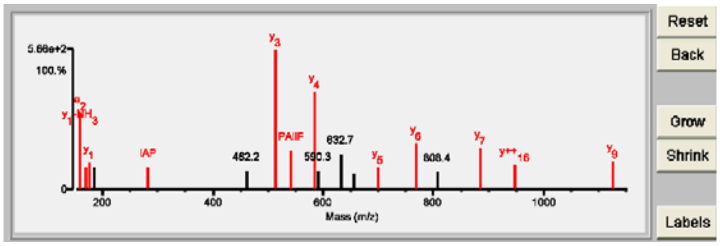
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.16	69.8	8	11/25	K312k	(K)NAPAIIFIDELDAIAPkR(E)	1967.0960	114.0525	4.6	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
2	4.26	51.9	4	16/25	K181k	(K)GKQYLELGTLLYVSVkR(F)	1967.1324	114.0161	-12.9	122491.7/5.10	HUMAN	RQ96RU2	REVERSE Ubiquitin carboxyl-terminal hydrolase 28 OS=Homo sapiens GN=USP28 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.16	69.8	8	11/25	K312k	(K) N A/P A I I F I D/E L/D/A/I/A/P k/R (E)	1967.0960	114.0525	4.6	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.060	86.097	88.042	113.072	116.072	120.079	141.065	158.092	169.095	175.115	185.114	282.183	462.223	514.305	542.333	585.350	590.322	632.694	655.445	698.452	769.444	808.438	884.499	948.523	1126.666
Frac. Inten.(% of TIC)	1.99	0.17	2.65	3.17	2.12	0.08	4.78	9.07	2.59	3.15	2.70	2.57	2.28	16.66	4.65	11.55	2.26	4.17	1.99	2.61	5.52	2.14	4.88	2.95	3.33
Rel. Inten.(% of BP)	11.93	1.00	15.88	19.04	12.70	0.50	28.72	54.43	15.52	18.90	16.24	15.42	13.66	100.00	27.92	69.30	13.56	25.03	11.97	15.67	33.11	12.82	29.28	17.71	19.98
Score	-0.12	0.22	-0.16	-0.19	-0.13	1.00	-0.29	0.50	0.75	1.50	-0.16	0.75	-0.14	1.50	0.75	1.50	-0.14	-0.25	-0.12	1.50	1.50	-0.13	1.50	1.50	1.50
Ion-type		LI				F		a_2 y_1-NH_3	AP	y_1		IAP		y_3	PAIIF	y_4				y_5	y_6		y_7	y^{++}_{16}	y_9
Delta ppm		3.2				-13.1		-1.9 -1.9	-13.9	-22.0		4.5		-8.4	-1.3	5.9				29.9	-30.9		5.2	-11.0	39.1



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Result Summary

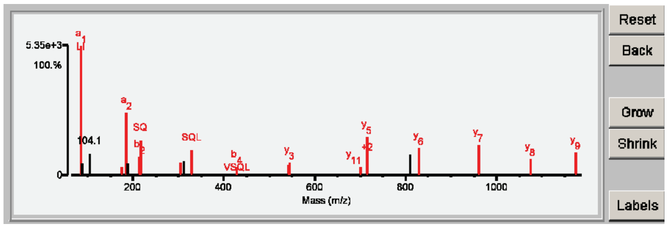
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.33	84.7	11	6/24	K336k	(R)IVSQLLTLMDGLkQR(A)	1714.9884	114.0644	11.8	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
2	8.46	64.8	3	12/24	K5439k	(K)LITINVITASGLkSER(E)	1715.0062	114.0467	2.1	692677.1/4.53	HUMAN	RQ8WXG9	REVERSE G-protein coupled receptor 98 OS=Homo sapiens GN=GPR98 PE=1 SV=1
3	6.14	52.4	3	13/24	None	(R)DPLVTPLHLQSLLVQR(Q)	1829.0643	-0.0115	-6.3	84082.7/8.38	HUMAN	RQ9BRB3	REVERSE Phosphatidylinositol N-acetylglucosaminyltransferase subunit Q OS=Homo sapiens GN=PIGQ PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.33	84.7	11	6/24	K336k	(R) I V|S Q|L\L/T/L/M/D/G L/k/Q/R (A)	1714.9884	114.0644	11.8	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	72.081	86.096	87.100	104.053	175.117	185.165	186.168	187.143	213.160	216.099	303.180	310.214
Frac. Inten.(% of TIC)	0.14	22.90	2.03	3.81	1.55	11.13	1.36	2.05	3.21	6.14	2.27	2.53
Rel. Inten.(% of BP)	0.60	100.00	8.87	16.64	6.78	48.59	5.96	8.93	14.00	26.82	9.90	11.03
Score	0.50	0.50 0.50	-0.09	-0.17	1.50	0.50	-0.06	-0.09	0.50	0.75	1.50	-0.11
Ion-type	V	a_1 LI			y_1	a_2			b_2	SQ	y_2	
Delta ppm	3.1	-13.0 -0.3			-10.6	-7.8			-2.6	0.1	8.5	

Fragment-ion (m/z)	329.186	428.253	541.343	545.321	701.404^{+2}	715.429	808.948	809.457	830.455	961.499	1074.583	1175.622
Frac. Inten.(% of TIC)	4.44	1.52	1.88	2.29	1.42	6.78	2.11	3.57	4.73	5.35	2.78	4.01
Rel. Inten.(% of BP)	19.40	6.66	8.22	10.00	6.20	29.62	9.21	15.58	20.63	23.38	12.12	17.50
Score	0.75	0.75	0.75	1.50	1.50	1.50	1.50	-0.16	1.50	1.50	1.50	1.50
Ion-type	SQL	b_4 VSQL	b_5 VSQLL	y_3	y_{11}^{+2}	y_5	y^{++}_{13}		y_6	y_7	y_8	y_9
Delta ppm	9.6	4.5 4.5	14.4 14.4	10.6	9.5	11.0	5.9		8.3	10.7	9.6	1.9



Result Summary

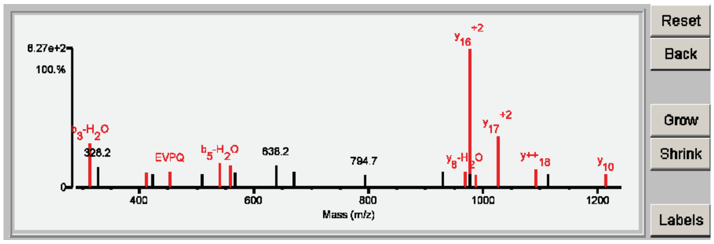
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.42	67.9	5	11/25	K486k	(R)ETVVEVPQVTWEDIGGLEDVkR(E)	2498.2773	114.0674	9.4	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.42	67.9	5	11/25	K486k	(R) E T V V/E|V/P Q V T W E/D I/G G L E D V k R (E)	2498.2773	114.0674	9.4	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.064	72.079	159.090	171.148	312.148	328.181^{+3}	411.227	423.195	454.220	509.238	540.270	558.285
Frac. Inten.(% of TIC)	0.00	0.12	0.12	3.74	8.04	3.80	2.64	2.41	2.98	2.43	4.44	3.95
Rel. Inten.(% of BP)	0.01	0.49	0.48	14.91	32.07	15.15	10.53	9.60	11.90	9.71	17.71	15.76
Score	0.20	0.50	2.00	-0.15	0.25	-0.15	0.25	-0.10	0.75	-0.10	0.25	0.50
Ion-type	PR	V	W		b_3-H_2O		b_4-H_2O		EVPQ		b_5-H_2O	b_5
Delta ppm	-10.4	-20.5	-12.4		-26.9		4.8		-23.2		4.8	13.1

Fragment-ion (m/z)	566.288	638.234	670.314	794.744	930.269	969.478	978.493^{+2}	978.607	987.524	1028.031^{+2}	1092.534	1113.071	1215.640
Frac. Inten.(% of TIC)	2.74	3.88	2.91	2.31	2.87	2.94	25.08	2.48	2.28	9.34	3.42	2.55	2.52
Rel. Inten.(% of BP)	10.90	15.45	11.59	9.20	11.42	11.73	100.00	9.90	9.08	37.24	13.65	10.15	10.03
Score	-0.11	-0.15	-0.12	-0.09	-0.11	0.50	1.50	-0.10	1.50	1.50	1.50	-0.10	1.50
Ion-type						y_8-H_2O	y_{16}^{+2}		y_8	y_{17}^{+2}	y++18		y_{10}
Delta ppm						-34.7	-1.6		2.8	1.7	-15.2		5.8



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Result Summary

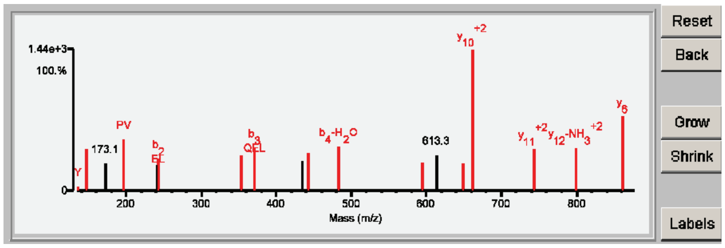
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.02	80.2	7	5/25	K502k	(R)ELQELVQYPVEHPDkFLK(F)	2212.1648	114.0581	6.5	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
2	13.23	75.1	6	6/25	K505k	(R)ELQELVQYPVEHPDKFLk(F)	2212.1648	114.0581	6.5	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
3	7.05	52.6	2	11/25	M829m	(R)LSQELDLGmEVPHEVKKAMR(I)	2310.1944	16.0285	14.4	102837.1/7.88	HUMAN	RQ7Z7L1	REVERSE Schlafen family member 11 OS=Homo sapiens GN=SLFN11 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.02	80.2	7	5/25	K502k	(R) E L\Q\E L V Q/Y/P V E H/P D/k F L/K (F)	2212.1648	114.0581	6.5	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.063	72.080	84.079	86.095	101.069	110.067	129.095	136.074	147.109	173.128	197.126	241.076	243.135
Frac. Inten.(% of TIC)	0.01	0.33	0.58	0.41	0.19	0.18	5.37	0.55	5.03	3.33	6.28	3.20	3.89
Rel. Inten.(% of BP)	0.03	1.93	3.36	2.41	1.09	1.06	31.24	3.19	29.28	19.36	36.52	18.63	22.66
Score	0.20	0.50	0.50	0.22		1.00	-0.31	1.00	1.50	-0.19	0.75	-0.19	0.75
Ion-type	PR	V	KQ	LI	KQ	H		Y	y_1		PV		b_2 EL
Delta ppm	-33.2	-5.2	-15.2	-11.9		-36.1		-13.2	-25.2		-15.5		-0.1 -0.1

Fragment-ion (m/z)	353.180	371.192	435.254	441.921^{+3}	482.221	595.294	613.322^{+2}	649.395	662.354^{+2}	743.890^{+2}	799.416^{+2}	861.484
Frac. Inten.(% of TIC)	4.34	5.26	3.66	4.56	5.33	3.45	4.26	3.32	17.19	5.04	5.25	8.99
Rel. Inten.(% of BP)	25.28	30.60	21.32	26.51	31.03	20.05	24.81	19.34	100.00	29.32	30.54	52.30
Score	0.50	0.75	-0.21	1.50	0.25	0.25	-0.25	1.50	1.50	1.50	0.50	1.50
Ion-type	b_3-H_2O QEL-H_2O	b_3 QEL		y_{10}^{+3}	b_4-H_2O	b_5-H_2O		y_4	y_{10}^{+2}	y_{11}^{+2}	y_{12}-NH_3^{+2}	y_6
Delta ppm	-7.2 -7.2	-5.1 -5.1		32.6	-9.2	-26.9		-12.0	-3.2	2.4	14.9	1.1



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Result Summary

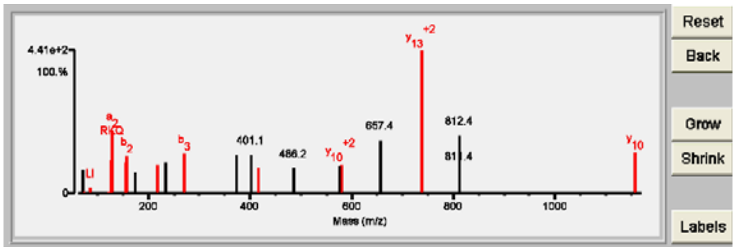
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.09	60.8	6	10/25	K524k	(K)GVLFYGPPGCGkTLLAK(A)	1777.9669	114.0565	7.2	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
2	9.39	57.5	5	11/25	K529k	(K)GVLFYGPPGCGKTLLAk(A)	1777.9669	114.0565	7.2	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.09	60.8	6	10/25	K524k	(K) G V\L\F|Y/G P/P G C G k T L L/A K (A)	1777.9669	114.0565	7.2	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.060	72.081	86.097	120.081	127.083	129.100	136.076	155.084	157.094	173.130	218.146	233.172
Frac. Inten.(% of TIC)	2.75	0.17	0.63	0.20	3.92	7.29	0.08	3.55	4.34	2.48	3.33	3.59
Rel. Inten.(% of BP)	16.68	1.01	3.86	1.19	23.84	44.29	0.47	21.54	26.38	15.06	20.22	21.84
Score	-0.17	0.50	0.22	1.00	0.50	0.50 0.50	1.00	0.75	0.50	-0.15	1.50	-0.22
Ion-type		V	LI	F	PG-28	a_2 RKQ	Y	PG	b_2		y_2	
Delta ppm		4.5	0.9	-1.5	-34.5	-25.1 -16.6	-0.7	10.3	-25.2		-16.6	

Fragment-ion (m/z)	270.183	372.224	401.145^{+2}	417.250	486.188	576.328	579.821^{+2}	656.849	657.367	738.396^{+2}	811.363	812.436^{+2}	1158.638
Frac. Inten.(% of TIC)	4.65	4.45	4.46	2.90	2.82	3.18	3.38	5.15	6.18	16.46	2.60	6.71	4.74
Rel. Inten.(% of BP)	28.24	27.04	27.06	17.61	17.13	19.31	20.52	31.27	37.54	100.00	15.77	40.74	28.81
Score	0.50	-0.27	-0.27	0.50	-0.17	-0.19	1.50	1.50	-0.38	1.50	-0.16	-0.41	1.50
Ion-type	b_3			b_4			y_{10}^{+2}	y^{++}_{12}		y_{13}^{+2}			y_{10}
Delta ppm	1.1			-1.3			3.6	-10.5		11.3			6.7



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Result Summary

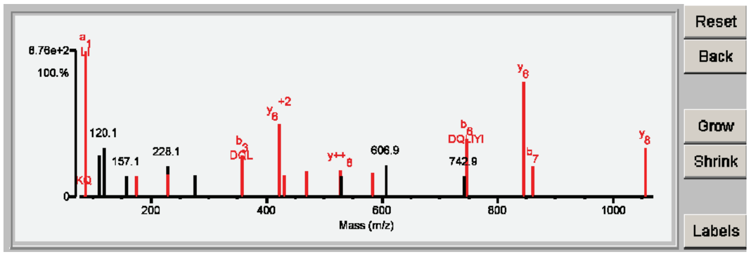
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.14	71.5	8	9/25	K651k	(R)LDQLIYIPLPDEkSR(V)	1799.9902	114.0470	2.1	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.14	71.5	8	9/25	K651k	(R) L D\Q\L\I\Y\I|P L/P D E k S/R (V)	1799.9902	114.0470	2.1	89322.3/5.14	HUMAN	P55072	773751	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.066	72.080	84.079	86.097	110.067	120.078	136.079	157.131	175.121	228.138	229.112	276.137
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.05 0.20 PR 15.3	2.79 17.69 -0.18	0.26 1.68 0.50 KQ -23.5	15.78 100.00 0.50 a_1 -10.7 0.50 LI 2.0	4.51 28.59 -0.29	5.36 34.00 -0.34	0.12 0.78 1.00 Y 23.6	2.21 14.01 -0.14	2.20 13.92 1.50 y_1 13.4	3.30 20.89 -0.21	2.50 15.87 0.50 b_2 -32.7	2.34 14.82 -0.15

Fragment-ion (m/z)	357.178	423.211^{+2}	430.251	470.266	528.290	528.769	583.340	606.948^{+3}	742.887	746.400	845.412	859.520	1055.549
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	4.55 28.81 0.75 b_3 -0.7 DQL -0.7	7.89 50.02 1.50 y_6^{+2} 4.0	2.37 15.04 0.50 $b{+}{+}_7$ 2.4	2.78 17.60 0.75 b_4 9.1 DQLI 9.1	2.93 18.57 1.50 $y{+}{+}_8$ 23.4	2.29 14.50 -0.15	2.68 16.99 0.50 b_5 -10.9	3.45 21.85 -0.22	2.26 14.32 -0.14	6.31 40.00 0.75 b_6 -12.2 DQLIYI -12.2	12.46 78.94 1.50 y_6 1.5	3.32 21.05 0.50 b_7 30.4	5.34 33.84 1.50 y_8 0.9



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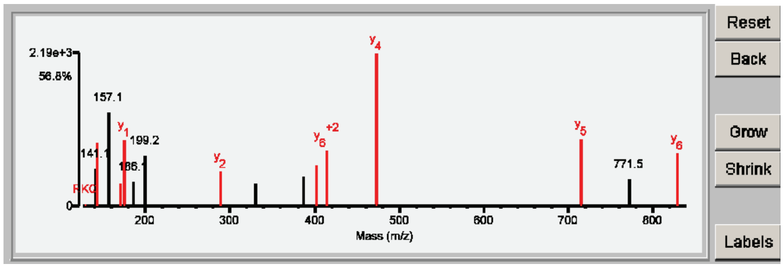
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.60	61.0	7	10/24	K658k	(R)VAILkANLR(K)	997.6517	114.0457	2.5	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.60	61.0	7	10/24	K658k	(R) V A\I/L/k/A/N/L/R (K)	997.6517	114.0457	2.5	89322.3/5.14	HUMAN	P55072	386876	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	70.066	72.081	84.081	86.096	87.058	87.097	120.081	129.102	141.102	143.117	157.133	171.112	175.119	186.102	199.178	288.205	329.700^{+2}	386.242^{+2}	402.246	414.760^{+2}	473.283	715.428	771.482	828.511
Frac. Inten.(% of TIC)	0.00	1.20	21.04	1.04	0.06	2.15	8.68	0.13	2.92	4.91	7.29	1.79	5.17	1.90	3.92	2.72	1.79	2.30	3.18	4.37	11.95	5.30	2.09	4.11
Rel. Inten.(% of BP)	0.02	5.69	100.00	4.93	0.31	10.21	41.27	0.63	13.89	23.34	34.64	8.49	24.56	9.01	18.63	12.95	8.48	10.92	15.10	20.77	56.82	25.19	9.94	19.51
Score	0.20	0.50	-0.53	0.22	0.33	-0.05	-0.22	0.20	-0.07	0.50	-0.18	0.50	1.50	-0.05	-0.10	1.50	-0.04	-0.06	1.50	1.50	1.50	1.50	-0.05	1.50
Ion-type	PR	a_1		LI	NR			RKQ		a_2		b_2	y_1			y_2			y_3	y_6^{+2}	y_4	y_5		y_6
Delta ppm	8.2	-16.3 0.50 V -1.0		-2.6	26.5			2.0		-11.1		-12.9	3.1			8.6			0.4	8.1	0.7	10.6		7.2



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Result Summary

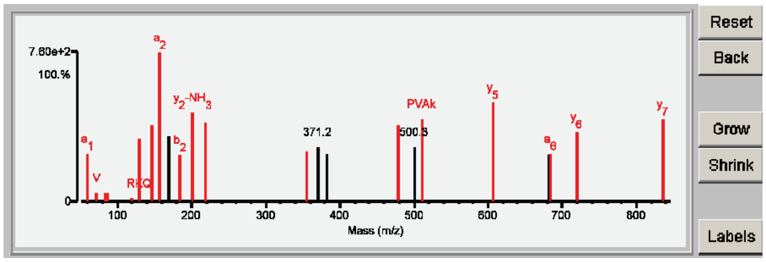
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.08	80.3	8	5/25	K668k	(K)SPVAkDVDLEFLAK(M)	1531.8366	114.0563	8.1	89322.3/5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.08	80.3	8	5/25	K668k	(K) S P\V A\k D V/D/L/E/F L/A/K (M)	1531.8366	114.0563	8.1	89322.3/5.14	HUMAN	P55072	386876	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Fragment-ion (m/z)	60.044	70.065	72.081	84.081	86.095	120.081	129.100	130.087	147.112	157.096	169.133	185.092
Frac. Inten.(% of TIC)	3.55	0.02	0.63	0.63	0.58	0.25	0.23	4.65	5.63	10.98	4.81	3.47
Rel. Inten.(% of BP)	32.30	0.16	5.75	5.74	5.28	2.30	2.08	42.32	51.26	100.00	43.82	31.56
Score	0.50	0.20	0.50	0.50	0.22	1.00	0.20	0.50	1.50	0.50	-0.44	0.50
Ion-type	a_1	PR	V	KQ	LI	F	RKQ	y_1-NH$_3$	y_1	a_2		b_2
Delta ppm	-24.8	-7.5	-2.4	-2.1	-11.9	3.5	-18.9	8.8	-2.7	-15.0		-5.8

Fragment-ion (m/z)	201.122	218.148	355.203	371.203	383.225	478.296	500.284	510.286	607.345	681.895^{+2}	684.377	720.429	835.459
Frac. Inten.(% of TIC)	6.53	5.81	3.68	3.96	3.49	5.61	3.97	6.07	7.30	3.42	3.49	5.15	6.09
Rel. Inten.(% of BP)	59.45	52.93	33.52	36.05	31.73	51.05	36.16	55.27	66.43	31.14	31.81	46.89	55.43
Score	0.50	1.50	0.50	-0.36	-0.32	1.50	-0.36	0.75	1.50	-0.31	0.50	1.50	1.50
Ion-type	y_2-NH$_3$	y_2	b_4			y_4		PVAk	y_5		a_6	y_6	y_7
Delta ppm	-6.8	-10.6	11.0			-13.6		-36.2	0.7		12.5	0.3	3.5



Result Summary

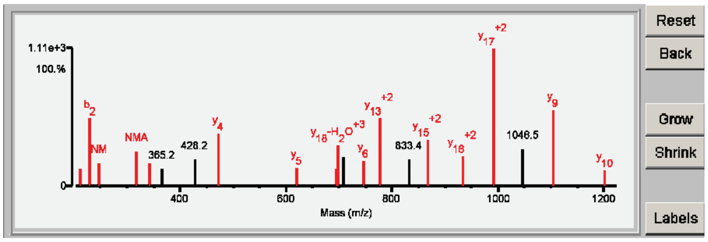
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.18	83.3	10	6/25	K73k	(R)VQNMALYADVGGkQFPVTR(G)	2094.0801	114.0603	7.9	18998.7/5.76	HUMAN	P51571	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.18	83.3	10	6/25	K73k	(R) V Q|N|M/A L/Y/A D/V/G G k/Q/F/P V T R (G)	2094.0801	114.0603	7.9	18998.7/5.76	HUMAN	P51571	366921	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1

Fragment-ion (m/z)	72.080	101.071	117.102	136.076	211.112	228.134	246.100	317.123	342.179	365.203	428.159	472.292
Frac. Inten.(% of TIC)	0.55	0.06	4.15	0.08	2.00	7.73	2.64	4.03	2.60	2.00	3.06	6.03
Rel. Inten.(% of BP)	3.49	0.37	26.31	0.51	12.69	48.99	16.75	25.53	16.51	12.70	19.38	38.24
Score	0.50 0.50	0.50	-0.23	1.00	0.25	0.50	0.75	0.75	0.50	-0.11	-0.17	1.50
Ion-type	a_1 V	QK		Y	b_2-NH_3	b_2	NM	NMA	b_3			y_4
Delta ppm	-28.8 -13.5	-0.4		0.1	14.1	-6.0	34.6	-18.3	2.1			9.7

Fragment-ion (m/z)	619.351	694.873	697.687^{+3}	709.396	747.428	776.395^{+2}	833.427^{+2}	868.472^{+2}	934.007^{+2}	991.007^{+2}	1046.527	1103.596	1202.681
Frac. Inten.(% of TIC)	2.06	1.94	4.72	3.26	2.92	7.79	3.02	5.32	3.46	15.77	4.22	8.72	1.87
Rel. Inten.(% of BP)	13.03	12.32	29.92	20.65	18.54	49.36	19.14	33.72	21.92	100.00	26.78	55.32	11.87
Score	1.50	1.50	0.50	-0.18	1.50	1.50	-0.16	1.50	1.50	1.50	-0.23	1.50	1.50
Ion-type	y_5	y^{++}_{12}	y_{18}-H_2O^{+3}		y_6	y_{13}^{+2}		y_{15}^{+2}	y_{16}^{+2}	y_{17}^{+2}		y_9	y_{10}
Delta ppm	-8.1	7.9	1.0		17.4	-5.2		14.0	28.5	5.6		0.3	13.9



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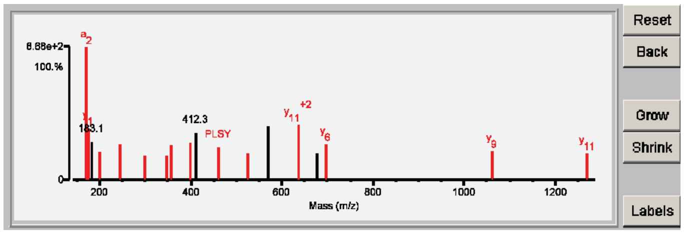
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.24	81.5	5	4/25	K116k	(R)VVAkLPFTPLSYIQGLSHR(N)	2126.2121	114.0665	10.5	21175.1/9.77	HUMAN	Q9UM00	Transmembrane and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=TMCO1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.24	81.5	5	4/25	K116k	(R) V V A k L P F T/P L/S Y I/Q G L/S H/R (N)	2126.2121	114.0665	10.5	21175.1/9.77	HUMAN	Q9UM00	786101	Transmembrane and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=TMCO1 PE=1 SV=1

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.065	0.01	0.07	0.20	PR	-1.8
72.079	0.58	3.29	0.50 0.50	a_1 V	-45.4 -30.2
84.078	0.22	1.22	0.50	KQ	-36.6
86.094	0.39	2.20	0.22	LI	-23.5
120.082	0.12	0.66	1.00	F	13.5
129.098	0.10	0.59	0.20	RKQ	-32.1
136.076	0.13	0.76	1.00	Y	3.7
171.147	17.69	100.00	0.50	a_2	-20.4
175.117	6.95	39.27	1.50	y_1	-14.0
183.148	5.08	28.70	-0.26		
199.102	3.73	21.09	0.75	TP	-32.2
245.125	4.73	26.74	0.75	PF	-20.2
298.182	3.18	18.00	0.75	PLS	14.7
346.173	3.29	18.59	0.75	FTP	-10.8
356.227	4.67	26.40	0.75	kL	-9.3
399.206	4.92	27.80	1.50	y_3	-10.3
412.284	6.30	35.59	-0.32		
461.239	4.33	24.47	0.75	PLSY	-4.0
526.315	3.54	19.99	0.75	VAkL	-39.2
569.305^{+2}	7.12	40.25	-0.37		
635.861^{+2}	7.31	41.31	1.50	y_{11}^{+2}	18.8
677.264	3.50	19.80	-0.18		
697.379	4.70	26.59	1.50	y_6	7.5
1060.564	3.85	21.78	1.50	y_9	10.0
1270.674	3.56	20.11	1.50	y_{11}	-12.7



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Result Summary

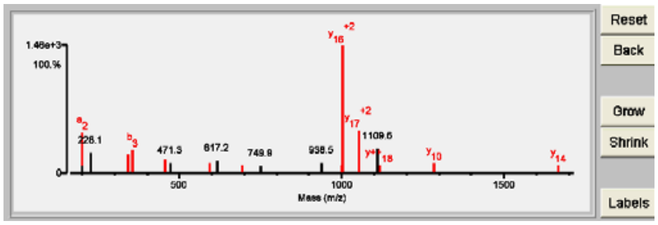
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.18	78.1	6	7/25	K68k	(R)LIQVPkGPVEGYEENEEFLR(T)	2346.1976	114.0591	6.6	14199.5/5.21	HUMAN	Q9UI30	TRM112-like protein OS=Homo sapiens GN=AD-001 PE=1 SV=1
2	5.87	61.5	2	14/25	None	(K)IQIVEFDSPYDSSPNNRPIIR(W)	2460.2518	0.0050	2.0	117749.2/8.91	HUMAN	RQ14703	REVERSE Membrane-bound transcription factor site-1 protease OS=Homo sapiens GN=MBTPS1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.18	78.1	6	7/25	K68k	(R) L I|Q|V|P k/G P V E/G Y E E N/E E F L R (T)	2346.1976	114.0591	6.6	14199.5/5.21	HUMAN	Q9UI30	791999	TRM112-like protein OS=Homo sapiens GN=AD-001 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.082	86.093	101.071	102.054	199.178	200.134	227.176	228.147	340.194	355.235	454.304	471.278
Frac. Inten.(% of TIC)	0.00	0.07	0.16	0.08	0.07	9.54	1.75	3.38	4.66	4.39	5.35	3.24	2.50
Rel. Inten.(% of BP)	0.01	0.22	0.53	0.27	0.24	32.18	5.92	11.40	15.72	14.80	18.07	10.92	8.42
Score	0.20		0.22	0.50	1.00	0.50	-0.06	0.50	-0.16	0.75	0.50	0.50	-0.08
Ion-type	PR	QK	LI	QK	E	a_2		b_2		Pk	b_3	b_4	
Delta ppm	-16.1		-35.1	2.6	-7.4	-16.0		-2.6		-15.4	0.1	0.2	

Fragment-ion (m/z)	593.329	617.191	693.379	749.908	938.486	999.496^{+2}	1003.971^{+2}	1053.515^{+2}	1109.550	1117.548	1285.579	1667.722
Frac. Inten.(% of TIC)	2.33	3.00	1.90	1.77	2.44	1.99	29.63	10.03	5.80	1.85	2.29	1.80
Rel. Inten.(% of BP)	7.87	10.12	6.41	5.98	8.24	6.73	100.00	33.85	19.57	6.24	7.72	6.08
Score	0.75	-0.10	1.50	-0.06	-0.08	0.50	1.50	1.50	-0.20	1.50	1.50	1.50
Ion-type	PkGPV		y_5			a_{17}^{+2}	y_{16}^{+2}	y_{17}^{+2}		$y{+}{+}_{18}$	y_{10}	y_{14}
Delta ppm	-20.7		32.6			1.5	-5.1	4.0		7.3	7.1	-19.5



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Result Summary

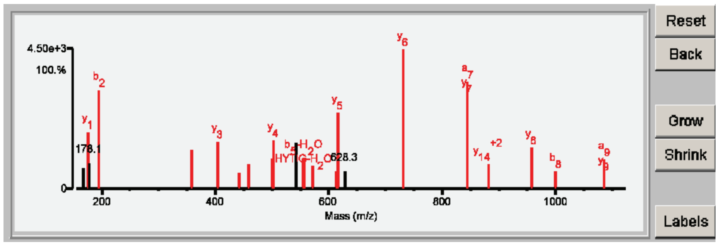
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.40	83.0	12	5/25	K112k	(R)GHYTIGkEIIDLVLDR(I)	1842.0120	114.0156	-14.0	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	17.40	83.0	12	5/25	K112k	(R)GHYTIGkEIIDLVLDR(I)	1842.0120	114.0156	-14.0	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	17.40	83.0	12	5/25	K112k	(R)GHYTIGkEIIDLVLDR(I)	1842.0120	114.0156	-14.0	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.40	83.0	12	5/25	K112k	(R) G H|Y\T\I\G k/E|I|I|D/L/V/L D/R (I)	1842.0120	114.0156	-14.0	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	17.40	83.0	12	5/25	K112k	(R) G H|Y\T\I\G k/E|I|I|D/L/V/L D/R (I)	1842.0120	114.0156	-14.0	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	17.40	83.0	12	5/25	K112k	(R) G H|Y\T\I\G k/E|I|I|D/L/V/L D/R (I)	1842.0120	114.0156	-14.0	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1

Fragment-ion (m/z)	84.078	86.094	167.086	175.113	178.057	195.083	358.144	403.224	441.176	459.193	500.734^{+2}
Frac. Inten.(% of TIC)	7.00	0.31	1.94	5.18	2.32	9.05	3.59	4.39	1.52	2.30	2.77
Rel. Inten.(% of BP)	54.30	2.39	15.03	40.19	17.96	70.15	27.84	34.02	11.81	17.86	21.47
Score	-0.54	0.22	-0.15	1.50	-0.18	0.50	0.50	1.50	0.25	0.50	0.50
Ion-type		LI		y_1		b_2	b_3	y_3	b_4-H_2O	b_4	b_8^{+2}
Delta ppm		-31.7		-36.3		-32.0	-22.0	-13.5	-29.2	-13.8	-25.6

Fragment-ion (m/z)	502.293	543.285	554.261	557.279^{+2}	572.266	613.815	615.369	628.317	730.399	843.475	881.476^{+2}	956.555	1000.463	1085.590
Frac. Inten.(% of TIC)	4.44	4.20	2.82	2.79	2.14	1.58	6.95	1.56	12.90	9.83	2.25	3.79	1.64	2.73
Rel. Inten.(% of BP)	34.43	32.57	21.86	21.65	16.58	12.25	53.89	12.09	100.00	76.22	17.46	29.37	12.69	21.13
Score	1.50	-0.33	0.50	0.50	0.75	0.50	1.50	-0.12	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type	y_4		b_5-H_2O HYTIG-H_2O	b_9^{+2}	b_5 HYTIG	b++10	y_5		y_6	a_7 y_7	y_{14}^{+2}	y_8	b_8	a_9 y_9
Delta ppm	-11.7		-21.8 -21.8	-17.5	-31.8 -31.8	-25.7	-21.8		-14.5	31.8 -21.7	-17.4	-23.9	-23.1	13.9 -27.7



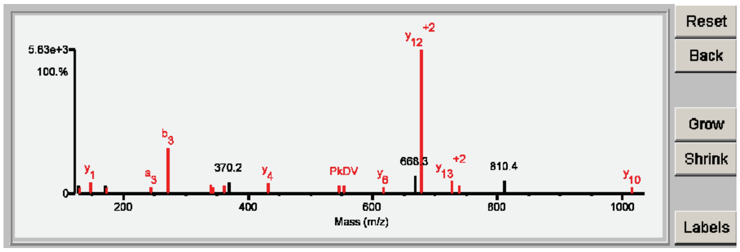
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.78	84.6	9	5/25	K326k	(R)GDVVPkDVNAAIATIK(T)	1610.9112	114.0506	4.5	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R)GDVVPkDVNAAIATIK(T)	1610.9112	114.0506	4.5	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R)GDVVPkDVNAAIATIK(T)	1610.9112	114.0506	4.5	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R)GDVVPkDVNAAIATIK(T)	1610.9112	114.0506	4.5	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	17.78	84.6	9	5/25	K326k	(R)GDVVPkDVNAAIATIK(T)	1610.9112	114.0506	4.5	49858.8/5.00	HUMAN	Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2
2	7.35	67.9	4	13/25	K336k	(R)GDVVPKDVNAAIATIk(T)	1610.9112	114.0506	4.5	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.78	84.6	9	5/25	K326k	(R) G D\V|V/P k/D V N A/A/I/A/T I/K (T)	1610.9112	114.0506	4.5	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R) G D\V|V/P k/D V N A/A/I/A/T I/K (T)	1610.9112	114.0506	4.5	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R) G D\V|V/P k/D V N A/A/I/A/T I/K (T)	1610.9112	114.0506	4.5	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	17.78	84.6	9	5/25	K326k	(R) G D\V|V/P k/D V N A/A/I/A/T I/K (T)	1610.9112	114.0506	4.5	49959.8/4.97	HUMAN	Q13748	770157	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	17.78	84.6	9	5/25	K326k	(R) G D\V|V/P k/D V N A/A/I/A/T I/K (T)	1610.9112	114.0506	4.5	49858.8/5.00	HUMAN	Q6PEY2	770159	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2

Fragment-ion (m/z)	70.065	72.082	84.080	86.096	127.051	130.089	147.112	171.149	173.054	244.131	272.125	340.199	343.190	361.241	370.189	432.277	545.374	554.300	616.400	668.340^{+2}	677.889^{+2}	727.408^{+2}	739.377	810.409	1015.583
Frac. Inten.(% of TIC)	0.00	0.90	0.14	0.34	2.02	1.81	3.16	2.03	1.96	1.85	12.53	2.52	1.87	2.02	3.22	2.67	2.06	2.29	1.89	4.66	38.94	3.55	2.29	3.51	1.76
Rel. Inten.(% of BP)	0.01	2.32	0.37	0.89	5.19	4.65	8.11	5.20	5.04	4.76	32.17	6.47	4.80	5.18	8.28	6.85	5.28	5.89	4.84	11.98	100.00	9.10	5.87	9.01	4.53
Score	0.20	0.50	0.50	0.22	-0.05	0.50	1.50	-0.05	0.50	0.50	0.50	0.75	0.50	1.50	-0.08	1.50	1.50	0.75	1.50	-0.12	1.50	1.50	0.75	-0.09	1.50
Ion-type	PR	V	KQ	LI		y_1-NH_3	y_1		b_2	a_3	b_3	Pk	a_4	y_3		y_4	y_5	PkDV	y_6		y_{12}^{+2}	y_{13}^{+2}	PkDVNA		y_{10}
Delta ppm	-0.4	10.0	-9.2	-2.6		20.3	-4.8		-14.9	2.9	0.0	1.1	-25.3	-9.5		-11.2	15.5	9.6	-4.4		1.4	-19.8	3.9		4.3



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Result Summary

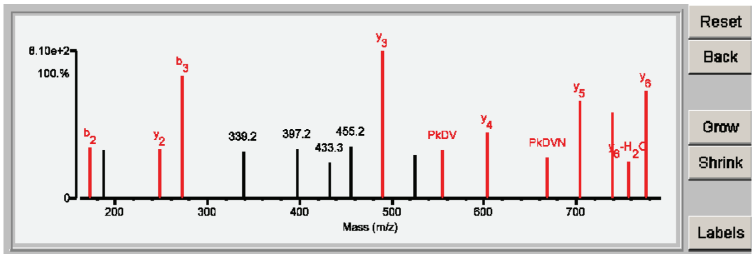
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.52	64.6	8	10/25	K326k K336k	(R)GDVVPkDVNAAIATIkTK(R)	1840.0538	228.1071	10.3	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R)GDVVPkDVNAAIATIkTK(R)	1840.0538	228.1071	10.3	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R)GDVVPkDVNAAIATIkTK(R)	1840.0538	228.1071	10.3	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R)GDVVPkDVNAAIATIkTK(R)	1840.0538	228.1071	10.3	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	10.52	64.6	8	10/25	K326k K336k	(R)GDVVPkDVNAAIATIkTK(R)	1840.0538	228.1071	10.3	49858.8/5.00	HUMAN	Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2
2	6.93	58.6	6	12/25	K326k K338k	(R)GDVVPkDVNAAIATIKTk(R)	1840.0538	228.1071	10.3	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.52	64.6	8	10/25	K326k K336k	(R) G D\V\V P k D V N A A I/A/T/I/k/T/K (R)	1840.0538	228.1071	10.3	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R) G D\V\V P k D V N A A I/A/T/I/k/T/K (R)	1840.0538	228.1071	10.3	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R) G D\V\V P k D V N A A I/A/T/I/k/T/K (R)	1840.0538	228.1071	10.3	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	10.52	64.6	8	10/25	K326k K336k	(R) G D\V\V P k D V N A A I/A/T/I/k/T/K (R)	1840.0538	228.1071	10.3	49959.8/4.97	HUMAN	Q13748	770157	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	10.52	64.6	8	10/25	K326k K336k	(R) G D\V\V P k D V N A A I/A/T/I/k/T/K (R)	1840.0538	228.1071	10.3	49858.8/5.00	HUMAN	Q6PEY2	770159	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2

Fragment-ion (m/z)	72.081	74.060	84.081	86.096	110.064	127.048	173.058	187.132	248.167	272.123	339.171	397.198
Frac. Inten.(% of TIC)	1.23	2.57	0.45	0.76	2.75	4.04	3.53	3.38	3.43	8.59	3.33	3.46
Rel. Inten.(% of BP)	12.02	25.06	4.40	7.36	26.83	39.40	34.46	32.98	33.46	83.72	32.46	33.77
Score	0.50	1.50	0.50	0.22	-0.27	-0.39	0.50	-0.33	1.50	0.50	-0.32	-0.34
Ion-type	V	y++$_1$	KQ	LI			b_2		y_2	b_3		
Delta ppm	-2.4	3.5	0.3	-2.6			4.7		28.3	-7.0		

Fragment-ion (m/z)	433.276	455.240^{+2}	490.301	525.271	554.291	603.383	668.332	704.434	739.367	757.467	775.463	810.406	887.513
Frac. Inten.(% of TIC)	2.53	3.63	10.26	3.05	3.40	4.63	2.84	6.82	6.03	2.56	7.47	6.46	2.79
Rel. Inten.(% of BP)	24.72	35.38	100.00	29.77	33.12	45.16	27.74	66.46	58.80	24.99	72.89	62.96	27.23
Score	-0.25	-0.35	1.50	-0.30	0.75	1.50	0.75	1.50	0.75	0.50	1.50	-0.63	-0.27
Ion-type			y_3		PkDV	y_4	PkDVN	y_5	PkDVNA	y_6-H_2O	y_6		
Delta ppm			4.3		-5.7	0.8	-8.5	5.5	-10.5	13.1	-5.7		



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Result Summary

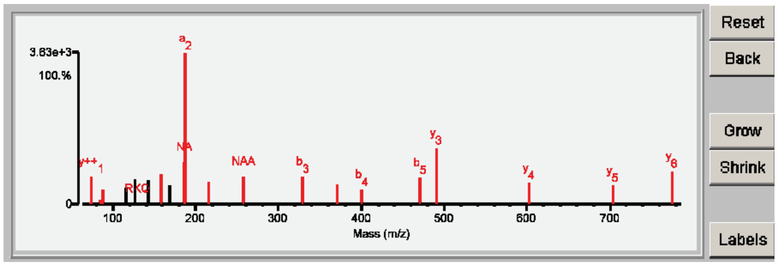
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.34	84.5	9	5/25	K336k	(K)DVNAAIATIkTK(R)	1244.7209	114.0517	6.4	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K)DVNAAIATIkTK(R)	1244.7209	114.0517	6.4	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K)DVNAAIATIkTK(R)	1244.7209	114.0517	6.4	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K)DVNAAIATIkTK(R)	1244.7209	114.0517	6.4	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	14.34	84.5	9	5/25	K336k	(K)DVNAAIATIkTK(R)	1244.7209	114.0517	6.4	49858.8/5.00	HUMAN	Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2
2	12.66	80.2	8	6/25	K338k	(K)DVNAAIATIKTk(R)	1244.7209	114.0517	6.4	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.34	84.5	9	5/25	K336k	(K) D V\N\A\A\I/A/T/I/k T/K (R)	1244.7209	114.0517	6.4	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K) D V\N\A\A\I/A/T/I/k T/K (R)	1244.7209	114.0517	6.4	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K) D V\N\A\A\I/A/T/I/k T/K (R)	1244.7209	114.0517	6.4	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	14.34	84.5	9	5/25	K336k	(K) D V\N\A\A\I/A/T/I/k T/K (R)	1244.7209	114.0517	6.4	49959.8/4.97	HUMAN	Q13748	770157	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	14.34	84.5	9	5/25	K336k	(K) D V\N\A\A\I/A/T/I/k T/K (R)	1244.7209	114.0517	6.4	49858.8/5.00	HUMAN	Q6PEY2	770159	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2

Fragment-ion (m/z)	72.080	74.061	84.080	86.096	87.056	88.040	115.054	127.086	129.102	142.085	157.132	158.091	169.067
Frac. Inten.(% of TIC)	0.33	4.22	0.63	0.76	0.10	2.23	2.48	3.90	0.11	3.70	2.50	4.67	2.97
Rel. Inten.(% of BP)	1.40	18.09	2.69	3.26	0.42	9.57	10.63	16.70	0.49	15.83	10.72	20.00	12.71
Score	0.50	1.50	0.50	0.22	0.33	0.50	-0.11	-0.17	0.20	-0.16	-0.11	0.50	-0.13
Ion-type	V	y^{++}_1	KQ	LI	NR	a_1			RKQ			NA-28	
Delta ppm	-13.5	15.7	-5.7	-6.1	8.2	-10.2			-0.3			-15.2	

Fragment-ion (m/z)	186.085	187.107	215.101	257.125	329.147	370.205	400.181	471.219	490.300	603.384	704.428	775.475
Frac. Inten.(% of TIC)	6.48	23.35	3.40	4.23	4.32	3.17	2.28	4.00	8.73	3.37	2.98	5.11
Rel. Inten.(% of BP)	27.75	100.00	14.55	18.13	18.51	13.56	9.78	17.12	37.39	14.42	12.77	21.87
Score	0.75	0.50	0.50	0.75	0.50	0.75	0.50	0.50	1.50	1.50	1.50	1.50
Ion-type	NA	a_2	b_2	NAA	b_3	NAAI	b_4	b_5	y_3	y_4	y_5	y_6
Delta ppm	-17.3	-8.1	-12.7	-2.4	0.4	-13.5	-5.9	-4.6	3.3	2.6	-3.4	10.1



Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	49858.8/5.00	HUMAN	Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	49924.7/4.95	HUMAN	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1
1	20.07	97.3	10	2/25	K370k	(K)VGINYQPPTVVPGGDLAkVQR(A)	2208.2135	114.0585	6.7	50093.8/4.94	HUMAN	Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1
2	3.32	69.0	1	17/25	K775k	(K)SLPGRSLVLDLPVSNVVVDTk(A)	2208.2598	114.0122	-13.2	193754.0/8.22	HUMAN	RQ460N5	REVERSE Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14 PE=2 SV=2

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH^+ Calculated (Da)</th><th>MH^+ Error (Da)</th><th>MH^+ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>50135.9/4.94</td><td>HUMAN</td><td>Q71U36</td><td>770033</td><td>Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>50151.9/4.94</td><td>HUMAN</td><td>P68363</td><td>770047</td><td>Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>49895.6/4.96</td><td>HUMAN</td><td>Q9BQE3</td><td>770065</td><td>Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>49959.8/4.97</td><td>HUMAN</td><td>Q13748</td><td>770157</td><td>Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>49858.8/5.00</td><td>HUMAN</td><td>Q6PEY2</td><td>770159</td><td>Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>49924.7/4.95</td><td>HUMAN</td><td>P68366</td><td>770185</td><td>Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1</td></tr>
<tr><td>1</td><td>20.07</td><td>97.3</td><td>10</td><td>2/25</td><td>K370k</td><td>(K) V G I N Y\Q|P P T\V|V|P/G G D/L/A/k/V Q R (A)</td><td>2208.2135</td><td>114.0585</td><td>6.7</td><td>50093.8/4.94</td><td>HUMAN</td><td>Q9NY65</td><td>770219</td><td>Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1</td></tr>
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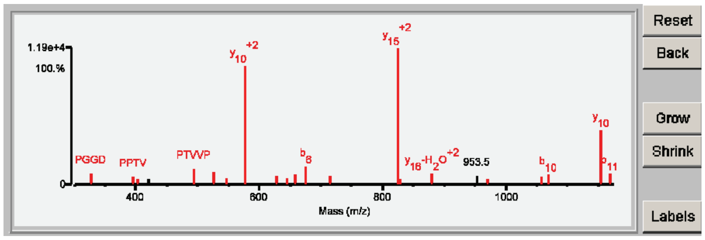
Fragment-ion (m/z)	70.064	72.080	86.097	327.128	395.230	402.242	419.141	494.296	526.286^{+2}	547.285	577.819^{+2}	627.364^{+2}
Frac. Inten.(% of TIC)	0.00	0.17	0.07	2.26	1.66	1.12	1.12	3.16	2.43	1.43	24.23	1.83
Rel. Inten.(% of BP)	0.01	0.60	0.26	8.07	5.92	4.01	4.01	11.29	8.66	5.09	86.48	6.52
Score	0.20	0.50 0.50	0.22	0.75	0.75	1.50	-0.04	0.75	0.25	0.50	1.50	1.50
Ion-type	PR	a_1 V	LI	PGGD	PPTV	y_3		PTVVP	b_{10}-H_2O^{+2}	b_5	y_{10}^{+2}	y_{11}^{+2}
Delta ppm	-11.8	-21.8 -6.6	2.0	-8.6	-1.0	-10.3		-4.9	5.4	-6.5	3.0	19.5

Fragment-ion (m/z)	644.389	658.321	675.345	715.427	824.464^{+2}	828.510	879.458^{+2}	953.474^{+2}	970.510	1057.584	1069.573	1154.630	1168.638
Frac. Inten.(% of TIC)	1.40	2.15	3.79	1.81	28.02	1.17	2.30	1.70	1.03	1.51	2.04	11.23	2.37
Rel. Inten.(% of BP)	4.99	7.66	13.53	6.46	100.00	4.17	8.19	6.07	3.68	5.40	7.29	40.08	8.44
Score	1.50	0.25	0.50	1.50	1.50	1.50	0.50	-0.06	0.50	1.50	0.50	1.50	0.50
Ion-type	y_4	b_6-NH_3	b_6	y_5	y_{15}^{+2}	y_6	y_{16}-H_2O^{+2}		b_9	y_9	b_{10}	y_{10}	b_{11}
Delta ppm	8.0	0.0	-3.8	8.2	2.2	6.1	-32.1		10.2	8.5	3.6	1.9	0.4



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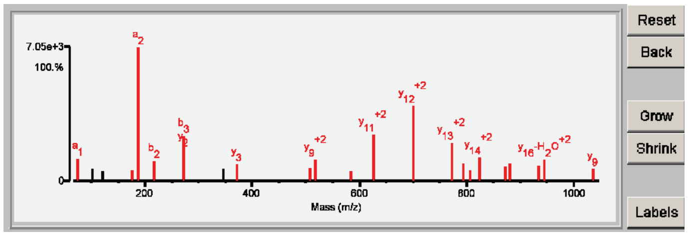
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.96	94.5	15	3/25	K60k	(K)TIGGGDDSFNTFFSETGAGkHVPR(A)	2497.1742	114.0391	-1.5	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K)TIGGGDDSFNTFFSETGAGkHVPR(A)	2497.1742	114.0391	-1.5	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K)TIGGGDDSFNTFFSETGAGkHVPR(A)	2497.1742	114.0391	-1.5	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K)TIGGGDDSFNTFFSETGAGkHVPR(A)	2497.1742	114.0391	-1.5	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	24.96	94.5	15	3/25	K60k	(K)TIGGGDDSFNTFFSETGAGkHVPR(A)	2497.1742	114.0391	-1.5	49858.8/5.00	HUMAN	Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2
2	5.61	54.1	1	13/25	M52m K53k	(K)DMKSFIKDVRQEPTLGDENmk(M)	2481.2112	130.0021	-13.7	22142.5/5.01	HUMAN	RP62760	REVERSE Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.96	94.5	15	3/25	K60k	(K) T I\G\G G D D S F/N/T/F/F/S/E/T/G A/G k/H/V/P/R (A)	2497.1742	114.0391	-1.5	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K) T I\G\G G D D S F/N/T/F/F/S/E/T/G A/G k/H/V/P/R (A)	2497.1742	114.0391	-1.5	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K) T I\G\G G D D S F/N/T/F/F/S/E/T/G A/G k/H/V/P/R (A)	2497.1742	114.0391	-1.5	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	24.96	94.5	15	3/25	K60k	(K) T I\G\G G D D S F/N/T/F/F/S/E/T/G A/G k/H/V/P/R (A)	2497.1742	114.0391	-1.5	49959.8/4.97	HUMAN	Q13748	770157	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	24.96	94.5	15	3/25	K60k	(K) T I\G\G G D D S F/N/T/F/F/S/E/T/G A/G k/H/V/P/R (A)	2497.1742	114.0391	-1.5	49858.8/5.00	HUMAN	Q6PEY2	770159	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2

Fragment-ion (m/z)	74.059	86.094	101.068	120.079	121.081	175.117	187.142	215.136	272.170	345.153	371.239	508.289	518.791^{+2}	583.302^{+2}	626.815^{+2}	700.356^{+2}	773.891^{+2}	793.685^{+3}	807.460	824.415^{+2}	872.922^{+2}	881.429^{+2}	935.511	945.960^{+2}	1036.564
Frac. Inten.(% of TIC)	3.54	0.09	1.94	0.60	1.63	1.80	21.35	3.21	7.26	1.97	2.56	2.14	3.47	1.63	7.46	11.87	6.13	2.82	1.76	3.72	2.30	2.91	2.54	3.32	1.97
Rel. Inten.(% of BP)	16.59	0.44	9.09	2.79	7.65	8.44	100.00	15.03	34.02	9.21	11.97	10.02	16.23	7.65	34.93	55.57	28.71	13.20	8.26	17.44	10.75	13.65	11.90	15.53	9.23
Score	0.50	0.22	-0.09	1.00	-0.08	1.50	0.50	0.50	1.50	-0.09	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50	0.50	1.50	1.50	0.50	1.50
Ion-type	a_1	LI		F		y_1	a_2	b_2	b_3 y_2		y_3	y_4	y_9^{+2}	y_{10}^{+2}	y_{11}^{+2}	y_{12}^{+2}	y_{13}^{+2}	y_{22}-H_2O^{+3}	y_6	y_{14}^{+2}	y_{15}-NH_3^{+2}	y_{15}^{+2}	y_8	y_{16}-H_2O^{+2}	y_9
Delta ppm	-30.2	-24.7		-14.8		-8.9	-18.2	-17.7	29.8 -7.4		-3.3	-19.6	10.3	-8.9	-12.9	-2.4	-1.4	-14.3	2.5	-1.1	-1.9	-9.5	-6.8	-6.3	-0.9



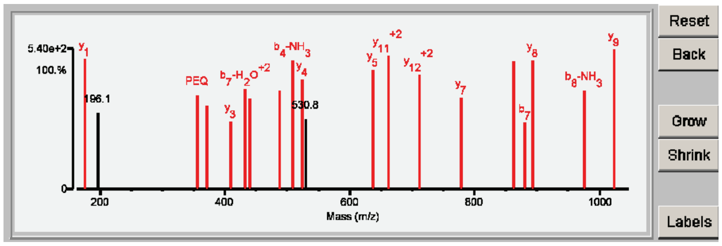
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	50135.9/4.94	HUMAN	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	50151.9/4.94	HUMAN	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	49895.6/4.96	HUMAN	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	49959.8/4.97	HUMAN	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	49924.7/4.95	HUMAN	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R)QLFHPEQLITGkEDAANNYAR(G)	2415.2051	114.0590	6.4	50093.8/4.94	HUMAN	Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	50135.9/4.94	HUMAN	Q71U36	770033	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	50151.9/4.94	HUMAN	P68363	770047	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	49895.6/4.96	HUMAN	Q9BQE3	770065	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	49959.8/4.97	HUMAN	Q13748	770157	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	49924.7/4.95	HUMAN	P68366	770185	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1
1	19.93	93.1	10	2/25	K96k	(R) Q L F H P E Q\L I/T/G k/E/D/A A/N/N/Y A/R (G)	2415.2051	114.0590	6.4	50093.8/4.94	HUMAN	Q9NY65	770219	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
84.044	0.10	1.51	1.00	E	-5.8
84.081	0.36	5.41	0.50	KQ	-0.9
86.096	0.96	14.44	0.22	LI	-4.9
110.070	0.21	3.13	1.00	H	-15.2
120.080	0.12	1.83	1.00	F	-8.1
175.115	6.16	92.75	1.50	y$_1$	-22.0
196.144	3.62	54.41	-0.54		
355.158	4.44	66.82	0.75	PEQ	-11.0
371.197	3.93	59.14	0.75	EQL	9.1
409.231	3.20	48.13	1.50	y$_3$	27.9
431.716^{+2}	4.74	71.33	0.25	b$_7$-H$_2$O^{+2}	3.5
440.711^{+2}	4.29	64.58	0.50	b$_7$$^{+2}$	-20.2
488.255^{+2}	4.71	70.90	0.25	b$_8$-H$_2$O^{+2}	-3.5
509.253	6.13	92.25	0.25	b$_4$-NH$_3$	1.8
523.264	5.23	78.67	1.50	y$_4$	3.6
530.797^{+2}	3.33	50.13	-0.50		
637.313	5.67	85.29	1.50	y$_5$	12.6
661.804^{+2}	6.32	95.09	1.50	y$_{11}$$^{+2}$	-5.6
712.330^{+2}	5.43	81.75	1.50	y$_{12}$$^{+2}$	-2.2
779.387	4.38	65.84	1.50	y$_7$	9.1
862.410	6.04	90.80	0.25	b$_7$-H$_2$O	-13.6
880.414	3.16	47.51	0.50	b$_7$	-20.5
894.418	6.13	92.25	1.50	y$_8$	13.4
976.493	4.69	70.59	0.25	b$_8$-NH$_3$	3.6
1023.460	6.65	100.00	1.50	y$_9$	10.2



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Result Summary

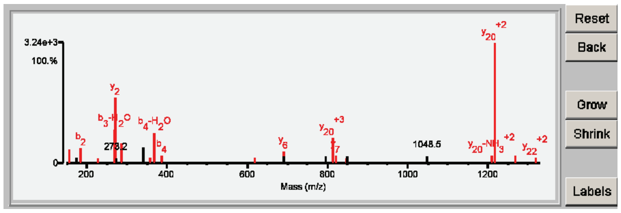
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.30	88.0	7	7/25	K297k	(R)ALTVPELTQQVFDAkNMMAACDPR(H)	2706.3048	114.0680	8.9	49671.1/4.78	HUMAN	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
2	8.35	69.0	3	14/25	None	(R)EREALAWAQREGQGPAVTEDSPGIPR(C)	2820.4023	-0.0295	-10.5	127495.3/6.67	HUMAN	O43593	Protein hairless OS=Homo sapiens GN=HR PE=1 SV=5
3	5.61	69.3	2	16/25	None	(R)SCVKQESVDWLVVSGDEYGALLLPR(S)	2820.4237	-0.0508	-18.0	35618.2/8.29	HUMAN	RQ9BYB4	REVERSE Guanine nucleotide-binding protein subunit beta-like protein 1 OS=Homo sapiens GN=GNB1L PE=1 SV=2
4	5.31	61.3	2	16/25	M286m M292m	(K)GRQAENEHIHmDNLAQmPMISIPR(V)	2788.3440	32.0289	13.8	35427.6/6.58	HUMAN	Q32ZL2	Lipid phosphate phosphatase-related protein type 5 OS=Homo sapiens GN=LPPR5 PE=2 SV=2
5	4.76	59.9	2	17/25	M286m M294m	(K)GRQAENEHIHmDNLAQMPmISIPR(V)	2788.3440	32.0289	13.8	35427.6/6.58	HUMAN	Q32ZL2	Lipid phosphate phosphatase-related protein type 5 OS=Homo sapiens GN=LPPR5 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.30	88.0	7	7/25	K297k	(R) A L|T|V|P E L T Q Q V F D A k N M/M/A/A C D/P R (H)	2706.3048	114.0680	8.9	49671.1/4.78	HUMAN	P07437	770563	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

Fragment-ion (m/z)	157.135	173.130	185.127	227.105	268.165	272.173	273.179	286.176	339.240	357.241	367.233	385.249	618.259	689.292
Frac. Inten.(% of TIC)	3.11	1.32	3.32	1.03	7.51	14.65	1.08	4.61	3.62	1.21	6.87	1.61	1.26	2.73
Rel. Inten.(% of BP)	11.53	4.89	12.32	3.82	27.85	54.33	4.01	17.09	13.43	4.47	25.49	5.99	4.66	10.12
Score	0.50	-0.05	0.50	0.75	0.25	1.50	-0.04	0.50	-0.13	0.50	0.25	0.50	1.50	1.50
Ion-type	a_2		b_2	PE	b_3-H_2O	y_2		b_3		a_4	b_4-H_2O	b_4	y_5	y_6
Delta ppm	4.9		-12.7	4.3	-4.7	4.4		-3.3		-25.8	-4.3	8.5	-12.3	-16.4

Fragment-ion (m/z)	690.326^{+2}	796.438	812.731^{+3}	820.323	845.749^{+3}	847.992	1048.477^{+2}	1210.036^{+2}	1218.564^{+2}	1268.102^{+2}	1318.622^{+2}
Frac. Inten.(% of TIC)	1.61	1.38	5.76	1.65	1.05	1.39	1.61	1.74	26.97	1.62	1.29
Rel. Inten.(% of BP)	5.97	5.13	21.35	6.12	3.89	5.15	5.97	6.46	100.00	6.00	4.78
Score	-0.06	-0.05	1.50	1.50	1.50	-0.05	-0.06	0.50	1.50	1.50	1.50
Ion-type			y_{20}^{+3}	y_7	y_{21}^{+3}			y_{20}-NH_3^{+2}	y_{20}^{+2}	y_{21}^{+2}	y_{22}^{+2}
Delta ppm			27.3	-25.9	20.7			-8.3	4.4	6.8	4.1



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Result Summary

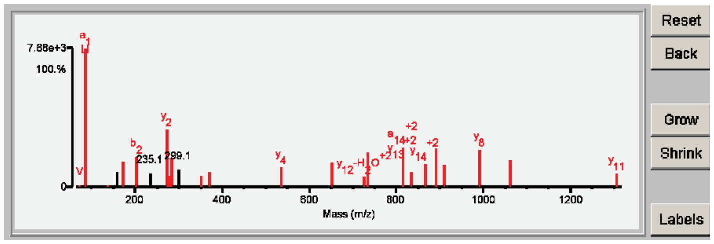
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.42	93.1	12	3/25	K58k	(R)ISVYYNEATGGkYVPR(A)	1816.9228	114.0502	3.8	49671.1/4.78	HUMAN	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.42	93.1	12	3/25	K58k	(R) I/S|V/Y/Y/N E/A/T/G/G k/Y/V/P R (A)	1816.9228	114.0502	3.8	49671.1/4.78	HUMAN	P07437	770563	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

Fragment-ion (m/z)	72.081	86.096	136.074	159.111	173.127	201.123	235.147	272.170	278.112	282.179	299.139	350.172
Frac. Inten.(% of TIC)	0.33	20.58	0.31	2.26	3.86	4.45	1.98	8.53	1.73	4.23	2.61	1.60
Rel. Inten.(% of BP)	1.60	100.00	1.52	10.96	18.78	21.64	9.64	41.44	8.38	20.53	12.69	7.78
Score	0.50	0.50 0.50	1.00	-0.11	0.50	0.50	-0.10	1.50	0.75	0.25	-0.13	0.75
Ion-type	V	a_1 LI	Y		a_2	b_2		y_2	YN	b_3-H_2O		SVY
Delta ppm	-1.0	-21.2 -8.4	-13.9		-14.2	-7.3		-5.6	-9.5	-12.1		-0.4

Fragment-ion (m/z)	371.238	534.303	653.336^{+2}	725.864^{+2}	734.864^{+2}	816.391^{+2}	833.465	865.939^{+2}	890.486	909.456^{+2}	991.533	1062.568	1305.654
Frac. Inten.(% of TIC)	2.19	2.93	3.55	1.57	5.14	5.93	2.16	3.35	5.72	3.33	5.60	3.94	2.11
Rel. Inten.(% of BP)	10.66	14.24	17.25	7.61	25.00	28.83	10.47	16.26	27.78	16.18	27.22	19.16	10.24
Score	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_3	y_4	y_{11}^{+2}	y_{12}-H_2O^{+2}	y_{12}^{+2}	a_{14}^{+2} y_{13}^{+2}	y_6	y_{14}^{+2}	y_7	y_{15}^{+2}	y_8	y_9	y_{11}
Delta ppm	-5.2	-1.4	7.6	9.2	1.8	-20.1 -4.0	3.1	11.8	2.5	12.8	1.5	-1.3	-0.8



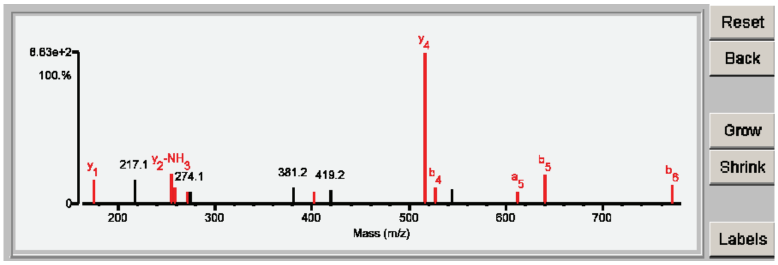
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	50327.2/5.06	HUMAN	Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49907.3/4.78	HUMAN	Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49953.4/4.78	HUMAN	Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49831.3/4.79	HUMAN	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	50433.0/4.83	HUMAN	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	48434.8/5.11	HUMAN	Q99867	Putative tubulin beta-4q chain OS=Homo sapiens GN=TUBB4Q PE=5 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49586.1/4.78	HUMAN	P04350	Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49671.1/4.78	HUMAN	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49857.4/4.77	HUMAN	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49572.9/4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain B OS=Homo sapiens PE=3 SV=1
1	9.61	60.6	6	9/23	K252k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	49776.3/4.79	HUMAN	Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2
1	9.61	60.6	6	9/23	K180k	(R)kLAVNMVPFPR(L)	1271.7293	114.0511	5.9	41775.3/4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	50327.2/5.06	HUMAN	Q9H4B7	770371	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49907.3/4.78	HUMAN	Q13885	770405	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49953.4/4.78	HUMAN	Q9BVA1	770415	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49831.3/4.79	HUMAN	P68371	770423	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	50433.0/4.83	HUMAN	Q13509	770503	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	48434.8/5.11	HUMAN	Q99867	770523	Putative tubulin beta-4q chain OS=Homo sapiens GN=TUBB4Q PE=5 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49586.1/4.78	HUMAN	P04350	770535	Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49671.1/4.78	HUMAN	P07437	770563	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49857.4/4.77	HUMAN	Q9BUF5	770597	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49572.9/4.75	HUMAN	A6NNZ2	770615	Tubulin beta-8 chain B OS=Homo sapiens PE=3 SV=1
1	9.61	60.6	6	9/23	K252k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	49776.3/4.79	HUMAN	Q3ZCM7	770619	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2
1	9.61	60.6	6	9/23	K180k	(R) k L A V\N\M\V/P F/P/R (L)	1271.7293	114.0511	5.9	41775.3/4.77	HUMAN	A6NKZ8	913329	Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2

Fragment-ion (m/z)	70.066	72.082	84.081	86.091	104.051	112.088	115.098	120.082	175.119	217.133	255.140	258.650	272.168	274.119	381.223	402.221	419.238^{+3}	516.295	526.337	544.238	612.372	640.378	771.427
Frac. Inten.(% of TIC)	0.00	0.92	12.70	2.41	7.33	0.07	2.18	0.16	4.51	4.32	5.54	3.06	2.17	2.35	2.92	2.23	2.53	27.79	3.07	2.67	2.21	5.36	3.50
Rel. Inten.(% of BP)	0.01	3.30	45.70	8.69	26.36	0.23	7.84	0.59	16.22	15.54	19.95	11.00	7.79	8.47	10.52	8.03	9.12	100.00	11.04	9.61	7.94	19.28	12.60
Score	0.20	0.50	-0.46	-0.09	-0.26	0.33	-0.08	1.00	1.50	-0.16	0.50	1.50	1.50	-0.08	-0.11	0.50	-0.09	1.50	0.50	-0.10	0.50	0.50	0.50
Ion-type	PR	V				R		F	y_1		y_2-NH_3	y^{++}_4	y_2			y_3-NH_3		y_4	b_4		a_5	b_5	b_6
Delta ppm	18.2	12.8				8.7		8.5	-2.0		-21.4	-0.3	-15.1			19.4		4.9	2.6		-18.6	-1.5	9.9



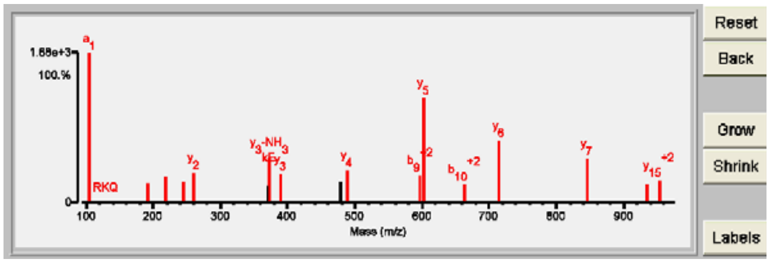
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.30	92.2	9	3/24	K324k	(R)MSMkEVDEQMLNVQNK(N)	1923.8973	114.0669	11.7	49907.3/4.78	HUMAN	Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R)MSMkEVDEQMLNVQNK(N)	1923.8973	114.0669	11.7	49953.4/4.78	HUMAN	Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R)MSMkEVDEQMLNVQNK(N)	1923.8973	114.0669	11.7	49831.3/4.79	HUMAN	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R)MSMkEVDEQMLNVQNK(N)	1923.8973	114.0669	11.7	49671.1/4.78	HUMAN	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
2	7.62	57.0	4	10/24	K336k	(R)MSMKEVDEQMLNVQNk(N)	1923.8973	114.0669	11.7	49907.3/4.78	HUMAN	Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.30	92.2	9	3/24	K324k	(R) M/S\M k E V D\E Q|M|L/N/V/Q/N K (N)	1923.8973	114.0669	11.7	49907.3/4.78	HUMAN	Q13885	770405	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R) M/S\M k E V D\E Q|M|L/N/V/Q/N K (N)	1923.8973	114.0669	11.7	49953.4/4.78	HUMAN	Q9BVA1	770415	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R) M/S\M k E V D\E Q|M|L/N/V/Q/N K (N)	1923.8973	114.0669	11.7	49831.3/4.79	HUMAN	P68371	770423	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1
1	17.30	92.2	9	3/24	K324k	(R) M/S\M k E V D\E Q|M|L/N/V/Q/N K (N)	1923.8973	114.0669	11.7	49671.1/4.78	HUMAN	P07437	770563	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

Fragment-ion (m/z)	61.011	72.081	84.044	84.080	86.096	101.069	104.052	129.101	191.086	219.082	245.075	261.159	370.176	372.196	389.216	478.750^{+2}	488.282	596.753^{+2}	602.331	662.295^{+2}	715.411	846.464	935.396	953.954^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.48 11.82 -0.12	0.15 0.71 0.50 V 8.7	0.15 0.74 1.00 E -4.6	0.22 1.07 0.50 KQ -12.8	0.17 0.80 0.22 LI -4.9	0.12 0.60 KQ	20.96 100.00 0.50 a_1 -13.9	0.13 0.60 0.20 RKQ -10.4	2.79 13.30 0.50 a_2 -1.4 SM-28 -1.4	3.63 17.34 0.75 b_2 4.6 SM 4.6	2.95 14.09 0.75 DE -10.2	4.21 20.10 1.50 y_2 11.4	2.38 11.36 -0.11	6.39 30.47 0.75 y_3-NH_3 22.7 kE 19.7	4.06 19.39 1.50 y_3 4.6	2.91 13.88 -0.14	4.65 22.18 1.50 y_4 -0.9	3.87 18.46 0.50 b_9^{+2} -0.4	14.53 69.31 1.50 y_5 9.5	2.67 12.74 0.50 b_{10}^{+2} 33.4	8.64 41.24 1.50 y_6 1.2	6.17 29.45 1.50 y_7 15.9	2.68 12.81 0.50 b_7 -1.1	3.08 14.72 1.50 y_{15}^{+2} 0.4



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Result Summary

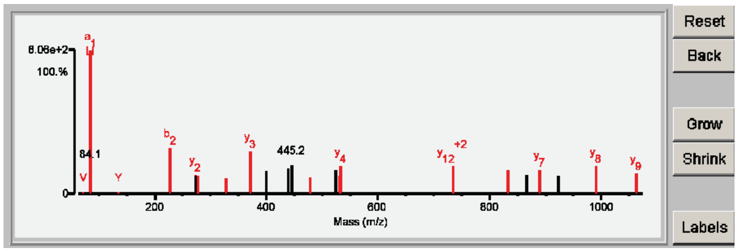
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.09	72.6	10	8/25	K58k	(R)INVYYNEATGGkYVPR(A)	1843.9337	114.0537	5.5	49831.3/4.79	HUMAN	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.09	72.6	10	8/25	K58k	(R) I N\V\Y/Y N E/A/T/G/G k/Y/V/P R (A)	1843.9337	114.0537	5.5	49831.3/4.79	HUMAN	P68371	770423	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1

Fragment-ion (m/z)	72.080	84.082	86.097	87.055	136.074	228.133	272.171	273.176	278.109	327.201	371.239	400.223
Frac. Inten.(% of TIC)	0.20	3.80	21.97	0.10	0.29	7.00	2.95	2.67	2.70	2.43	6.56	3.45
Rel. Inten.(% of BP)	0.90	17.31	100.00	0.45	1.31	31.84	13.44	12.16	12.28	11.08	29.87	15.71
Score	0.50	-0.17	0.50	0.33	1.00	0.50	1.50	-0.12	0.75	0.50	1.50	-0.16
Ion-type	**V**		a_1	**NR**	**Y**	b_2	y_2		**YN**	b_3	y_3	
Delta ppm	-13.5		-6.1	-5.6	-13.2	-10.4	-1.5		-20.2	-8.2	-2.5	
			0.50									
			LI									
			6.7									

Fragment-ion (m/z)	439.250	445.240	478.201	524.732^{+2}	531.790^{+2}	534.303	734.858^{+2}	833.460	865.963^{+2}	890.502	923.452	991.526	1062.590
Frac. Inten.(% of TIC)	3.76	4.47	2.55	3.71	2.73	4.27	4.30	3.58	2.88	3.64	2.65	4.30	3.04
Rel. Inten.(% of BP)	17.14	20.33	11.59	16.89	12.45	19.46	19.58	16.29	13.10	16.55	12.06	19.56	13.84
Score	-0.17	-0.20	0.75	-0.17	1.50	1.50	1.50	1.50	-0.13	1.50	-0.12	1.50	1.50
Ion-type			**YNEA**		y_9^{+2}	y_4	y_{12}^{+2}	y_6		y_7		y_8	y_9
Delta ppm			13.1		2.9	-1.6	-6.1	-3.4		19.9		-5.6	19.8



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Result Summary

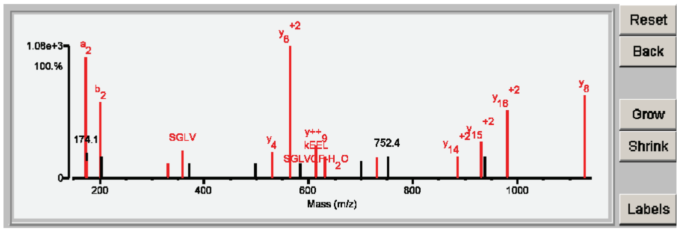
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.81	82.2	7	8/25	K412k	(R)TVVSGLVQFVPkEELQDR(L)	2044.1073	114.0542	5.2	59143.8/6.61	HUMAN	P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4
2	5.12	52.3	2	14/25	K56k K70k	(K)WIkGLVSNPLKSTVMEk(K)	1930.0830	228.0785	-3.4	61175.5/6.34	HUMAN	RQ9H223	REVERSE EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1
3	4.87	52.3	2	14/25	K56k K64k	(K)WIkGLVSNPLkSTVMEK(K)	1930.0830	228.0785	-3.4	61175.5/6.34	HUMAN	RQ9H223	REVERSE EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1
4	4.50	55.9	2	15/25	None	(K)LSLDDVQKLIKDREDKSR(S)	2158.1826	-0.0211	-9.8	316052.8/8.09	HUMAN	Q6KC79	Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2
5	4.11	59.9	2	14/25	K179k	(K)DTVALNYkHVKEKIEEK(S)	2044.1073	114.0542	5.2	27562.4/7.17	HUMAN	RQ86WH2	REVERSE Ras association domain-containing protein 3 OS=Homo sapiens GN=RASSF3 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.81	82.2	7	8/25	K412k	(R) T V|V/S/G L V Q F/V/P k E E/L Q D/R (L)	2044.1073	114.0542	5.2	59143.8/6.61	HUMAN	P54577	764461	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4

Fragment-ion (m/z)	72.079	84.079	86.096	173.127	174.130	175.122	201.123	202.123	329.209	357.211	370.725^{+2}	497.232	531.295
Frac. Inten.(% of TIC)	0.19	0.10	0.14	14.11	2.90	2.04	8.90	2.57	1.75	3.26	1.72	1.84	3.05
Rel. Inten.(% of BP)	1.26	0.67	0.91	91.75	18.86	13.27	57.89	16.71	11.39	21.21	11.19	11.94	19.81
Score	0.50	0.50	0.22	0.50	-0.19	1.50	0.50	-0.17	0.50	0.75	-0.11	-0.12	1.50
Ion-type	V	KQ	LI	a_2		y_1	b_2		SGLV-28	SGLV			y_4
Delta ppm	-20.5	-16.4	-3.8	-15.3		19.7	-8.8		-30.8	-9.6			12.9

Fragment-ion (m/z)	564.788^{+2}	584.317	614.328	632.335	701.449	731.430	752.394^{+2}	886.455^{+2}	929.980^{+2}	936.510	979.525^{+2}	1128.550
Frac. Inten.(% of TIC)	15.38	1.72	3.84	2.50	1.99	2.43	2.60	2.54	4.26	2.51	8.00	9.66
Rel. Inten.(% of BP)	100.00	11.17	25.00	16.24	12.92	15.83	16.91	16.54	27.69	16.31	52.03	62.80
Score	1.50	-0.11	1.50	0.75	-0.13	0.75	-0.17	1.50	1.50	-0.16	1.50	1.50
Ion-type	y_8^{+2}		y^{++}_9 kEEL SGLVQF-H_2O	SGLVQF		SGLVQFV		y_{14}^{+2}	y_{15}^{+2}		y_{16}^{+2}	y_8
Delta ppm	3.1		12.8 20.2 -4.7	-10.8		28.2		-17.7	-7.5		4.1	-12.5



Result Summary

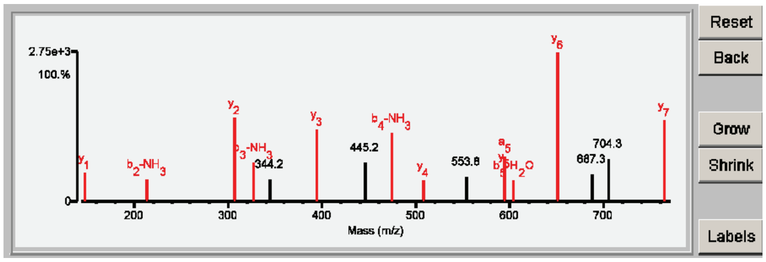
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.10	72.3	7	9/25	K513k	(K)QTNFMTkLGSISCK(S)	1614.7978	114.0481	3.0	59143.8/6.61	HUMAN	P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.10	72.3	7	9/25	K513k	(K) Q T N F M T k/L/G/S/I/S/C/K (S)	1614.7978	114.0481	3.0	59143.8/6.61	HUMAN	P54577	764461	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4

Fragment-ion (m/z)	70.066	84.045	84.081	86.096	87.056	120.081	129.099	140.071	141.102	147.112	213.088	307.144	327.131
Frac. Inten.(% of TIC)	0.13	5.26	0.66	0.37	0.07	0.12	0.09	2.49	2.47	3.16	2.54	9.40	4.42
Rel. Inten.(% of BP)	0.76	31.39	3.93	2.21	0.41	0.73	0.55	14.88	14.72	18.86	15.17	56.08	26.36
Score	-0.01	-0.31	0.50	0.22	0.33	1.00	0.20	-0.15	-0.15	1.50	0.25	1.50	0.25
Ion-type			KQ	LI	NR	F	RKQ			y_1	b_2-NH_3	y_2	b_3-NH_3
Delta ppm			1.5	-2.6	11.6	3.5	-28.2			-4.8	1.0	1.1	1.2

Fragment-ion (m/z)	344.176	394.175	445.225	474.201	507.249	553.802^{+2}	594.293	604.266	651.317	687.284	704.317	764.396
Frac. Inten.(% of TIC)	2.49	8.08	4.36	7.69	2.39	2.77	5.08	2.33	16.75	3.01	4.77	9.11
Rel. Inten.(% of BP)	14.84	48.24	26.02	45.93	14.24	16.55	30.31	13.89	100.00	17.96	28.45	54.38
Score	-0.15	1.50	-0.26	0.25	1.50	-0.17	1.50	0.25	1.50	-0.18	-0.28	1.50
Ion-type		y_3		b_4-NH_3	y_4		a_5 y_5	b_5-H_2O	y_6			y_7
Delta ppm		-0.5		2.7	-20.6		36.4 2.7	16.1	5.6			-1.8



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Result Summary

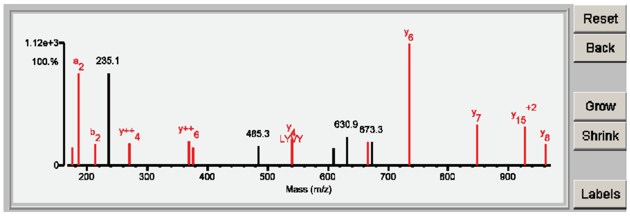
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.08	72.9	9	8/25	K329k	(K)VLYVYDMLAGkLIPVHQVR(G)	2214.2467	114.0642	9.1	62003.9/8.93	HUMAN	Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3
2	3.91	50.7	2	15/25	None	(R)QQVLPLDSIYKKTLPDWKR(S)	2328.3074	0.0035	1.5	226374.8/6.95	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.08	72.9	9	8/25	K329k	(K) V L\Y\V/Y D M L/A G k/L/I/P V/H Q V/R (G)	2214.2467	114.0642	9.1	62003.9/8.93	HUMAN	Q9Y5J1	826587	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3

Fragment-ion (m/z)	72.079	84.080	86.096	104.050	110.067	136.075	137.074	141.098	175.117	185.163	213.161	235.144	270.164
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.72 4.31 0.50 a_1 -34.3 0.50 V -19.1	0.19 1.15 0.50 KQ -4.5	0.44 2.62 0.22 LI -9.6	2.37 14.18 -0.10	0.12 0.70 1.00 H -37.9	0.54 3.21 1.00 Y -7.3	3.77 22.51 -0.16	2.46 14.69 -0.10	2.46 14.69 1.50 y_1 -12.9	12.66 75.73 0.50 a_2 -17.5	2.93 17.51 0.50 b_2 1.6	12.69 75.86 -0.53	3.12 18.66 1.50 y^{++}_4 30.5

Fragment-ion (m/z)	368.219	376.235	485.297	539.300	608.391	630.914^{+2}	666.390	673.347^{+3}	735.421	848.511	927.493^{+2}	961.596
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.33 19.88 1.50 y^{++}_6 6.4	2.54 15.18 0.75 b_3 29.6 LYV 29.6	2.67 15.98 -0.11	3.62 21.66 1.50 y_4 -9.7 LYVY 22.4	2.32 13.88 -0.10	3.99 23.88 -0.17	3.23 19.30 1.50 y^{++}_{11} -13.0	3.21 19.18 -0.13	16.72 100.00 1.50 y_6 -7.0	5.59 33.43 1.50 y_7 1.7	5.40 32.31 1.50 y_{15}^{+2} -14.0	2.92 17.45 1.50 y_8 2.2



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Result Summary

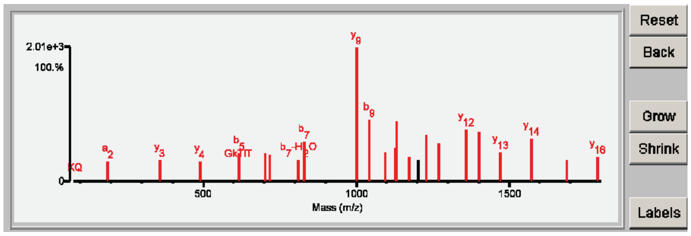
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	25.09	97.6	14	1/25	K11k	(K)TLTGkTITLEVEPSDTIENVK(A)	2288.2231	114.0612	7.6	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Detailed Results

<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>25.09</td><td>97.6</td><td>14</td><td>1/25</td><td>K11k</td><td>(K) T L/T/G k|T|I|T/L|E|V|E|P S D/T I/E/N V\K (A)</td><td>2288.2231</td><td>114.0612</td><td>7.6</td><td>8564.9/6.56</td><td>HUMAN</td><td>P62988</td><td>814891</td><td>Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1</td></tr>
</table>

Fragment-ion (m/z)	84.080	187.144	360.229	489.264	615.347	703.396	716.397	811.486	829.490	1002.505	1043.601	1044.059	1094.569^{+2}
Frac. Inten.(% of TIC)	0.13	2.24	2.42	2.30	3.17	3.08	2.94	2.36	4.41	14.96	6.88	2.26	3.29
Rel. Inten.(% of BP)	0.85	14.97	16.18	15.35	21.21	20.62	19.67	15.77	29.47	100.00	46.01	15.12	22.01
Score	0.50	0.50	1.50	1.50	0.75	1.50	0.75	0.25	0.50	1.50	0.50	1.50	1.50
Ion-type	KQ	a_2	y_3	y_4	b_5	y_6	b_6	b_7-H_2O	b_7	y_9	b_9	y^{++}_{18}	y_{19}^{+2}
Delta ppm	-14.0	-7.0	14.3	-4.8	-0.6	-2.8	2.5	21.9	13.6	-4.9	-9.6	11.6	-1.9
					GkTIT		TGkTIT						
					-0.6		2.5						

Fragment-ion (m/z)	1128.586^{+2}	1131.544	1172.655	1204.404	1230.608	1271.688	1359.666	1400.763	1472.747	1573.810	1686.872	1787.916
Frac. Inten.(% of TIC)	3.82	6.71	2.71	2.41	5.12	4.23	5.78	5.50	3.32	4.86	2.38	2.72
Rel. Inten.(% of BP)	25.53	44.88	18.15	16.13	34.25	28.29	38.65	36.80	22.17	32.48	15.91	18.16
Score	0.50	1.50	0.50	-0.16	1.50	0.50	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	b_{20}^{+2}	y_{10}	b_{10}		y_{11}	b_{11}	y_{12}	b_{12}	y_{13}	y_{14}	y_{15}	y_{16}
Delta ppm	1.7	-7.6	1.8		-10.9	-26.3	1.5	-1.0	-0.9	9.0	-4.4	-6.5



Result Summary

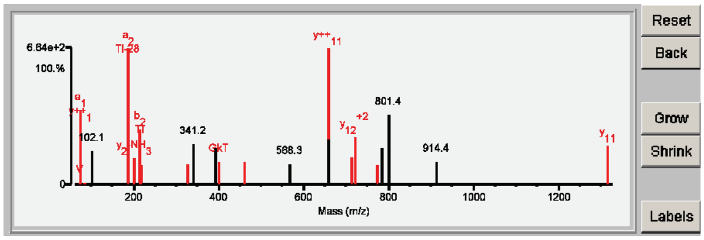
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.45	68.3	7	8/25	K11k K27k	(K)TLTGkTITLEVEPSDTIENVkAK(I)	2487.3552	228.1077	8.1	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	10.11	63.5	5	10/25	K11k K29k	(K)TLTGkTITLEVEPSDTIENVKAk(I)	2487.3552	228.1077	8.1	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
3	4.18	57.3	2	13/25	K170k K183k	(R)kQETISMLDVVKAkSETQARPK(S)	2487.3599	228.1030	6.3	139988.7/6.05	HUMAN	RP78312	REVERSE Uncharacterized protein C4orf8 OS=Homo sapiens GN=C4orf8 PE=1 SV=2
4	3.93	57.3	2	13/25	K170k K181k	(R)kQETISMLDVVkAKSETQARPK(S)	2487.3599	228.1030	6.3	139988.7/6.05	HUMAN	RP78312	REVERSE Uncharacterized protein C4orf8 OS=Homo sapiens GN=C4orf8 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.45	68.3	7	8/25	K11k K27k	(K) T L\T G k T I T L E/V/E/P S D T I E N V/k/A/K (I)	2487.3552	228.1077	8.1	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.066	72.079	74.058	84.083	86.094	102.051	187.142	201.118	215.135	218.149	326.172	341.152	392.243^{+2}
Frac. Inten.(% of TIC)	0.00	0.22	7.79	0.20	0.21	3.43	14.15	2.71	5.75	2.05	2.19	4.21	3.83
Rel. Inten.(% of BP)	0.03	1.55	54.66	1.38	1.50	24.09	99.23	18.98	40.31	14.40	15.35	29.53	26.83
Score	0.20	0.50	1.50	0.50	0.22	-0.24	0.50	0.50	0.75	1.50	0.75	-0.30	-0.27
Ion-type	PR	V	a_1 y^{++}_1	KQ	LI		a_2 TI-28	y_2-NH_3	b_2 TI	y_2	VEP		
Delta ppm	6.8	-26.0	-43.7 -28.9	22.9	-30.5		-15.5 -15.5	-28.2	-25.2 -25.2	-3.7	-0.8		

Fragment-ion (m/z)	401.208	460.286	568.251^{+2}	658.356	658.850	713.865^{+2}	722.842^{+2}	772.393^{+2}	785.428^{+2}	801.438	914.449	1315.694
Frac. Inten.(% of TIC)	2.41	2.38	2.13	14.26	4.75	2.86	4.91	2.06	3.81	7.21	2.38	4.11
Rel. Inten.(% of BP)	16.93	16.72	14.91	100.00	33.31	20.05	34.42	14.46	26.71	50.57	16.66	28.85
Score	0.75	1.50	-0.15	1.50	-0.33	0.50	1.50	1.50	-0.27	-0.51	-0.17	1.50
Ion-type	GkT	y_3		y^{++}_{11}		y_{12}-H_2O^{+2}	y_{12}^{+2}	y_{13}^{+2}				y_{11}
Delta ppm	-19.5	-3.9		15.0		3.6	-35.2	-11.5				6.9



Result Summary

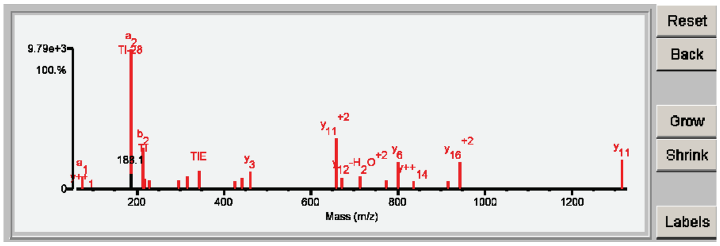
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.06	96.9	11	1/25	K27k	(K)TITLEVEPSDTIENVkAK(I)	1987.0594	114.0494	3.1	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	20.49	94.8	9	2/25	K29k	(K)TITLEVEPSDTIENVKAk(I)	1987.0594	114.0494	3.1	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
3	11.89	70.6	5	11/25	None	(K)GPVLCMKGQTLNELVENAK(S)	2101.0780	0.0307	14.6	128881.4/6.74	HUMAN	RQ7Z392	REVERSE UPF0636 protein C4orf41 OS=Homo sapiens GN=C4orf41 PE=1 SV=2
4	9.24	59.7	5	13/25	None	(R)LTTIEDELQVLEAKLEEK(E)	2101.1275	-0.0187	-8.9	22449.2/5.45	HUMAN	RQ16890	REVERSE Tumor protein D53 OS=Homo sapiens GN=TPD52L1 PE=1 SV=1
5	8.69	72.0	1	9/25	K50k	(K)AkVNEITDSPEVELTITK(G)	1987.0594	114.0494	3.1	8564.9/6.80	HUMAN	RP62988	REVERSE Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.06	96.9	11	1/25	K27k	(K) T I|T\L/E/V E/P S D T/I/E/N V/k/A/K (I)	1987.0594	114.0494	3.1	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.064	72.079	74.060	84.078	86.096	187.142	188.145	215.136	218.146	229.118	298.173	316.186	344.182
Frac. Inten.(% of TIC)	0.00	0.06	2.58	0.16	0.22	28.57	3.13	8.48	2.06	1.76	1.78	2.52	3.77
Rel. Inten.(% of BP)	0.01	0.23	9.02	0.57	0.76	100.00	10.94	29.69	7.23	6.17	6.22	8.80	13.19
Score	0.20	0.50	1.50	0.50	0.22	0.50	-0.11	0.75	1.50	0.75	0.25	0.50	0.75
Ion-type	PR	V	a_1	KQ	LI	a_2		b_2	y_2	VE	b_3-H_2O	b_3	TIE
Delta ppm	-20.3	-21.9	-20.8	-29.4	-9.6	-15.0		-18.7	-18.4	-5.2	-15.9	-5.0	-2.9
			y^{++}_1			TI-28		TI				TIE-28	
			-5.9			-15.0		-18.7				-5.0	

Fragment-ion (m/z)	425.238	443.249	460.287	658.346^{+2}	673.398	713.857^{+2}	772.390^{+2}	802.442	836.917	915.517	943.987^{+2}	1315.682
Frac. Inten.(% of TIC)	1.68	2.42	3.64	10.44	2.30	2.62	1.73	5.42	1.65	1.60	5.45	5.96
Rel. Inten.(% of BP)	5.87	8.47	12.73	36.53	8.04	9.16	6.04	18.98	5.77	5.59	19.08	20.85
Score	0.50	0.75	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	TLEV-H_2O	y_3-NH_3	y_3	y_{11}^{+2}	y_5	y_{12}-H_2O^{+2}	y_{13}^{+2}	y_6	y^{++}_{14}	y_7	y_{16}^{+2}	y_{11}
Delta ppm	-5.3	-28.6	-1.1	-1.0	-1.6	-7.5	-15.9	0.8	-7.5	-10.1	-1.8	-2.1
		TLEV										
		-5.7										



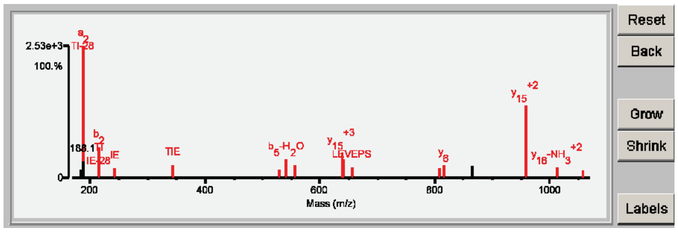
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.15	91.6	6	3/24	K27k K33k	(K)TITLEVEPSDTIENVkAKIQDk(E)	2471.3239	228.1114	9.5	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
1	17.15	91.6	6	3/24	K27k K29k	(K)TITLEVEPSDTIENVkAkIQDK(E)	2471.3239	228.1114	9.5	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	15.55	88.6	5	4/24	K29k K33k	(K)TITLEVEPSDTIENVKAkIQDk(E)	2471.3239	228.1114	9.5	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
3	7.32	68.1	2	11/24	K751k	(K)ERMAKARETELAIAkELLTLNGK(T)	2585.4443	113.9910	-19.2	133100.3/4.87	HUMAN	RQ9UL68	REVERSE Myelin transcription factor 1-like protein OS=Homo sapiens GN=MYT1L PE=2 SV=2
4	7.21	55.6	2	10/24	M485m K497k	(R)mALQRAELVGNAkKAGEVLDTINK(R)	2569.4130	130.0223	-5.7	80152.2/8.93	HUMAN	RQ8IWA5	REVERSE Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=2

Detailed Results

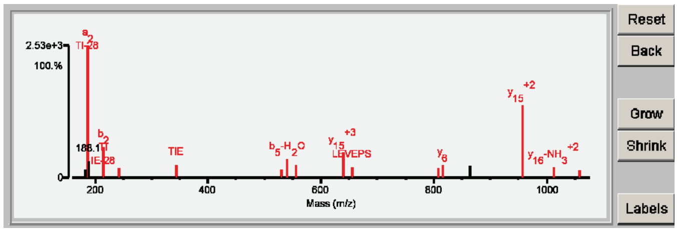
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.15	91.6	6	3/24	K27k K33k	(K) T\I\T L E V E/P S D/T I E N V/k/A K I Q D k (E)	2471.3239	228.1114	9.5	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.064	72.080	84.043	84.080	86.095	102.053	183.110	187.143	188.147	215.141	243.135	344.180	529.811^{+2}	540.307	556.333	638.668^{+3}	639.353	655.330	807.946^{+2}	816.449	864.495	957.503^{+2}	1013.515^{+2}	1058.597
Frac. Inten.(% of TIC)	0.01	0.16	0.11	0.19	0.44	0.15	2.03	30.46	3.74	7.04	2.20	2.89	1.86	4.40	2.90	5.80	4.17	2.40	2.26	3.05	2.61	16.78	2.54	1.82
Rel. Inten.(% of BP)	0.02	0.52	0.37	0.62	1.43	0.50	6.66	100.00	12.28	23.12	7.22	9.49	6.11	14.44	9.52	19.03	13.69	7.88	7.43	10.02	8.56	55.09	8.33	5.96
Score	0.20	0.50	1.00	0.50	0.22	1.00	-0.07	0.50	-0.12	0.75	0.75	0.75	1.50	0.25	0.75	1.50	0.25	0.75	1.50	1.50	-0.09	1.50	0.50	1.50
Ion-type	PR	V	b_1-H_2O	KQ	LI	b_1		a_2		b_2	IE	TIE	y_7^{+2}	b_5-H_2O	ITLEV	y_{15}^{+3}	b_6-H_2O	LEVEPS	y_{12}^{+2}	y_6		y_{15}^{+2}	y_{16}-NH_3^{+2}	y_7
Delta ppm	-8.9	-12.1	-28.4	-5.7	-11.9	-27.0		-13.9		2.2	0.3	-7.0	17.4	5.0	-3.8	-2.5	-30.2	-1.1	2.6	-10.0		3.6	7.2	1.4
						1.00		TI-28		TI														
			E			E		-13.9		2.2														
						-16.2				IE-28														
										2.2														



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.15	91.6	6	3/24	K27k K29k	(K) T\I\T L E V E/P S D/T I E N V/k/A k I Q D K (E)	2471.3239	228.1114	9.5	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.064	72.080	84.043	84.080	86.095	102.053	183.110	187.143	188.147	215.141	243.135	344.180	529.811^{+2}	540.307	556.333	638.668^{+3}	639.353	655.330	807.946^{+2}	816.449	864.495	957.503^{+2}	1013.515^{+2}	1058.597
Frac. Inten.(% of TIC)	0.01	0.16	0.11	0.19	0.44	0.15	2.03	30.46	3.74	7.04	2.20	2.89	1.86	4.40	2.90	5.80	4.17	2.40	2.26	3.05	2.61	16.78	2.54	1.82
Rel. Inten.(% of BP)	0.02	0.52	0.37	0.62	1.43	0.50	6.66	100.00	12.28	23.12	7.22	9.49	6.11	14.44	9.52	19.03	13.69	7.88	7.43	10.02	8.56	55.09	8.33	5.96
Score	0.20	0.50	1.00	0.50	0.22	1.00	-0.07	0.50	-0.12	0.75	0.75	0.75	1.50	0.25	0.75	1.50	0.25	0.75	1.50	1.50	-0.09	1.50	0.50	1.50
Ion-type	PR	V	b_1-H_2O	KQ	LI	b_1		a_2		b_2	IE	TIE	y_7^{+2}	b_5-H_2O	kAk	y_{15}^{+3}	b_6-H_2O	LEVEPS	y_{12}^{+2}	y_6		y_{15}^{+2}	y_{16}-NH_3^{+2}	y_7
Delta ppm	-8.9	-12.1	-28.4	-5.7	-11.9	-27.0		-13.9		2.2	0.3	-7.0	17.4	5.0	21.3	-2.5	-30.2	-1.1	2.6	-10.0		3.6	7.2	1.4
						1.00		TI-28		TI														
			E			E		-13.9		2.2														
						-16.2				IE-28														
										2.2														



Result Summary

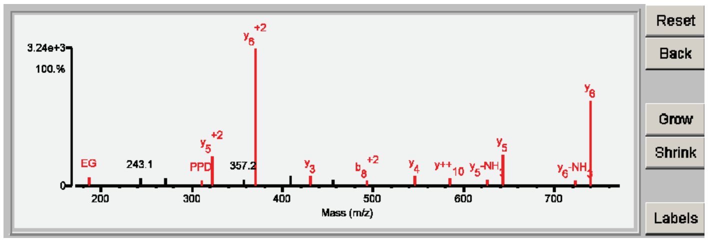
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.69	84.2	6	9/25	K29k	(K)AkIQDKEGIPPDQQR(L)	1722.9133	114.0232	-10.7	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	13.14	82.4	5	10/25	K33k	(K)AKIQDkEGIPPDQQR(L)	1722.9133	114.0232	-10.7	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
3	8.11	74.2	2	15/25	M324m K332k	(R)HHLVGAAAGmAGGHPSTk(G)	1706.8635	130.0731	4382.0	87928.2/9.72	HUMAN	RQ6ZVC0	REVERSE Uncharacterized protein C7orf51 OS=Homo sapiens GN=C7orf51 PE=1 SV=1
4	5.60	73.0	1	16/25	None	(R)GRGSDPTGVTELSNKYR(K)	1836.9199	0.0167	9.1	45501.6/9.29	HUMAN	RO43581	REVERSE Synaptotagmin-7 OS=Homo sapiens GN=SYT7 PE=1 SV=3
5	5.45	59.6	2	17/25	M98m K94k	(K)QIkFYRmRHHYK(S)	1706.9060	130.0305	-4.0	28192.8/6.49	HUMAN	Q8WVD3	E3 ubiquitin-protein ligase RNF138 OS=Homo sapiens GN=RNF138 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.69	84.2	6	9/25	K29k	(K) A k I Q D/K E G\I/P/P/D/Q Q R (L)	1722.9133	114.0232	-10.7	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.064	84.078	86.096	143.116	187.071	243.142	271.140	310.140	322.161^{+2}	357.173	357.233	369.678^{+2}
Frac. Inten.(% of TIC)	0.00	0.11	0.40	2.46	1.98	1.77	1.70	1.35	7.18	1.34	1.69	1.18
Rel. Inten.(% of BP)	0.00	0.34	1.21	7.45	5.99	5.36	5.15	4.09	21.76	4.06	5.12	3.57
Score	0.20	0.50	0.22	-0.07	0.75	-0.05	-0.05	0.75	1.50	0.75	-0.05	-0.04
Ion-type	PR	KQ	LI		EG			PPD	y_5^{+2}	IQD		
Delta ppm	-21.8	-36.6	-10.8		-8.2			-4.0	-2.6	-13.3		

Fragment-ion (m/z)	370.687^{+2}	409.233^{+2}	431.231	455.166^{+2}	492.751^{+2}	546.256	584.300	626.298	643.304	723.353	740.367	909.421	984.466
Frac. Inten.(% of TIC)	33.00	2.32	2.43	1.62	1.31	2.34	1.77	1.60	7.55	1.28	20.58	1.20	1.86
Rel. Inten.(% of BP)	100.00	7.03	7.36	4.90	3.97	7.08	5.37	4.83	22.89	3.89	62.35	3.63	5.64
Score	1.50	-0.07	1.50	-0.05	0.50	1.50	1.50	0.50	1.50	0.50	1.50	-0.04	-0.06
Ion-type	y_6^{+2}		y_3		b_8^{+2}	y_4	y^{++}_{10}	y_5-NH_3	y_5	y_6-NH_3	y_6		
Delta ppm	-1.4		-13.0		-17.3	-13.1	-15.5	13.5	-18.8	15.0	-1.9		



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Result Summary

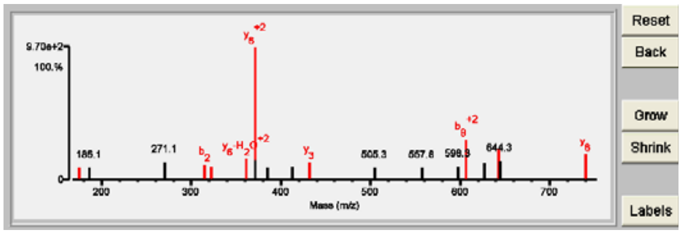
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.01	62.4	5	13/25	K29k K33k	(K)AkIQDkEGIPPDQQR(L)	1722.9133	228.0820	-2.0	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	4.82	50.8	1	15/25	K15k	(R)CDIAkPTPMQARRHR(L)	1836.9432	114.0522	4.7	163847.7/6.88	HUMAN	RO75064	REVERSE DENN domain-containing protein 4B OS=Homo sapiens GN=DENND4B PE=1 SV=4
2	4.82	50.8	1	15/25	K1482k	(R)HRRAQMPTPkAIDCR(K)	1836.9432	114.0522	4.7	163847.7/6.86	HUMAN	O75064	DENN domain-containing protein 4B OS=Homo sapiens GN=DENND4B PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.01	62.4	5	13/25	K29k K33k	(K) A k\I Q D k E G I|P/P D/Q Q/R (L)	1722.9133	228.0820	-2.0	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.066	71.080	84.082	86.096	140.007	175.116	186.090	271.142	314.189	322.169^{+2}	361.673^{+2}	370.688^{+2}
Frac. Inten.(% of TIC)	0.01	2.63	0.31	0.14	3.32	2.36	2.38	3.43	3.16	2.62	4.18	26.56
Rel. Inten.(% of BP)	0.05	9.91	1.18	0.53	12.49	8.87	8.98	12.90	11.89	9.86	15.73	100.00
Score	0.20	-0.10	0.50	0.22	-0.12	1.50	-0.09	-0.13	0.50	1.50	0.50	1.50
Ion-type	PR		KQ	LI		y_1			b_2	y_5^{+2}	$y_6\text{-}H_2O^{+2}$	y_6^{+2}
Delta ppm	8.2		12.2	-9.6		-16.9			18.8	22.9	-27.5	0.7

Fragment-ion (m/z)	371.698	385.224^{+3}	413.232	431.226	505.268	557.759	598.339	606.338^{+2}	626.305^{+3}	643.323	644.316^{+2}	740.367	768.381
Frac. Inten.(% of TIC)	3.89	2.46	2.56	3.52	2.41	2.46	2.72	8.03	3.19	6.32	3.83	5.17	2.34
Rel. Inten.(% of BP)	14.65	9.28	9.64	13.26	9.09	9.24	10.24	30.23	12.02	23.80	14.40	19.47	8.81
Score	-0.15	-0.09	-0.10	1.50	-0.09	-0.09	-0.10	0.50	-0.12	1.50	-0.14	1.50	-0.09
Ion-type				y_3				b_9^{+2}		y_5		y_6	
Delta ppm				-23.7				24.9		10.5		-2.1	



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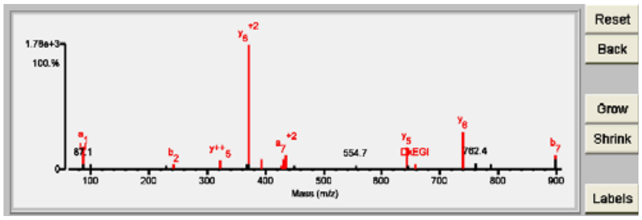
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.50	83.3	5	11/25	K33k	(K)IQDkEGIPPDQQR(L)	1523.7812	114.0441	0.7	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	4.62	59.6	2	18/25	M1770m M1775m	(R)LPGGNEVGmVAFKmR(F)	1605.8240	32.0014	7.0	276556.5/6.06	HUMAN	O00763	Acetyl-CoA carboxylase 2 OS=Homo sapiens GN=ACACB PE=1 SV=2
3	4.06	53.8	2	20/25	M186m M189m	(R)SALYLLmAEmAQHK(K)	1605.8127	32.0126	13.9	162192.4/5.86	HUMAN	RQ96P48	REVERSE Arf-GAP, Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3
4	4.05	55.1	1	18/25	K1511k	(R)ASESSLSSGQLRSSk(T)	1523.7660	114.0594	10.0	311647.5/7.93	HUMAN	RP25054	REVERSE Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2
5	3.88	58.2	2	18/25	None	(R)YYWKVNMLLHDR(K)	1637.8257	-0.0003	-0.2	172424.5/7.48	HUMAN	RQ9P2R6	REVERSE Arginine-glutamic acid dipeptide repeats protein OS=Homo sapiens GN=RERE PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.50	83.3	5	11/25	K33k	(K) I Q\D k E G|I|P/P D/Q Q R (L)	1523.7812	114.0441	0.7	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	70.066	84.080	86.096	87.063	99.048	228.110	242.146	322.160	367.824	370.690^{+2}	370.857^{+2}	393.193	427.221	431.243	435.738^{+2}	449.990	554.750^{+2}	643.327	644.708^{+2}	657.321	740.363	762.374^{+2}	786.347	898.463	898.565
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR 5.3	0.06 0.16 0.50 KQ -5.7	6.81 18.28 0.50 a_1 -4.9 0.50 LI -4.9	1.55 4.16 -0.04	1.42 3.80 -0.04	1.23 3.29 -0.03	1.48 3.97 0.50 b_2 -15.4	2.74 7.36 1.50 y++$_5$ -4.2	1.34 3.59 -0.04	37.27 100.00 1.50 y_6^{+2} 4.8	1.53 4.10 -0.04	2.87 7.71 0.50 b++$_6$ -1.1	1.10 2.95 1.50 y++$_7$ -19.8	3.03 8.13 1.50 y_3 16.0	4.16 11.15 0.50 a_7^{+2} 0.7	1.13 3.04 -0.03	1.11 2.97 -0.03	6.64 17.81 1.50 y_5 16.6	1.20 3.22 -0.03	1.42 3.82 0.75 DkEGI 0.4	11.31 30.36 1.50 y_6 -7.5	1.66 4.47 -0.04	1.50 4.01 -0.04	4.43 11.87 0.50 b_7 -0.2	3.02 8.09 -0.08



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Result Summary

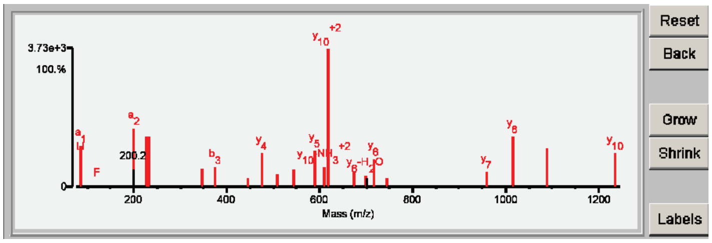
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.82	96.6	10	2/25	K48k	(R)LIFAGkQLEDGR(T)	1346.7427	114.0498	4.7	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	14.98	71.2	5	9/25	None	(R)ILFAGTANGEAQLR(R)	1460.7856	0.0069	4.7	51834.5/6.55	HUMAN	RQ13882	REVERSE Tyrosine-protein kinase 6 OS=Homo sapiens GN=PTK6 PE=1 SV=1
3	11.83	73.8	6	9/25	K70k	(R)ILMCAQkQVGAK(Q)	1346.7283	114.0642	14.6	54142.2/5.83	HUMAN	RQ6NXE6	REVERSE Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2
4	10.81	68.0	3	11/25	S83s K88k	(K)LIFDsFIKRk(V)	1266.7569	194.0357	18.1	34222.3/8.74	HUMAN	Q8NH49	Olfactory receptor 4X1 OS=Homo sapiens GN=OR4X1 PE=2 SV=1
5	10.74	63.9	5	12/25	T305t K311k	(K)ILIPVtDLAAlk(Q)	1266.8032	193.9894	-13.6	65331.6/6.24	HUMAN	A6NK59	Ankyrin repeat and SOCS box-containing protein 14 OS=Homo sapiens GN=ASB14 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.82	96.6	10	2/25	K48k	(R) L/I|F|A|G/k|Q/L/E/D/G R (T)	1346.7427	114.0498	4.7	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	84.082	86.096	120.080	199.181	200.187	227.176	232.140	347.173	374.240	445.286	476.207	508.771^{+2}	544.278^{+2}
Frac. Inten.(% of TIC)	0.08	5.66	0.09	7.99	2.28	6.93	6.86	2.43	2.60	1.16	4.58	1.63	2.33
Rel. Inten.(% of BP)	0.42	29.87	0.49	42.11	12.02	36.52	36.17	12.83	13.71	6.13	24.13	8.59	12.29
Score	0.50	0.50	1.00	0.50	-0.12	0.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	KQ	a_1	F	a_2		b_2	y_2	y_3	b_3	b_4	y_4	y_8^{+2}	y_9^{+2}
Delta ppm	18.1	-20.0	-8.1	-5.0		-3.5	-3.9	16.8	-12.3	8.0	-7.2	22.0	-0.1
		0.50											
		LI											
		-7.3											

Fragment-ion (m/z)	589.285	609.300^{+2}	617.807^{+2}	674.368^{+2}	699.320	702.414^{+2}	717.344	744.444	959.463	1016.516	1087.555	1234.605
Frac. Inten.(% of TIC)	4.90	2.65	18.96	2.21	1.55	1.15	3.88	1.17	2.08	6.83	5.32	4.69
Rel. Inten.(% of BP)	25.81	13.98	100.00	11.63	8.18	6.08	20.44	6.15	10.98	36.00	28.07	24.73
Score	1.50	0.50	1.50	1.50	0.50	-0.06	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	y_5	$y_{10}\text{-}NH_3^{+2}$	y_{10}^{+2}	y_{11}^{+2}	$y_6\text{-}H_2O$		y_6	b_6	y_7	y_8	y_9	y_{10}
Delta ppm	-14.8	1.5	-8.4	20.6	-30.9		-11.4	3.6	-29.1	3.8	5.4	-10.4



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Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	28.38	97.9	14	1/25	K63k	(R)TLSDYNIQkESTLHLVLR(L)	2130.1553	114.0609	8.0	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	8.39	69.0	2	13/25	None	(K)LTEYYHGPLDRILKRLTR(M)	2244.2611	-0.0449	-20.0	162192.8/9.31	HUMAN	RQ9P227	REVERSE Rho GTPase-activating protein 23 OS=Homo sapiens GN=ARHGAP23 PE=1 SV=2
3	8.19	64.0	3	14/25	M188m	(K)TIVmQKEAPLYQFPFLFR(W)	2228.1936	16.0226	12.3	209292.0/5.93	HUMAN	RQ2WGJ9	REVERSE Fer-1-like protein 6 OS=Homo sapiens GN=FER1L6 PE=2 SV=1
4	8.19	64.0	3	14/25	M270m K267k	(R)TLIYYLDEIPPkFSmKR(L)	2114.1355	130.0808	19.1	35709.6/9.14	HUMAN	P09758	Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3
4	8.19	64.0	3	14/25	M270m K271k	(R)TLIYYLDEIPPKFSmkR(L)	2114.1355	130.0808	19.1	35709.6/9.14	HUMAN	P09758	Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3

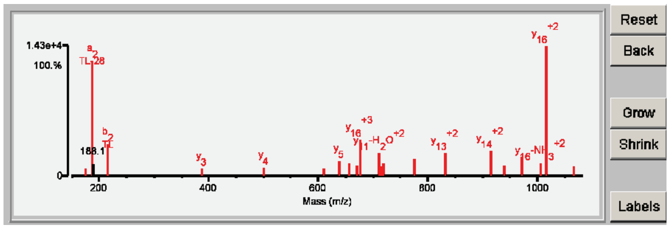
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	28.38	97.9	14	1/25	K63k	(R) T/L|S/D/Y/N/I/Q/k/E/S T L/H/L/V L/R (L)	2130.1553	114.0609	8.0	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	86.096	101.071	136.074	175.117	187.143	188.145	215.138	387.274	500.352
Frac. Inten.(% of TIC)	0.10	0.06	0.08	1.32	20.75	2.11	5.66	1.38	1.45
Rel. Inten.(% of BP)	0.41	0.24	0.35	5.64	88.46	8.98	24.13	5.88	6.17
Score	0.22	0.50	1.00	1.50	0.50	-0.09	0.75	1.50	1.50
Ion-type	LI	QK	Y	y_1	a_2 TL-28		b_2 TL	y_3	y_4
Delta ppm	-4.9	-0.4	-10.2	-12.9	-13.4 -13.4		-8.4 -8.4	6.1	-6.8

Fragment-ion (m/z)	610.014^{+3}	637.411	655.383^{+2}	671.366^{+3}	677.362^{+3}	710.407^{+2}	715.056^{+3}	719.410
Frac. Inten.(% of TIC)	1.26	2.66	2.25	1.91	6.50	4.04	1.77	2.32
Rel. Inten.(% of BP)	5.38	11.32	9.59	8.15	27.74	17.23	7.56	9.90
Score	1.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y_{14}^{+3}	y_5	y_{10}^{+2}	$y_{16}\text{-}H_2O^{+3}$	y_{16}^{+3}	$y_{11}\text{-}H_2O^{+2}$	y_{17}^{+3}	$y{+}{+}_{11}$
Delta ppm	10.6	-5.2	0.4	14.3	2.6	-0.7	0.9	-2.4

Fragment-ion (m/z)	775.967^{+2}	832.978^{+2}	914.507^{+2}	938.577	972.016^{+2}	1007.042^{+2}	1015.539^{+2}	1067.623
Frac. Inten.(% of TIC)	3.03	4.05	4.57	1.88	3.45	2.35	23.45	1.61
Rel. Inten.(% of BP)	12.92	17.27	19.47	8.02	14.70	10.02	100.00	6.89
Score	1.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	y_{12}^{+2}	y_{13}^{+2}	y_{14}^{+2}	y_8	y_{15}^{+2}	$y_{16}\text{-}NH_3^{+2}$	y_{16}^{+2}	y_9
Delta ppm	15.7	2.7	-0.0	-1.3	-5.4	18.1	1.7	1.8



Result Summary

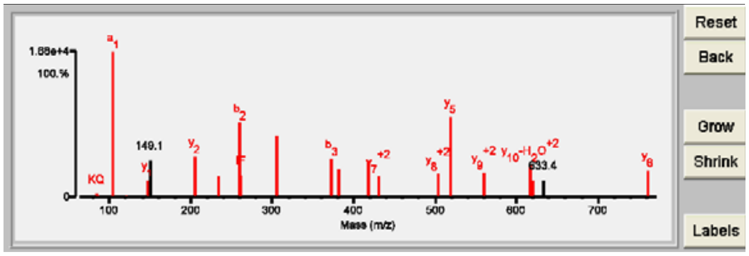
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.80	93.0	9	2/24	K6k	(-)MQIFVkTLTGK(T)	1265.7286	114.0424	-0.4	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	12.43	62.4	5	7/24	K11k	(-)MQIFVKTLTGk(T)	1265.7286	114.0424	-0.4	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.80	93.0	9	2/24	K6k	(-) M Q|I|F/V|k/T/L/T/G/K (T)	1265.7286	114.0424	-0.4	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	72.081	84.082	86.097	104.053	120.080	129.102	147.113	149.074	204.135	233.166	260.106	261.153
Frac. Inten.(% of TIC)	0.12	0.39	0.22	18.89	0.18	0.13	2.22	4.83	5.25	2.71	9.67	2.81
Rel. Inten.(% of BP)	0.63	2.09	1.15	100.00	0.96	0.68	11.73	25.59	27.80	14.34	51.21	14.89
Score	0.50	0.50	0.22	0.50	1.00	0.20	1.50	-0.26	1.50	0.50	0.50	0.75
Ion-type	V	KQ	LI	a$_1$	F	RKQ	y$_1$		y$_2$	IF-28	b$_2$	IF
Delta ppm	8.7	8.6	7.8	-8.1	-3.1	-2.6	-0.7		3.6	-1.0	-4.0	-30.4

Fragment-ion (m/z)	305.182	373.191	381.229^{+2}	418.265	430.761^{+2}	504.301^{+2}	519.313	560.837^{+2}	615.866^{+2}	619.322	633.365^{+2}	761.450
Frac. Inten.(% of TIC)	8.04	4.97	3.69	4.71	2.66	2.91	10.44	3.22	4.12	2.12	2.14	3.54
Rel. Inten.(% of BP)	42.57	26.33	19.55	24.94	14.08	15.41	55.26	17.03	21.81	11.23	11.35	18.73
Score	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	0.50	0.50	-0.11	1.50
Ion-type	y$_3$	b$_3$	y$_6^{+2}$	y$_4$	y$_7^{+2}$	y$_8^{+2}$	y$_5$	y$_9^{+2}$	y$_{10}$-H$_2$O^{+2}	b$_5$		y$_6$
Delta ppm	0.5	-1.1	-2.2	-1.7	-5.4	5.7	-1.1	-5.5	4.1	-9.9		-1.8



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Result Summary

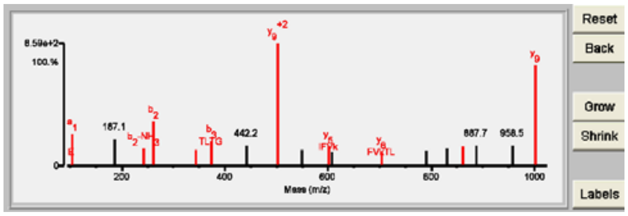
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	9.89	68.3	6	11/25	K6k K11k	(-)MQIFVkTLTGkTITLEVEPSDTIENVK(A)	3034.6381	228.1097	7.3	8564.9/6.56	HUMAN	P62988	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
2	3.06	51.5	0	16/25	K99k	(R)AFSLEKPRGGTGKAEFLQLGRETLVCRk(R)	3148.7048	114.0430	0.0	13891.2/9.72	HUMAN	RQ9Y5J5	REVERSE Pleckstrin homology-like domain family A member 3 OS=Homo sapiens GN=PHLDA3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.89	68.3	6	11/25	K6k K11k	(-) M Q\I\F V k\T L T G k T I T L E V E/P S D/T/I E N V K (A)	3034.6381	228.1097	7.3	8564.9/6.56	HUMAN	P62988	814891	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1

Fragment-ion (m/z)	60.045	72.079	84.081	86.097	102.053	104.052	187.145	243.078	260.106	344.194	373.197	442.156
Frac. Inten.(% of TIC)	2.48	0.27	0.11	0.20	0.19	5.28	4.35	2.92	7.25	2.71	4.03	3.37
Rel. Inten.(% of BP)	12.34	1.32	0.56	1.00	0.96	26.26	21.65	14.51	36.04	13.49	20.06	16.78
Score	-0.12	0.50	0.50	0.22	1.00	0.50	-0.22	0.25	0.50	0.75	0.75	-0.17
Ion-type		V	KQ	LI	E	a_1		b_2-NH_3	b_2	TIE	b_3 TLTG	
Delta ppm		-27.4	-2.1	6.7	-22.1	-14.8		-10.2	-4.8	31.9	14.5 -33.1	

Fragment-ion (m/z)	501.763^{+2}	548.981^{+4}	602.347	608.288	703.405	790.890	831.444	861.484	887.722^{+3}	958.501	1002.507	1071.462	1131.602
Frac. Inten.(% of TIC)	20.11	2.66	3.15	2.26	2.32	2.51	2.87	3.10	3.33	3.29	16.62	2.29	2.29
Rel. Inten.(% of BP)	100.00	13.25	15.67	11.26	11.54	12.50	14.27	15.40	16.54	16.38	82.67	11.41	11.40
Score	1.50	-0.13	1.50	-0.11	1.50	-0.13	-0.14	0.50	-0.17	-0.16	1.50	-0.11	-0.11
Ion-type	y_9^{+2}		y_5 IFVk		y_6 FVkTL			b_6			y_9		
Delta ppm	8.5		-6.0 -33.1		8.8 -14.4			20.8			-2.8		



Result Summary

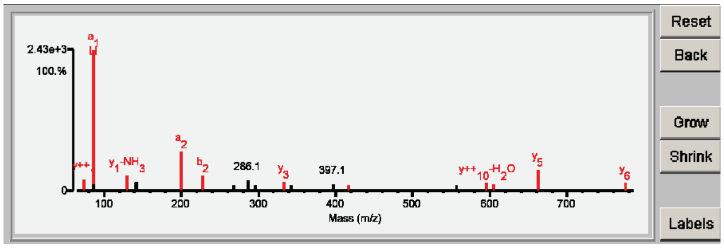
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.92	79.0	5	11/25	K421k	(K)LIEDSTLSkSVK(N)	1319.7417	114.0501	5.0	294366.9/5.79	HUMAN	Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3
2	8.17	69.2	3	14/25	K424k	(K)LIEDSTLSKSVk(N)	1319.7417	114.0501	5.0	294366.9/5.79	HUMAN	Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3
3	8.09	72.1	3	14/25	None	(K)LSENSKILISMAK(E)	1433.8032	-0.0115	-8.0	141751.4/6.26	HUMAN	Q1MSJ5	Centrosome and spindle pole-associated protein 1 OS=Homo sapiens GN=CSPP1 PE=1 SV=2
4	7.93	69.6	2	13/25	K118k	(R)LLCIEkVTTDK(D)	1319.7239	114.0678	17.4	63445.4/7.02	HUMAN	Q96JP5	Zinc finger protein 91 homolog OS=Homo sapiens GN=ZFP91 PE=1 SV=1
5	7.39	68.9	4	14/25	None	(R)LIDSLVTACKVSK(V)	1433.8032	-0.0115	-8.0	133471.2/7.04	HUMAN	RQ9HCJ5	REVERSE Zinc finger SWIM domain-containing protein 6 OS=Homo sapiens GN=ZSWIM6 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.92	79.0	5	11/25	K421k	(K) L I|E D S T/L/S k/S V/K (N)	1319.7417	114.0501	5.0	294366.9/5.79	HUMAN	Q9UPU5	815197	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3

Fragment-ion (m/z)	74.061	84.041	84.081	86.095	87.052	87.097	129.103	130.087	141.096	143.082	199.180	227.065
Frac. Inten.(% of TIC)	3.14	0.07	0.27	39.48	1.98	1.67	0.16	4.05	2.04	2.43	10.95	1.86
Rel. Inten.(% of BP)	7.96	0.19	0.68	100.00	5.02	4.23	0.39	10.27	5.16	6.16	27.72	4.71
Score	1.50	1.00	0.50	0.50	-0.05	-0.04	0.20	0.50	-0.05	-0.06	0.50	-0.05
Ion-type	y++$_1$	E	KQ	a$_1$			RKQ	y$_1$-NH$_3$			a$_2$	
Delta ppm	11.6	-36.8	-2.1	-24.7			4.3	1.9			-6.5	
				0.50								
				LI								
				-11.9								

Fragment-ion (m/z)	227.172	268.089	286.102	296.089	333.217	342.209	397.137	417.209	557.259	595.309	604.298	662.385	775.465
Frac. Inten.(% of TIC)	4.25	1.56	3.03	1.42	2.60	1.47	1.89	1.57	1.64	2.26	1.95	5.92	2.33
Rel. Inten.(% of BP)	10.76	3.96	7.67	3.60	6.58	3.71	4.79	3.98	4.16	5.73	4.93	15.00	5.90
Score	0.50	-0.04	-0.08	-0.04	1.50	-0.04	-0.05	0.75	-0.04	0.50	1.50	1.50	1.50
Ion-type	b$_2$				y$_3$			SkS		y++$_{10}$-H$_2$O	y++$_{10}$	y$_5$	y$_6$
Delta ppm	-21.6				11.3			-4.4		4.7	-22.3	3.1	-2.4



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Result Summary

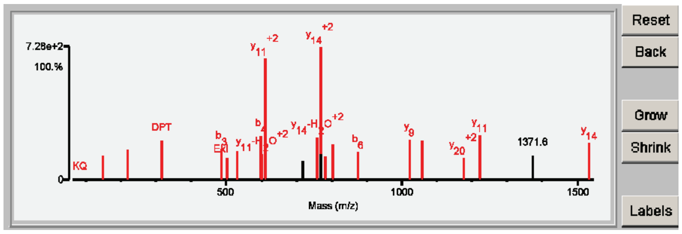
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.66	92.2	11	3/25	K360k	(K)LEkIFQNAPTDPTQDFSTQVAK(L)	2478.2511	114.0573	5.5	95786.8/4.91	HUMAN	P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2
2	5.54	52.9	3	14/25	M1499m K1490k	(K)kNRALPFVPmSYQLSQTYYR(I)	2462.2649	130.0434	2.2	238876.1/7.01	HUMAN	Q12789	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4
3	5.32	57.1	2	13/25	K5296k	(R)LYWFkDGQPLTASAHIRMTDK(K)	2478.2598	114.0485	2.2	868488.4/5.69	HUMAN	Q5VST9	Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3
4	4.38	51.4	2	15/25	K16k	(-)MWPQPRFPPHPAMSEkTQQGK(L)	2478.2169	114.0914	18.7	58854.6/4.80	HUMAN	A6NEF3	Putative golgin subfamily A member 6-like protein 4 OS=Homo sapiens PE=5 SV=2
5	3.36	51.1	1	15/25	K21k	(-)MWPQPRFPPHPAMSEKTQQGk(L)	2478.2169	114.0914	18.7	58854.6/4.80	HUMAN	A6NEF3	Putative golgin subfamily A member 6-like protein 4 OS=Homo sapiens PE=5 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.66	92.2	11	3/25	K360k	(K) L E/k\I\F Q\N/A|P T D/P T/Q D/F S T Q V/A/K (L)	2478.2511	114.0573	5.5	95786.8/4.91	HUMAN	P45974	407680	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2

Fragment-ion (m/z)	70.063	84.082	86.094	147.108	218.147	314.136	485.265	503.267	529.790^{+2}	598.365	602.314^{+2}	611.301^{+2}
Frac. Inten.(% of TIC)	0.00	0.12	0.09	2.81	3.39	4.50	3.58	2.46	3.29	4.96	2.95	13.65
Rel. Inten.(% of BP)	0.02	0.77	0.57	18.71	22.54	29.92	23.81	16.38	21.90	33.00	19.63	90.85
Score	0.20	0.50	0.22	1.50	1.50	0.75	0.75	0.75	0.50	0.50	0.50	1.50
Ion-type	PR	KQ	LI	y_1	y_2	DPT	b_3 EkI	IFQN	b_8^{+2}	b_4	$y_{11}\text{-}H_2O^{+2}$	y_{11}^{+2}
Delta ppm	-24.6	8.6	-34.0	-31.3	-12.5	0.1	-16.7 -16.7	8.4	7.8	13.6	17.5	-13.8

Fragment-ion (m/z)	716.354	758.874^{+2}	767.871^{+2}	768.893^{+3}	780.420	803.414^{+2}	873.464	1023.501	1058.559	1175.578^{+2}	1221.597	1371.618	1534.755
Frac. Inten.(% of TIC)	2.16	4.87	15.02	2.87	2.62	4.05	3.09	4.58	4.49	2.50	5.10	2.74	4.13
Rel. Inten.(% of BP)	14.35	32.40	100.00	19.09	17.46	26.94	20.56	30.49	29.87	16.63	33.97	18.27	27.52
Score	-0.14	0.50	1.50	-0.19	1.50	1.50	0.50	1.50	0.50	1.50	1.50	-0.18	1.50
Ion-type		$y_{14}\text{-}H_2O^{+2}$	y_{14}^{+2}		y_7	y_{15}^{+2}	b_6	y_9	b_8	y_{20}^{+2}	y_{11}		y_{14}
Delta ppm		7.9	-2.4		-7.0	27.9	-22.5	-9.8	-4.7	-7.8	-11.5		10.5



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Result Summary

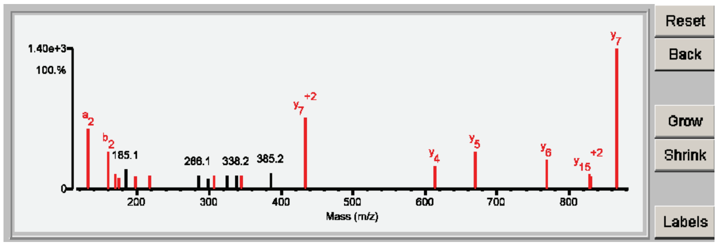
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.07	81.0	7	7/25	K793k	(R)SAADSISESVPVGPkVR(D)	1698.9021	114.0555	6.9	95786.8/4.91	HUMAN	P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2
2	3.43	52.1	1	18/25	K2292k K2297k	(K)kSGSAkCYEKSLVK(N)	1584.8414	228.1161	16.7	248073.6/8.45	HUMAN	RQ5D862	REVERSE Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1
3	3.42	56.9	1	15/25	K19k	(K)LPSARLQQLSIEESk(E)	1698.9385	114.0191	-13.2	60459.2/8.63	HUMAN	RA6NK97	REVERSE Solute carrier family 22 member 20 OS=Homo sapiens GN=SLC22A20 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.07	81.0	7	7/25	K793k	(R) S A|A D\S I S E S V/P/V/G/P k V/R (D)	1698.9021	114.0555	6.9	95786.8/4.91	HUMAN	P45974	815359	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2

Fragment-ion (m/z)	70.065	72.079	84.078	86.096	131.079	159.076	169.130	175.112	185.091	197.124	217.084	286.099
Frac. Inten.(% of TIC)	0.01	0.20	4.93	0.11	9.59	5.92	2.45	1.79	3.07	2.00	2.15	2.27
Rel. Inten.(% of BP)	0.02	0.91	22.07	0.51	42.94	26.50	10.96	8.00	13.72	8.96	9.61	10.17
Score	0.20	0.50	-0.22	0.22	0.50	0.50	0.50	1.50	-0.14	0.75	0.75	-0.10
Ion-type	PR	V		LI	a_2	b_2	PV-28	y_1		PV	ES	
Delta ppm	3.9	-21.9		-1.5	-29.0	-11.4	-28.0	-38.0		-29.7	3.7	

Fragment-ion (m/z)	298.172	307.185^{+2}	324.149	338.171	345.141	385.176^{+2}	433.759^{+2}	613.384	670.411	769.473	827.932^{+2}	830.370	866.525
Frac. Inten.(% of TIC)	1.65	2.12	2.20	2.26	2.23	2.65	11.38	3.69	5.94	4.69	2.46	1.92	22.33
Rel. Inten.(% of BP)	7.38	9.50	9.84	10.13	9.99	11.85	50.97	16.52	26.62	20.99	11.02	8.58	100.00
Score	-0.07	1.50	-0.10	-0.10	0.75	-0.12	1.50	1.50	1.50	1.50	1.50	0.25	1.50
Ion-type		y_4^{+2}			b_4 AADS		y_7^{+2}	y_4	y_5	y_6	y_{15}^{+2}	b_9-H_2O	y_7
Delta ppm		-23.6			-2.2 -2.2		-10.8	10.4	17.8	6.4	-11.6	19.0	5.1



Result Summary

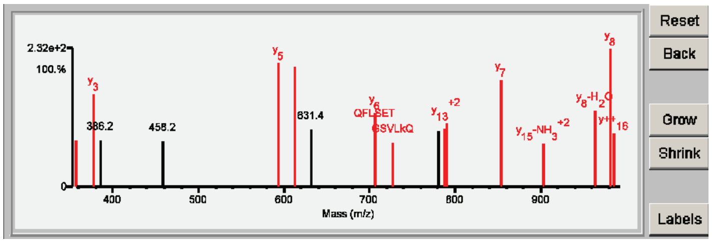
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.68	66.6	8	9/25	K115k	(K)LGFEDGSVLkQFLSETEK(M)	2027.0332	114.0647	10.2	24824.5/5.33	HUMAN	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.68	66.6	8	9/25	K115k	(K) L G/F E D/G S V L/k/Q/F/L/S E/T E K (M)	2027.0332	114.0647	10.2	24824.5/5.33	HUMAN	P09936	815711	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2

Fragment-ion (m/z)	84.083	86.097	120.081	153.060	171.104	177.102	353.139	356.238	377.193	386.193	458.230	593.281
Frac. Inten.(% of TIC)	0.26	4.08	0.31	3.83	4.03	3.28	3.21	2.77	5.52	2.78	2.72	7.38
Rel. Inten.(% of BP)	3.13	49.63	3.77	46.65	49.03	39.91	39.05	33.74	67.21	33.87	33.13	89.76
Score	0.50	0.50 0.50	1.00	-0.47	-0.49	-0.40	-0.39	0.75	1.50	-0.34	-0.33	1.50
Ion-type	**KQ**	a_1 **LI**	**F**					**Lk**	y_3			y_5
Delta ppm	22.9	-2.6 10.2	1.0					21.0	-26.2			5.7

Fragment-ion (m/z)	612.324^{+2}	631.398	706.344	727.407	781.370^{+2}	787.363	790.404^{+2}	853.427	903.942^{+2}	963.454	981.486	986.001	1015.007^{+2}
Frac. Inten.(% of TIC)	7.13	3.44	4.38	2.67	3.37	3.50	3.75	6.36	2.55	4.53	8.22	3.19	6.74
Rel. Inten.(% of BP)	86.70	41.90	53.30	32.44	40.95	42.55	45.62	77.41	30.97	55.16	100.00	38.79	82.03
Score	1.50	-0.42	1.50	0.75	-0.41	0.25	1.50	1.50	0.50	0.50	1.50	1.50	-0.82
Ion-type	y_9^{+2}		y_6 **QFLSET**	**GSVLkQ**		$b_8\text{-}H_2O$	y_{13}^{+2}	y_7	$y_{15}\text{-}NH_3^{+2}$	$y_8\text{-}H_2O$	y_8	y^{++}_{16}	
Delta ppm	11.8		-24.7 3.6	-5.5		0.1	-20.8	-3.6	0.2	-24.9	-3.1	12.3	



Result Summary

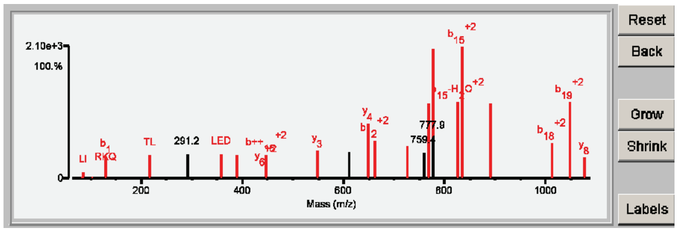
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.84	88.5	13	4/25	K210k	(R)KPFPINHGETSDETLLEDAIEVCkK(F)	2870.4241	114.0553	4.2	26182.7/4.84	HUMAN	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1
1	15.84	88.5	13	4/25	K211k	(R)KPFPINHGETSDETLLEDAIEVCKk(F)	2870.4241	114.0553	4.2	26182.7/4.84	HUMAN	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.84	88.5	13	4/25	K210k	(R) K\P F P I N H G E T S D\E\T\L\L\E/D\A|I/E/V/C/k K (F)	2870.4241	114.0553	4.2	26182.7/4.84	HUMAN	P15374	815725	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1

Fragment-ion (m/z)	72.081	84.080	86.095	102.053	129.101	215.137	291.194	358.157	389.244	445.744^{+2}	549.274	611.365	648.344
Frac. Inten.(% of TIC)	0.07	0.15	0.59	0.13	2.20	2.31	2.38	2.35	2.23	2.33	2.70	2.63	5.38
Rel. Inten.(% of BP)	0.55	1.16	4.56	0.98	16.86	17.67	18.23	18.01	17.12	17.83	20.65	20.17	41.24
Score	0.50	0.50	0.22	1.00	0.50 0.50	0.75	-0.18	0.75	1.50	1.50	1.50	-0.20	1.50
Ion-type	V	KQ	LI	E	b_1 RKQ	TL		LED	y_2	$b{+}{+}_{16}^{+2}$ y_6^{+2}	y_3		y_4
Delta ppm	-1.0	-8.0	-14.2	-16.2	-21.2 -12.7	-13.6		-14.2	-18.0	35.6 5.7	-13.9		-9.0

Fragment-ion (m/z)	662.320^{+2}	726.836^{+2}	759.366^{+2}	768.354^{+2}	777.380	777.863	824.910^{+2}	833.904^{+2}	890.461^{+2}	1012.484^{+2}	1048.006^{+2}	1076.518
Frac. Inten.(% of TIC)	3.69	3.14	2.51	7.39	12.74	3.93	7.49	13.05	7.43	3.56	7.49	2.12
Rel. Inten.(% of BP)	28.30	24.06	19.25	56.61	97.59	30.15	57.36	100.00	56.95	27.30	57.42	16.24
Score	0.50	0.50	-0.19	0.25	1.50	-0.30	0.25	0.50	0.50	0.50	0.50	1.50
Ion-type	b_{12}^{+2}	b_{13}^{+2}		$b_{14}\text{-}H_2O^{+2}$	$b{+}{+}_{14}$ y_5		$b_{15}\text{-}H_2O^{+2}$	b_{15}^{+2}	b_{16}^{+2}	b_{18}^{+2}	b_{19}^{+2}	y_8
Delta ppm	-1.3	-7.5		-8.3	18.2 -16.0		9.7	-4.1	12.2	-0.6	2.6	-21.0



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Result Summary

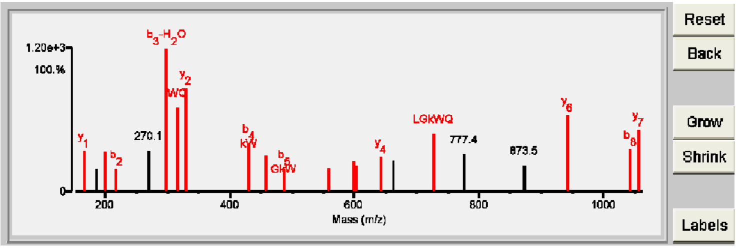
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.90	85.1	8	5/25	K529k	(K)DTVLGkWQYF(-)	1256.6310	114.0525	7.0	57295.2/9.46	HUMAN	O14562	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.90	85.1	8	5/25	K529k	(K) D T\V/L|G\k/W/Q|Y|F (-)	1256.6310	114.0525	7.0	57295.2/9.46	HUMAN	O14562	812689	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=1 SV=1

Fragment-ion (m/z)	72.080	120.080	136.074	166.082	185.165	199.075	217.082	270.146	298.140	315.147	329.149	429.234
Frac. Inten.(% of TIC)	0.12	0.09	0.30	3.87	2.17	3.71	2.19	3.84	13.53	7.87	9.76	4.61
Rel. Inten.(% of BP)	0.87	0.69	2.25	28.58	16.03	27.42	16.19	28.36	100.00	58.19	72.17	34.10
Score	0.50	1.00	1.00	1.50	-0.16	0.25	0.50	-0.28	0.25	0.75	1.50	0.75
Ion-type	V	F	Y	y_1		b_2-H_2O	b_2		b_3-H_2O	WQ	y_2	b_4 kW
Delta ppm	-10.8	-3.1	-15.4	-23.8		18.4	0.5		0.5	6.5	-3.3	-1.8 21.2

Fragment-ion (m/z)	457.207	486.255	557.288	599.340	603.295^{+2}	643.290	661.326	727.388	777.366	873.477	942.446	1042.508	1055.531
Frac. Inten.(% of TIC)	3.38	2.17	2.27	2.83	2.52	3.35	2.94	5.48	3.55	2.45	7.17	4.01	5.81
Rel. Inten.(% of BP)	24.99	16.05	16.76	20.95	18.63	24.76	21.69	40.49	26.25	18.11	53.02	29.65	42.93
Score	1.50	0.75	0.75	0.75	0.50	1.50	-0.22	0.75	-0.26	-0.18	1.50	0.50	1.50
Ion-type	y_3	b_5 GkW	kWQ	LGkW	b_9^{+2}	y_4		LGkWQ			y_6	b_8	y_7
Delta ppm	-1.4	-1.5 18.8	8.2	16.0	-9.5	4.7		-0.9			-0.7	-22.3	-0.2



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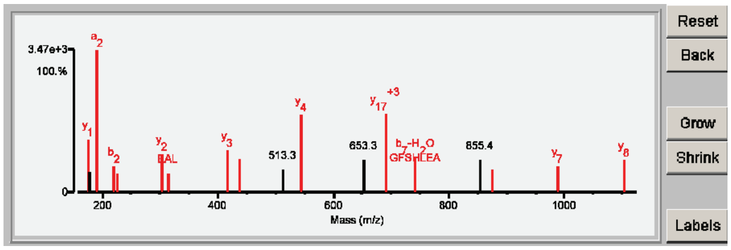
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.93	83.2	8	5/25	K109k	(R)AFGFSHLEALLDDSkELQR(F)	2176.1033	114.0681	11.0	31284.2/4.85	HUMAN	Q96FW1	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.93	83.2	8	5/25	K109k	(R) A F|G F S H L E A L L/D/D/S k/E/L/Q/R (F)	2176.1033	114.0681	11.0	31284.2/4.85	HUMAN	Q96FW1	474231	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2

Fragment-ion (m/z)	70.066	84.080	86.096	110.072	120.081	121.083	129.102	175.119	177.102	191.117	219.113	225.101	303.180	314.171	416.263	437.740^{+2}	513.258	545.310	653.343^{+3}	691.361^{+3}	742.348	855.438	874.480	989.517	1104.532
Frac. Inten.(% of TIC)	0.00	0.30	0.64	0.17	1.35	3.20	0.07	6.56	2.56	17.83	3.32	2.41	4.74	2.41	5.20	4.25	2.86	9.65	4.05	9.78	4.40	4.10	2.85	3.30	3.99
Rel. Inten.(% of BP)	0.01	1.71	3.58	0.93	7.58	17.94	0.40	36.76	14.33	100.00	18.64	13.52	26.59	13.52	29.17	23.85	16.02	54.13	22.72	54.82	24.68	22.97	15.97	18.51	22.40
Score	0.20	0.50	0.22	1.00	1.00	-0.18	0.20	1.50	-0.14	0.50	0.50	0.75	1.50	0.75	1.50	1.50	-0.16	1.50	-0.23	1.50	0.75	-0.23	1.50	1.50	1.50
Ion-type	PR	KQ	LI	H	F		RKQ	y_1		a_2	b_2	SH	y_2	EAL	y_3	y_6^{+2}		y_4		y_{17}^{+3}	b_7-H_2O GFSHLEA		y_6	y_7	y_8
Delta ppm	5.3	-8.0	-0.3	5.7	-2.3		-3.4	-0.9		-8.8	-3.2	7.0	8.8	-3.3	3.4	-0.9		10.3		13.7	-26.6 -6.0		6.9	15.7	3.5



Result Summary

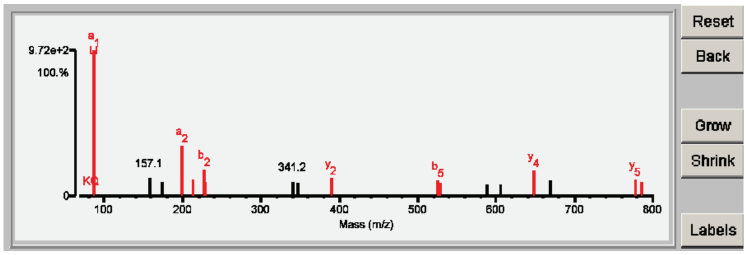
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.77	76.9	6	8/24	K178k	(K)LLALNPDAVELFkK(A)	1570.9203	114.0566	8.1	45338.7/4.82	HUMAN	Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1
1	11.77	76.9	6	8/24	K179k	(K)LLALNPDAVELFKk(A)	1570.9203	114.0566	8.1	45338.7/4.82	HUMAN	Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.77	76.9	6	8/24	K178k	(K) L/L\A L N\P D A V/E/L F/k K (A)	1570.9203	114.0566	8.1	45338.7/4.82	HUMAN	Q9BSL1	812199	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1

Fragment-ion (m/z)	70.063	72.080	84.081	86.096	87.055	157.133	173.131	199.177	213.089	227.176	228.129	229.111
Frac. Inten.(% of TIC)	0.00	0.19	0.25	30.23	0.07	3.66	2.99	10.56	3.37	5.43	2.86	2.74
Rel. Inten.(% of BP)	0.01	0.62	0.81	100.00	0.24	12.11	9.91	34.94	11.16	17.95	9.45	9.05
Score	0.20	0.50	0.50	0.50 0.50	0.33	-0.12	-0.10	0.50	0.75	0.50	0.75	0.75
Ion-type	PR	V	KQ	a_1 LI	NR			a_2	PD	b_2	LN	VE
Delta ppm	-31.8	-6.6	6.2	-17.7 -4.9	-1.0			-21.0	6.2	-1.3	-27.0	-38.3

Fragment-ion (m/z)	341.215	346.681^{+2}	389.257	525.332	528.267	588.327	606.638	649.415	668.847	778.429	786.467^{+2}	838.509^{+2}
Frac. Inten.(% of TIC)	3.02	2.66	3.68	3.26	2.68	2.49	2.50	5.33	3.16	3.38	2.86	2.63
Rel. Inten.(% of BP)	9.99	8.79	12.19	10.77	8.88	8.24	8.26	17.64	10.46	11.19	9.47	8.69
Score	-0.10	-0.09	1.50	0.50	0.75	-0.08	-0.08	1.50	-0.10	1.50	1.50	-0.09
Ion-type			y_2	b_5	DAVEL			y_4		y_5	y_{13}^{+2}	
Delta ppm			16.7	-17.1	-1.1			17.6		-21.8	30.1	



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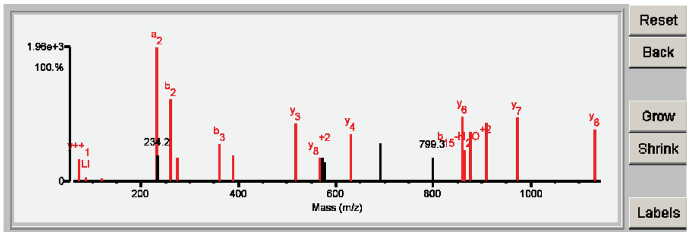
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.21	85.8	8	5/25	K119k	(K)FLTPCYHPNVDTQGNICLDILkEK(W)	2875.4117	114.0597	5.6	19652.4/6.83	HUMAN	O00762	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1
2	18.54	83.4	8	6/25	K121k	(K)FLTPCYHPNVDTQGNICLDILKEk(W)	2875.4117	114.0597	5.6	19652.4/6.83	HUMAN	O00762	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1
3	8.53	51.2	5	13/25	M803m	(R)SCNLRAKmFTTWTDELLFRGGIDNK(C)	2973.4710	16.0004	1.8	120616.1/7.07	HUMAN	RQ13591	REVERSE Semaphorin-5A OS=Homo sapiens GN=SEMA5A PE=1 SV=3
4	7.27	58.3	2	11/25	K321k K324k	(K)GTRFALKELFDEANEWSDIkYTk(S)	2761.3832	228.0882	0.8	83655.3/9.27	HUMAN	RQ13823	REVERSE Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1
5	5.29	51.3	1	12/25	K411k K431k	(K)TYkIDSWENAEDFLEKLAFRTGk(L)	2761.3832	228.0882	0.8	83655.3/9.27	HUMAN	Q13823	Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.21	85.8	8	5/25	K119k	(K) F L|T|P C Y H P N V D T Q G N I/C/L/D I/L/k E/K (W)	2875.4117	114.0597	5.6	19652.4/6.83	HUMAN	O00762	812551	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1

Fragment-ion (m/z)	70.065	74.059	84.080	86.096	110.071	120.080	233.165	234.166	261.158	274.122	362.209	389.154	518.296	566.807^{+2}	571.601	576.264	631.372	692.289^{+2}	799.348^{+2}	859.490	863.882^{+2}	876.762^{+3}	910.433^{+3}	972.582	1132.604
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.03 0.20 PR -4.6	2.39 16.25 1.50 y^{++}_1 -15.4	0.07 0.45 0.50 KQ -8.0	0.43 2.92 0.22 LI -0.3	0.07 0.47 1.00 H -1.6	0.35 2.35 1.00 a_1 -13.9 1.00 F -4.8	14.71 100.00 0.50 a_2 -6.2	2.81 19.13 -0.19	9.02 61.33 0.50 b_2 -10.5	2.59 17.58 0.75 CL -5.4	4.13 28.08 0.50 b_3 0.5	2.80 19.06 0.75 CLD 9.7	6.30 42.86 1.50 y_3 5.8	2.54 17.28 1.50 y_8^{+2} 3.6	2.53 17.21 -0.17	2.08 14.13 -0.14	5.28 35.88 1.50 y_4 -9.0	4.18 28.45 -0.28	2.59 17.58 -0.18	7.14 48.55 1.50 y_6 2.1	3.45 23.44 0.25 $b_{15}\text{-}H_2O^{+2}$ -4.9	5.41 36.77 1.50 y_{21}^{+3} 6.6	6.42 43.68 1.50 y_{22}^{+3} -6.6	7.01 47.63 1.50 y_7 9.6	5.70 38.73 1.50 y_8 1.3



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Result Summary

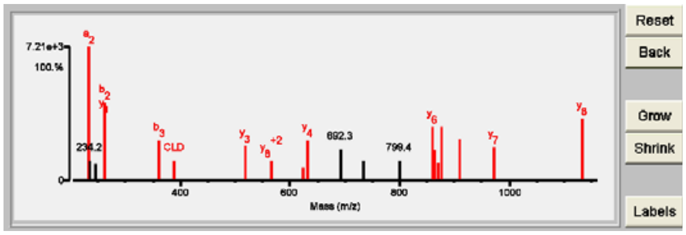
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.97	84.3	9	6/25	K121k	(K)FLTPCYHPNVDTQGNICLDILKEk(W)	2875.4117	114.0765	11.2	19652.4/6.83	HUMAN	O00762	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1
2	17.97	84.3	8	6/25	K119k	(K)FLTPCYHPNVDTQGNICLDILkEK(W)	2875.4117	114.0765	11.2	19652.4/6.83	HUMAN	O00762	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1
3	6.36	57.9	2	12/25	K321k K324k	(K)GTRFALKELFDEANEWSDIkYTk(S)	2761.3832	228.1050	6.4	83655.3/9.27	HUMAN	RQ13823	REVERSE Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1
4	5.92	54.7	4	12/25	M265m K289k	(R)mKLATKDAKELFPREPNESGEIPMk(L)	2859.4743	130.0139	-8.0	80685.0/8.90	HUMAN	RO60563	REVERSE Cyclin-T1 OS=Homo sapiens GN=CCNT1 PE=1 SV=1
5	5.32	57.1	2	12/25	K770k	(K)DKEFLSRCVNNYISLTFHDIIYk(I)	2875.4447	114.0434	0.2	470773.9/6.05	HUMAN	RQ8TD57	REVERSE Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.97	84.3	9	6/25	K121k	(K) F L|T|P C Y H P N V D T Q G N/I/C/L/D I/L/K E|k (W)	2875.4117	114.0765	11.2	19652.4/6.83	HUMAN	O00762	812551	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1

Fragment-ion (m/z)	70.065	84.080	86.096	120.080	133.042	233.164	234.169	246.126	261.160	362.206	389.147	518.291
Frac. Inten.(% of TIC)	0.00	0.14	0.54	0.43	2.31	16.48	2.42	2.11	9.68	4.94	2.40	4.30
Rel. Inten.(% of BP)	0.01	0.83	3.27	2.63	14.05	100.00	14.70	12.78	58.73	29.97	14.55	26.11
Score	0.20	0.50	0.22	1.00 1.00	-0.14	0.50	-0.15	-0.13	1.50	0.50	0.75	1.50
Ion-type	PR	KQ	LI	a_1 F		a_2			b_2 y_1	b_3	CLD	y_3
Delta ppm	1.1	-14.0	-4.9	-18.1 -9.0		-6.6			-4.4 15.2	-7.3	-8.8	-4.6

Fragment-ion (m/z)	566.811^{+2}	623.346^{+2}	631.379	692.285^{+2}	734.311^{+2}	799.361^{+2}	859.494	863.896^{+2}	871.079^{+3}	876.766^{+3}	910.454^{+3}	972.574	1132.602
Frac. Inten.(% of TIC)	2.46	1.64	5.02	3.88	2.44	2.51	6.74	3.77	2.24	6.62	5.07	4.21	7.64
Rel. Inten.(% of BP)	14.92	9.93	30.49	23.52	14.83	15.25	40.92	22.88	13.60	40.20	30.78	25.58	46.39
Score	1.50	1.50	1.50	-0.24	-0.15	-0.15	1.50	0.25	0.50	1.50	1.50	1.50	1.50
Ion-type	y_8^{+2}	y_9^{+2}	y_4				y_6	b_{15}-H_2O^{+2}	y_{21}-NH_3^{+3}	y_{21}^{+3}	b_{23}^{+3} y_{22}^{+3}	y_7	y_8
Delta ppm	10.3	-1.3	2.8				6.9	11.7	-1.8	11.1	14.3 16.2	1.4	-1.2



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Result Summary

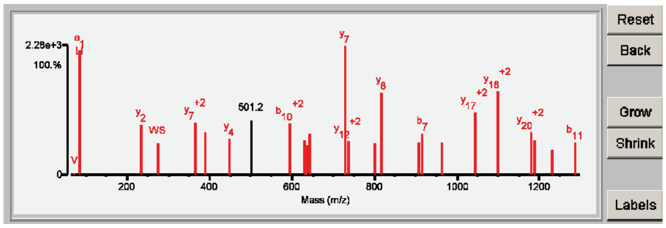
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.83	95.5	14	1/25	K136k	(R)IYHCNINSQGVICLDILkDNWSPALTISK(V)	3372.7079	114.0787	10.3	21404.3/8.77	HUMAN	P51965	Ubiquitin-conjugating enzyme E2 E1 OS=Homo sapiens GN=UBE2E1 PE=1 SV=1
1	23.83	95.5	14	1/25	K144k	(R)IYHCNINSQGVICLDILkDNWSPALTISK(V)	3372.7079	114.0787	10.3	22255.2/7.59	HUMAN	Q96LR5	Ubiquitin-conjugating enzyme E2 E2 OS=Homo sapiens GN=UBE2E2 PE=1 SV=1
1	23.83	95.5	14	1/25	K150k	(R)IYHCNINSQGVICLDILkDNWSPALTISK(V)	3372.7079	114.0787	10.3	22912.7/6.73	HUMAN	Q969T4	Ubiquitin-conjugating enzyme E2 E3 OS=Homo sapiens GN=UBE2E3 PE=1 SV=1
2	11.92	64.6	9	7/25	K147k	(R)IYHCNINSQGVICLDILKDNWSPALTISk(V)	3372.7079	114.0787	10.3	21404.3/8.77	HUMAN	P51965	Ubiquitin-conjugating enzyme E2 E1 OS=Homo sapiens GN=UBE2E1 PE=1 SV=1
2	11.92	64.6	9	7/25	K155k	(R)IYHCNINSQGVICLDILKDNWSPALTISk(V)	3372.7079	114.0787	10.3	22255.2/7.59	HUMAN	Q96LR5	Ubiquitin-conjugating enzyme E2 E2 OS=Homo sapiens GN=UBE2E2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.83	95.5	14	1/25	K136k	(R) I Y H C N I\N\S Q/G\V|I/C/L/D I L/k/D N W/S/P A L/T I/S K (V)	3372.7079	114.0787	10.3	21404.3/8.77	HUMAN	P51965	811963	Ubiquitin-conjugating enzyme E2 E1 OS=Homo sapiens GN=UBE2E1 PE=1 SV=1
1	23.83	95.5	14	1/25	K144k	(R) I Y H C N I\N\S Q/G\V|I/C/L/D I L/k/D N W/S/P A L/T I/S K (V)	3372.7079	114.0787	10.3	22255.2/7.59	HUMAN	Q96LR5	811967	Ubiquitin-conjugating enzyme E2 E2 OS=Homo sapiens GN=UBE2E2 PE=1 SV=1
1	23.83	95.5	14	1/25	K150k	(R) I Y H C N I\N\S Q/G\V|I/C/L/D I L/k/D N W/S/P A L/T I/S K (V)	3372.7079	114.0787	10.3	22912.7/6.73	HUMAN	Q969T4	811973	Ubiquitin-conjugating enzyme E2 E3 OS=Homo sapiens GN=UBE2E3 PE=1 SV=1

Fragment-ion (m/z)	72.080	86.096	234.145	274.125	365.228^{+2}	389.148	448.281	501.231^{+2}	594.271^{+2}	629.806^{+2}	634.781^{+2}	643.787^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.11 1.00 0.50 V -6.6	10.26 96.51 0.50 a_1 -16.5 0.50 LI -3.8	4.18 39.31 1.50 y_2 2.0	2.59 24.37 0.75 WS 17.5	4.29 40.37 1.50 y_7^{+2} -3.0	3.51 33.01 0.75 CLD -4.4	2.99 28.09 1.50 y_4 9.6	4.46 41.95 -0.42	4.25 39.92 0.50 b_{10}^{+2} 6.9	2.86 26.94 0.50 a_{11}^{+2} 2.5	2.43 22.88 0.25 $b_{11}\text{-}H_2O^{+2}$ -24.2	3.37 31.73 0.50 b_{11}^{+2} -21.9

Fragment-ion (m/z)	729.446	737.390^{+2}	801.378	816.484	907.993^{+2}	915.403	964.510^{+2}	1044.555^{+2}	1101.086^{+2}	1179.142^{+2}	1187.551	1231.642	1286.596
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	10.63 100.00 1.50 y_7 -5.9	2.79 26.24 1.50 y_{12}^{+2} 1.4	2.56 24.03 0.50 b_6 6.7	6.78 63.74 1.50 y_8 2.1	2.70 25.35 1.50 y_{15}^{+2} 8.1	3.41 32.03 0.50 b_7 -13.4	2.71 25.48 1.50 y_{16}^{+2} -18.5	5.10 47.93 1.50 y_{17}^{+2} 11.1	6.90 64.89 1.50 y_{18}^{+2} 0.8	3.51 32.98 1.50 y_{20}^{+2} 9.5	2.84 26.72 0.50 b_{10} 20.0	2.07 19.47 1.50 y_{11} 8.6	2.71 25.51 0.50 b_{11} -0.1



Result Summary

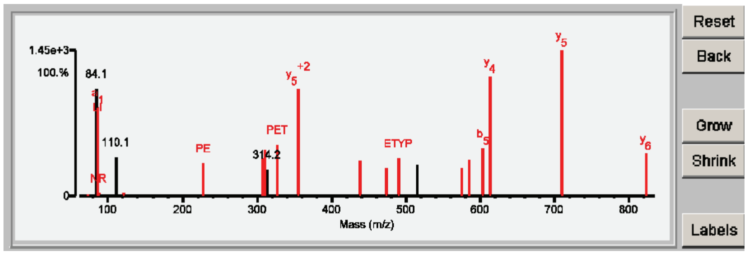
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.87	81.4	4	4/25	K72k	(K)IPETYPFNPPkVR(F)	1557.8424	114.0540	6.6	22406.8/5.33	HUMAN	P61086	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.87	81.4	4	4/25	K72k	(K) I P E T Y\P F/N/P/P k V R (F)	1557.8424	114.0540	6.6	22406.8/5.33	HUMAN	P61086	812583	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3

Fragment-ion (m/z)	70.065	72.081	84.046	84.080	86.095	87.054	110.071	120.079	136.077	227.104	307.191
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.02 0.18 0.20 **PR** -4.6	0.14 1.09 0.50 **V** 3.1	0.11 0.83 1.00 **E** 14.4	9.71 73.84 -0.74	8.03 61.03 0.50 a_1 -31.6 0.50 **LI** -18.9	0.33 2.51 0.33 **NR** -20.6	3.59 27.31 -0.27	0.32 2.41 1.00 **F** -15.6	0.09 0.71 1.00 **Y** 7.4	2.98 22.62 0.75 **PE** 1.2	3.44 26.19 1.50 $y++_4$ -6.0

Fragment-ion (m/z)	310.140	314.151	328.147	355.719^{+2}	439.271	473.208	491.216	514.930	576.312	586.299	604.306	613.379	710.436	824.476
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	4.22 32.09 0.50 **PET**-H_2O -1.8	2.46 18.67 -0.19	4.66 35.47 0.75 **PET** -15.0	9.74 74.05 1.50 y_5^{+2} -0.1	3.17 24.08 0.75 **PkV** 8.1	2.50 18.99 0.50 **ETYP**-H_2O 8.9	3.47 26.34 0.75 **ETYP** 2.4	2.88 21.89 -0.22	2.49 18.91 0.50 a_5 13.6	3.32 25.26 0.25 b_5-H_2O 18.9	4.38 33.33 0.50 b_5 12.6	10.87 82.61 1.50 y_4 1.3	13.15 100.00 1.50 y_5 7.3	3.93 29.90 1.50 y_6 2.7



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Result Summary

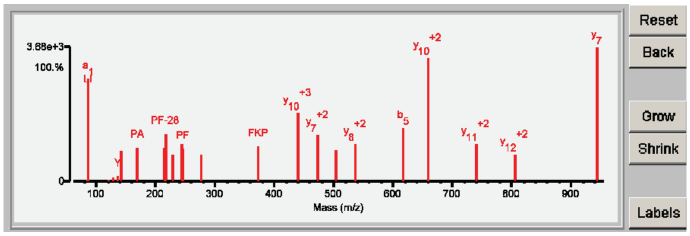
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.40	100.0	7	0/25	K71k	(R)IEINFPAEYPFKPPKITFk(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
1	22.40	100.0	7	0/25	K67k	(R)IEINFPAEYPFKPPkITFK(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
2	16.09	75.2	6	4/25	K64k	(R)IEINFPAEYPFkPPKITFK(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
3	10.62	65.7	2	9/25	M2875m K2884k	(K)EVmGKANAPYIkQIFPVTEK(E)	2263.2155	130.0783	16.9	470773.9/6.05	HUMAN	RQ8TD57	REVERSE Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1
4	8.55	52.4	5	11/25	M456m	(R)TIKmVCGDRIMKWALLATNR(S)	2377.2665	16.0273	13.5	77401.1/9.11	HUMAN	RA8K979	REVERSE Exonuclease domain-containing protein 1 OS=Homo sapiens GN=EXOD1 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.40	100.0	7	0/25	K71k	(R) I E\I N F\P A/E/Y/P F/K/P P K I T F k (T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	812013	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.080	86.095	102.054	120.079	129.100	136.073	141.099	169.095	215.136	217.130	228.132	243.132
Frac. Inten.(% of TIC)	0.02	0.17	10.46	0.11	0.20	0.37	0.55	3.16	3.45	3.44	4.81	2.77	3.78
Rel. Inten.(% of BP)	0.17	1.26	76.36	0.84	1.46	2.69	3.99	23.05	25.17	25.13	35.09	20.21	27.56
Score	0.20	0.50	0.50	1.00	1.00	0.20	1.00	0.50	0.75	0.75	0.50	0.75	0.75
Ion-type	PR	KQ	a_1	E	F	RKQ	Y	PA-28	PA	a_2	PF-28	IN	b_2
Delta ppm	-17.5	-9.2	-30.5 0.50 LI -17.7	-11.3	-15.6	-14.2	-17.6	-27.9	-21.6	-19.6 IT -19.6 EI-28 -19.6	-20.9	-12.6	-12.5 EI -12.5

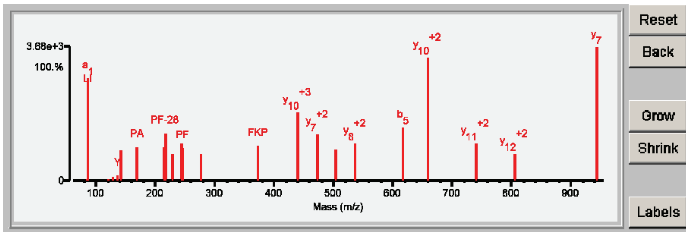
Fragment-ion (m/z)	245.127	276.168	373.218	439.595^{+3}	472.780^{+2}	504.246	536.828^{+2}	617.326	658.886^{+2}	740.412^{+2}	804.933^{+2}	944.546
Frac. Inten.(% of TIC)	3.38	2.79	3.57	7.00	4.76	3.17	3.82	5.48	12.54	3.78	2.74	13.70
Rel. Inten.(% of BP)	24.70	20.35	26.05	51.12	34.74	23.13	27.85	39.99	91.51	27.59	19.98	100.00
Score	0.75	0.75	0.75	1.50	1.50	0.75	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	PF	FK	FKP	y_{10}^{+3}	y_7^{+2}	EINF	y_8^{+2}	b_5	y_{10}^{+2}	y_{11}^{+2}	y_{12}^{+2}	y_7
Delta ppm	-11.2	-13.2	-17.5	-0.9	-3.7	-1.3	-3.0	-7.0	-6.4	-12.8	-12.8	-10.9



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.40	100.0	7	0/25	K67k	(R) I E\I N F\P A/E/Y/P F/K/P P k I T F K (T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	812013	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.080	86.095	102.054	120.079	129.100	136.073	141.099	169.095	215.136	217.130	228.132	243.132
Frac. Inten.(% of TIC)	0.02	0.17	10.46	0.11	0.20	0.37	0.55	3.16	3.45	3.44	4.81	2.77	3.78
Rel. Inten.(% of BP)	0.17	1.26	76.36	0.84	1.46	2.69	3.99	23.05	25.17	25.13	35.09	20.21	27.56
Score	0.20	0.50	0.50	1.00	1.00	0.20	1.00	0.50	0.75	0.75	0.50	0.75	0.75
Ion-type	PR	KQ	a_1	E	F	RKQ	Y	PA-28	PA	a_2	PF-28	IN	b_2
Delta ppm	-17.5	-9.2	-30.5 0.50 LI -17.7	-11.3	-15.6	-14.2	-17.6	-27.9	-21.6	-19.6 IT -19.6 EI-28 -19.6	-20.9	-12.6	-12.5 EI -12.5

Fragment-ion (m/z)	245.127	276.168	373.218	439.595^{+3}	472.780^{+2}	504.246	536.828^{+2}	617.326	658.886^{+2}	740.412^{+2}	804.933^{+2}	944.546
Frac. Inten.(% of TIC)	3.38	2.79	3.57	7.00	4.76	3.17	3.82	5.48	12.54	3.78	2.74	13.70
Rel. Inten.(% of BP)	24.70	20.35	26.05	51.12	34.74	23.13	27.85	39.99	91.51	27.59	19.98	100.00
Score	0.75	0.75	0.75	1.50	1.50	0.75	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	PF	FK	FKP	y_{10}^{+3}	y_7^{+2}	EINF	y_8^{+2}	b_5	y_{10}^{+2}	y_{11}^{+2}	y_{12}^{+2}	y_7
Delta ppm	-11.2	-13.2	-17.5	-0.9	-3.7	-1.3	-3.0	-7.0	-6.4	-12.8	-12.8	-10.9



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Result Summary

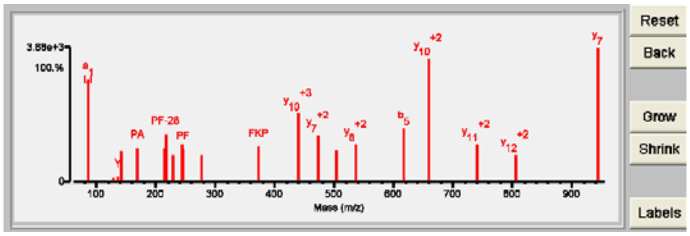
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.40	100.0	7	0/25	K71k	(R)IEINFPAEYPFKPPKITFk(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
1	22.40	100.0	7	0/25	K67k	(R)IEINFPAEYPFKPPkITFK(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
2	16.09	75.2	6	4/25	K64k	(R)IEINFPAEYPFkPPKITFK(T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1
3	10.62	65.7	2	9/25	M2875m K2884k	(K)EVmGKANAPYIkQIFPVTEK(E)	2263.2155	130.0783	16.9	470773.9/6.05	HUMAN	RQ8TD57	REVERSE Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1
4	8.55	52.4	5	11/25	M456m	(R)TIKmVCGDRIMKWALLATNR(S)	2377.2665	16.0273	13.5	77401.1/9.11	HUMAN	RA8K979	REVERSE Exonuclease domain-containing protein 1 OS=Homo sapiens GN=EXOD1 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.40	100.0	7	0/25	K71k	(R) I E\I N F\P A/E/Y/P F/K/P P K I T F k (T)	2279.2475	114.0463	1.4	17861.7/8.68	HUMAN	P68036	812013	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1

Fragment-ion (m/z)	70.064	84.080	86.095	102.054	120.079	129.100	136.073	141.099	169.095	215.136	217.130	228.132	243.132
Frac. Inten.(% of TIC)	0.02	0.17	10.46	0.11	0.20	0.37	0.55	3.16	3.45	3.44	4.81	2.77	3.78
Rel. Inten.(% of BP)	0.17	1.26	76.36	0.84	1.46	2.69	3.99	23.05	25.17	25.13	35.09	20.21	27.56
Score	0.20	0.50	0.50	1.00	1.00	0.20	1.00	0.50	0.75	0.75	0.50	0.75	0.75
Ion-type	PR	KQ	a_1	E	F	RKQ	Y	PA-28	PA	a_2	PF-28	IN	b_2
Delta ppm	-17.5	-9.2	-30.5 0.50 LI -17.7	-11.3	-15.6	-14.2	-17.6	-27.9	-21.6	-19.6 IT -19.6 EI-28 -19.6	-20.9	-12.6	-12.5 EI -12.5

Fragment-ion (m/z)	245.127	276.168	373.218	439.595^{+3}	472.780^{+2}	504.246	536.828^{+2}	617.326	658.886^{+2}	740.412^{+2}	804.933^{+2}	944.546
Frac. Inten.(% of TIC)	3.38	2.79	3.57	7.00	4.76	3.17	3.82	5.48	12.54	3.78	2.74	13.70
Rel. Inten.(% of BP)	24.70	20.35	26.05	51.12	34.74	23.13	27.85	39.99	91.51	27.59	19.98	100.00
Score	0.75	0.75	0.75	1.50	1.50	0.75	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	PF	FK	FKP	y_{10}^{+3}	y_7^{+2}	EINF	y_8^{+2}	b_5	y_{10}^{+2}	y_{11}^{+2}	y_{12}^{+2}	y_7
Delta ppm	-11.2	-13.2	-17.5	-0.9	-3.7	-1.3	-3.0	-7.0	-6.4	-12.8	-12.8	-10.9



Result Summary

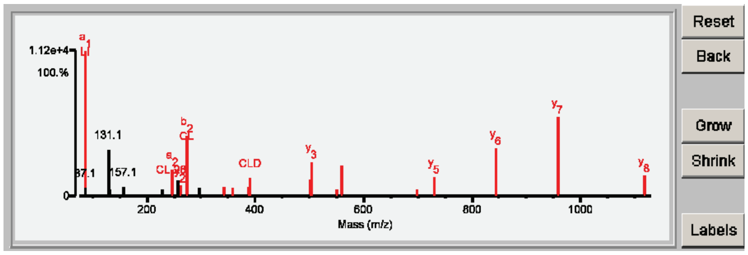
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.81	84.5	6	7/25	K92k	(R)ICLDILkDK(W)	1117.6286	114.0490	4.9	17137.9/6.13	HUMAN	P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1
2	14.18	81.7	5	9/25	K94k	(R)ICLDILKDk(W)	1117.6286	114.0490	4.9	17137.9/6.13	HUMAN	P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1
3	7.30	62.0	3	14/25	None	(R)ICDDELILIK(N)	1231.6603	0.0173	14.0	60343.9/5.80	HUMAN	P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.81	84.5	6	7/25	K92k	(R) I/C|L|D|I L/k/D K (W)	1117.6286	114.0490	4.9	17137.9/6.13	HUMAN	P61088	812593	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1

Fragment-ion (m/z)	84.081	86.096	87.099	131.117	133.041	157.133	229.109	246.126	257.096	262.141	274.123	296.198
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.11 0.48 0.50 KQ 0.3	22.37 100.00 0.50 a_1 -16.5 0.50 LI -3.8	1.28 5.70 -0.06	7.13 31.86 -0.32	1.03 4.61 -0.05	1.38 6.16 -0.06	1.01 4.50 -0.04	4.19 18.72 0.50 a_2 -8.4 CL-28 -8.4	2.44 10.90 -0.11	1.72 7.68 1.50 y_2 3.3	9.25 41.37 0.75 b_2 -1.0 CL -1.0	1.25 5.58 -0.06

Fragment-ion (m/z)	342.200	358.173	387.200	389.150	502.233	504.278	550.791^{+2}	559.802^{+2}	697.429	730.442	845.473	958.560	1118.585
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.37 6.13 0.75 DIL -11.2	1.15 5.14 0.75 kD -1.1	1.41 6.29 0.50 b_3 -18.7	2.70 12.06 0.75 CLD -0.3	2.54 11.36 0.75 b_4 -3.2 CLDI -3.2	5.19 23.20 1.50 y_3 0.5	0.99 4.43 0.50 $y_8\text{-}H_2O^{+2}$ -2.7	4.77 21.30 1.50 y_8^{+2} 7.4	1.10 4.91 0.75 LDILk 5.9	2.98 13.30 1.50 y_5 -5.3	7.28 32.53 1.50 y_6 0.6	12.15 54.31 1.50 y_7 3.5	3.24 14.50 1.50 y_8 -2.0



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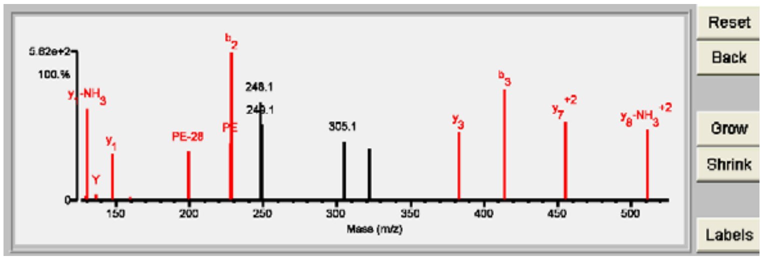
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	13.22	70.6	5	7/25	K132k	(R)VQWYPEGVkQHVK(E)	1597.8485	114.0528	5.8	141294.2/5.01	HUMAN	Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.22	70.6	5	7/25	K132k	(R) V Q\W\Y P E/G V k Q/H V/K (E)	1597.8485	114.0528	5.8	141294.2/5.01	HUMAN	Q9C0C9	812603	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3

Fragment-ion (m/z)	70.064	71.068	72.081	84.046	84.081	86.095	102.053	110.072	117.102	129.101	130.082	136.075	147.110	159.091	199.108	227.101	228.134	248.108	249.100	305.128	322.160	383.245	414.220	455.266^{+2}	511.292^{+2}
Frac. Inten.(% of TIC)	0.03	3.68	1.37	0.13	0.73	10.00	0.16	0.16	7.44	0.33	6.91	0.38	3.48	0.25	3.63	4.34	11.12	7.37	5.67	4.43	3.82	5.05	8.35	5.88	5.28
Rel. Inten.(% of BP)	0.31	33.11	12.34	1.14	6.54	89.94	1.47	1.46	66.92	2.93	62.17	3.43	31.33	2.29	32.67	39.04	100.00	66.32	51.02	39.86	34.40	45.47	75.15	52.88	47.48
Score	0.20	-0.08	0.50		0.50	-0.22	1.00	1.00	-0.16	0.20	0.50	1.00	1.50	2.00	0.50	0.75	0.50	-0.16	-0.12	-0.10	-0.08	1.50	0.50	1.50	0.50
Ion-type	**PR**		a_1	**E**	**KQ**		**E**	**H**		**RKQ**	y_1-NH_3	**Y**	y_1	**W**	**PE**-28	**PE**	b_2					y_3	b_3	y_7^{+2}	y_8-NH_3^{+2}
Delta ppm	-8.9		-14.9		-0.9		-15.2	10.2		-8.8	-30.4	-5.1	-20.4	-1.7	-5.1	-12.5	-7.3					13.0	12.4	-2.6	33.5
			0.50																						
			V																						
			0.3																						



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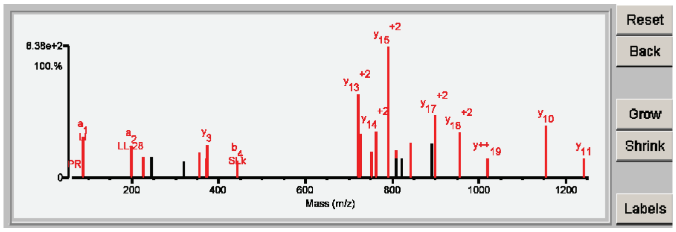
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.86	87.6	13	5/25	K825k	(K)ILESLkNMTVEQLLTGSPTSPTVEPEKPTR(E)	3295.7454	114.0696	7.8	141294.2/5.01	HUMAN	Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.86	87.6	13	5/25	K825k	(K) I L\E S\L k N M T V E/Q|L|L/T/G/S/P T/S/P T V E/P E K/P T R (E)	3295.7454	114.0696	7.8	141294.2/5.01	HUMAN	Q9C0C9	812603	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3

Fragment-ion (m/z)	70.064	86.096	199.177	227.171	243.147	319.136	355.193	371.185	373.224	443.253	719.886^{+2}	727.406	750.894^{+2}	763.399^{+2}	791.904^{+2}	807.412^{+2}	808.023	820.399	842.438	889.993	898.958^{+2}	955.515^{+2}	1019.522	1153.609	1240.648
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.03 0.20 PR -8.9	4.60 31.30 0.50 a_1 -15.4 0.50 LI -2.6	3.61 24.57 0.50 a_2 -21.5 LL-28 -21.5	2.35 16.00 0.75 b_2 -26.4 LL -26.4	2.28 15.51 -0.16	1.86 12.66 -0.13	2.79 18.98 0.75 EKP -17.2	2.26 15.35 0.75 EQL -22.4	3.70 25.16 1.50 y_3 11.0	1.93 13.12 0.75 b_4 4.7 SLk -20.7	9.34 63.50 1.50 y_{13}^{+2} 7.2	4.94 33.61 1.50 y_6 -4.7	2.90 19.70 0.50 b_{12}^{+2} 4.0	5.26 35.80 1.50 y_{14}^{+2} 3.1	14.70 100.00 1.50 y_{15}^{+2} -4.4	3.10 21.09 0.50 b_{13}^{+2} -26.1	2.15 14.61 -0.15	2.18 14.85 -0.15	3.92 26.65 1.50 y++$_{16}$ 8.7	3.89 26.46 -0.26	7.02 47.73 1.50 y_{17}^{+2} -16.4	5.09 34.62 1.50 y_{18}^{+2} -0.0	2.17 14.73 1.50 y++$_{19}$ -22.0	5.82 39.58 1.50 y_{10} -10.2	2.14 14.55 1.50 y_{11} -4.3



Result Summary

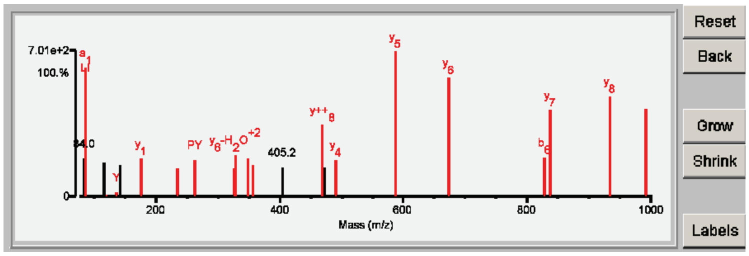
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	16.49	83.4	8	6/25	K63k	(R)LkFPIDYPYSPPAFR(F)	1810.9527	114.0486	2.9	26736.9/4.41	HUMAN	P49427	Ubiquitin-conjugating enzyme E2 R1 OS=Homo sapiens GN=CDC34 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.49	83.4	8	6/25	K63k	(R) L k\F P I D\Y|P/Y/S/P/P A F/R (F)	1810.9527	114.0486	2.9	26736.9/4.41	HUMAN	P49427	812035	Ubiquitin-conjugating enzyme E2 R1 OS=Homo sapiens GN=CDC34 PE=1 SV=2

Fragment-ion (m/z)	70.066	72.082	84.044	86.096	115.085	120.081	136.074	141.102	175.120	233.133	261.127	326.167	328.678^{+2}
Frac. Inten.(% of TIC)	0.02	3.94	2.99	10.11	2.68	0.16	0.34	2.46	3.01	2.23	2.89	2.22	3.29
Rel. Inten.(% of BP)	0.14	34.57	26.23	88.74	23.56	1.44	2.96	21.59	26.38	19.56	25.36	19.48	28.87
Score	0.20	-0.35	-0.26	0.50 0.50	-0.24	1.00	1.00	-0.22	1.50	0.50	0.75	0.75	0.50
Ion-type	PR			a_1 LI		F	Y		y_1	PY-28	PY	PID	y_6-H_2O^{+2}
Delta ppm	13.9			-14.2 -1.5		-2.3	-10.2		8.3	14.8	10.5	-16.4	-3.0

Fragment-ion (m/z)	348.162	356.225	405.181^{+2}	467.742	473.243^{+2}	490.273	587.329	674.361	828.468	837.433	934.468	991.525
Frac. Inten.(% of TIC)	2.98	2.49	2.29	5.60	2.26	2.85	11.40	9.33	3.07	6.78	7.81	6.83
Rel. Inten.(% of BP)	26.14	21.83	20.08	49.10	19.81	24.97	100.00	81.84	26.98	59.46	68.52	59.92
Score	0.75	0.50	-0.20	1.50	-0.20	1.50	1.50	1.50	0.50	1.50	1.50	0.50
Ion-type	YSP	b_2		y^{++}_8		y_4	y_5	y_6	b_6	y_7	y_8	b_7
Delta ppm	15.5	-15.0		-0.9		-9.3	-2.1	-1.5	7.0	9.5	-10.3	-0.7



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Result Summary

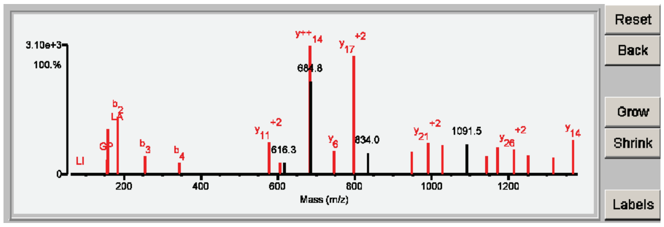
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	22.21	81.5	12	4/25	K197k	(R)ALASGTEASSTDPGAPGGPGGAEGPMAkK(H)	2569.2199	114.0743	11.7	23845.4/8.46	HUMAN	Q16763	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2
1	22.21	81.5	12	4/25	K198k	(R)ALASGTEASSTDPGAPGGPGGAEGPMAKk(H)	2569.2199	114.0743	11.7	23845.4/8.46	HUMAN	Q16763	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.21	81.5	12	4/25	K197k	(R) A L|A|S|G/T E/A/S/S T D/P G A|P G/G/P G G A E/G P M A k K (H)	2569.2199	114.0743	11.7	23845.4/8.46	HUMAN	Q16763	812611	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2

Fragment-ion (m/z)	70.064	86.096	155.082	157.133	185.128	256.166	343.200	578.793^{+2}	607.313^{+2}	616.288	684.345	684.848	745.411	796.899^{+2}
Frac. Inten.(% of TIC)	0.00	0.05	1.71	5.43	6.87	2.19	1.42	3.88	1.32	1.42	15.21	10.95	2.83	14.03
Rel. Inten.(% of BP)	0.01	0.34	11.27	35.69	45.14	14.42	9.34	25.48	8.65	9.36	100.00	71.98	18.62	92.23
Score	0.20	0.22	0.75	0.50	0.75	0.50	0.50	1.50	1.50	-0.09	1.50	-0.72	1.50	1.50
Ion-type	PR	LI	GP	a_2 LA-28	b_2 LA	b_3	b_4	y_{11}^{+2}	y_{12}^{+2}		$y{+}{+}_{14}$		y_6	y_{17}^{+2}
Delta ppm	-18.9	-2.6	-4.5	-12.3 -12.3	-7.8 -7.8	-1.8	2.3	0.7	16.8		7.0		11.6	3.7

Fragment-ion (m/z)	834.049^{+3}	948.450^{+2}	991.964^{+2}	1027.504^{+2}	1091.491^{+2}	1142.525^{+2}	1171.045^{+2}	1214.549^{+2}	1250.041^{+2}	1316.601	1367.681
Frac. Inten.(% of TIC)	2.56	2.70	3.74	3.43	3.54	2.19	3.24	2.88	2.30	2.01	4.08
Rel. Inten.(% of BP)	16.81	17.72	24.58	22.57	23.30	14.40	21.31	18.91	15.09	13.24	26.84
Score	-0.17	1.50	1.50	1.50	-0.23	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type		y_{20}^{+2}	y_{21}^{+2}	y_{22}^{+2}		y_{24}^{+2}	y_{25}^{+2}	y_{26}^{+2}	y_{27}^{+2}	b_{15}	y_{14}
Delta ppm		0.8	-1.7	19.8		-3.4	4.4	-5.9	-27.2	2.9	5.4



Result Summary

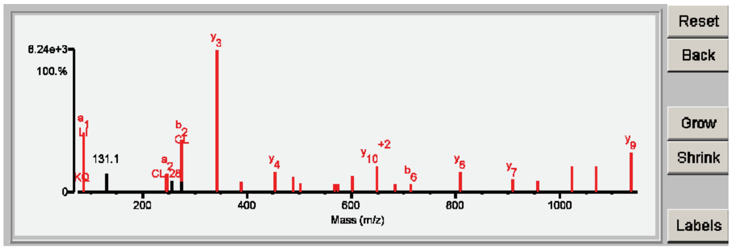
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.22	93.3	9	3/25	K91k	(R)ICLDVLkLPPK(G)	1295.7756	114.0544	8.1	22521.0/7.78	HUMAN	Q9NPD8	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens GN=UBE2T PE=1 SV=1
2	4.68	52.5	2	16/25	K257k	(R)QIVLCPGKPRk(S)	1295.7616	114.0683	18.0	36462.8/9.08	HUMAN	RQ5MJ70	REVERSE Speedy protein A OS=Homo sapiens GN=SPDYA PE=1 SV=2
2	4.68	52.5	2	16/25	K254k	(R)QIVLCPGkPRK(S)	1295.7616	114.0683	18.0	36462.8/9.08	HUMAN	RQ5MJ70	REVERSE Speedy protein A OS=Homo sapiens GN=SPDYA PE=1 SV=2
3	4.57	56.3	2	17/25	None	(R)CLIRASLPVKPR(A)	1409.8410	-0.0110	-7.8	39945.6/5.50	HUMAN	Q02833	Ras association domain-containing protein 7 OS=Homo sapiens GN=RASSF7 PE=1 SV=1
4	3.57	56.3	1	17/25	None	(-)MAAALQVLPRLAR(A)	1409.8410	-0.0110	-7.8	55252.9/6.25	HUMAN	Q8IVS8	Glycerate kinase OS=Homo sapiens GN=GLYCTK PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.22	93.3	9	3/25	K91k	(R) I/C|L/D|V|L\k|L|P/P K (G)	1295.7756	114.0544	8.1	22521.0/7.78	HUMAN	Q9NPD8	812617	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens GN=UBE2T PE=1 SV=1

Fragment-ion (m/z)	84.080	86.095	131.116	244.167	246.126	257.094	274.122	275.125	341.218	389.147	454.304	488.224
Frac. Inten.(% of TIC)	0.07	10.07	3.08	3.03	3.13	1.91	8.96	1.68	23.86	1.79	3.47	2.45
Rel. Inten.(% of BP)	0.31	42.19	12.89	12.69	13.13	8.02	37.55	7.04	100.00	7.50	14.52	10.26
Score	0.50	0.50	-0.13	1.50	0.50	-0.08	0.75	-0.07	1.50	0.75	1.50	0.75
Ion-type	KQ	a_1		y_2	a_2		b_2		y_3	CLD	y_4	CLDV
Delta ppm	-9.2	-24.7		7.1	-10.0		-2.9		0.2	-7.8	3.3	12.0
		0.50			CL-28		CL					
		LI			-10.0		-2.9					
		-11.9										

Fragment-ion (m/z)	502.236	568.382	573.304	601.307	648.885^{+2}	683.409	714.389	809.529	908.586	956.535	1023.621	1069.609	1136.701
Frac. Inten.(% of TIC)	1.52	1.26	1.27	2.69	4.34	1.27	1.36	3.46	2.08	1.95	4.29	4.34	6.68
Rel. Inten.(% of BP)	6.37	5.28	5.31	11.27	18.20	5.30	5.71	14.50	8.70	8.17	17.96	18.18	28.00
Score	0.50	0.75	0.50	0.75	1.50	0.75	0.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type	b_4	VLkL	a_5	b_5	y_{10}^{+2}	DVLkL	b_6	y_6	y_7	b_7	y_8	b_8	y_9
Delta ppm	2.8	-0.9	-5.7	7.1	21.8	-1.1	3.3	6.2	-8.0	10.6	1.7	0.2	-2.3
			CLDVL-28	CLDVL									
			-5.7	7.1									



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Result Summary

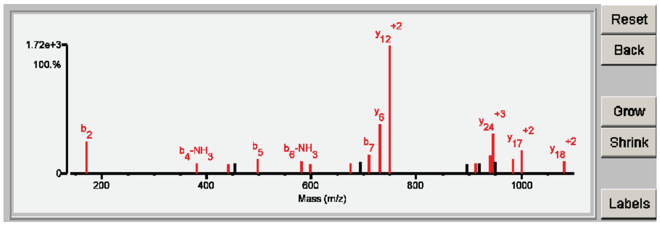
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	15.85	85.1	9	6/25	K627k	(K)GNVQVVIPFLTESYSSSQDPPEkSIPICTLK(N)	3433.7560	114.0670	6.8	117849.6/5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3
2	13.96	74.9	8	7/25	K635k	(K)GNVQVVIPFLTESYSSSQDPPEKSIPICTLk(N)	3433.7560	114.0670	6.8	117849.6/5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.85	85.1	9	6/25	K627k	(K) G N\V Q V\V|I|P F L T E S/Y/S S/S Q D/P P E k S I/P I C T L K (N)	3433.7560	114.0670	6.8	117849.6/5.49	HUMAN	P22314	406046	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Fragment-ion (m/z)	70.064	84.043	86.096	172.069	382.174	441.235	454.203	498.274	580.310	597.335	675.332	692.367
Frac. Inten.(% of TIC)	0.00	0.06	0.17	6.69	2.17	1.98	2.20	2.96	2.58	1.97	2.15	2.44
Rel. Inten.(% of BP)	0.01	0.25	0.65	25.64	8.32	7.57	8.43	11.33	9.88	7.54	8.25	9.34
Score	0.20	1.00	0.22	0.50	0.25	0.75	-0.08	0.50	0.25	0.50	0.75	-0.09
Ion-type	PR	E	LI	b_2	b_4-NH$_3$	NVQV		b_5	b_6-NH$_3$	b_6	PFLTES	
Delta ppm	-14.6	-15.4	-0.3	-20.7	2.3	-25.9		12.1	0.6	-2.5	-5.8	

Fragment-ion (m/z)	710.415	731.411	748.907^{+2}	896.955	913.956^{+2}	919.415^{+2}	941.159^{+3}	946.795^{+3}	949.981	984.490^{+3}	1001.008^{+2}	1082.520^{+2}	1126.596^{+2}
Frac. Inten.(% of TIC)	3.88	10.26	26.10	1.79	2.07	2.12	3.57	8.25	2.24	2.98	4.80	2.49	4.08
Rel. Inten.(% of BP)	14.88	39.31	100.00	6.87	7.93	8.13	13.69	31.63	8.58	11.40	18.40	9.53	15.64
Score	0.50	1.50	1.50	-0.07	1.50	-0.08	0.50	1.50	-0.09	1.50	1.50	1.50	-0.16
Ion-type	b_7	y_6	y_{12}^{+2}		y_{15}^{+2}		y_{24}-NH$_3^{+3}$	y_{24}^{+3}		y_{25}^{+3}	y_{17}^{+2}	y_{18}^{+2}	
Delta ppm	-8.5	-1.7	-4.7		-14.5		36.3	-6.0		-5.7	6.7	-12.3	



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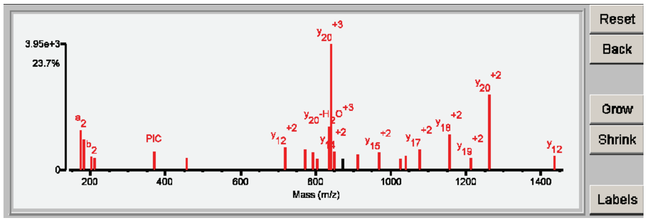
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	26.90	98.9	11	1/25	K635k	(K)SIPICTLkNFPNAIEHTLQWAR(D)	2609.3657	114.0406	-0.9	117849.6/5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3
2	14.64	85.3	6	9/25	K607k	(K)AEPISSSISNMELELNIHNSKAPk(K)	2609.3239	114.0823	14.5	207721.9/5.29	HUMAN	P38398	Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2
2	14.64	85.3	7	9/25	K604k	(K)AEPISSSISNMELELNIHNSkAPK(K)	2609.3239	114.0823	14.5	207721.9/5.29	HUMAN	P38398	Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2
3	10.94	74.0	4	14/25	K83k	(K)LSNGKKFDSSHDRNEPFVFSLGk(G)	2609.3107	114.0956	19.3	51212.5/5.71	HUMAN	Q13451	FK506-binding protein 5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2
4	9.44	73.9	3	15/25	K123k	(R)ISVkTSASASLEATAMGTEKGAVLMR(G)	2609.3637	114.0425	-0.1	22452.8/10.05	HUMAN	Q8TAG6	Uncharacterized protein C8orf46 OS=Homo sapiens GN=C8orf46 PE=2 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	26.90	98.9	11	1/25	K635k	(K) S I|P/I/C/T/L/k/N/F/P N A I/E/H T L Q W A R (D)	2609.3657	114.0406	-0.9	117849.6/5.49	HUMAN	P22314	812091	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Fragment-ion (m/z)	70.064	86.095	173.127	183.146	201.119	211.141	371.164	456.238^{+2}	718.375^{+2}	771.752^{+3}	791.906^{+2}	803.758^{+3}	835.751^{+3}	841.764^{+3}	848.920^{+2}	870.772^{+3}	911.468	969.968^{+2}	1026.540^{+2}	1040.519	1077.049^{+2}	1157.067^{+2}	1213.597^{+2}	1262.137^{+2}	1435.703
Frac. Inten.(% of TIC)	0.00	0.05	3.94	2.99	1.33	1.24	1.85	1.17	2.21	2.00	1.72	1.08	4.27	51.79	1.82	1.05	1.50	1.77	1.13	1.45	2.03	3.50	1.25	7.45	1.39
Rel. Inten.(% of BP)	0.00	0.09	7.60	5.78	2.56	2.40	3.57	2.25	4.26	3.87	3.32	2.09	8.25	100.00	3.52	2.03	2.91	3.42	2.18	2.80	3.93	6.77	2.42	14.38	2.69
Score	0.20	0.22	0.50	0.50	0.50	0.75	0.75	1.50	1.50	1.50	1.50	0.50	0.50	1.50	1.50	-0.02	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	PR	LI	a_2	PI-28	b_2	PI	PIC	y_7^{+2}	y_{12}^{+2}	y_{18}^{+3}	y_{13}^{+2}	$y_{19}\text{-}NH_3^{+3}$	$y_{20}\text{-}H_2O^{+3}$	y_{20}^{+3}	y_{14}^{+2}		y_7	y_{15}^{+2}	y_{16}^{+2}	y_8	y_{17}^{+2}	y_{18}^{+2}	y_{19}^{+2}	y_{20}^{+2}	y_{12}
Delta ppm	-18.9	-20.0	-15.9	-22.9	-25.2	-18.5	-33.0	-16.8	-1.5	37.2	-4.7	18.7	-16.9	-6.0	-13.6		-18.2	-33.4	-2.2	-7.5	-15.6	-12.2	-21.8	-10.0	-28.5



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Result Summary

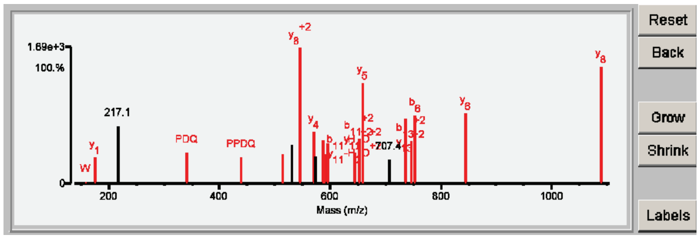
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	19.59	86.7	10	4/25	K746k	(R)QLLHNFPPDQLTSSGAPFWSGPkR(C)	2680.3630	114.0743	11.2	117849.6/5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.59	86.7	10	4/25	K746k	(R) Q L L H N F\P P D Q\L|T S|S G A/P F/W/S/G/P k/R (C)	2680.3630	114.0743	11.2	117849.6/5.49	HUMAN	P22314	812091	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Fragment-ion (m/z)	70.064	86.096	120.080	159.091	175.118	217.134	341.141	438.196	514.307	531.278^{+2}	544.793^{+2}	571.332
Frac. Inten.(% of TIC)	0.01	0.15	0.07	0.21	2.36	5.18	2.80	2.39	2.66	3.49	12.32	4.70
Rel. Inten.(% of BP)	0.09	1.24	0.59	1.69	19.19	42.07	22.70	19.44	21.56	28.31	100.00	38.11
Score	0.20	0.22	1.00	2.00	1.50	-0.42	0.75	0.75	1.50	-0.28	1.50	1.50
Ion-type	PR	LI	F	W	y_1		PDQ	PPDQ	y_3		y_8^{+2}	y_4
Delta ppm	-11.8	-3.8	-8.1	-1.7	-4.3		-16.3	-8.7	-5.5		14.3	1.5

Fragment-ion (m/z)	572.333^{+2}	586.818^{+2}	589.306	595.803^{+2}	643.343^{+2}	652.330^{+2}	658.363	707.358	736.372	746.374^{+2}	753.409	844.442	1088.578
Frac. Inten.(% of TIC)	2.51	3.94	2.66	3.58	2.78	4.09	9.13	2.16	5.89	3.83	6.11	6.34	10.62
Rel. Inten.(% of BP)	20.36	31.99	21.61	29.08	22.59	33.21	74.15	17.57	47.80	31.10	49.63	51.45	86.19
Score	-0.20	0.25	0.25	0.50	0.50	1.50	1.50	-0.18	0.25	1.50	0.50	1.50	1.50
Ion-type		$b_{10}\text{-}H_2O^{+2}$	$b_5\text{-}NH_3$	b_{10}^{+2}	$b_{11}\text{-}H_2O^{+2}$ $y_{11}\text{-}H_2O^{+2}$	b_{11}^{+2} y_{11}^{+2}	y_5		$b_6\text{-}NH_3$	b_{13}^{+2} y_{13}^{+2}	b_6	y_6	y_8
Delta ppm		36.6	-6.7	1.3	7.3 27.8	-21.6 -1.4	-0.6		-9.2	-13.3 4.3	4.3	-0.3	13.1



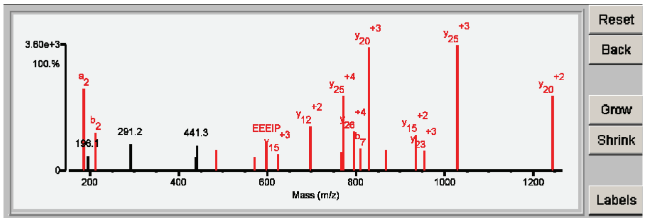
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	20.80	91.2	8	4/25	K628k	(R)DPPEEEIPFCTLkSFPAAIEHTIQWAR(D)	3182.5615	114.1002	17.4	117970.6/5.76	HUMAN	A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1
2	4.89	64.4	2	14/25	K233k	(K)DPNMKGAMLTNTGKYAIPTIDAEAYAIGKk(E)	3182.6224	114.0393	-1.1	201565.3/9.65	HUMAN	Q7Z6E9	Retinoblastoma-binding protein 6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1
2	4.89	64.4	2	14/25	K232k	(K)DPNMKGAMLTNTGKYAIPTIDAEAYAIGkK(E)	3182.6224	114.0393	-1.1	201565.3/9.65	HUMAN	Q7Z6E9	Retinoblastoma-binding protein 6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1
3	4.02	63.0	1	14/25	None	(K)LVVPDIHKLDPHDLVAEDAQADLLSQFAAR(L)	3296.7274	-0.0656	-19.9	22151.2/5.63	HUMAN	RQ9UBI1	REVERSE COMM domain-containing protein 3 OS=Homo sapiens GN=COMMD3 PE=1 SV=1
4	3.75	62.7	1	14/25	M50m	(K)LVEAAERSPLIPPKQTRPEEVYLAGmEEK(R)	3280.7246	15.9372	-17.5	131655.0/6.87	HUMAN	RO60290	REVERSE Zinc finger protein 862 OS=Homo sapiens GN=ZNF862 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.80	91.2	8	4/25	K628k	(R) D/P|PE/EE/I|PFCTL/kS/F/PAAIEHTIQWAR (D)	3182.5615	114.1002	17.4	117970.6/5.76	HUMAN	A0AVT1	812189	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.079	86.097	185.092	196.060	213.088	291.196	438.277	441.286	485.188	570.280	598.276	623.665^{+3}	696.880^{+2}	767.394^{+4}	770.412^{+2}	771.892^{+4}	796.163^{+4}	810.363	829.766^{+3}	867.455^{+3}	935.013^{+2}	953.509^{+3}	1028.854^{+3}	1244.146^{+2}
Frac. Inten.(% of TIC)	0.01	0.08	0.05	9.15	1.57	4.25	2.91	1.52	2.76	2.33	1.52	3.27	1.86	4.94	2.06	2.03	8.37	4.35	2.42	13.72	2.34	3.97	2.18	14.04	8.31
Rel. Inten.(% of BP)	0.05	0.59	0.38	65.20	11.16	30.31	20.73	10.86	19.67	16.58	10.84	23.27	13.24	35.18	14.66	14.47	59.65	31.00	17.24	97.75	16.66	28.26	15.50	100.00	59.20
Score	0.20	0.50	0.22	0.50	-0.11	0.50	-0.21	-0.11	-0.20	0.75	0.50	0.75	1.50	1.50	0.50	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	PR	KQ	LI	a_2		b_2				PEEE	EEEIP-28	EEEIP	y_{15}^{+3}	y_{12}^{+2}	$y_{25}\text{-}H_2O^{+4}$	y_{13}^{+2}	y_{25}^{+4}	y_{26}^{+4}	b_7	y_{20}^{+3}	y_{21}^{+3}	y_{15}^{+2}	y_{23}^{+3}	y_{25}^{+3}	y_{20}^{+2}
Delta ppm	-0.4	-27.1	11.3	-6.8		-0.8				-1.3	4.3	4.4	1.4	10.2	12.9	6.8	7.1	16.4	12.5	8.9	2.3	22.1	28.8	7.5	9.8



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Result Summary

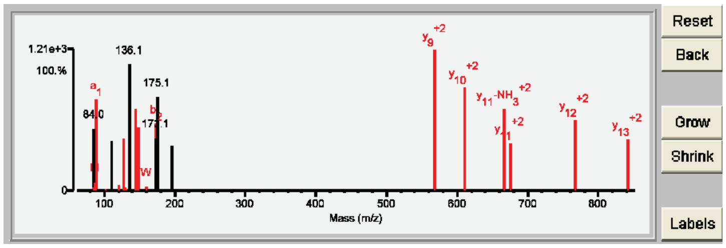
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.83	67.2	7	6/25	K739k	(K)DGSLFWQSPkRPPSPIK(F)	1940.0389	114.0793	17.7	117970.6/5.76	HUMAN	A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1
2	10.88	62.3	6	7/25	K746k	(K)DGSLFWQSPKRPPSPIk(F)	1940.0389	114.0793	17.7	117970.6/5.76	HUMAN	A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.83	67.2	7	6/25	K739k	(K) D G\S L/F/W/Q/S/P k R P P S P I/K (F)	1940.0389	114.0793	17.7	117970.6/5.76	HUMAN	A0AVT1	812189	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1

Fragment-ion (m/z)	70.065	84.045	84.081	86.096	88.039	101.070	110.071	120.081	127.049	129.102	130.070	136.075
Frac. Inten.(% of TIC)	0.01	4.72	0.30	0.65	6.97	0.11	3.80	0.46	3.96	0.19	0.14	9.63
Rel. Inten.(% of BP)	0.11	43.82	2.74	6.08	64.69	0.99	35.24	4.24	36.80	1.78	1.31	89.34
Score	0.20	-0.44	0.50	0.22	0.50		-0.35	1.00	0.50	0.20		-0.89
Ion-type	PR		KQ	LI	a_1	KQ		F	GS-H_2O	RKQ	W	
Delta ppm	-0.4		0.3	-0.3	-1.2			4.4	-5.5	-4.2		

Fragment-ion (m/z)	145.061	147.113	159.090	173.054	173.128	175.088	196.073	567.351^{+2}	610.861^{+2}	666.382^{+2}	674.895^{+2}	767.946^{+2}	841.462^{+2}
Frac. Inten.(% of TIC)	6.19	4.86	0.34	5.07	4.00	7.17	3.47	10.78	7.91	6.25	3.65	5.43	3.93
Rel. Inten.(% of BP)	57.48	45.14	3.14	47.07	37.09	66.54	32.24	100.00	73.44	58.02	33.87	50.41	36.47
Score	0.75	1.50	2.00	0.50	-0.37	-0.67	-0.32	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	a_2 GS	y_1	W	b_2				y_9^{+2}	y_{10}^{+2}	y_{11}-NH_3^{+2}	y_{11}^{+2}	y_{12}^{+2}	y_{13}^{+2}
Delta ppm	2.3 2.3	-0.0	-7.4	-7.4				13.4	3.6	10.6	10.1	23.5	-0.5



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Result Summary

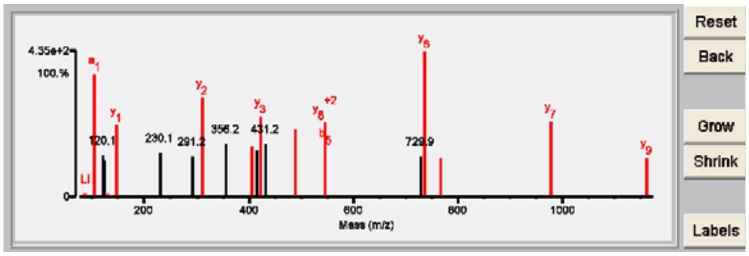
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	14.47	72.2	9	8/24	K71k	(R)MDNNAAAIkALELYK(I)	1664.8676	114.0531	5.7	100688.2/5.12	HUMAN	Q05086	Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.47	72.2	9	8/24	K71k	(R) M D/N N A\A/A/I/k/A L E/L/Y/K (I)	1664.8676	114.0531	5.7	100688.2/5.12	HUMAN	Q05086	812649	Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4

Fragment-ion (m/z)	84.080	86.095	104.051	120.082	123.081	129.102	136.075	147.111	230.100	291.190	310.175	356.165^{+2}
Frac. Inten.(% of TIC)	0.27	0.29	9.54	3.25	2.83	0.19	0.19	5.62	3.48	3.19	7.70	4.10
Rel. Inten.(% of BP)	2.37	2.55	84.07	28.63	24.93	1.72	1.64	49.51	30.70	28.08	67.87	36.09
Score	0.50	0.22	0.50	-0.29	-0.25	0.20	1.00	1.50	-0.31	-0.28	1.50	-0.36
Ion-type	KQ	LI	a_1			RKQ	Y	y_1			y_2	
Delta ppm	-10.4	-15.4	-29.3			-5.0	-2.1	-14.3			-3.3	

Fragment-ion (m/z)	405.905^{+3}	414.711^{+2}	423.250	431.155	489.785	546.204	546.330^{+2}	729.876	736.419	766.917^{+2}	978.552	1162.654
Frac. Inten.(% of TIC)	3.95	3.62	6.23	4.15	5.25	3.85	5.79	3.19	11.35	3.02	5.92	3.03
Rel. Inten.(% of BP)	34.78	31.85	54.89	36.59	46.24	33.95	51.02	28.08	100.00	26.58	52.15	26.70
Score	0.50	-0.32	1.50	-0.37	1.50	0.50	1.50	-0.28	1.50	1.50	1.50	1.50
Ion-type	$y_{10}\text{-}H_2O^{+3}$		y_3		$y{++}_7$	b_5	y_8^{+2}		y_6	y_{13}^{+2}	y_7	y_9
Delta ppm	-8.5		-24.1		0.3	10.1	5.7		-6.1	-10.8	-10.6	-24.6



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Result Summary

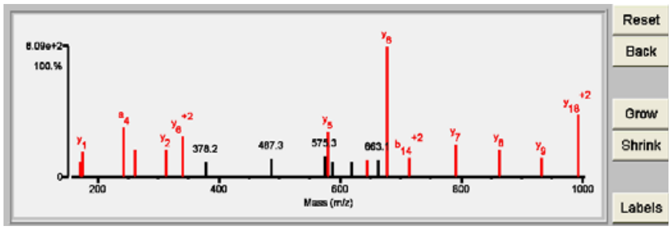
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.49	81.7	10	7/25	K67k	(R)GGGVGGFLPAMkQIGNVAALPGIVHR(S)	2516.3918	114.0511	3.1	55210.6/6.77	HUMAN	Q9Y3I0	UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1
2	4.72	56.9	2	14/25	K595k	(R)DFLkRIFVEAKLRPSADELLR(H)	2516.4348	114.0082	-13.2	69741.2/8.04	HUMAN	Q9Y2U5	Mitogen-activated protein kinase kinase kinase 2 OS=Homo sapiens GN=MAP3K2 PE=1 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.49	81.7	10	7/25	K67k	(R) G G G\V G G F L|P A M k Q I\G N V/A/A/L/P/G I V/H/R (S)	2516.3918	114.0511	3.1	55210.6/6.77	HUMAN	Q9Y3I0	132681	UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1

Fragment-ion (m/z)	72.081	86.097	120.080	129.101	143.111	172.072	175.122	243.141	262.116	312.170	339.698^{+2}	378.211^{+2}
Frac. Inten.(% of TIC)	0.33	0.35	0.25	0.08	3.15	2.27	3.83	7.41	4.02	4.08	6.05	2.24
Rel. Inten.(% of BP)	1.66	1.78	1.26	0.41	16.11	11.63	19.61	37.91	20.55	20.89	30.93	11.45
Score	0.50	0.22	1.00	0.20	-0.16	0.75	1.50	0.50	0.75	1.50	1.50	-0.11
Ion-type	V	LI	F	RKQ		b_3 GN	y_1	a_4	GGF	y_2	y_6^{+2}	
Delta ppm	-2.4	5.5	-9.0	-8.8		0.2 0.2	15.1	-15.5	-8.1	-24.5	-23.7	

Fragment-ion (m/z)	487.288	575.304	581.345	587.304	619.336^{+2}	645.321	663.058	678.407	714.372^{+2}	791.472	862.540	933.548	993.556^{+2}
Frac. Inten.(% of TIC)	2.69	3.04	6.78	2.29	2.27	2.63	2.64	19.54	2.94	4.89	4.08	2.88	9.28
Rel. Inten.(% of BP)	13.76	15.53	34.71	11.70	11.64	13.48	13.50	100.00	15.05	25.03	20.85	14.73	47.46
Score	-0.14	-0.16	1.50	-0.12	-0.12	0.50	-0.14	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type			y_5			b_8		y_6	b_{14}^{+2}	y_7	y_8	y_9	y_{18}^{+2}
Delta ppm			-11.5			-22.6		3.4	-6.9	-20.8	16.4	-15.8	-0.5



Result Summary

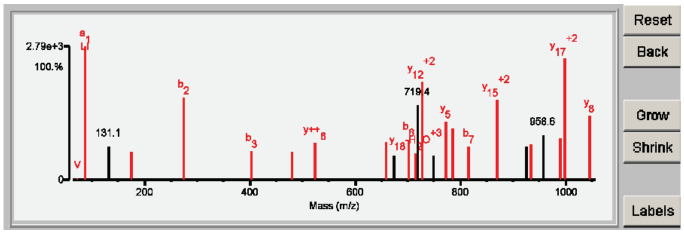
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	18.73	81.4	10	6/25	K65k	(R)LCEQGINPEALSSVIkELR(K)	2156.1380	114.0520	4.0	8478.8/4.76	HUMAN	Q08AG7	UPF0582 protein C13orf37 OS=Homo sapiens GN=C13orf37 PE=2 SV=2

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.73	81.4	10	6/25	K65k	(R) L C|E|Q/G I|N|P E A L/S/S V/I/k E L/R (K)	2156.1380	114.0520	4.0	8478.8/4.76	HUMAN	Q08AG7	108329	UPF0582 protein C13orf37 OS=Homo sapiens GN=C13orf37 PE=2 SV=2

Fragment-ion (m/z)	72.082	86.097	131.117	175.119	274.123	403.166	479.792^{+2}	523.304	659.396	673.361	701.327	713.708^{+3}
Frac. Inten.(% of TIC)	0.10	10.56	2.68	2.24	6.56	2.26	2.17	2.91	3.02	1.90	3.17	2.08
Rel. Inten.(% of BP)	0.97	100.00	25.40	21.21	62.17	21.37	20.53	27.56	28.60	17.96	30.00	19.66
Score	0.50	0.50 0.50	-0.25	1.50	0.50	0.50	1.50	1.50	1.50	-0.18	0.50	0.50
Ion-type	V	a_1 LI		y_1	b_2	b_3	y_7^{+2}	$y{+}{+}_8$	y_4		b_6	$y_{18}\text{-}H_2O^{+3}$
Delta ppm	14.2	-7.2 5.5		2.0	-1.8	0.3	8.7	1.6	18.5		-4.0	10.6

Fragment-ion (m/z)	719.372^{+3}	728.414^{+2}	750.071^{+3}	772.469	785.436^{+2}	815.364	870.483^{+2}	925.997	934.501^{+2}	958.572^{+2}	990.021^{+2}	999.033^{+2}	1045.598
Frac. Inten.(% of TIC)	5.91	7.82	1.96	4.62	4.09	2.65	6.35	2.65	2.85	3.55	3.28	9.57	5.06
Rel. Inten.(% of BP)	55.98	74.06	18.55	43.75	38.73	25.12	60.19	25.14	27.02	33.62	31.09	90.67	47.93
Score	-0.56	1.50	-0.19	1.50	1.50	0.50	1.50	-0.25	1.50	-0.34	0.50	1.50	1.50
Ion-type		y_{12}^{+2}		y_5	y_{13}^{+2}	b_7	y_{15}^{+2}		y_{16}^{+2}		$y_{17}\text{-}H_2O^{+2}$	y_{17}^{+2}	y_8
Delta ppm		2.3		1.9	2.8	-10.8	-4.0		-15.6		-10.6	-3.8	-2.0



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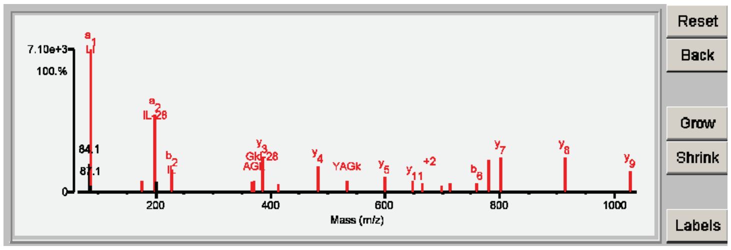
Result Summary

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	23.43	92.3	11	3/25	K53k	(K)LIYAGkILSDDVPIR(D)	1672.9632	114.0554	7.0	39609.4/4.56	HUMAN	P54725	UV excision repair protein RAD23 homolog A OS=Homo sapiens GN=RAD23A PE=1 SV=1
2	11.40	68.6	5	11/25	K502k K506k	(R)IIGkHPAkETVPIR(S)	1558.9428	228.0759	-5.6	465750.9/5.71	HUMAN	RQ86WI1	REVERSE Fibrocystin-L OS=Homo sapiens GN=PKHD1L1 PE=2 SV=1
3	8.19	62.0	3	13/25	K193k	(K)LLkMLGELQVMLER(R)	1672.9488	114.0698	15.0	83901.5/6.44	HUMAN	RQ9Y4J8	REVERSE Dystrobrevin alpha OS=Homo sapiens GN=DTNA PE=1 SV=2
4	5.05	59.2	2	16/25	M943m K940k	(K)IlkNPmDLSTIKKR(L)	1656.9829	130.0357	-1.2	116831.9/6.73	HUMAN	O15164	Transcription intermediary factor 1-alpha OS=Homo sapiens GN=TRIM24 PE=1 SV=3
5	4.82	55.1	2	13/25	K302k	(R)VSDALLEKkKLMAAR(E)	1672.9778	114.0408	-1.2	43568.3/8.96	HUMAN	P28222	5-hydroxytryptamine receptor 1B OS=Homo sapiens GN=HTR1B PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.43	92.3	11	3/25	K53k	(K) L I|Y/A/G k|I/L/S/D/D/V/P I/R (D)	1672.9632	114.0554	7.0	39609.4/4.56	HUMAN	P54725	562945	UV excision repair protein RAD23 homolog A OS=Homo sapiens GN=RAD23A PE=1 SV=1

Fragment-ion (m/z)	72.079	84.080	86.096	87.098	136.075	175.118	199.178	200.181	227.173	368.231	371.204	385.256	413.252	484.320	534.262	599.350	647.351	663.880^{+2}	699.398^{+2}	714.379	760.437	780.926^{+2}	801.408	914.493	1027.579
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.04 0.18 0.50 V -24.6	4.79 19.76 -0.20	24.23 100.00 0.50 a_1 -20.0 0.50 LI -7.3	1.17 4.83 -0.05	0.13 0.53 1.00 Y -2.1	1.90 7.86 1.50 y_1 -5.4	13.11 54.11 0.50 a_2 -16.0 IL-28 -16.0	1.79 7.38 -0.07	3.82 15.77 0.75 b_2 -13.2 IL -13.2	1.84 7.59 0.50 y_3-NH_3 4.3	1.92 7.94 0.75 AGk -3.1	6.02 24.84 1.50 y_3 1.1 GkI-28 -1.8	1.34 5.53 0.75 GkI 1.5	4.43 18.28 1.50 y_4 -7.8	1.99 8.20 0.75 YAGk -11.2	2.57 10.63 1.50 y_5 -2.4	1.96 8.10 0.75 YAGkI -1.8	1.62 6.69 1.50 y_{11}^{+2} 11.1	1.20 4.94 1.50 y_{12}^{+2} 9.9	1.55 6.38 1.50 y_6 0.6	1.65 6.80 0.50 b_6 1.3	5.58 23.02 1.50 y_{13}^{+2} 4.0	5.95 24.54 1.50 y_7 -2.5	5.87 24.23 1.50 y_8 -1.1	3.53 14.58 1.50 y_9 0.8



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Result Summary

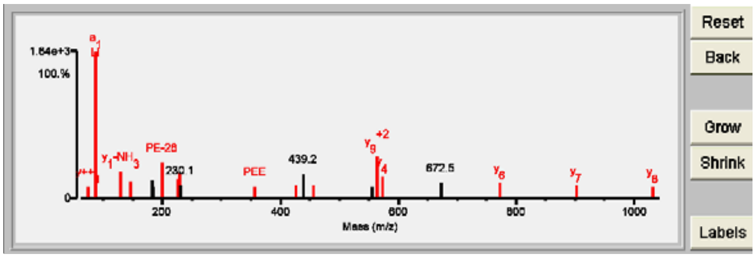
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	17.05	81.8	7	6/25	K24k	(K)IDIDPEETVkALK(E)	1470.8050	114.0502	4.6	43171.4/4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1
2	12.33	68.8	6	10/25	K27k	(K)IDIDPEETVKALk(E)	1470.8050	114.0502	4.6	43171.4/4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.05	81.8	7	6/25	K24k	(K) I D\I D|P/E/E/T V/k A L/K (E)	1470.8050	114.0502	4.6	43171.4/4.79	HUMAN	P54727	562953	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

Fragment-ion (m/z)	70.064	72.082	74.060	84.079	86.096	102.053	130.083	147.114	183.117	185.084	199.106	227.100	229.121
Frac. Inten.(% of TIC)	0.01	0.10	2.24	0.37	27.95	0.09	5.23	3.13	3.42	2.22	6.92	3.59	4.92
Rel. Inten.(% of BP)	0.03	0.36	8.00	1.33	100.00	0.34	18.71	11.21	12.24	7.95	24.76	12.86	17.61
Score	0.20	0.50	1.50	0.50	0.50	1.00	0.50	1.50	-0.12	-0.08	0.50	0.75	0.75
Ion-type	PR	V	y^{++}_1	KQ	a_1	E	y_1-NH_3	y_1			PE-28	PE	b_2
Delta ppm	-21.8	22.5	3.5	-17.5	-21.2	-16.2	-26.6	11.5			-16.2	-14.7	5.8
					0.50								
					LI								ID
					-8.4								5.8

Fragment-ion (m/z)	230.113	356.151	427.260	439.174	457.216	555.287^{+2}	564.813^{+2}	573.378	672.473	773.481	902.557	1031.609
Frac. Inten.(% of TIC)	2.60	2.37	2.40	4.78	2.58	2.23	8.12	4.10	2.96	2.91	2.48	2.26
Rel. Inten.(% of BP)	9.31	8.48	8.60	17.10	9.23	7.98	29.04	14.68	10.58	10.40	8.88	8.07
Score	-0.09	0.75	0.75	-0.17	0.50	-0.08	1.50	1.50	-0.11	1.50	1.50	1.50
Ion-type		PEE	kAL		b_4		y_9^{+2}	y_4		y_6	y_7	y_8
Delta ppm		12.6	-16.2		-31.7		-5.5	11.2		-9.1	29.3	34.7



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Result Summary

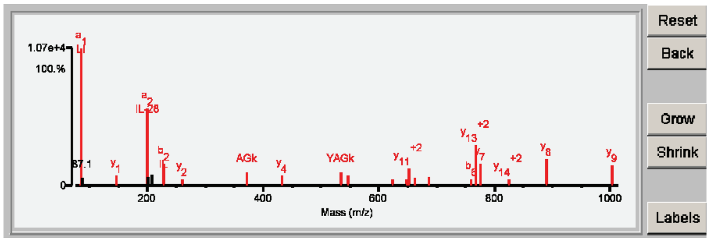
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	25.30	94.4	13	3/25	K51k	(K)LIYAGkILNDDTALK(E)	1647.9316	114.0514	4.8	43171.4/4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1
2	11.10	68.1	6	14/25	K60k	(K)LIYAGKILNDDTALk(E)	1647.9316	114.0514	4.8	43171.4/4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1
3	8.82	68.8	4	14/25	K136k	(R)ILGKGSFGIVIEATDk(E)	1647.9316	114.0514	4.8	57831.2/6.61	HUMAN	Q9BYT3	Serine/threonine-protein kinase 33 OS=Homo sapiens GN=STK33 PE=1 SV=1
4	8.48	66.2	5	14/25	K48k	(K)ILVEFVVDSQkKDK(L)	1647.9316	114.0514	4.8	31293.6/5.10	HUMAN	O95229	ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2
5	7.60	59.7	5	15/25	K298k	(R)ILNVDNPHVSAIVEk(W)	1647.9064	114.0766	19.1	104037.7/7.28	HUMAN	Q13003	Glutamate receptor, ionotropic kainate 3 OS=Homo sapiens GN=GRIK3 PE=1 SV=3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	25.30	94.4	13	3/25	K51k	(K) L/I|Y/A/G/k|I/L/N/D/D/T A/L/K (E)	1647.9316	114.0514	4.8	43171.4/4.79	HUMAN	P54727	562953	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

Fragment-ion (m/z)	84.081	86.097	87.100	136.075	147.113	199.180	200.182	207.113	227.176	260.198	371.203	432.280	534.266
Frac. Inten.(% of TIC)	0.27	27.69	1.54	0.14	2.11	15.45	1.74	2.29	4.27	1.29	2.67	1.92	2.66
Rel. Inten.(% of BP)	0.99	100.00	5.54	0.50	7.60	55.79	6.30	8.28	15.42	4.64	9.66	6.94	9.61
Score	0.50	0.50	-0.06	1.00	1.50	0.50	-0.06	-0.08	0.75	1.50	0.75	1.50	0.75
Ion-type	KQ	a_1		Y	y_1	a_2			b_2	y_2	AGk	y_4	YAGk
Delta ppm	-2.1	-11.9 0.50 LI 0.9		-5.8	-2.1	-8.5 IL-28 -8.5			-4.0 IL -4.0	3.6	-4.7	-4.3	-3.7

Fragment-ion (m/z)	547.311	622.842^{+2}	647.349	651.363^{+2}	662.335	686.874^{+2}	760.430	768.413^{+2}	776.377	824.962^{+2}	889.461	1002.548
Frac. Inten.(% of TIC)	1.93	1.31	1.27	3.40	1.57	1.87	1.33	8.12	4.35	1.21	5.40	4.20
Rel. Inten.(% of BP)	6.99	4.73	4.59	12.26	5.67	6.74	4.79	29.34	15.70	4.39	19.50	15.15
Score	1.50	1.50	0.75	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_5	y_{10}^{+2}	YAGkI	y_{11}^{+2}	y_6	y_{12}^{+2}	b_6	y_{13}^{+2}	y_7	y_{14}^{+2}	y_8	y_9
Delta ppm	5.1	-5.4	-5.0	10.1	-1.4	-2.3	-8.5	7.5	-1.8	16.5	-2.0	1.0



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Result Summary

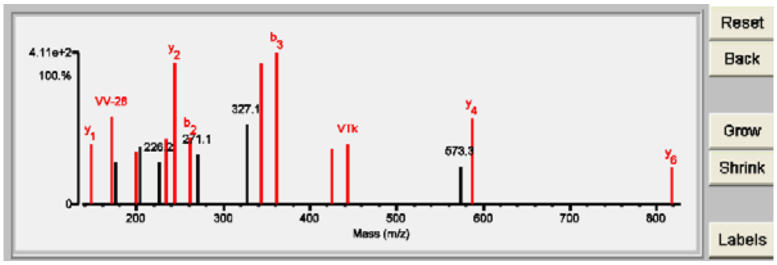
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	10.04	71.3	6	8/23	K76k	(K)NFVVVMVTkPK(A)	1261.7337	114.0453	1.7	43171.4/4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.04	71.3	6	8/23	K76k	(K) N F\V\V V/M V/T k/P/K (A)	1261.7337	114.0453	1.7	43171.4/4.79	HUMAN	P54727	562953	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

Fragment-ion (m/z)	72.081	84.080	104.053	105.050	120.080	147.113	171.145	175.083	199.145	203.117	226.152	234.126
Frac. Inten.(% of TIC)	0.66	0.41	4.04	2.98	0.22	4.18	6.09	2.97	3.64	4.06	2.97	4.52
Rel. Inten.(% of BP)	6.20	3.88	38.22	28.20	2.10	39.59	57.66	28.15	34.43	38.39	28.13	42.80
Score	0.50	0.50	-0.38	-0.28	1.00	1.50	0.50	-0.28	0.75	-0.38	-0.28	0.50
Ion-type	V	KQ			F	y_1	VV-28		VV			a_2
Delta ppm	5.9	-11.6			-4.8	0.7	-22.7		5.5			8.5

Fragment-ion (m/z)	244.164	262.118	271.140	327.127	344.189	361.188	425.245	443.259	573.327	587.343	817.451
Frac. Inten.(% of TIC)	9.87	4.68	3.46	5.52	9.80	10.57	3.90	4.21	2.65	6.00	2.59
Rel. Inten.(% of BP)	93.45	44.28	32.75	52.29	92.73	100.00	36.91	39.85	25.11	56.81	24.55
Score	1.50	0.50	-0.33	-0.52	0.75	0.50	0.50	0.75	-0.25	1.50	1.50
Ion-type	y_2	b_2			Tk	b_3	VTk-H_2O	VTk		y_4	y_6
Delta ppm	-4.8	-4.3			-10.9	2.4	-13.2	-4.6		-13.5	-10.7



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Result Summary

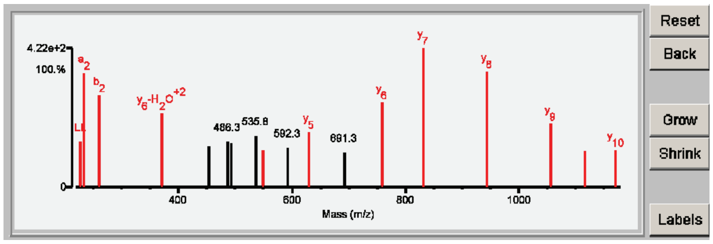
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	11.11	71.5	7	9/25	K129k	(R)FLEQQNkILLAELEQLK(G)	2057.1641	114.0615	8.6	53651.9/5.06	HUMAN	P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.11	71.5	7	9/25	K129k	(R) F L\E Q Q N k/I|L/L/A/E/L E Q L K (G)	2057.1641	114.0615	8.6	53651.9/5.06	HUMAN	P08670	837031	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Fragment-ion (m/z)	84.080	86.096	101.072	120.076	157.134	201.079	215.135	227.175	233.162	261.159	371.225^{+2}	453.214^{+2}	486.303
Frac. Inten.(% of TIC)	0.25	0.53	0.10	0.14	2.83	2.80	2.77	3.63	9.04	7.21	5.85	3.20	3.60
Rel. Inten.(% of BP)	2.32	4.84	0.90	1.28	25.95	25.62	25.40	33.20	82.75	66.04	53.53	29.29	33.01
Score	0.50	0.22		1.00	-0.26	-0.26	-0.25	0.75	0.50	0.50	0.50	-0.29	-0.33
Ion-type	KQ	LI	KQ	F				LL	a_2	b_2	y_6-H_2O^{+2}		
Delta ppm	-5.7	-9.6		-36.4				-8.4	-18.6	-5.6	37.5		

Fragment-ion (m/z)	493.219^{+2}	535.759^{+2}	549.786^{+2}	592.323^{+2}	630.375	691.349	759.430	830.472	943.522	1056.621	1115.569	1169.702
Frac. Inten.(% of TIC)	3.48	4.02	2.98	3.08	4.31	2.76	6.63	10.92	9.12	4.95	2.89	2.91
Rel. Inten.(% of BP)	31.85	36.80	27.32	28.25	39.45	25.26	60.71	100.00	83.53	45.36	26.42	26.64
Score	-0.32	-0.37	0.25	-0.28	1.50	-0.25	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type			b_8-NH_3^{+2}		y_5		y_6	y_7	y_8	y_9	b_8	y_{10}
Delta ppm			6.0		-10.5		6.6	12.6	-25.1	-8.9	-14.4	-10.2



Result Summary

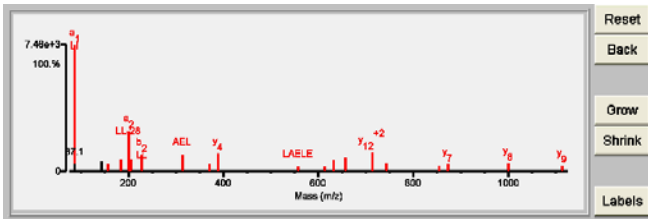
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	21.82	94.0	9	3/25	K139k	(K)ILLAELEQLkGQGK(S)	1539.9105	114.0585	9.4	53651.9/5.06	HUMAN	P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4
2	18.58	85.8	7	5/25	K143k	(K)ILLAELEQLKGQGk(S)	1539.9105	114.0585	9.4	53651.9/5.06	HUMAN	P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4
3	7.39	54.3	3	13/25	K795k	(K)kELLKALLNEIAGK(Q)	1539.9469	114.0221	-12.6	122521.8/6.23	HUMAN	RQ9UPN9	REVERSE E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33 PE=1 SV=2
3	7.39	54.3	3	13/25	K799k	(K)KELLkALLNEIAGK(Q)	1539.9469	114.0221	-12.6	122521.8/6.23	HUMAN	RQ9UPN9	REVERSE E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33 PE=1 SV=2
4	6.61	63.7	2	16/25	K1015k K1023k	(K)ILLSkAIVNEVVk(L)	1425.9039	228.0650	-12.6	182623.1/7.30	HUMAN	RQ70Z35	REVERSE Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens GN=PREX2 PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.82	94.0	9	3/25	K139k	(K) I L|L/A E/L/E/Q/L/k/G Q/G K (S)	1539.9105	114.0585	9.4	53651.9/5.06	HUMAN	P08670	837031	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Fragment-ion (m/z)	84.079	86.096	87.098	102.053	143.117	157.132	185.128	199.180	200.181	201.087	204.135	227.174
Frac. Inten.(% of TIC)	0.18	33.71	1.73	0.04	2.80	1.93	3.34	10.88	1.43	1.54	3.45	4.47
Rel. Inten.(% of BP)	0.53	100.00	5.13	0.13	8.30	5.74	9.91	32.29	4.24	4.58	10.25	13.26
Score	0.50	0.50	-0.05	1.00	-0.08	0.50	0.75	0.50	-0.04	0.75	1.50	0.75
Ion-type	KQ	a_1		E		LA-28	LA	a_2		AE	y_2	b_2
Delta ppm	-22.3	-7.3 0.50 LI -7.3		-19.2		-8.5	-0.3	-0.5 LL-28 -0.5		0.6	1.6	-4.0 LL -4.0

Fragment-ion (m/z)	314.173	371.188	389.215	556.306	613.344^{+2}	631.348	657.870^{+2}	714.399^{+2}	744.444	855.475	872.495	1001.534	1114.621
Frac. Inten.(% of TIC)	4.33	1.79	4.80	1.41	1.38	2.94	3.71	5.00	2.15	1.45	1.78	2.15	1.60
Rel. Inten.(% of BP)	12.83	5.31	14.24	4.19	4.11	8.71	10.99	14.85	6.38	4.30	5.28	6.37	4.75
Score	0.75	0.75	1.50	0.75	0.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	AEL	EQL	y_4	LAELE	$y_{10}\text{-}H_2O^{+2}$	y_5	y_{11}^{+2}	y_{12}^{+2}	y_6	$y_7\text{-}NH_3$	y_7	y_8	y_9
Delta ppm	7.8	-11.3	2.0	15.1	22.8	-6.3	23.4	3.1	10.9	8.3	0.2	-3.6	-0.4



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Result Summary

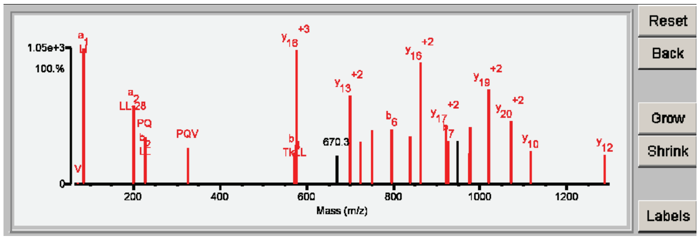
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	24.97	94.9	15	2/25	K396k	(K)ILTkLLEVSDDPQVLAVAAHDVGEYVR(H)	2950.5884	114.0746	10.3	55883.4/6.07	HUMAN	Q9UI12	V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.97	94.9	15	2/25	K396k	(K) I L\T k\L L\E|V/S/D/D/P Q/V/L/A V/A A/H/D/V G E Y V R (H)	2950.5884	114.0746	10.3	55883.4/6.07	HUMAN	Q9UI12	832021	V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1

Fragment-ion (m/z)	72.081	84.080	86.095	199.179	226.113	227.177	325.187	570.365	575.301^{+3}	670.320	700.378^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.13 1.37 0.50 V 1.7	0.06 0.65 0.50 KQ -14.0	9.75 100.00 0.50 a_1 -30.5 0.50 LI -17.7	5.61 57.58 0.50 a_2 -12.5 LL-28 -12.5	3.37 34.61 0.75 PQ -27.5	2.35 24.15 0.75 b_2 -0.0 LL -0.0	2.66 27.28 0.75 PQV -5.0	2.28 23.40 0.75 b_4 5.7 TkLL 5.7	9.66 99.06 1.50 y_{16}^{+3} -13.3	2.03 20.78 -0.21	6.34 65.07 1.50 y_{13}^{+2} 10.8

Fragment-ion (m/z)	722.369	749.904^{+2}	796.533	837.441	862.467^{+2}	919.982^{+2}	925.565	947.172	974.479	977.479^{+2}	1021.015^{+2}	1070.522^{+2}	1116.553	1286.669
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.03 31.04 1.50 y_6 -19.7	3.88 39.83 1.50 y_{14}^{+2} -0.6	3.97 40.75 0.50 b_6 3.6	3.42 35.07 1.50 y_7 36.4	8.73 89.59 1.50 y_{16}^{+2} 8.8	4.25 43.57 1.50 y_{17}^{+2} 9.9	3.15 32.32 0.50 b_7 -8.5	3.12 31.96 -0.32	2.19 22.45 1.50 y_8 10.2	4.14 42.42 1.50 y_{18}^{+2} -8.3	6.80 69.77 1.50 y_{19}^{+2} 11.6	4.53 46.49 1.50 y_{20}^{+2} -14.4	2.40 24.59 1.50 y_{10} 9.0	2.13 21.89 1.50 y_{12} 16.0



Result Summary

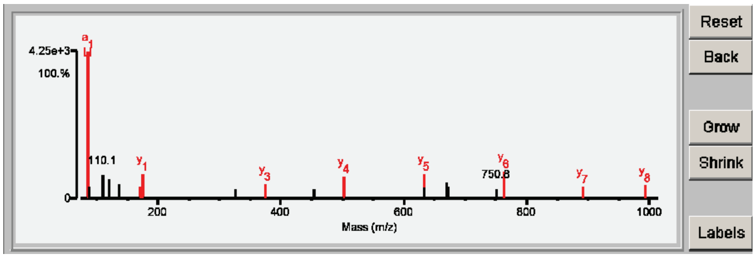
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	Protein Name
1	12.31	63.9	8	12/25	K116k	(K)IGLTkALTQMEEAQR(K)	1688.9000	114.0445	0.9	31293.6/5.10	HUMAN	O95229	ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2

Detailed Results

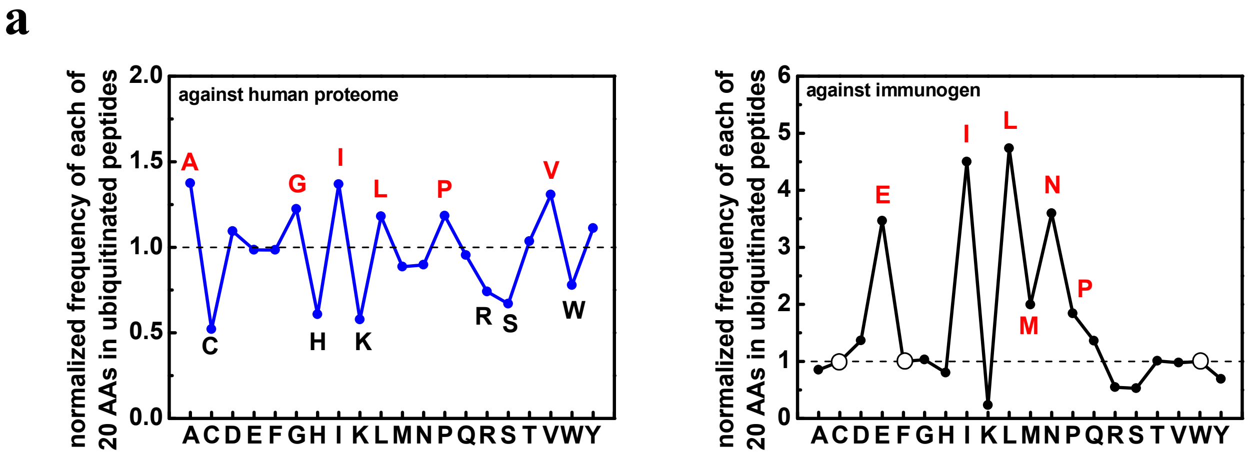
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.31	63.9	8	12/25	K116k	(K) I G\L T k A L/T/Q/M/E/E/A Q/R (K)	1688.9000	114.0445	0.9	31293.6/5.10	HUMAN	O95229	933375	ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2

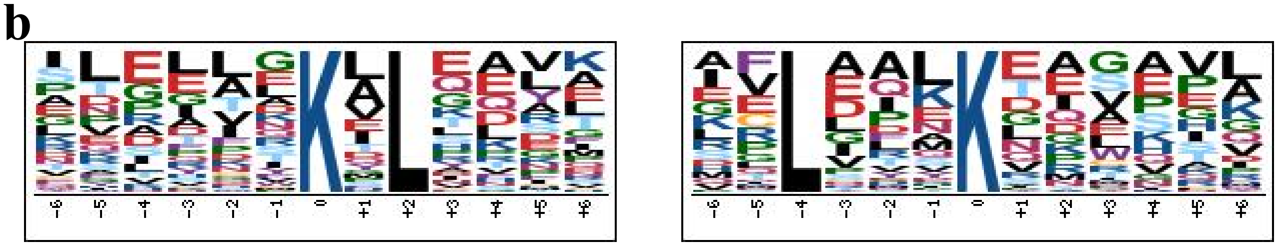
Fragment-ion (m/z)	70.066	72.080	84.044	84.082	86.097	87.100	101.072	110.072	120.080	136.076	171.108	175.119
Frac. Inten.(% of TIC)	0.01	3.69	0.12	0.13	31.72	2.59	0.15	4.99	4.14	3.24	2.46	5.21
Rel. Inten.(% of BP)	0.04	11.64	0.39	0.42	100.00	8.18	0.47	15.73	13.07	10.21	7.75	16.41
Score	0.20	-0.12	1.00		0.50	-0.08	0.50	-0.16	-0.13	-0.10	0.75	1.50
Ion-type	PR		E	QK	a_1		QK				b_2	y_1
Delta ppm	5.3		-1.1		-10.7		5.5				-31.6	-2.0
					0.50						GL	
					LI						-31.6	
					2.0							

Fragment-ion (m/z)	325.201	374.215	452.926^{+3}	503.274	632.299	633.297^{+2}	670.303	670.644	670.985^{+2}	750.838	763.348	891.396	992.461
Frac. Inten.(% of TIC)	2.09	3.04	2.12	4.63	5.25	2.38	2.73	3.46	2.53	2.09	5.74	2.63	2.85
Rel. Inten.(% of BP)	6.59	9.59	6.67	14.60	16.56	7.51	8.59	10.91	7.97	6.58	18.10	8.28	9.00
Score	-0.07	1.50	-0.07	1.50	1.50	-0.08	-0.09	-0.11	-0.08	-0.07	1.50	1.50	1.50
Ion-type		y_3		y_4	y_5						y_6	y_7	y_8
Delta ppm		1.0		33.9	-0.7						9.8	-3.6	14.2



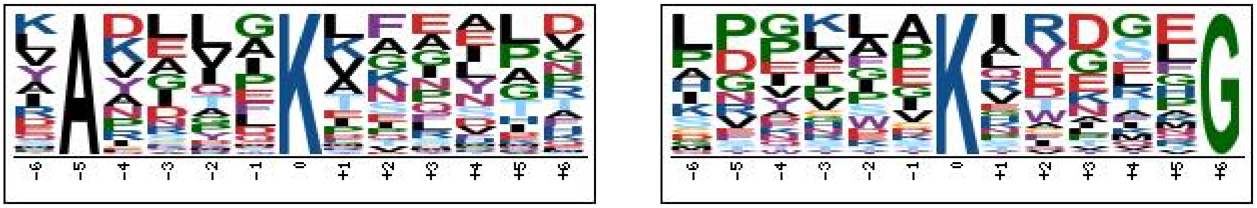
Supplementary Fig. 7





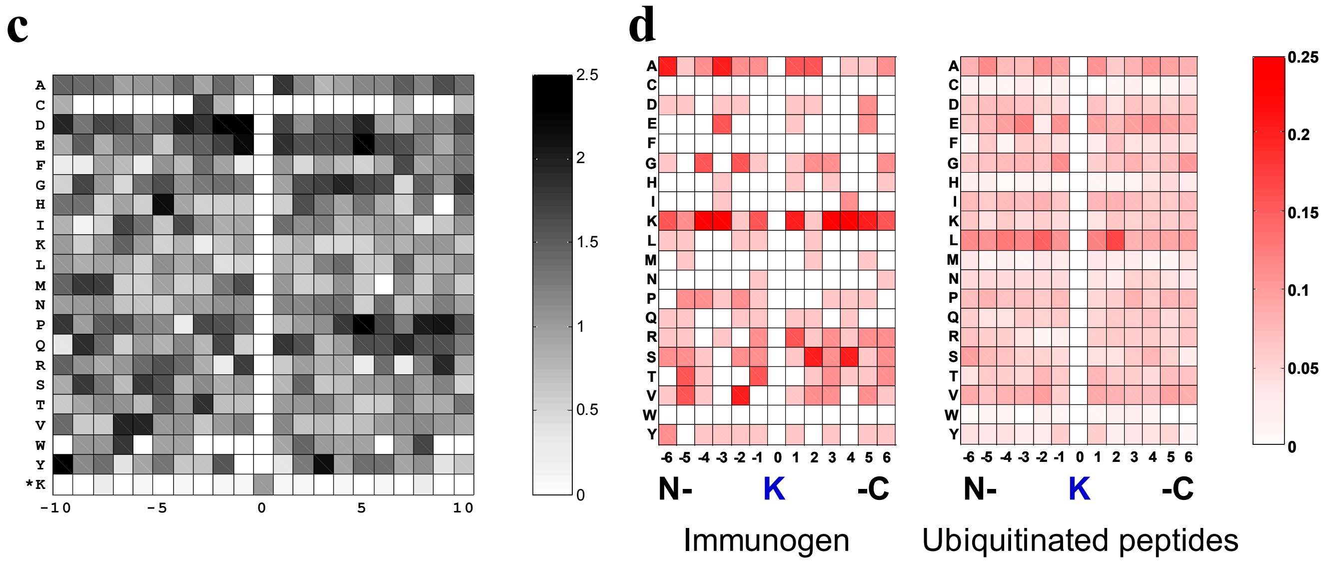
$p < 10^{-5}$ (68 matches, 1.8 fold increase)

$p < 10^{-3}$ (42 matches, 1.8 fold increase)



$p < 10^{-4}$ (38 matches, 2.1 fold increase)

$p < 10^{-3}$ (24 matches, 2.1 fold increase)



Supplementary Fig. 7 Ubiquitinated peptides have little preference for backbone amino acid sequences.

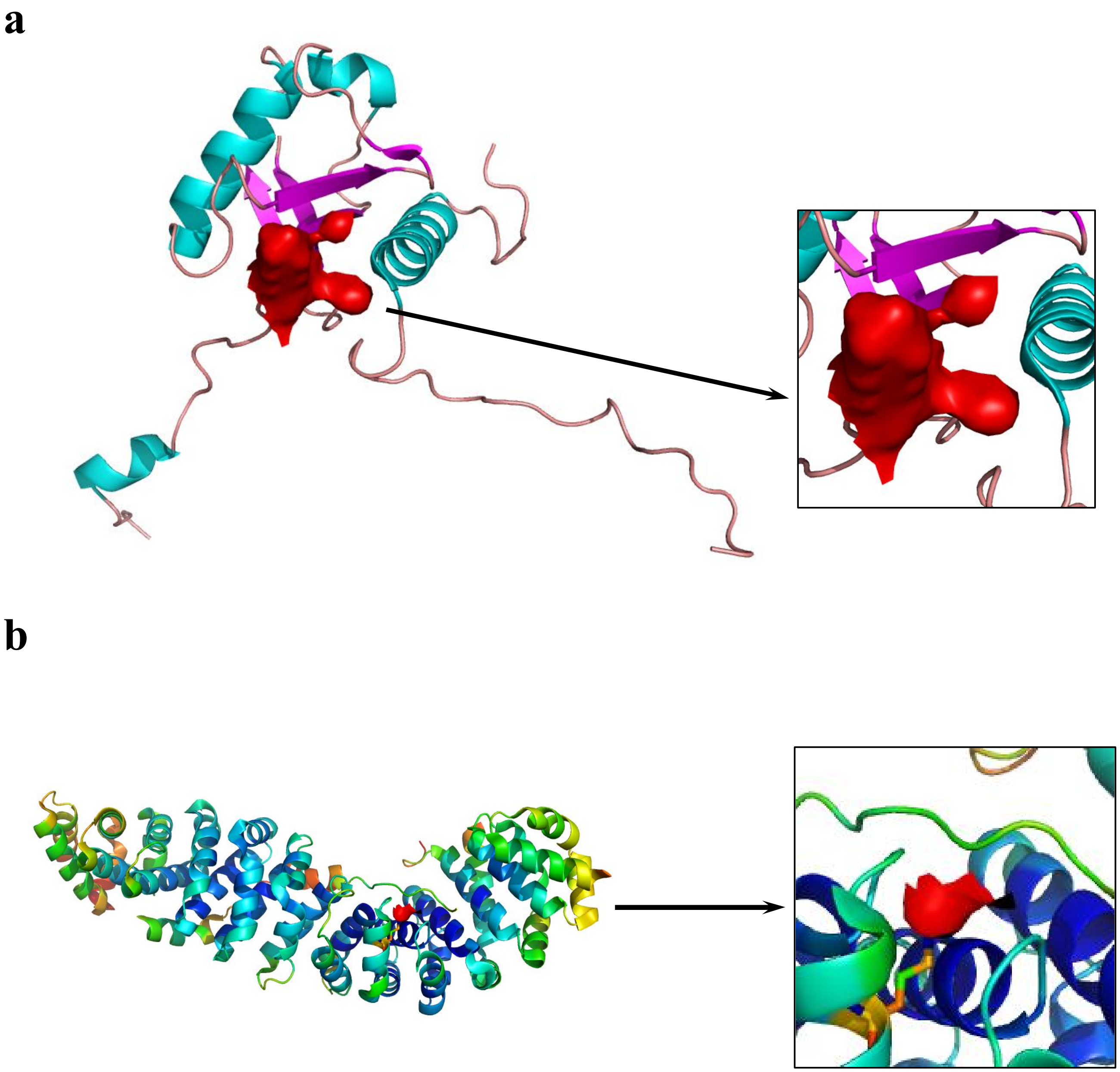
(**a**) Normalized frequency of each of the 20 amino acids within a six amino acid span on either side of the ubiquitinated lysines. Normalization was carried out against the frequency calculated for each amino acid using all lysines in all human proteins in the Swiss-Prot database (v57.2, May 5, 2009) (left panel) or against the immunogen (bovine histone III-S) used for the antibody production (right panel). Note that (**1**) there are no Cys (C), Phe (F), and Trp (W) in the immunogen so that the normalized frequency for these amino acids is artificially set to 1.0 and plotted with open circles; and (**2**) the ubiquitinated lysines were not counted in this analysis. In the left panel showing residues adjacent to the modified lysine in ubiquitin remnant peptides, Ala, Gly, Ile, Leu, Pro, and Val, are slightly enriched (studentôs *t* test, $p < 0.0001$) and Cys, His, Lys, Arg, Ser, and Trp are slightly depleted (studentôs t test, $p < 0.0001$).

(**b**) Sequence logo representations of extracted motifs for the ubiquitinated peptides obtained using the Motif-x[4] search algorithm. The significance, number of matches, and the fold increase of the motif were shown below each logo. Sequence logos were automatically generated by Motif-x using Weblogo[5, 6]. In sequence logos, the height of each residue is proportional to the frequency in the subset of peptides[4].

(**c**) Backbone amino acid sequence analysis of ubiquitinated peptides detected in yeast. A density map was prepared as described in **Fig. 3b** except we used the proteins found to be ubiquitinated in yeast described in a previous proteomic study[7]. Unlike in mammalian proteins, Asp, Glu, His, and Pro are highly enriched (>2.3 times of the expected value in the yeast proteome) at some positions.

(**d**) The frequency of each of the 20 amino acids at the indicated positions of the N- or C-termini of the lysines in the immunogen or in the ubiquitinated peptides. The difference between these density maps from the one in **Fig. 3b** is that here the data are not normalized to the frequency of each of 20 amino acids at the same position using all lysines in the human Swiss-Prot database. As can be seen, the two density maps clearly show that amino acids that surround the modified lysines in the immunogen are not similar to the amino acids that surround the modified lysines in the ubiquitin remnant peptides. This confirms that there is no major bias or preference for amino acid context surrounding the diglycine-modified lysine in the peptides that are immunoprecipitated by the GX41 antibody.

Supplementary Fig. 8

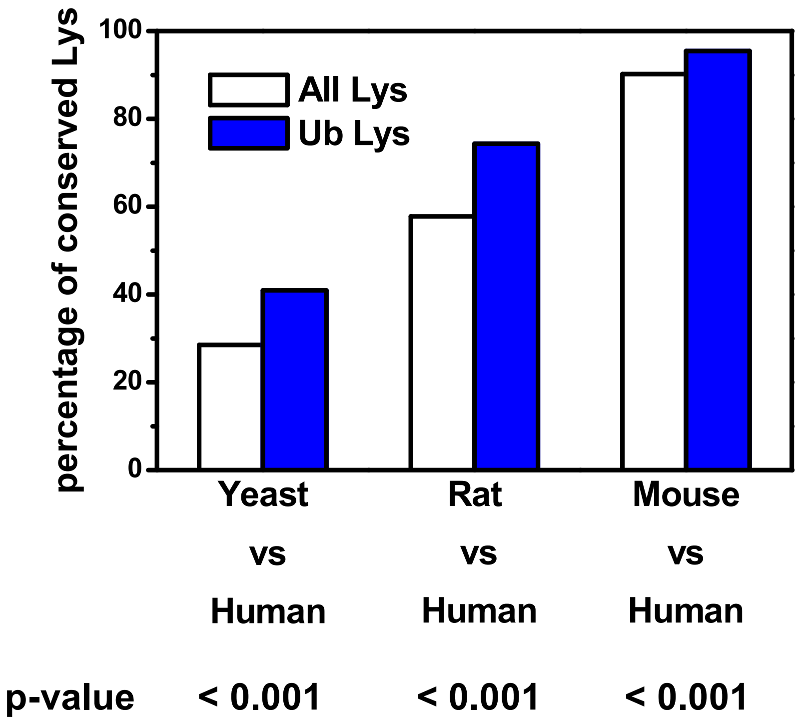


Supplementary Fig. 8 Both solvent exposed and buried lysines can be ubiquitinated.

(**a**) A solvent exposed ubiquitination site, lysine 76, from UV excision repair protein RAD23 homolog B (PDB:1UEL). The solvent-accessible area of lysines is shown in red.

(**b**) A solvent buried ubiquitination site, lysine 435, from β-catenin (PDB:1JDH). The snapshots were prepared using PyMOL[8]. Buried lysines are interesting since some mechanism must exist to increase their solvent exposure in order for them to be ubiquitinated.

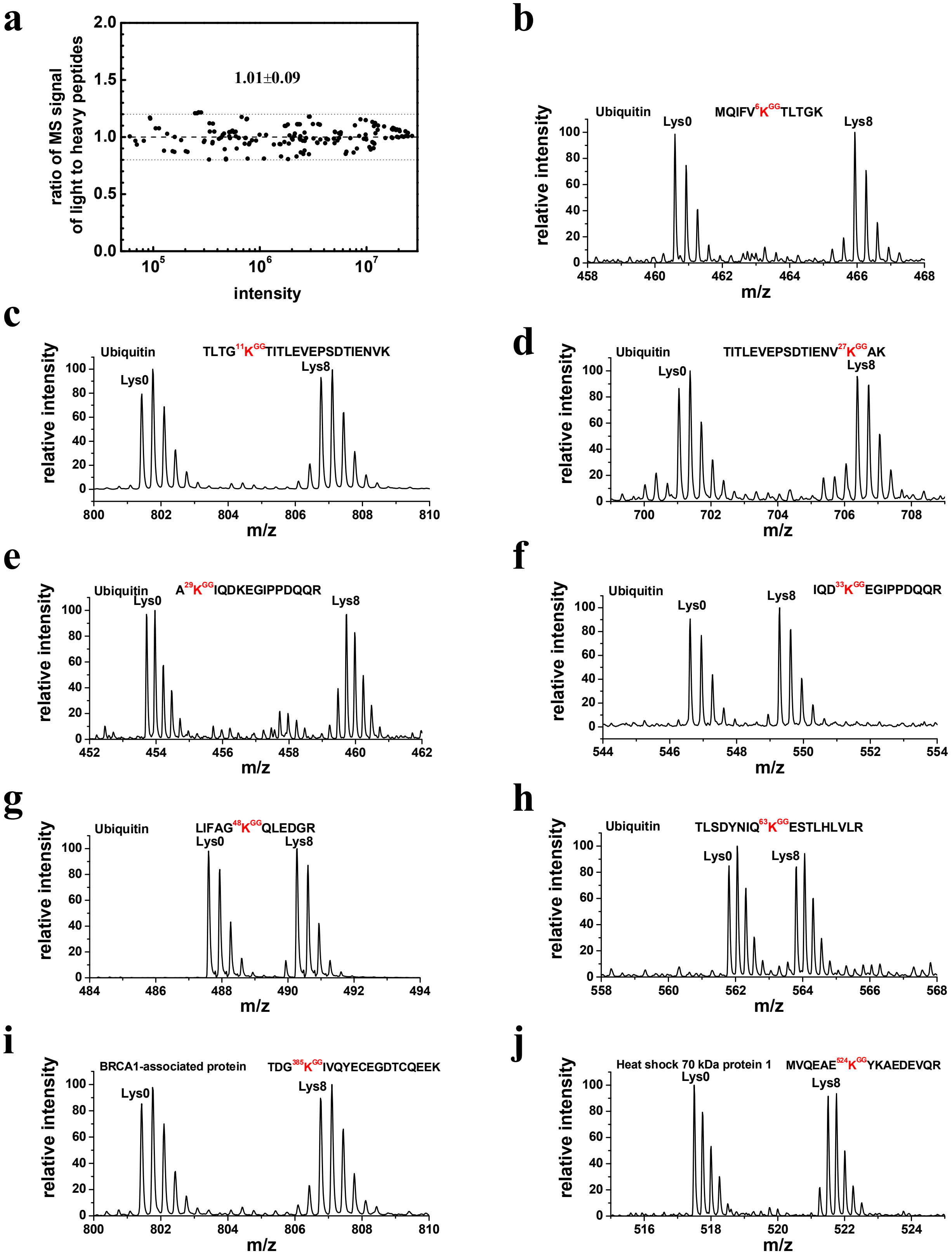
Supplementary Fig. 9



Supplementary Fig. 9 Ubiquitinated lysines are highly conserved in different organisms.

Lysine conservation in human, mouse, rat and yeast for all lysine residues (All Lys) and ubiquitinated lysine residues (Ub Lys) for the ubiquitinated proteins identified in our experiments. The sequence alignment of human proteins is performed by Basic Local Alignment Search Tool (BLAST) and the best hit for each human ubiquitinated protein in three organisms, mouse, rat and yeast, is used for the analysis of lysine conservation. Matches are found for all the ubiquitinated proteins in the mouse and the rat proteome, while matches were found for all but four proteins in the yeast proteome. This analysis showed that the ubiquitinated lysines are more conserved than lysines in general in three organisms.

Supplementary Fig. 10



Supplementary Fig. 10 The anti-diglycyl-lysine monoclonal antibody can quantitatively enrich for and quantitate ubiquitinated peptides in SILAC experiment.

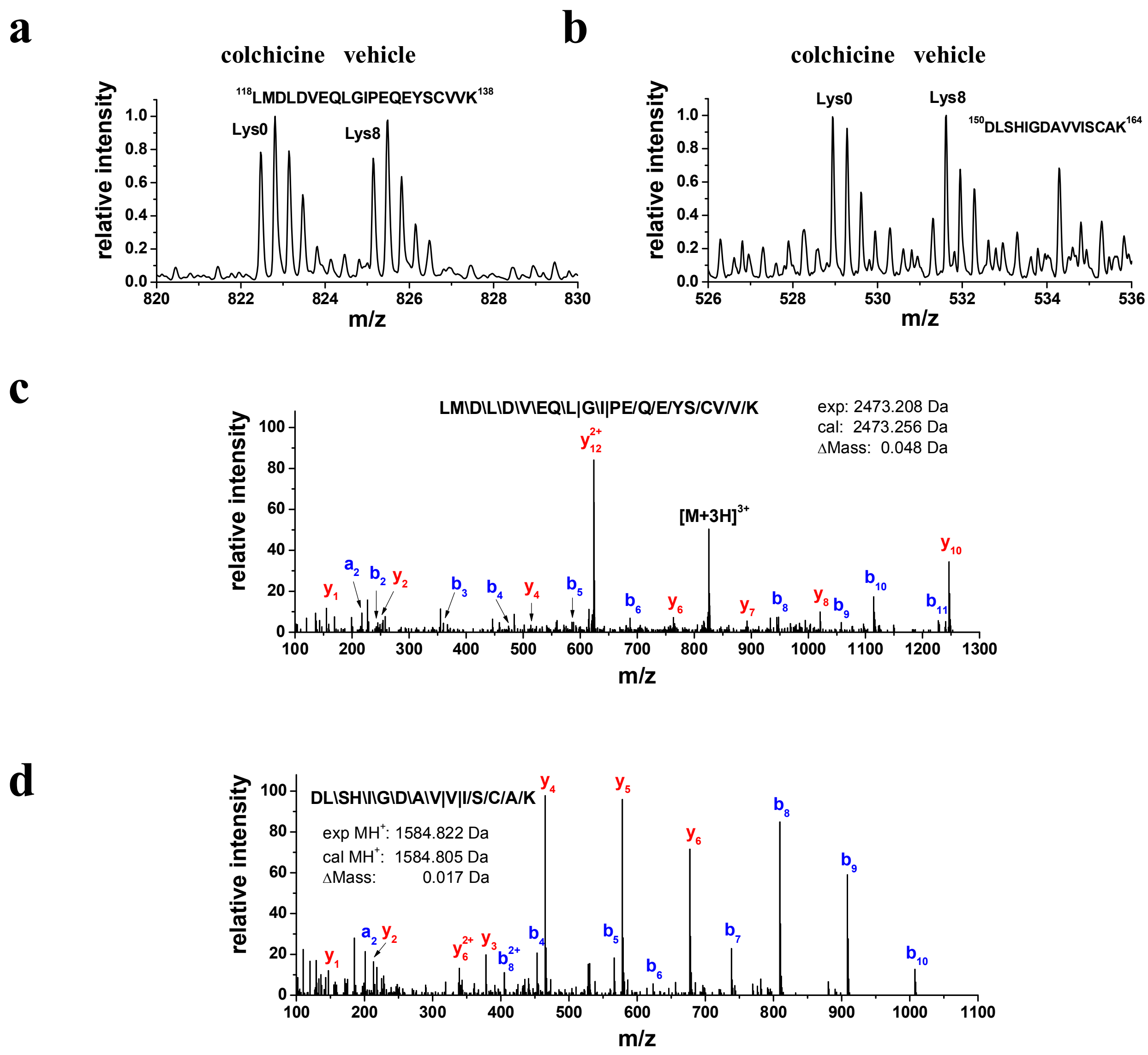
(**a**) The anti-diglycyl-lysine antibody immunoprecipitation can be used for the quantification of ubiquitinated peptides in connection with SILAC approach. Cells were metabolically labeled with light or heavy lysine and cells were mixed prior to Ni-NTA affinity purification, trypsin digestion and immunoaffinity purification. We selected peptides at a range of MS intensity to determine the ratio of light to heavy. An approximate 1:1 ratio was seen over the entire range of selected ion intensities. The average ratio (1.01) and 2X of its standard deviation (2X 0.09) are indicated with dotted lines in the figure.

HEK293 cells were labeled with either light or heavy lysines in SILAC medium and transfected with a plasmid expressing His_6-tagged ubiquitin. An equal amount of cells from each of the labeled condition both treated with 25 μM LLnL for 16 hours, are mixed, lysed, and purified using Ni-NTA resin followed by trypsin digestion, anti-diglycyl-lysine antibody immunoprecipitation, and LC-MS/MS analysis.

(**b-j**) Examples of MS spectra of nine ubiquitinated peptides from ubiquitin, BRCA1 associated protein, and heat shock 70kD protein 1 obtained from the sample described above.

Almost all the ubiquitinated peptides have a ratio within 20% of the expected value, 1.0. The ratios of the representative ubiquitinated peptides in light and heavy forms are very close to 1.0. These results demonstrated that the monoclonal antibody can be used for peptide quantification in SILAC approach and also confirmed the labeled cells are equally mixed prior to affinity purification.

Supplementary Fig. 11



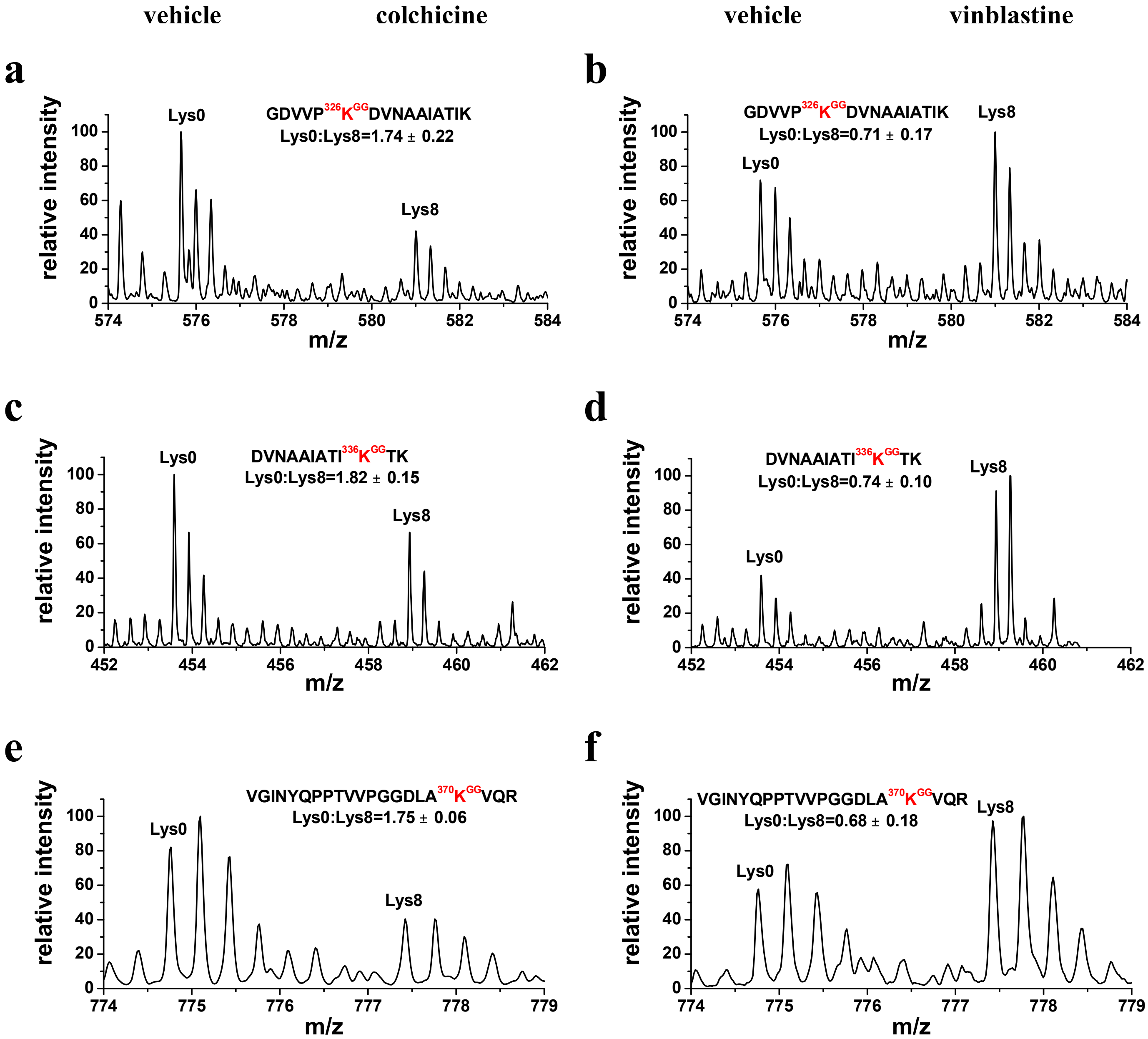
Supplementary Fig. 11 MS and MS/MS of peptides from non-ubiquitinated PNCA used to normalize ubiquitinated PNCA peptides in SILAC quantification.

(**a**) and (**b**) The cell lysate from the mixture of light and heavy lysine-labeled cells, treated with colchicine and vehicle, respectively, contains an approximately equal amount of light and heavy lysine-labeled non-ubiquitinated PCNA peptides. Typical MS spectra of two non-ubiquitinated PNCA peptides from the initial cell lysate mixed with same amount of light and heavy lysine-labeled cells prior to the affinity purification by Ni-NTA resin. These data suggest that total PCNA levels do not change substantially as a result of colchicine treatment. The average ratio of these light and heavy lysine-labeled peptides was used for the normalization of ubiquitinated PNCA peptides from colchicine- and vehicle-treated samples.

(**c**) and (**d**) MS/MS spectra of non-ubiquitinated PCNA peptides used for normalization to confirm their identity in **(a)** and **(b)**, respectively. Note that the peptide in **(c)** contains a heavy lysine (Lys8) at the C-termini.

HEK293 cells were grown in SILAC medium with either light (Lys0) or heavy lysines and transfected with His_6-tagged ubiquitin. Light and heavy lysine-labeled HEK293 cells were treated with colchicine (10 μM) and vehicle, respectively, in the presence of proteasome inhibitor (LLnL, 25 μM), for 16 hours. An equal amount of differently labeled cells were mixed, lysed, digested by trypsin, and analyzed by LC-MS/MS.

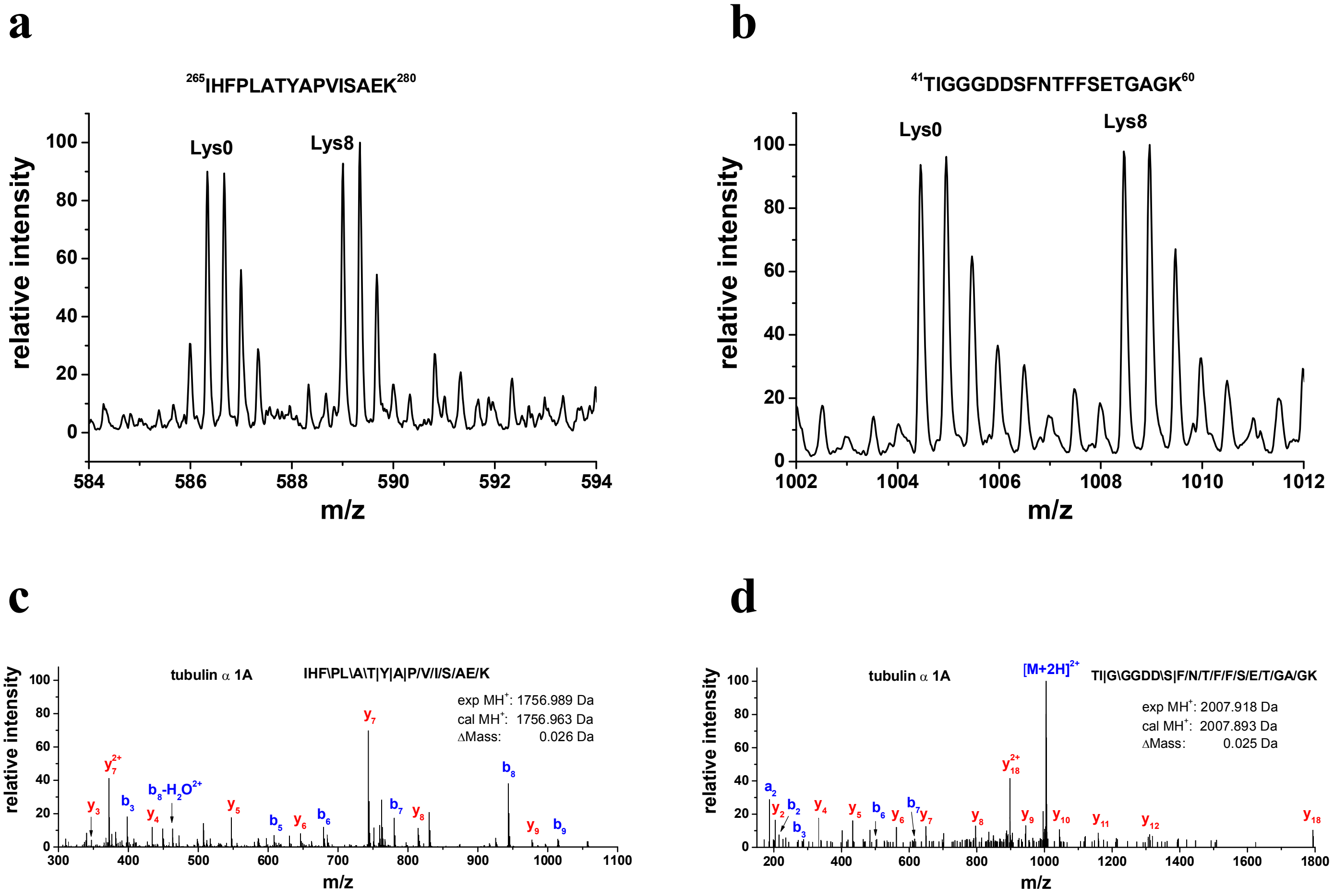
Supplementary Fig. 12



Supplementary Fig. 12 Analysis of the change in tubulin α-1A ubiquitination at three different lysines upon drug treatment.

HEK293 cells were grown in SILAC media containing either light (Lys0) or heavy (Lys8) lysine, and transfected with His$_6$-ubiquitin plasmid. Lys0-labeled cells were treated with 50 µM LLnL (vehicle) while Lys8-labeled cells were treated with 50 µM LLnL and 10 µM colchicine (**a**, **c**, **e**) or 1 µM vinblastine (**b**, **d**, **f**) for 30 min. The same amount of cells from vehicle and drug (colchicine or vinblastine) treated samples were mixed and ubiquitinated peptides were obtained as described in the text. The relative MS ratio between Lys0- and Lys8-labeled ubiquitinated peptides was used for the quantification of ubiquitination level in vehicle or drug treated sample. This ratio is normalized by the average ratio of two unmodified tubulin peptides (**Supplementary Fig. 13**) detected in the initial cell lysate. All the experiments were repeated three times.

Supplementary Fig. 13



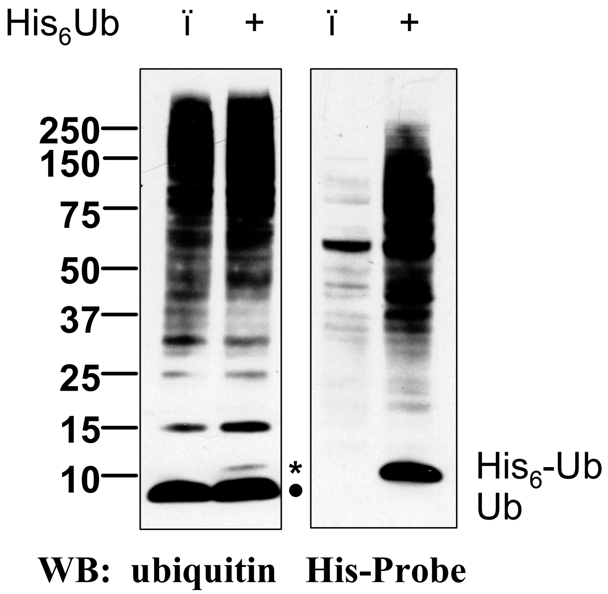
Supplementary Fig. 13 MS and MS/MS of peptides from non-ubiquitinated tubulin α-1A used for SILAC normalization of ubiquitinated tubulin peptides quantified in Supplementary Fig. 12.

(**a**) and (**b**) Typical MS spectra of non-ubiquitinated tubulin peptides obtained from the initial cell lysate mixed with same amount of light and heavy lysine-labeled cells prior to affinity purification by Ni-NTA resin. These peptides were used for the normalization of the ratio of ubiquitinated tubulin peptides from vehicle or drug treated samples.

(**c**) and (**d**) MS/MS spectra, corresponding to the non-ubiquitinated peptides in (**a**) and (**b**) respectively, used to confirm their identity.

HEK293 cells were grown in SILAC medium with either light lysine (Lys0) or heavy lysine (Lys8) and transfected with His$_6$-tagged ubiquitin. Light and heavy HEK293 cells were treated with vehicle and drugs (10 μM colchicine or 1 μM vinblastine), respectively, in the presence of the proteasome inhibitor (LLnL, 50 μM) for 30 min. An equal amount of differently labeled cells were mixed, lysed, digested by trypsin, and analyzed by LC-MS/MS.

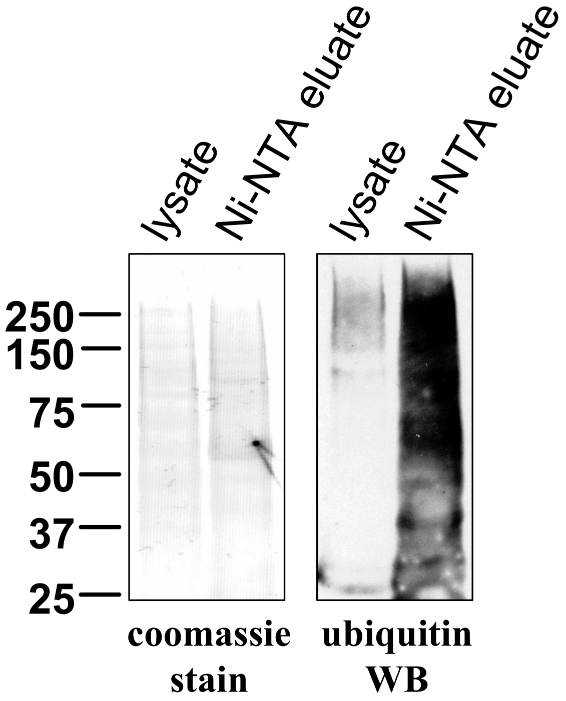
Supplementary Fig. 14



Supplementary Fig. 14 Features of His$_6$-Ub expression in HEK293 cells.

In this experiment we assessed the degree of His$_6$-Ub expression relative to endogenous ubiquitin. Non-transfected and His$_6$-Ub-transfected HEK293 cells treated with LLnL were lysed and the lysates were separated by SDS-PAGE and blotted with anti-ubiquitin antibody (left panel). As can be seen, ubiquitin is readily apparent (solid circle), as well as higher molecular weight ubiquitin-conjugated proteins. Lysates from cells expressing His$_6$-Ub show the heterologously expressed protein (indicated with an asterisk). Only a small amount of this protein is expressed relative to the endogenous amount of ubiquitin, reducing the likelihood that this protein might perturb endogenous ubiquitin pathways. In the right panel, cell lysates are blotted with His-Probe HRP (right panel) to detect His$_6$-Ub and His$_6$-Ub-conjugated proteins. Note that the His-Probe HRP can also detect endogenous histidine rich proteins.

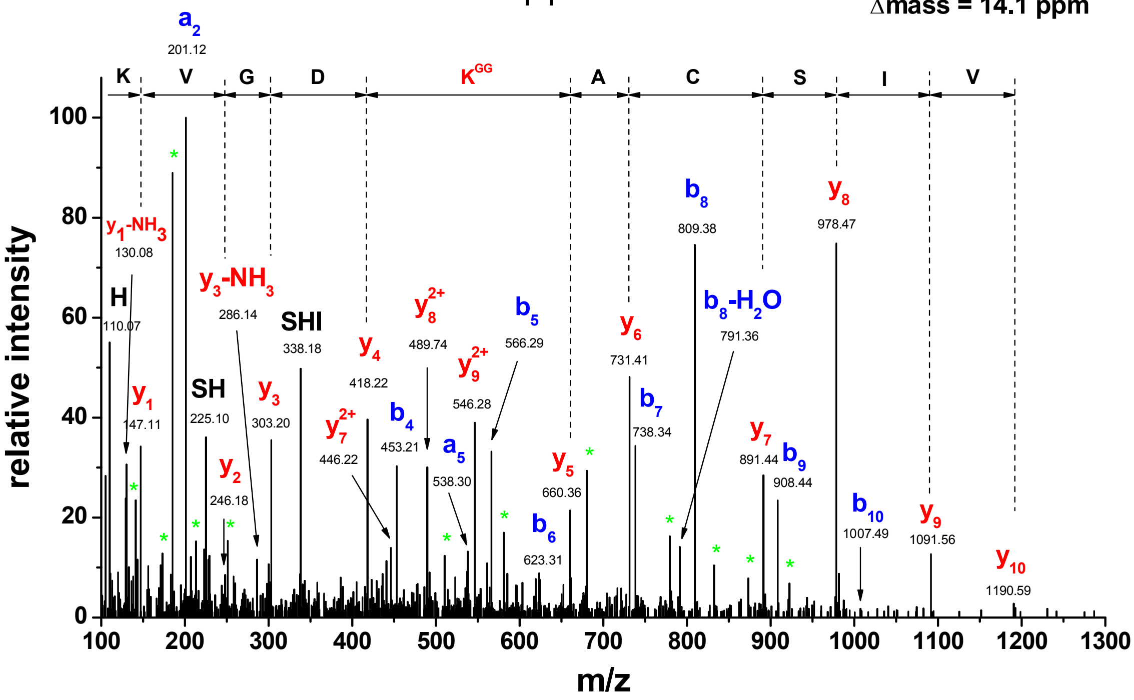
Supplementary Fig. 15



Supplementary Fig. 15 Ubiquitinated proteins are significantly enriched after Ni-NTA resin purification.

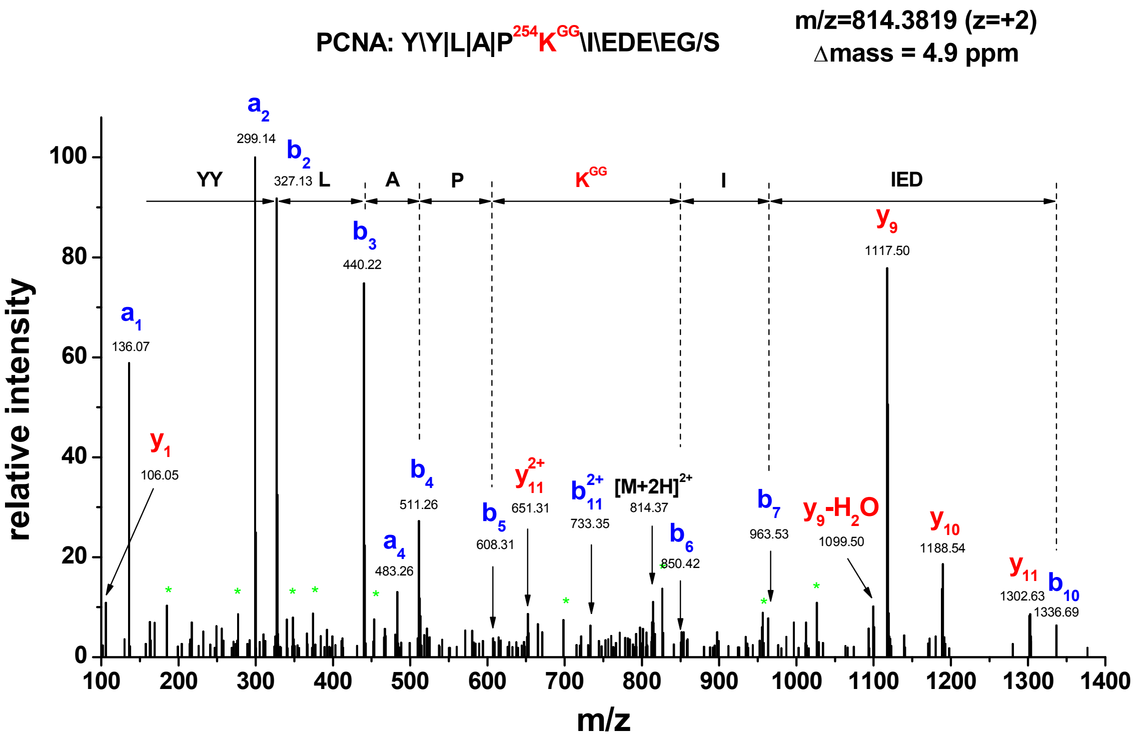
The use of His$_6$-Ub expression allows for the enrichment of ubiquitinated proteins prior to trypsin digestion and ubiquitin remnant peptide immunopurification. In addition to reducing the likelihood that diglycine-modified peptides might derive from modifications other than ubiquitin, this approach can also enrich for otherwise low abundance proteins, thereby facilitating their detection. In the experiment above, the same amount of proteins from cell lysate and Ni-NTA eluate from His$_6$-Ub expressing HEK293 cells were separated by SDS-PAGE and stained with Coomassie blue (left panel) or blotted with anti-ubiquitin antibody (right panel). Ubiquitinated proteins were significantly enriched in the sample after Ni-NTA resin purification.

Supplementary Figure 16



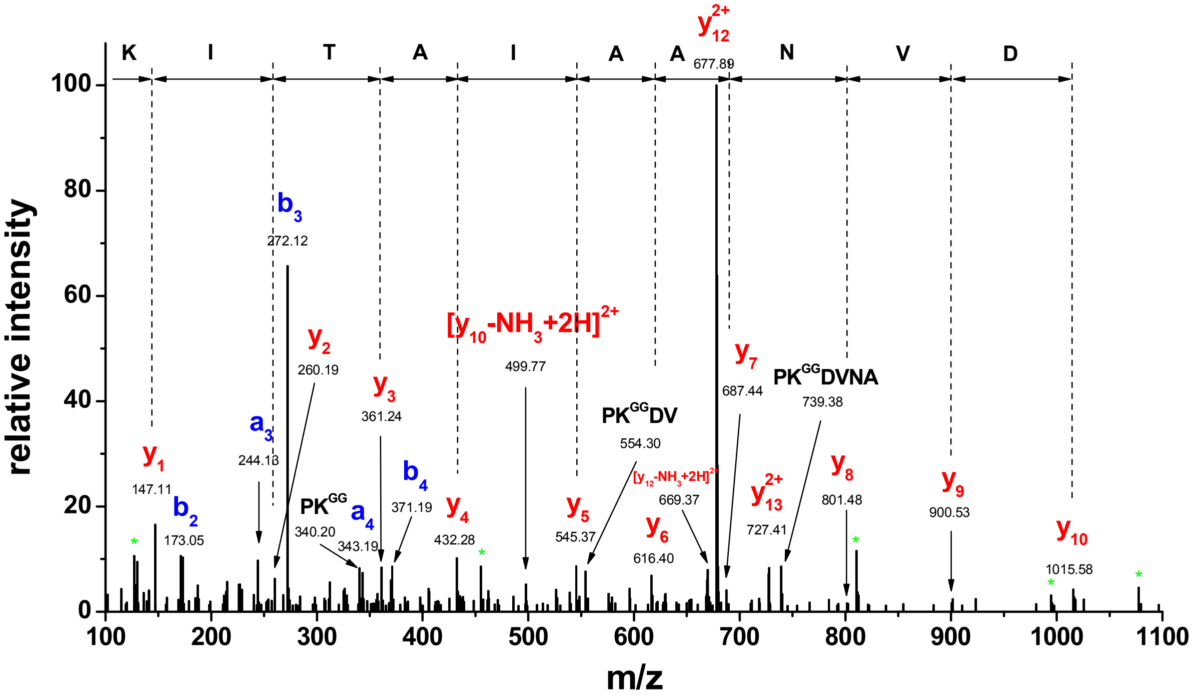
PCNA: DL\SH\I\G\D\A\V|V|I/S/C/A/^{164}K^{GG}/D/G/V/K

m/z=525.2778 (z=+4)
Δmass = 14.1 ppm



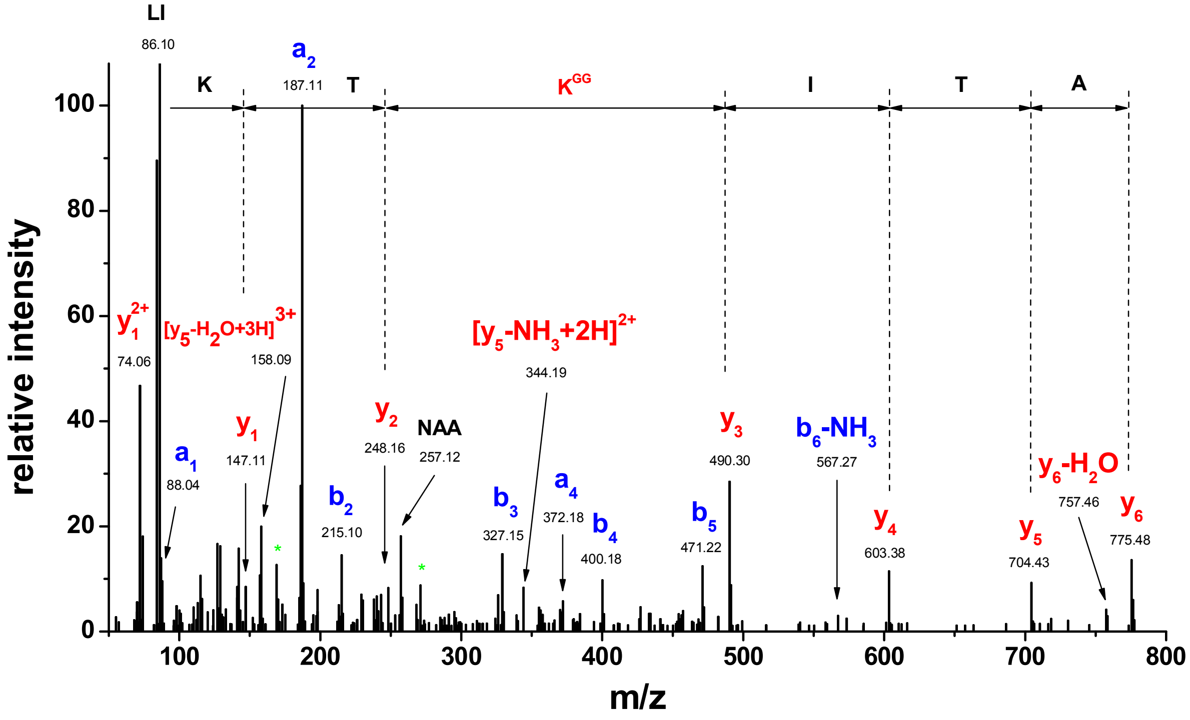
PCNA: Y\Y|L|A|P^{254}K^{GG}\I\EDE\EG/S

m/z=814.3819 (z=+2)
Δmass = 4.9 ppm



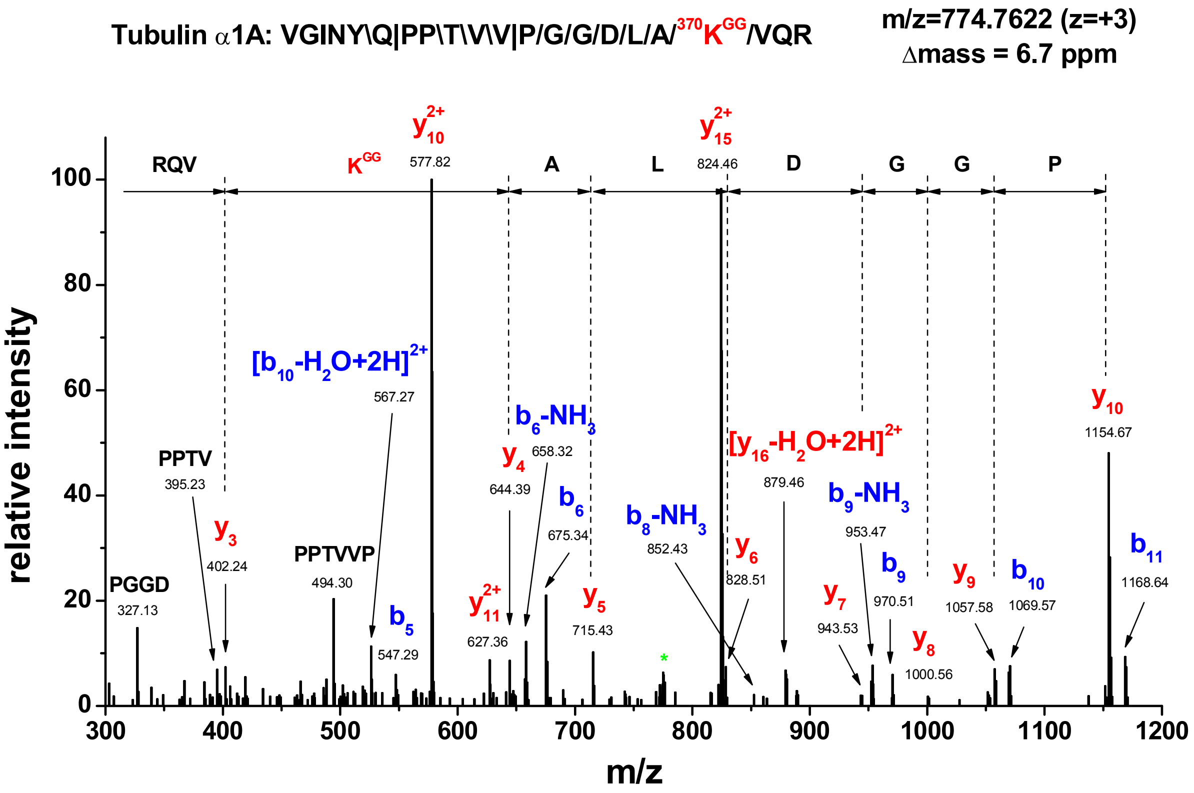
Tubulin α1A: GD\V|V|P^{326}K^{GG}/D/V/N/A/A/I/A/T/I/K

m/z=575.6588 (z=+3)
Δmass = 4.5 ppm



Tubulin α1A: D\V\N\A\A\I|A/T/I/^{336}K^{GG}/T/K

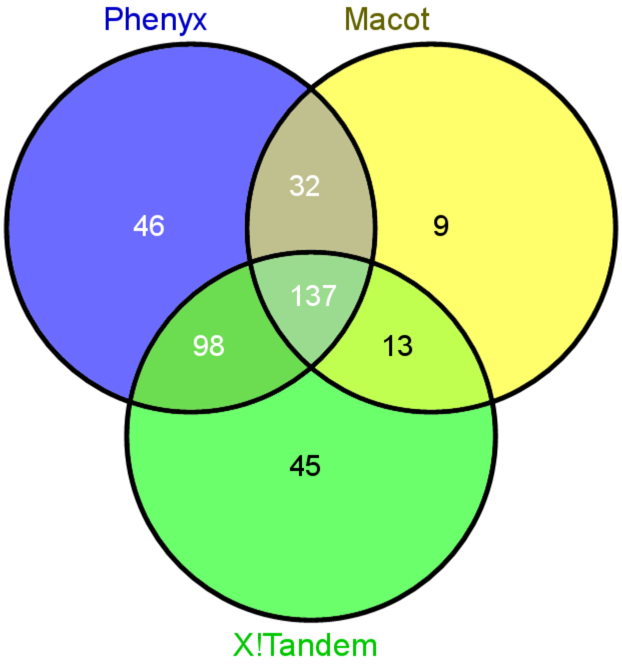
m/z=453.5957 (z=+3)
Δmass = 6.4 ppm



Supplementary Fig. 16 Manually annotated MS/MS spectra of ubiquitinated peptides associated with microtubule inhibitor studies.

In these spectra, the *y*-ions and *b*-ions are labeled in red and blue, respectively. The peaks associated with parental ions are labeled in black. The unmatched peaks are indicated by green asterisks (*). The m/z values for *y*, *b* ions and parental ions are provided for each matched peak. The m/z, charge state, the mass error of the precursor ions, and the fragmentation pattern of the peptides are shown in the spectra. As expected, all the major peaks are matched while only a few peaks with very low intensity are not matched.

Supplementary Fig. 17

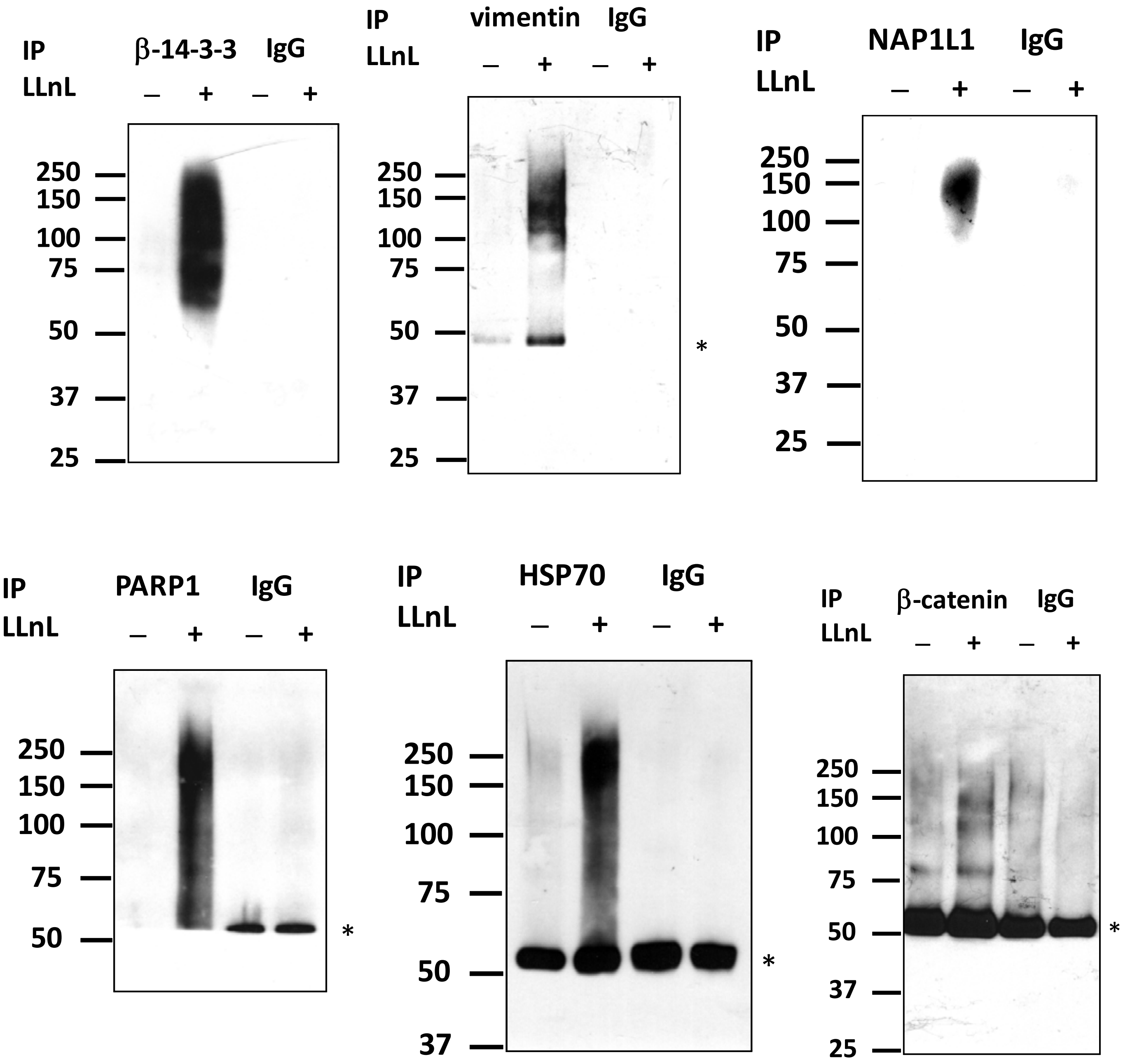


Supplementary Fig. 17 A Venn diagram shows the overlap of the Spectrum Mill-identified ubiquitinated peptides (<1% false positive rate) based on their concurrent identification using other search programs: Mascot, X!Tandem, and Phenyx.

The mgf file containing MS/MS fragments of all the ubiquitinated peptides identified by Spectrum Mill was submitted for online database searching by the three search programs listed above.

Websites for online search programs:
Mascot: http://www.matrixscience.com/search_form_select.html
X!Tandem: http://ppp.thegpm.org/tandem/ppp.html
Phenyx: http://www.genebio.com/products/phenyx/phenyx_online.html

Supplementary Fig. 18



Supplementary Fig. 18 Full-length blots for Fig. 2d. The bands labeled with asterisks are likely IgG bands. Note: The original PVDF membrane for PARP1 blotting was cut at about 55 kDa after transferring the proteins to the membrane.

Supplementary Table 1. List of LC-MS/MS identified ubiquitin-remnant peptides with diglycine-modified lysines. The listed information includes charge state, score, Forward-Reverse score, the percentage of the scored peak intensity (SPI), modification sites, start amino acid number in the protein sequence, sequence map, measured mass, matched mass, mass shift, delta mass, molecular weight, uniprot accession #, protein name, Phenyx p-value, Mascot score and expectation value, X!Tandem log(e) value if available. The symbols, \, / and |, represent b-ions, y-ions, and both b-ions and y-ions, respectively. Diglycine modified lysines are indicated as "k". In the treatment column: Vehicle for no treatment, LLnL for LLnL treatment, and Both for both vehicle and LLnL treatment.

#	z	Score	Fwd-Rev Score	SPI (%)	Variable Sites	Start AA Position	Sequence Map	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)	Protein MW (Da)	Accession #	Protein Name	Treatment	p value from Phenyx	Mascot Score	Mascot Expectation Value	X!Tandem log(e) value	Lysine Acetylation Site
1	3	19.31	11.91	80.4	K51k	44	(R)NL|L\SV/A/Y/k/N/V/V/GA/R(R)	539.9755	1503.864	114.0478	3	28082.5	P31946	14-3-3 protein beta/alpha	LLnL	5.17E-11	52	2.9E-04	-8.7	Y
2	4	21.38	21.38	89.2	K106k	95	(K)LI/CCD\I|L/DVLDkHL/I/P/AA/N/TGE/SK(V)	703.1151	2695.379	114.0592	5.8	29174.1	P62258	14-3-3 protein epsilon	Both	1.40E-14			-4.8	
3	3	23.12	23.12	93.4	K196k	194	(R)LA\kAAFDD\A\I|A/E|L/D/T/L/S/E/E/S/YK(D)	838.751	2400.182	114.0568	5.5	29174.1	P62258	14-3-3 protein epsilon	Both	1.37E-42	69	7.0E-06	-16.6	
4	3	12.54	12.54	62.0	K50k	43	(R)NL/L\SVA/Y/k/N/V/I/GA/R(R)	544.6462	1517.88	114.0442	0.8	29174.1	P62258	14-3-3 protein epsilon	LLnL	4.67E-07	42	2.3E-03	-2.4	Y
5	3	17.93	17.93	88.4	K258k	250	(R)VV|GSEL/I/Q/k/Y/L/GD/GPK(L)	606.3363	1702.937	114.0569	7.7	49184.8	P62191	26S protease regulatory subunit 4	LLnL	1.17E-17	49	7.5E-04		Y
6	3	21.06	21.06	96.0	K210k	201	(R)FV|N\L|GIE/P/PkGV/L/L/F/G/PPGTGK(T)	784.442	2237.269	114.0422	-0.3	48634.1	P35998	26S protease regulatory subunit 7	LLnL	2.25E-14	44	1.3E-03	-7.5	
7	4	10.94	10.94	65.2	K210k K222k	201	(R)FV\N\LGIE/PPkGVL/L/F/G/P/PGTGkTLCAR(A)	767.4216	2838.57	228.0947	2.9	48634.1	P35998	26S protease regulatory subunit 7	LLnL				-1.3	
8	3	13.24	8.16	76.9	K222k	211	(K)GV\L|L/F/G/P/P/GTGkTLCAR(A)	620.0099	1743.957	114.0577	8	48634.1	P35998	26S protease regulatory subunit 7	LLnL				-2	
9	3	17.56	11.00	85.3	K248k	240	(R)VI|GSELV/Q/k/Y/V/GE/GA/R(M)	607.0052	1704.928	114.0731	16.6	48634.1	P35998	26S protease regulatory subunit 7	LLnL	5.21E-09	31	3.3E-02	-4	
10	3	12.49	12.49	69.4	K310k	303	(K)TSSAF/V/Gk/T/PEASPE/P/K(D)	616.311	1732.875	114.0432	0.2	105836.9	Q99460	26S proteasome non-ATPase regulatory subunit 1	LLnL	2.19E-05			-2.4	Y
11	3	15.10	11.38	73.2	K122k	109	(R)II|A|F|V/GS/PVEDNEkD/L/VK(L)	696.3765	1973.059	114.056	6.2	40736.9	P55036	26S proteasome non-ATPase regulatory subunit 4	LLnL		43	2.9E-03	-1.4	
12	4	17.20	17.20	72.3	K40k	26	(R)LQ\A\QQD\A/V/N/I/V/CH/SkT/R(S)	521.272	1968.008	114.0582	7.3	40736.9	P55036	26S proteasome non-ATPase regulatory subunit 4	LLnL	3.70E-10			-10.4	
13	3	12.70	8.25	60.5	K119k	107	(R)AI\AYL/F/P/SGLFE/k/R(A)	575.9879	1611.889	114.0598	9.8	45835.1	P82933	28S ribosomal protein S9, mitochondrial	LLnL				-4.3	
14	3	10.75	4.62	73.2	K135k	128	(K)LI\E\G\L\PEkVL/S/LV/DD/PR(N)	669.7122	1893.069	114.0529	5	48117.7	Q9BZE1	39S ribosomal protein L37, mitochondrial	LLnL	4.60E-06				
15	4	9.31	4.54	61.8	K138k K139k	130	(R)SA\V|PPGADkkAEAGAGSA/T/E/F/QFR(G)	655.8234	2392.189	228.0826	-1.2	18897.9	P46783	40S ribosomal protein S10	LLnL	7.01E-07			-3.6	
16	3	10.75	10.75	69.7	K43k	43	(K)kGL\TPS/Q/I/GV/ILR(D)	499.3034	1381.853	114.0431	0.1	17222.4	P62277	40S ribosomal protein S13	LLnL	6.84E-07			-3.2	
17	3	14.88	14.88	74.3	K50k	46	(R)TL\Q\YkL\L/E/PV/L/L/L/GK(E)	614.711	1728.067	114.0515	4.6	16445.4	P62249	40S ribosomal protein S16	LLnL	1.08E-09	23	3.2E-02	-4.9	
18	3	14.04	14.04	73.0	K19k	15	(R)VI|I/E/k/Y/Y/T/R(L)	433.5779	1184.667	114.0518	6.8	15550.2	P08708	40S ribosomal protein S17	LLnL	8.44E-16	32	2.3E-02	-2.6	Y
19	3	14.47	9.31	64.0	K18k	11	(K)FV|ADGI/Fk/A/EL/N/E/F/LTR(E)	695.3736	1970.038	114.0681	12.1	26688.5	P23396	40S ribosomal protein S3	LLnL	1.97E-05			-7.1	
20	3	17.79	17.79	77.5	K197k	188	(K)IM|L/P/W/D/PTGk/IGPK(K)	556.3076	1552.856	114.0526	5.8	26688.5	P23396	40S ribosomal protein S3	Both	9.70E-09	34	1.6E-02	-3.4	
21	3	21.40	17.15	80.5	K90k	77	(R)F/G|F/PEGSV/EL/Y/A/EkV/ATR(G)	705.3619	2000.012	114.0588	7.5	26688.5	P23396	40S ribosomal protein S3	LLnL	1.16E-07			-8.1	
22	4	10.37	10.37	60.6	K142k	121	(R)TLTAVHDA\I\LED\LV/F/P/SEIVGk/R(I)	660.1066	2523.382	114.0229	-7.6	22127	P62081	40S ribosomal protein S7	LLnL	9.43E-06			-1.5	
23	3	16.64	16.64	76.5	K49k	42	(R)ELN|I/TAA/k/E/I/E/V/GGG/R(K)	590.9872	1656.892	114.0555	7.1	22127	P62081	40S ribosomal protein S7	LLnL	1.34E-06	35	2.2E-02	-5	
24	3	18.77	4.31	93.2	K128k	126	(K)GAk\L\T\PE/E/E/E/I/L/N/K(K)	562.3016	1570.832	114.058	8.9	24205.3	P62241	40S ribosomal protein S8	LLnL	6.09E-09			-3	
25	2	11.43	11.43	71.9	K344k K347k	339	(R)VLGF|VkVA|k|EQGAK(V)	851.4906	1473.879	228.0951	5.5	53802.2	P49189	4-trimethylaminobutyraldehyde dehydrogenase	LLnL				-6.1	
26	3	10.47	10.47	61.2	K292k	291	(R)LkVG\LQ/V/V/A/V/K(A)	423.2744	1153.767	114.0419	-0.8	61055	P10809	60 kDa heat shock protein, mitochondrial	LLnL	1.69E-05	26	1.4E-02	-1.2	
27	2	18.01	18.01	96.3	K49k	34	(K)AAGV|N\V|E|PF/W|PGL/F|A/k(A)	908.9757	1702.895	114.049	3.3	11514	P05386	60S acidic ribosomal protein P1	LLnL	1.72E-23	68	1.0E-05	-9.5	
28	3	20.91	20.91	82.6	K21k	3	(R)YV|A|SY/L/L/AA/L/GGNSS/PSA/k/D/IK(K)	780.4125	2225.181	114.0417	-0.5	11665	P05387	60S acidic ribosomal protein P2	Vehicle		31	4.9E-02	-4.7	Y
29	3	10.66	10.66	75.3	K41k	39	(R)LN\k\V|I/SEL/N/GK(N)	443.589	1214.71	114.0421	-0.6	11665	P05387	60S acidic ribosomal protein P2	Both	4.12E-11	35	2.1E-02	-2	
30	4	17.22	17.22	81.7	K61k	50	(K)NIEDV\IAQGIGkLAS\V|PAGGAVAVSA/A|PGSA/A/PAA/GSA/PAAAEEK(K)	1032.2902	4012.099	114.0404	-0.6	11665	P05387	60S acidic ribosomal protein P2	LLnL				-4.7	
31	3	16.61	16.61	73.4	K169k	165	(R)WF\QQkY/D/GI/I/L/P/G/K(-)	602.9926	1692.911	114.0524	5.3	20252.5	P62913	60S ribosomal protein L11	LLnL				-2.5	
32	3	11.91	11.91	73.8	K38k	36	(R)AAk\VL\E\QL|T/GQ/T/P\V/F/SK(A)	644.3597	1817.017	114.0478	2.5	20252.5	P62913	60S ribosomal protein L11	LLnL	4.21E-20			-4.5	
33	4	15.00	15.00	70.7	K140k	129	(K)FF\E\V\I/LI/D/P/F/H/k/AI/R(R)	490.529	1845.042	114.052	4.6	24146.2	P61313	60S ribosomal protein L15	Both	4.36E-10				
34	3	10.85	10.85	63.6	K13k	4	(R)YSL/D/PE/N/P/Tk/SCK(S)	551.5956	1538.716	114.0567	8.3	21397.2	P18621	60S ribosomal protein L17	LLnL				-2	
35	3	15.94	15.94	87.0	K119k	116	(R)AG\Gk\I\L\T\F/DQ|LA/L/D/S/PK(G)	630.0122	1773.975	114.0475	2.4	21634.6	Q07020	60S ribosomal protein L18	Both	6.77E-22	41	4.5E-03	-6.9	
36	2	15.72	8.52	79.4	K152k	140	(R)LA/PDYD\A\L|DV\A/Nk/IG/II(-)	958.0189	1800.974	114.0563	7	17695.1	P62750	60S ribosomal protein L23a	Both	4.74E-09			-4.6	
37	4	15.93	12.54	68.3	K12k	3	(K)VE|LCSFS/GYk/I/YP/GH/G/R(R)	521.7611	1969.959	114.0637	10	17779.1	P83731	60S ribosomal protein L24	LLnL	3.35E-09			-1.5	
38	3	10.72	5.29	66.3	K27k	24	(R)TDGkV\F/Q/FL/NA/K(C)	494.5992	1367.732	114.0513	5.6	17779.1	P83731	60S ribosomal protein L24	both	1.52E-09				Y
39	3	19.09	12.97	80.8	K93k	81	(R)AI|TG/AS/L/A/D/I/M/A/k/R(N)	511.2838	1417.783	114.0537	7	17779.1	P83731	60S ribosomal protein L24	Both				-1.8	Y
40	4	13.95	8.06	81.5	K134k	129	(K)AK\DQT/kAQAAAPA\SV/P/AQ/A/PK(R)	541.5496	2049.109	114.0678	11.5	17752.2	P47914	60S ribosomal protein L29	Vehicle				-1.7	
41	3	16.01	16.01	76.3	K149k	135	(K)AQ\AA/A|PA/SV|PA/Q/A/PkR(T)	549.9682	1533.85	114.0404	-1.5	17752.2	P47914	60S ribosomal protein L29	LLnL	3.99E-17			-5.2	
42	4	13.22	13.22	62.8	K131k	126	(K)GDV/P/T/k/R/P/PV/L/R(A)	362.9671	1334.79	114.0563	9.2	29995.8	P62424	60S ribosomal protein L7a	LLnL				-1.4	
43	3	18.45	18.45	86.5	K217k	213	(K)GA|L|A|k|L|V/E/AI/R(T)	418.9225	1140.71	114.043	0.1	29995.8	P62424	60S ribosomal protein L7a	LLnL	1.15E-08	61	1.7E-05	-4	Y
44	3	13.40	13.40	65.8	K302k	296	(R)VW|TSQ/Lk/STI/Q/TA/EAL/R(L)	682.7085	1932.055	114.056	6.4	59609.5	Q16875	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	LLnL	6.56E-05				
45	3	11.93	11.93	74.5	K59k	52	(K)VV|GAQ/SL/kE/MV/S/K(L)	497.2807	1375.761	114.0662	15.6	53140.3	P52209	6-phosphogluconate dehydrogenase, decarboxylating	LLnL	6.33E-11			-3.9	Y
46	5	16.48	16.48	65.3	K86k	71	(K)Y/PIEHGII/TNW/D/D/M/Ek/IWHHTFYNE/LR(V)	715.1473	3457.642	114.0651	6.2	42019.2	P68032	Actin, alpha cardiac muscle 1	LLnL	9.62E-05				
47	3	16.27	8.97	78.8	K193k	186	(R)DL|TD/YL/M/k/I/L/TE/R(G)	575.6383	1610.846	114.0545	6.7	42009.2	P62736	Actin, aortic smooth muscle	LLnL	2.61E-11				Y
48	3	13.37	9.06	80.6	K328k	318	(K)EITALA/P/S/T/MkI/K(I)	506.2871	1402.797	114.0493	4.2	42009.2	P62736	Actin, aortic smooth muscle	Both	3.07E-10			-2.3	
49	3	11.50	11.50	63.6	K330k	329	(K)Ik\I\I/A/P/PE/R(K)	384.2395	1036.651	114.0526	8.4	42009.2	P62736	Actin, aortic smooth muscle	LLnL	5.49E-05	35	2.7E-03	-3	Y
50	4	13.67	6.40	78.9	K113k	96	(R)VA\PEEHPVLLTEA/PL/N/PkANR(E)	603.0837	2295.246	114.0674	10.2	41737	P60709	Actin, cytoplasmic 1	LLnL				-3.3	
51	3	17.04	17.04	74.6	K291k	291	(R)kDLYANT\V|L/S/G/GT/T/M/Y/PGI/AD/R(M)	819.7483	2343.165	114.0654	9.2	41737	P60709	Actin, cytoplasmic 1	LLnL	8.25E-12	63	2.8E-04	-7.3	
52	4	14.06	10.22	75.6	K196k K209k	195	(K)EkGST\LD\LS/DLEAEk/L/V/M/FQ/R(R)	660.0925	2409.233	228.1152	11.1	41522.9	O00767	Acyl-CoA desaturase	LLnL				-4.4	
53	3	19.65	19.65	80.6	K209k	197	(K)GST/L/D/L/SDLEAE/k/L/V/M/F/Q/R(R)	756.0563	2152.095	114.0589	7	41522.9	O00767	Acyl-CoA desaturase	LLnL	5.12E-11	33	2.6E-02	-7.1	
54	3	12.98	12.98	66.2	K12k	5	(R)LL|L/NNGAk/M/PI/L/GLGTWK(S)	685.0626	1939.12	114.0535	5.1	35853.6	P15121	Aldose reductase	LLnL	5.39E-05				
55	4	16.24	16.24	85.8	K153k	141	(K)AIAHYE\QSAD\Y/Y/k/GEES/N/S/SANK(C)	669.8034	2562.138	114.0539	4.1	33232.9	P54920	Alpha-soluble NSF attachment protein	LLnL	2.09E-13			-2.9	
56	3	17.23	11.41	85.4	K239k	227	(R)LT|S/PV/I/NTSLDTk/NI/A/FE/R(T)	745.0643	2119.139	114.039	-1.8	67619.4	Q8IZ07	Ankyrin repeat domain-containing protein 13A	LLnL	2.45E-12	45	1.9E-03		
57	3	13.19	13.19	64.4	K1209k	1202	(K)AQ\EE/P/P/AkL/L/D/D/LF/R(K)	619.3324	1741.912	114.0707	15	151888.2	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus	LLnL				-1.8	
58	3	12.81	6.16	67.4	K134k	129	(R)FL|A\AQkGA\Y/PI/I/F/TAWK(L)	680.3761	1925.068	114.0454	1.2	54142.2	Q6NXE6	Armadillo repeat-containing protein 6	LLnL	1.56E-06				
59	4	13.37	7.76	72.3	K221k	209	(R)DVPLHALYDNVEkL|F/P/G/FE/IETVK(N)	722.6337	2773.445	114.0683	8.8	64370.3	P08243	Asparagine synthetase [glutamine-hydrolyzing]	LLnL	3.59E-06			-1	
60	4	17.98	14.42	82.0	K504k	484	(K)I/L|Q/EYVEHQV/DDA|MMANAAQ/k/F/P/FN/T/PK(T)	838.1635	3235.555	114.0771	10.2	64370.3	P08243	Asparagine synthetase [glutamine-hydrolyzing]	LLnL	1.54E-05			-5.5	
61	3	15.15	15.15	74.0	K262k	254	(K)I/T|SDE/PL/Tk/DD/I/PVFL/R(H)	691.706	1959.043	114.0601	8.3	53489.1	Q9UBB4	Ataxin-10	LLnL	1.91E-06			-6.1	
62	4	23.10	23.10	77.8	K117k	111	(R)SF|I/C/N/Y/k/E/H/W/FTV/R(K)	500.9942	1886.901	114.0543	5.7	43417.8	P54252	Ataxin-3	LLnL	1.93E-13	48	4.6E-04	-4.6	
63	3	19.91	11.93	91.8	K200k	191	(K)LI|GEE/L|A/Q/L/k/E/QR(V)	547.6405	1526.854	114.0533	6.3	43417.8	P54252	Ataxin-3	LLnL	6.55E-17	55	1.3E-04	-2.6	
64	4	15.38	15.38	80.1	K195k	185	(R)LGGHG\PSF|PL/k/GI/TE\QQ/K(E)	502.7747	1894.018	114.0588	7.9	82705	P13010	ATP-dependent DNA helicase 2 subunit 2	Both	5.87E-10			-5.5	Y
65	3	16.37	16.37	81.6	K137k	119	(R)LV|T|L/I/SQQATL/L/A/S/NEAFk/K(Q)	763.7705	2175.238	114.0586	6.8	27991.8	P51572	B-cell receptor-associated protein 31	LLnL	1.89E-11	33	1.1E-02	-3.9	
66	5	13.62	13.62	69.4	K95k	80	(K)VN|L\QNN/P/GAMEH/F/HMk/LF/R(A)	480.2443	2283.127	114.065	9.2	27991.8	P51572	B-cell receptor-associated protein 31	LLnL	2.61E-09	32	3.4E-02		
67	3	24.06	15.66	96.0	K1460k	1456	(R)LI|V/N/k/N/A/G/E/T/L/L/Q/R(A)	561.6626	1568.912	114.0614	11	192189.6	Q6W2J9	BCL-6 corepressor	Both	3.39E-09	52	2.7E-04		
68	3	18.07	11.02	81.6	K509k	508	(K)WkALF\EE\V|P/E/L/L/T/EAE/K(K)	716.037	2032.064	114.0327	-4.8	64616.2	P31939	Bifunctional purine biosynthesis protein PURH	LLnL	1.27E-10			-5.6	
69	4	23.35	16.36	91.6	K381k K385k	377	(R)LV|ASkTDGkIVQYE|C/E/G/D/T/C/QE/E/K(I)	754.6045	2787.281	228.115	9.7	67291	Q7Z569	BRCA1-associated protein	LLnL	1.86E-14	75	7.0E-07		
70	3	19.31	19.31	82.4	K385k	382	(K)TD\GkIV\Q\Y|E/C/E/G/D/T/CQ/E/EK(I)	801.675	2288.965	114.0459	1.2	67291	Q7Z569	BRCA1-associated protein	LLnL	4.06E-16	30	3.9E-03		
71	3	13.41	13.41	69.9	K31k	23	(K)DG\D\GTI/TT/k/E/L/GTV/M/R(S)	603.3033	1693.843	114.0528	5.5	16837.7	P62158	Calmodulin	Vehicle	7.32E-17			-4.5	
72	3	13.06	13.06	70.8	K95k	92	(R)VFDkDGNG\Y/I/S/A/A/E/L/R(H)	623.6444	1754.871	114.0479	2.6	16837.7	P62158	Calmodulin	Vehicle	2.23E-11	41	3.3E-03	-3.8	Y
73	3	19.92	19.92	82.7	K261k	253	(K)V/S\I/L/E/SL/D/k/W/E/R(L)	530.2839	1474.79	114.0471	2.6	43210.1	P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit	LLnL	1.19E-21	42	4.3E-03	-5.8	
74	4	15.26	15.26	77.7	K122k	108	(R)TP\AL/VFEH\VN\NTDF\kQLYQ/TL/T/D/YD/IR(F)	839.6777	3241.616	114.0726	8.8	45143.8	P68400	Casein kinase II subunit alpha	LLnL	6.16E-08			-1.3	
75	4	23.73	23.73	91.0	K170k	159	(K)LL|NDE/DQ/V/V/V/Nk/A/A/V/M/V/HQLSK(K)	641.8491	2450.307	114.0674	9.5	85497.1	P35222	Catenin beta-1	LLnL	7.04E-16	34	2.0E-02	-3.4	
76	5	20.20	20.20	91.8	K345k	343	(R)VLk\VLSV\CSSNKPA\I\V|E/A/G/G/M/Q/AL/GL/HLTD/PSQR(L)	738.8045	3575.904	114.0898	12.7	85497.1	P35222	Catenin beta-1	LLnL	4.91E-04				
77	3	10.37	10.37	64.8	K435k	434	(K)Nk\M\MV\CQ\V/G/GI/E/ALV/R(T)	640.3362	1804.923	114.071	14.6	85497.1	P35222	Catenin beta-1	LLnL	6.42E-16	34	2.0E-02	-6	
78	4	12.75	12.75	72.0	K508k	497	(K)LLH\PPSH\WPL\Ik/A/TV/GLI/R(N)	566.3419	2148.28	114.0653	9.9	85497.1	P35222	Catenin beta-1	LLnL	2.19E-09	33	3.0E-03	-4.2	
79	2	11.33	7.91	65.2	K220k	214	(K)DY/P/FQ/GkV/R(A)	612.319	1109.574	114.0569	11.4	42099.3	P56202	Cathepsin W	LLnL				-3	
80	4	13.78	13.78	69.5	K166k	159	(R)EQFYHSCkQY/GI/TG/ENV/R(G)	583.2769	2216.019	114.0668	10.3	56921	Q96JB5	CDK5 regulatory subunit-associated protein 3	LLnL	7.45E-07				
81	3	13.07	7.80	80.8	K103k	95	(R)GF\S\I/PE/CQkL/L/P/K(A)	544.2965	1516.819	114.0557	7.9	51712.7	O75390	Citrate synthase, mitochondrial	LLnL	3.48E-09	33	6.1E-02	-3.1	
82	3	24.20	24.20	100.0	K382k	376	(K)LV|AQLY/k\I|V/P/N/V/L/LEQGK(A)	713.7651	2025.211	114.0701	12.7	51712.7	O75390	Citrate synthase, mitochondrial	LLnL	1.30E-29	52	4.9E-05	-9.2	Y
83	3	15.56	7.35	86.2	K43k	35	(K)DI\L\A\DL/I/P/k/E/QA/R(I)	532.6308	1481.832	114.0456	1.7	51712.7	O75390	Citrate synthase, mitochondrial	Both	9.20E-13	43	1.8E-03	-4.6	
84	3	11.38	11.38	56.3	K459k	451	(K)SM|STE/GL/Mk/FV/D/SK(S)	558.603	1559.744	114.0501	4.3	51712.7	O75390	Citrate synthase, mitochondrial	LLnL	2.31E-07			-1.9	
85	4	17.74	17.74	87.8	K265k	246	(K)DS\G\Y|PETLVNL/I/V/L/SQHLGk/PPEVTNR(Y)	773.4159	2976.579	114.0629	6.4	34482.2	O14579	Coatomer subunit epsilon	LLnL				-1.4	
86	4	13.52	13.52	71.7	K112k	96	(K)KEDL\V\F\I\FWA/PESA/PLk/SK(M)	580.5702	2205.195	114.0636	8.9	18502.6	P23528	Cofilin-1	LLnL	6.58E-11				
87	3	18.40	5.75	93.7	K63k	59	(K)EL\VEk/L/L/E/GY/L/K(E)	516.6298	1433.825	114.0498	4.5	39446.9	Q96G28	Coiled-coil domain-containing protein 104	LLnL	3.36E-06	29	4.4E-02		
88	2	11.75	2.67	77.9	K289k	282	(R)I/S|L/P/ESLk/R(I)	578.8305	1042.626	114.0282	-12.7	187149.1	P01024	Complement C3	LLnL	7.76E-05			-4.3	
89	3	13.83	13.83	78.5	K243k	238	(K)VQ\Q|L|Pk/Y/T/SQ/I/VGR(F)	577.6563	1616.912	114.0425	-0.3	47873.4	Q9UNS2	COP9 signalosome complex subunit 3	LLnL	1.88E-08			-4.2	
90	4	19.49	19.49	84.5	K116k	97	(K)GVT\IASGGV/L/PNI/H/PEL/L/A/k/K(R)	557.8324	2114.233	114.0746	14.2	39617.3	O75367	Core histone macro-H2A.1	Both	9.77E-05	32	1.5E-02		
91	4	21.61	13.97	97.7	K117k	97	(K)GV\T\I/A/S/G\G\V/L/PNI/H/PE/LLA/K/k(R)	557.8233	2114.233	114.0382	-2.1	39617.3	O75367	Core histone macro-H2A.1	LLnL	2.03E-13				
92	5	17.55	17.55	77.5	K292k	272	(K)FVIH\CNS\PV/W/GADKCEEL/L/EkT/V/K(N)	595.501	2859.417	114.0591	5.4	39617.3	O75367	Core histone macro-H2A.1	Both	2.12E-04				
93	3	18.63	10.19	83.6	K16k	7	(R)V/V|D|F/DET/W/Nk/L/L/TTI/K(A)	679.3648	1922.027	114.0529	4.9	86983.6	Q13617	Cullin-2	LLnL	5.01E-11				
94	4	13.59	13.59	77.7	K63k	47	(R)IYD\AQNE/L/S/AATH/LTSkLL/K(E)	583.3215	2216.192	114.072	12.5	79663.9	Q9UKG1	DCC-interacting protein 13-alpha	LLnL	8.14E-05			-1.2	
95	3	12.91	12.91	66.2	K109k	106	(R)T\N\Ek\VE/L/Q/E/L/ND/R(F)	567.9509	1587.797	114.0409	-1.2	53536	P17661	Desmin	Both	5.06E-11	32	2.7E-02	-1.9	Y
96	3	14.55	14.55	72.4	K159k	159	(K)k\I\I\E\N\E|L/E/G/F/GI/R(L)	544.6343	1517.832	114.0561	8.1	40542.4	Q9Y295	Developmentally-regulated GTP-binding protein 1	LLnL	1.54E-21	30	5.4E-02	-6.6	
97	3	14.62	14.62	72.2	K123k	116	(R)QYTSLLGkMNSEEEDE/V/W/Q/V|I/I/G/A/R(A)	1003.831	2895.419	114.0591	5.4	27131	Q9NR28	Diablo homolog, mitochondrial	LLnL	8.08E-10			-6.3	
98	5	16.80	16.80	82.4	K191k	185	(R)NH\I\Q\L\V/kLQ/VEE/V/H/Q/LS/R(K)	457.659	2170.209	114.0568	6.1	27131	Q9NR28	Diablo homolog, mitochondrial	Both	6.04E-12	46	9.1E-04		
99	3	19.34	12.52	88.9	K158k	157	(K)YkLL|PE|Y|P/GV/L/S/DVQEEK(G)	741.0581	2107.096	114.064	9.5	21452.9	P00374	Dihydrofolate reductase	LLnL	1.07E-21			-6.6	

100	4	12.30	9.05	68.7	K158k K174k	157	(K)YkLL\PE\Y/P/GVLSDVQ/E/EkGI/K(Y)	659.1031	2405.296	228.0943	3.2	21452.9	P00374	Dihydrofolate reductase	LLnL	2.68E-06				
101	3	14.32	14.32	64.8	K1121k	1105	(K)MQ/EV/V/A/N\LQ/Y/DD/GS/GMkR(E)	719.0064	2040.948	114.0569	6.5	126968.6	Q16531	DNA damage-binding protein 1	LLnL	2.20E-06			-1.7	
102	3	14.96	14.96	80.8	K1131k	1123	(R)EATADDL/I\k/V/V/E/E/LTR(I)	639.3408	1801.954	114.0537	5.6	126968.6	Q16531	DNA damage-binding protein 1	LLnL	3.98E-17			-3.2	
103	4	21.81	21.81	87.6	K600k	585	(R)SVLHEV\M\E\QQ/T|L/SI/A/k/A/GI/I/C/Q/L/NAR(T)	756.6606	2909.534	114.087	14.6	96558.4	P33991	DNA replication licensing factor MCM4	LLnL	1.30E-16	52	2.7E-04	-15.7	
104	4	14.11	14.11	76.9	K145k	133	(R)RFE\L\Y\FQ/GP/S/S/Nk/P/R(V)	485.7544	1825.934	114.0614	9.5	81308.4	P33993	DNA replication licensing factor MCM7	LLnL	5.61E-12	46	1.2E-03	-4.6	
105	3	12.54	12.54	67.0	K75k	73	(R)YAkLFAD\A\VQ/E|L/L/PQYK(E)	704.3831	1997.074	114.0605	8.3	81308.4	P33993	DNA replication licensing factor MCM7	LLnL	1.45E-05				
106	3	14.63	8.22	81.0	K252k	249	(K)LS|PkAEEV/A/TFF/A/K(M)	551.2996	1537.826	114.0582	9.2	90726.2	P11387	DNA topoisomerase 1	LLnL	7.98E-06			-1.8	
107	3	22.58	11.81	93.5	K129k	117	(R)LL|M/PSQLV/SQ/V/Gk/EL/L/R(L)	675.7267	1911.11	114.056	6.4	25370.7	Q9NX09	DNA-damage-inducible transcript 4 protein	LLnL		41	1.8E-03		
108	3	18.95	12.68	87.9	K344k	339	(K)L/S\L/L/E\k/L|L/P/E/R(K)	475.6231	1310.804	114.0505	5.3	45610.1	P31689	DnaJ homolog subfamily A member 1	Vehicle	1.25E-10	41	1.1E-03	-5.7	
109	3	17.18	17.18	77.9	K82k	75	(R)IQ|I|N/PQNk/A/DF/Q/G/I/S/PE/R(A)	723.7129	2055.062	114.0624	9	12496.8	P61803	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	LLnL	1.24E-08			-2.1	
110	4	17.04	17.04	66.9	K67k	59	(R)FL/AE/EGF/Y/k/FH/NWF/D/D/R(A)	584.5247	2221.014	114.0632	8.7	80530.1	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	LLnL	1.62E-07				
111	3	15.97	15.97	69.9	K255k	240	(R)MA|A|A/G/GTV/S/G/P/SSA/Ck/PGR(S)	625.9685	1761.837	114.0539	5.8	289596.3	Q9ULT8	E3 ubiquitin-protein ligase HECTD1	LLnL	1.80E-24	46	6.8E-04	-4.9	
112	4	21.48	21.48	92.2	K3345k	3335	(R)HV\LDT\L\I|Q|L/A/k/V/F/PSH/FTQQR(T)	648.8605	2478.362	114.0586	6	481893.3	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	LLnL	9.53E-17	36	1.0E-02	-12.6	
113	3	15.92	15.92	76.2	K446k	433	(K)EF/D/P/L/G\P\L|P/PGWEkR(T)	617.9902	1737.896	114.0602	9.3	102803.3	Q96J02	E3 ubiquitin-protein ligase Itchy homolog	LLnL	9.47E-06				
114	4	16.40	16.40	63.8	K28k	26	(K)WGkQ/D/GGE/G/H/V/GTV/R(S)	424.9607	1582.772	114.0489	3.5	110136.6	Q86YT6	E3 ubiquitin-protein ligase MIB1	LLnL				-1.9	
115	3	17.90	10.70	89.2	K421k	421	(K)kL\F\E\TQ|E|S/GDL/N/E/E/LV/K(A)	698.3573	1978.997	114.0606	8.4	110136.6	Q86YT6	E3 ubiquitin-protein ligase MIB1	LLnL	1.33E-23	43	2.3E-03		
116	3	13.52	13.52	80.5	K197k	187	(K)RP|E\P\PS\T\S/T|L/kQV/T/K(V)	594.9971	1668.928	114.0488	3.3	56194.9	Q9NS91	E3 ubiquitin-protein ligase RAD18	LLnL	1.24E-25	34	2.0E-02		
117	3	23.47	13.51	100.0	K309k	296	(K)SA|A\E|I|VQ/E/I/E/N/IE/kT/R(M)	648.6796	1829.96	114.0639	10.8	56194.9	Q9NS91	E3 ubiquitin-protein ligase RAD18	Both	9.54E-33	65	2.3E-05		
118	3	14.42	6.21	75.1	K318k	314	(R)LE|ASkLNE/S/V/MV/F/T/K(D)	603.9905	1695.899	114.0584	8.5	56194.9	Q9NS91	E3 ubiquitin-protein ligase RAD18	LLnL	3.04E-10				
119	4	18.78	12.87	86.4	K334k	329	(R)LG\E/TQk/A/MLD/P/P/K/PS/R(G)	471.2606	1767.942	114.0784	18.8	51219	Q96BH1	E3 ubiquitin-protein ligase RNF25	Both	5.08E-09	32	3.0E-02		
120	4	14.45	6.37	77.7	K334k K341k	329	(R)LGETQkAMLD|P/P|k/P/S/R(G)	499.766	1767.942	228.1	7.1	51219	Q96BH1	E3 ubiquitin-protein ligase RNF25	LLnL		30	5.1E-02	-1.4	
121	3	12.33	9.21	72.9	K172k	167	(R)YE\E\IV/kEV/S/TY/I/K(K)	572.3043	1600.847	114.0515	5	50141.1	P68104	Elongation factor 1-alpha 1	LLnL	3.07E-10			-1.4	Y
122	4	15.43	15.43	74.4	K244k	220	(K)DGN\ASGTTLL/EAL/D/C/I/L/P/PTR/PTD/kPLR(L)	784.6663	3021.567	114.076	10.6	50141.1	P68104	Elongation factor 1-alpha 1	LLnL				-2	
123	3	14.91	14.91	77.9	K255k	248	(R)LP\LQDV\Y/kI/G/G/I/G/TV/PVGR(V)	699.4021	1982.143	114.0484	2.6	50141.1	P68104	Elongation factor 1-alpha 1	LLnL	1.53E-06			-3.4	Y
124	3	13.04	8.14	71.2	K273k	267	(R)VE\TGVLk\PGMVV/T/F/A/PV/NVTTEVK(S)	877.1524	2515.384	114.0586	6	50141.1	P68104	Elongation factor 1-alpha 1	LLnL	2.05E-05			-1.5	
125	3	14.09	6.08	71.7	K147k	138	(R)IL/G\L/L/DAY/L/k/T/R(T)	497.3001	1375.831	114.055	8.1	50119.1	P26641	Elongation factor 1-gamma	LLnL	3.79E-06			-2.4	Y
126	3	15.38	15.38	73.7	K239k	236	(K)FA\Ak/GEGQ|L/G/P/AE/R(A)	515.6027	1430.739	114.0549	7.7	95338.7	P13639	Elongation factor 2	Vehicle				-1.7	Y
127	3	17.65	17.65	77.4	K42k	33	(K)ST|L/TD/SLV/Ck/A/GI/I/A/SA/R(A)	659.6908	1863	114.0574	7.3	95338.7	P13639	Elongation factor 2	LLnL	6.99E-12	41	4.5E-03	-4.7	
128	3	14.58	14.58	71.4	K845k	843	(K)GLkE\GI|P/A/L/D/NF/L/D/KL(-)	619.6801	1742.969	114.057	7.6	95338.7	P13639	Elongation factor 2	Both	1.02E-11	35	1.8E-02	-4.5	
129	3	12.86	12.86	65.3	K256k	253	(R)DLE/kPFLL|PV\EA/V/Y/S/V/PGR(G)	748.4104	2129.164	114.0525	4.3	49541.8	P49411	Elongation factor Tu, mitochondrial	LLnL	2.70E-06			-1.9	Y
130	3	11.84	11.84	67.1	K133k	124	(R)VS/AAL/E/E/AD/kMFL/R(T)	565.2947	1579.815	114.0547	6.9	20875.7	Q9Y6B2	EP300-interacting inhibitor of differentiation 1	LLnL	1.17E-10	33	2.3E-02		
131	3	20.25	20.25	83.8	K107k	98	(K)EN\M/Y/A/V/Q/T/L/k/D/F/Q/YV/D/R(D)	745.3607	2120.012	114.0558	5.8	57575.6	Q9Y6I3	Epsin-1	Both	2.56E-08	39	3.8E-03		
132	4	18.52	18.52	81.4	K146k	142	(R)AE\VQ/kLQ/MEA/PH/I/I/V/GT/PG/R(V)	572.8169	2174.175	114.0707	12.2	46154.2	P60842	Eukaryotic initiation factor 4A-I	LLnL	8.61E-06	45	1.5E-03	-4.9	
133	3	14.08	14.08	65.9	K177k	175	(K)YIk\MFVL/D/E/A/D/E/ML/SR(G)	692.0114	1959.955	114.0642	10.3	46154.2	P60842	Eukaryotic initiation factor 4A-I	LLnL	1.09E-26	51	3.9E-04	-6	
134	3	10.53	10.53	69.6	K193k	191	(R)GFk\DQ\I/Y/DI/FQ/K(L)	539.2815	1501.769	114.0614	11.4	46154.2	P60842	Eukaryotic initiation factor 4A-I	LLnL	9.56E-10			-2.3	Y
135	3	25.87	25.87	98.1	K54k	46	(R)GI|Y|A|Y/G/FE/k/P/S/A/I/QQR(A)	647.999	1827.939	114.0436	0.4	46154.2	P60842	Eukaryotic initiation factor 4A-I	LLnL	1.44E-24	51	3.9E-04	-9.2	Y
136	3	19.96	14.92	89.4	K69k	63	(R)AI|I|PCIkGYDV|I/A/Q/A/Q/S/GT/GK(T)	768.7464	2190.159	114.0659	10	46402.5	Q14240	Eukaryotic initiation factor 4A-II	Both	1.32E-16	43	3.1E-03	-3.9	
137	4	18.38	12.01	78.3	K68k	68	(K)kY\ED\I|C/P/S/T/HNM/DV/PNI/K(R)	569.5195	2161.005	114.0509	3.5	16832.4	P63241	Eukaryotic translation initiation factor 5A-1	LLnL	2.60E-12			-8.1	Y
138	4	12.40	12.40	64.6	K85k	69	(K)YE\D\ICPSTHNMDV/P/N/I/k/R(N)	576.521	2189.011	114.0508	3.4	16832.4	P63241	Eukaryotic translation initiation factor 5A-1	LLnL	6.93E-08	34	7.3E-03	-5.2	
139	2	11.09	2.32	82.0	K224k	218	(K)YL|S|FLEkRQ/K(L)	713.3881	1311.742	114.027	-11.2	58305.1	Q8NHP7	Exonuclease 3'-5' domain-like-containing protein 1	LLnL				-4.1	
140	4	12.97	12.97	70.9	K157k	147	(K)T\G\D\VEDST/V/Lk/SLHL/P/K(N)	489.0165	1838.986	114.0584	7.9	73954.5	Q9UNN5	FAS-associated factor 1	LLnL	1.04E-07			-3.6	
141	3	13.98	10.00	79.2	K457k	445	(K)TDQ/FPLF|L|I/I/M/GkR(S)	598.3349	1678.935	114.0552	6.9	73954.5	Q9UNN5	FAS-associated factor 1	LLnL	1.91E-18	29	4.8E-02	-3	
142	3	21.54	16.95	91.2	K28k	23	(R)IV|A|PGk\G/IL/A/A/D/E/S/T/GSI/AK(R)	671.3761	1898.059	114.0544	5.7	39420.2	P04075	Fructose-bisphosphate aldolase A	LLnL	8.18E-11	41	3.4E-03	-5.2	
143	3	13.70	8.69	72.6	K42k	29	(K)GI|L|AADE/S/T/G/SI/Ak/R(L)	534.9567	1488.802	114.0539	6.8	39420.2	P04075	Fructose-bisphosphate aldolase A	LLnL	3.96E-05	43	3.2E-03	-3.4	Y
144	3	11.39	11.39	69.3	K55k	52	(R)GFFkVL\GQLTE|T/G/V/V/S/PEQFMK(S)	852.7833	2442.274	114.0616	7.3	20749.2	Q96EK6	Glucosamine 6-phosphate N-acetyltransferase	LLnL	7.13E-04				
145	3	12.77	12.77	63.1	K194k	187	(K)TV/D/G/P/S/G/k/LW/R(D)	443.9044	1215.648	114.0506	5.8	36053.4	P04406	Glyceraldehyde-3-phosphate dehydrogenase	LLnL	8.38E-09	45	1.9E-03	-1	Y
146	3	17.41	12.97	87.2	K215k	201	(R)GAL\QN\I/I/PAST/GA/Ak/AV/GK(V)	627.6945	1767.012	114.0566	7.3	36053.4	P04406	Glyceraldehyde-3-phosphate dehydrogenase	LLnL	9.75E-12	45	7.9E-04	-9.3	
147	3	16.01	6.84	80.1	K219k	201	(R)GAL\Q|N\I/I/PA/S/T/G\A/A/KAVG/k(V)	627.6939	1767.012	114.0548	6.3	36053.4	P04406	Glyceraldehyde-3-phosphate dehydrogenase	LLnL	1.93E-06			-2.9	Y
148	3	9.02	2.95	67.4	K216k	214	(K)LTkAICG\L|I/D/DY/SMV/R(F)	657.0086	1854.945	114.066	11.7	32761.5	Q9UHW5	GPN-loop GTPase 3	LLnL	1.01E-11	33	2.2E-02		
149	4	16.26	16.26	78.5	K18k K29k	16	(R)MDkV\GDA\L/E/EV/L/S/k/A|L/SQR(T)	580.0538	2089.096	228.0976	5.1	18335.9	P24522	Growth arrest and DNA-damage-inducible protein GADD45 alpha	LLnL		38	1.0E-02		
150	3	17.20	17.20	82.9	K29k	19	(K)V/G|DALEEV|L/S/k/A/L/SQR(T)	610.3338	1714.933	114.0535	5.8	18335.9	P24522	Growth arrest and DNA-damage-inducible protein GADD45 alpha	LLnL	3.34E-13	38	1.1E-02		
151	3	16.97	16.97	69.7	K159k	153	(K)SN\YN/FEk/P/F/L/W/L/AR(K)	633.6607	1784.912	114.0557	6.7	24423.2	P62826	GTP-binding nuclear protein Ran	LLnL	1.31E-06			-5.5	Y
152	3	12.23	6.86	76.4	K829k	825	(K)ID\V\I|kQADY\V/P/SD/QDLL\R(C)	734.7257	2088.097	114.0654	10.2	111025.1	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	LLnL	1.03E-12			-3	
153	3	16.33	16.33	76.0	K917k	909	(R)LQ|EALNL|F/k/S/I/W/N/NR(W)	654.0232	1845.997	114.0581	7.7	111025.1	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	LLnL	4.73E-13	32	3.5E-02	-1.2	
154	3	11.77	11.77	61.7	K950k	949	(K)Sk\IED\Y\F/PE/FA/R(Y)	539.2699	1501.732	114.063	12.4	111025.1	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	LLnL	6.10E-05				
155	3	15.17	10.44	80.5	K130k	128	(K)TI\kLWN/T/L/G/V/C/K(Y)	516.2881	1432.798	114.0517	5.6	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL	2.83E-07	40	4.8E-03	-1.3	Y
156	3	23.03	13.91	93.9	K172k	156	(R)FS|PN/SSN/PII/V/S/C/GWD/kLV/K(V)	788.0759	2248.143	114.0701	11.5	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL				-2.2	
157	3	17.36	17.36	87.8	K175k	173	(K)LV|k\VW/N/L/A/N/C/K(L)	486.9427	1344.746	114.0679	17.1	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL	4.66E-14	57	1.2E-04	-3.4	
158	5	18.40	18.40	89.1	K185k	184	(K)LkTNHIGHTGY\L\N\T\V\TVS/PD/GSL/C/A/S/GG/K(D)	620.5192	2984.489	114.0774	11.1	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL	4.43E-05	44	2.5E-03		
159	3	24.95	17.83	89.9	K257k	246	(R)YW|L|CA/A/T/G/PSI/k/I/W/DLE/GK(I)	774.7275	2208.116	114.0522	4	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL	1.33E-09	51	4.8E-04	-6	
160	3	22.88	16.16	92.6	K271k	265	(K)I/I|V/D/E|L/k/Q/E/VI/ST/SSK(A)	635.0194	1788.995	114.0483	2.8	35076.9	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	LLnL	9.52E-18	73	2.4E-06	-6.9	
161	3	17.82	17.82	84.2	K112k	109	(K)GE\TkAF/Y|PE/E/I/S/SMV/LTK(M)	715.366	2030.015	114.0684	11.9	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	3.63E-13			-1.7	
162	3	16.96	16.96	79.7	K126k	113	(K)AF|Y|PEEI/SSM/V/L/T/k/MK(E)	663.3378	1873.944	114.055	6.1	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	2.66E-06	30	4.6E-02	-1.5	
163	3	14.85	14.85	74.3	K128k	113	(K)AF|Y/PEEI/SS/MV/L/T/KMk(E)	663.3408	1873.944	114.064	10.6	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	3.53E-05			-1.7	
164	4	20.79	20.79	94.4	K524k	518	(R)MVQ/E/AE/kY/K/A/E/D/E/V/Q/R(E)	517.5066	1952.938	114.0664	11.3	70052.6	P08107	Heat shock 70 kDa protein 1	Both	2.16E-16	46	8.5E-04	-10.9	Y
165	4	10.09	10.09	63.3	K524k K526k	518	(R)MVQEAEkY/kAE/D/E/VQ/R(E)	546.0159	1952.938	228.1036	8.1	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	9.54E-13			-1.6	Y
166	4	11.78	11.78	79.3	K526k	518	(R)MV\QEAEKY\k/AED/E/V/Q/R(E)	517.5051	1952.938	114.0604	8.4	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	2.54E-07			-3.4	Y
167	3	10.21	10.21	60.3	K550k	540	(K)NA|L|E/SYA/FNMk/SAV/ED/EGLK(G)	777.3802	2216.054	114.0721	12.5	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL				-4	
168	4	22.54	17.99	97.1	K597k	596	(K)RkELEQVCN\P\I\I\SGL\Y\Q/G\A/G|G|P/G/PGGF/GAQ/GPK(G)	864.1928	3339.69	114.0591	4.7	70052.6	P08107	Heat shock 70 kDa protein 1	LLnL	2.20E-06	70	8.0E-07	-17.7	
169	3	11.43	11.43	70.3	K126k	113	(K)SF|Y/PEEV\SSMV/L/T/k/M/K(E)	664	1875.923	114.0624	9.8	70898.4	P11142	Heat shock cognate 71 kDa protein	LLnL				-1.7	
170	3	15.15	15.15	75.4	K388k	375	(R)GC\A\LQCA|I|L/S/P/A/F/kVR(E)	635.6709	1790.94	114.0577	7.8	96865.5	Q92598	Heat shock protein 105 kDa	LLnL	2.94E-11			-4.8	
171	3	16.65	16.65	86.3	K188k	173	(R)II|NE/PTA\A\A\I/A/Y/G/LD/k/K(G)	634.6861	1787.99	114.0536	5.6	70021.3	P54652	Heat shock-related 70 kDa protein 2	LLnL	1.06E-15	52	2.9E-04	-6	
172	3	13.40	13.40	66.8	K350k	337	(R)SSGP/YGGGGQ/Y/F/A/k/P/R(N)	581.6176	1628.782	114.0567	7.9	38846	P09651	Heterogeneous nuclear ribonucleoprotein A1	Both		43	1.4E-03		Y
173	4	13.18	13.18	67.4	K57k	53	(R)EH\F\EkWGTLTD/C/V/V/M/R(D)	531.2553	2007.941	114.0578	7	39595.1	P51991	Heterogeneous nuclear ribonucleoprotein A3	LLnL				-1.1	
174	3	20.93	15.64	87.4	K197k	184	(K)IF|V/GGL/S/PD/T/PE/E/kI/R(E)	624.671	1757.943	114.0552	6.6	38434.4	Q14103	Heterogeneous nuclear ribonucleoprotein D0	Both		49	7.7E-04	-5.7	
175	3	28.72	19.72	95.9	K22k	10	(K)L/F|I/G/G/L/N/TE/TNEk/A/L/E/A/V/F/GK(Y)	789.0932	2251.197	114.0682	10.7	42332	P38159	Heterogeneous nuclear ribonucleoprotein G	Both	1.58E-11	73	2.4E-06	-11.4	
176	3	18.01	18.01	74.4	K167k	151	(R)ST|GE/A/F/VQ/FA/SQEI/A/E/k/ALK(K)	756.7258	2154.108	114.0551	5.4	49229.7	P31943	Heterogeneous nuclear ribonucleoprotein H	LLnL	6.69E-05	34	1.9E-02		Y
177	5	18.38	18.38	91.6	K62k	61	(R)LkTDNAGDQHGGGGG\G\G\G\G\AG\A/A/G/GGGGGE/NY/DD/PH/K(T)	668.0941	3222.382	114.0598	5.1	64133.1	P14866	Heterogeneous nuclear ribonucleoprotein L	LLnL		19	5.7E-03		
178	3	18.08	11.29	78.3	K667k	659	(R)NL|P/F/D/F/T/W/k/ML/K(D)	551.9573	1539.803	114.0545	7	77516.1	P52272	Heterogeneous nuclear ribonucleoprotein M	LLnL	1.85E-12	42	3.2E-03	-2.3	
179	3	16.11	9.90	84.4	K83k	73	(R)AF|I/TN/I/PFDVkWQ/SLK(D)	674.3694	1907.043	114.0511	4	77516.1	P52272	Heterogeneous nuclear ribonucleoprotein M	LLnL	8.95E-05			-1.2	
180	3	16.90	9.96	82.5	K463k	462	(K)EkPYFPI|PEEY\TF|I/Q/N/V/PLE/D/R(V)	946.8129	2724.356	114.0686	9	90513.8	Q00839	Heterogeneous nuclear ribonucleoprotein U	Vehicle		39	7.3E-03	-3.7	Y
181	4	16.46	16.46	86.3	K523k	516	(K)HA\AE\N\PG\kYNI\L/GT/NTI/M/D/K(M)	576.0431	2187.086	114.0643	9.3	90513.8	Q00839	Heterogeneous nuclear ribonucleoprotein U	Both	7.37E-19	47	9.9E-04	-4.8	Y
182	3	19.51	19.51	85.0	K46k	39	(R)NY|Y/EQW/Gk/L/T/D/CV/V/MR(D)	726.0075	2061.952	114.0559	5.9	37429.9	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	Vehicle	1.87E-12	31	1.6E-02	-9.3	
183	3	14.01	5.79	75.2	K15k	10	(K)FL\V/EY/k/SA/VE/K(K)	476.2603	1312.715	114.0516	6.1	49512.9	O14929	Histone acetyltransferase type B catalytic subunit	LLnL	3.04E-05				
184	3	12.42	12.42	63.8	K74k	68	(K)ELTSLV/k/E/V/Y/PE/AR(K)	583.3162	1633.88	114.0545	6.6	17561.2	O00422	Histone deacetylase complex subunit SAP18	LLnL	2.17E-07				
185	3	9.48	9.48	68.4	K100k	94	(K)GTL/VQ/Tk/GT/GA/SGSFK(L)	551.6271	1538.817	114.0494	3.9	21842.2	Q02539	Histone H1.1	LLnL	6.04E-10	29	6.2E-02	-7.8	
186	3	19.93	19.93	95.4	K67k	67	(K)kA\L\A|A|A/G|Y/D/V/E/K(N)	450.5788	1235.663	114.0588	11.8	21842.2	Q02539	Histone H1.1	Vehicle		53	2.3E-04	-8.2	
187	3	25.77	25.77	97.9	K46k	35	(K)AS|G/P/PV/SEL/I/T/k/A/V/AA/SK(E)	614.0109	1725.975	114.0436	0.4	21364.9	P16403	Histone H1.2	Both	1.53E-11	71	3.8E-06	-7.4	Y
188	3	27.25	27.25	100.0	K119k	97	(K)LL/GGV|T/I/AQ/GGV|L|PNI|Q/A|V/L/L/Pk/K(T)	838.5118	2399.475	114.046	1.2	14233.6	Q96QV6	Histone H2A type 1-A	Both	2.25E-24	48	3.0E-05	-5.7	Y
189	3	19.97	19.97	89.9	K119k	101	(R)VTIA|Q/GGVL|PNI|Q/A|VL/L/Pk/K(T)	725.1125	2059.264	114.0592	7.5	14135.6	P04908	Histone H2A type 1-B/E	Both	2.89E-17	37	7.0E-04	-7.2	Y
190	5	20.16	12.79	92.3	K119k K120k	101	(R)VTIAQGGV/L/PNI/Q/AV/L/L/PkkTESH/HK(A)	602.1481	2778.599	228.1125	8.9	14135.6	P04908	Histone H2A type 1-B/E	Both	2.15E-08				Y
191	2	23.75	23.75	100.0	K120k	101	(R)VT/I/A|Q|G/GV|L|PNIQA/V/L|L|PKk(T)	1087.1575	2059.264	114.044	0.5	14135.6	P04908	Histone H2A type 1-B/E	LLnL	3.95E-28	65	1.5E-06	-14.1	Y
192	3	16.35	16.35	85.6	K100k	97	(K)LLGkVT\IAQGGV|L|PNI/QAVLL/PK(K)	819.5056	2342.453	114.0489	2.4	14107.5	P20671	Histone H2A type 1-D	Vehicle	3.49E-17	24	6.6E-03	-3.8	
193	5	17.20	17.20	84.5	K119k	101	(K)VTIAQGGVL/PNIQA/VL/L/Pk/KTE/SHK(A)	551.931	2641.54	114.0859	15.6	13988.4	Q16777	Histone H2A type 2-C	Vehicle	3.32E-06				Y
194	5	13.66	13.66	77.6	K120k K125k	101	(K)VT\IA\QG\GVL|PNIQ/A/VL/L/P/K/kTE/SHk(A)	574.7343	2641.54	228.1024	5.8	13988.4	Q16777	Histone H2A type 2-C	Vehicle	5.21E-07				Y (K120)
195	4	25.83	14.55	97.5	K110k	102	(R)LL|L/P/G/E/L/Ak/H/A/V/SE/GT/K(A)	470.0203	1763.006	114.0532	5.5	14167.6	Q96A08	Histone H2B type 1-A	Both	1.94E-14	50	3.4E-04	-7	Y
196	4	11.83	11.83	59.7	K122k	111	(K)HA\VSEG/TK/A\VTk/Y/T/S/S/K(-)	477.753	1793.939	114.051	4.2	14167.6	Q96A08	Histone H2B type 1-A	LLnL	6.60E-13			-1.2	Y
197	3	11.49	11.49	66.2	K123k	118	(R)VT\I/M/Pk/D/IQL/A/R(R)	500.289	1384.798	114.0544	7.6	15508.3	Q16695	Histone H3.1t	LLnL	1.79E-08			-3.6	Y
198	3	15.12	15.12	78.0	K57k	55	(R)YQ\k/S/T/E/L/L/I/R(K)	455.5921	1250.71	114.0514	6.2	15508.3	Q16695	Histone H3.1t	Both	3.11E-13	58	5.3E-05	-4.4	Y
199	3	16.85	8.29	75.2	K80k	74	(R)EI/AQ/D/F/k/T/D/L/R(F)	483.919	1335.69	114.0521	6.4	15508.3	Q16695	Histone H3.1t	Both		39	5.8E-03		Y
200	3	15.91	7.31	85.5	K32k	25	(R)DN\I\QGI/T/k/P/AI/R(R)	480.6102	1325.754	114.0625	13.6	11367.4	P62805	Histone H4	LLnL	7.29E-06	39	4.4E-03	-5.6	Y
201	3	17.47	6.94	71.9	K60k	57	(R)GV|L/k/V/F/L/ENVI/R(D)	500.9721	1386.847	114.055	8	11367.4	P62805	Histone H4	Both	1.23E-10	35	4.7E-03	-4.8	Y
202	3	14.22	8.57	66.7	K92k	81	(K)TV\TAM/DV/V/Y/A/L/k/R(Q)	527.625	1466.804	114.0569	8.8	11367.4	P62805	Histone H4	LLnL	1.47E-14			-2	Y
203	3	15.30	15.30	72.9	K199k	192	(R)ESVE/L/A/L/k/L/L/DEDEI/R(G)	662.6891	1871.996	114.0567	6.9	85853.2	O43719	HIV Tat-specific factor 1	LLnL	1.12E-12			-2.4	
204	3	15.95	8.51	84.6	K175k	171	(R)SV|GY/k/PDFV/GFE/I/PD/K(F)	637.9922	1797.906	114.0563	7	24579.5	P00492	Hypoxanthine-guanine phosphoribosyltransferase	LLnL	1.65E-09			-3.9	
205	3	14.58	14.58	79.7	K240k	239	(R)Nk\N\PA|PPIDA\V|E/Q/I|L/PTLVR(L)	767.1031	2185.234	114.0608	7.8	57862.2	P52292	Importin subunit alpha-2	LLnL	6.35E-06			-5.7	

206	3	13.79	13.79	68.8	K300k	292	(K)T\GV\V|PQLVkLLGASE/L/PI/V/TPALR(A)	862.5227	2471.496	114.0576	5.7	57862.2	P52292	Importin subunit alpha-2	LLnL	1.10E-06			-1.3	
207	3	15.62	15.62	86.9	K459k	454	(K)LGE\TEk\L\S\I|M|I/E/E/C/GGLDK(I)	746.0351	2122.041	114.0501	3.2	57862.2	P52292	Importin subunit alpha-2	LLnL	1.36E-23	49	5.4E-04	-11	
208	3	11.43	11.43	62.5	K537k	526	(R)SSA/YE/SLM/EI/V/k/NS/A/K(D)	624.3175	1756.879	114.0594	8.8	97170.8	Q14974	Importin subunit beta-1	LLnL	5.57E-14				
209	3	19.41	19.41	90.5	K730k	730	(K)kYLEVV|LNT\L/Q/Q|A/SQA/Q/V/D/K(S)	797.103	2275.229	114.0652	9.3	97170.8	Q14974	Importin subunit beta-1	LLnL	7.62E-16	43	2.8E-03	-9.8	
210	3	22.96	10.29	92.3	K213k	200	(R)LL|V|PT/Q/YV/GAI/I/Gk/E/GATIR(N)	738.4289	2099.222	114.0498	3.1	63456.8	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1	LLnL	9.47E-05	45	6.4E-04	-5	
211	3	18.12	11.62	83.4	K450k	441	(K)IA|P/PET/P/D/Sk/V/R(M)	475.2556	1309.711	114.0412	-1.2	63456.8	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1	LLnL	2.98E-08	43	2.0E-03	-2.3	
212	3	18.88	10.79	82.1	K141k	128	(K)IL|PTL/EAV/AAL/GNk|V/V/ESL/R(A)	736.4418	2093.233	114.078	15.9	43290.6	Q12905	Interleukin enhancer-binding factor 2	LLnL				-5.1	
213	3	11.12	11.12	61.7	K328k	328	(R)kIL\GQEGDASYLASEI/STW/DGV/I/V/T/P/SEK(A)	1069.8804	3093.563	114.064	6.6	43062.4	Q12905	Interleukin enhancer-binding factor 2	LLnL	4.68E-07	43	2.9E-03	-4.4	
214	4	12.03	12.03	60.6	K804k	798	(R)IADLQGkTSY/H/L/V/L/R(A)	457.7636	1713.965	114.0679	13.7	123743.8	P42702	Leukemia inhibitory factor receptor	LLnL				-7.8	
215	3	15.38	15.38	83.8	K118k	113	(R)NV\N\I\Fk/F/I/I/PNVV/K(Y)	587.019	1644.984	114.0589	9.1	36688.9	P00338	L-lactate dehydrogenase A chain	Both	1.35E-11	28	2.3E-02	-4.2	Y
216	3	13.39	9.48	74.7	K14k	6	(K)DQ|L|IYN/LL/kE/EQ/T/PQNK(I)	730.0517	2074.081	114.059	7.4	36688.9	P00338	L-lactate dehydrogenase A chain	LLnL	1.96E-15	32	3.6E-02	-4.6	Y
217	3	12.47	12.47	72.7	K243k	233	(K)QVVESAY/E/V/I/k/LK(G)	540.6431	1505.857	114.0574	8.9	36688.9	P00338	L-lactate dehydrogenase A chain	LLnL				-1.8	
218	3	15.86	15.86	73.3	K81k	77	(K)IVSG/k/D/YN/V/T/A/N/SK(L)	537.2795	1495.775	114.0488	3.7	36688.9	P00338	L-lactate dehydrogenase A chain	LLnL	5.42E-08				Y
219	3	14.77	5.61	82.0	K244k	234	(K)MV\VESAY/E/V/I/k/L/K(G)	541.6362	1508.839	114.0548	7.3	36638.7	P07195	L-lactate dehydrogenase B chain	LLnL	1.59E-12	30	3.6E-02	-3.4	
220	3	19.36	14.87	94.0	K308k	300	(R)GL|T|S/V|I/N/Q/kL/K/DDEVAQLK(K)	738.4119	2099.171	114.0505	3.4	36638.7	P07195	L-lactate dehydrogenase B chain	LLnL	1.52E-09	31	3.9E-02	-4.8	
221	4	18.24	7.15	93.2	K310k	300	(R)GL\TSV/I/NQKL/kDDE/V/AQ/L/K(K)	554.0608	2099.171	114.0507	3.5	36638.7	P07195	L-lactate dehydrogenase B chain	LLnL				-3.3	
222	3	10.58	10.58	72.0	K152k	149	(R)VGCkYQ/AE/I/PD/R(L)	517.2565	1435.7	114.0551	7.9	75023.5	O94776	Metastasis-associated protein MTA2	LLnL	7.60E-17	31	2.8E-02	-4.7	Y
223	3	15.34	9.81	75.5	K241k	235	(K)SF\E|A/PIkL/V/F/PQDLLE/K(G)	696.7211	1974.095	114.0541	5.4	41488.6	Q8TCT9	Minor histocompatibility antigen H13	LLnL	5.48E-05			-2.5	
224	3	23.78	23.78	90.7	K27k	17	(K)LD/PGL|I|M\EQV\kVQI/AV/A/N/A/Q/E/L/L/Q/R(M)	964.2062	2776.539	114.0651	7.7	10500.1	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	LLnL	9.90E-34	77	5.0E-07	-16.1	
225	4	13.70	13.70	63.3	K312k	296	(R)TV\LEHYALEDDPL/A/A/F/k/Q/R(Q)	583.3081	2216.135	114.076	14.2	39646.4	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50	LLnL	1.25E-06				
226	2	17.64	17.64	86.7	K80k	74	(R)FA\Q|I|V/Q/k/G/G/Q(-)	595.3212	1075.59	114.0457	2.3	9343.6	Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B	Both	5.34E-11	46	1.3E-03	-6	
227	3	18.66	18.66	77.0	K209k	194	(K)IA\Q/DLEMY/GV/NY/F/SI/k/N/K(K)	749.7138	2133.068	114.0583	6.9	67820.4	P26038	Moesin	LLnL	5.05E-09	30	5.4E-02	-3	Y
228	3	12.43	12.43	69.9	K109k	106	(K)EIA\kMAE/M/L/V/E/LV/R(R)	582.6562	1631.886	114.0681	14.4	14649.7	Q9Y605	MORF4 family-associated protein 1	Both	4.74E-13	52	3.4E-04		
229	3	11.70	11.70	62.2	K107k	95	(R)AL\GQ/N/P/TNAE/VL/k/VL/GN/PK(S)	693.0558	1963.097	114.0557	6.2	22764.1	P14649	Myosin light chain 6B	LLnL		33	2.2E-02	-2.9	Y
230	4	15.64	15.64	82.8	K91k	86	(R)LG\IGTk/M/LNH/V/L/NI/CE/K(D)	514.2813	1940.046	114.0578	7.2	19398.5	Q9GZZ1	N-acetyltransferase 13	LLnL	1.07E-04			-4.6	
231	3	14.99	5.65	68.1	K126k	120	(R)TL|A\EI/A/k/V/EL/DNM/PL/R(G)	643.0199	1812.989	114.0564	7	54231.9	Q15233	Non-POU domain-containing octamer-binding protein	LLnL	5.55E-07	31	4.0E-02	-3.9	
232	4	15.49	15.49	79.5	K371k	365	(R)RQ\Q\E\G\F\k/GTF/P/D/A/R(E)	438.4748	1636.819	114.0583	8.8	54231.9	Q15233	Non-POU domain-containing octamer-binding protein	LLnL	2.90E-13	46	1.3E-03	-5.5	
233	3	14.23	14.23	78.5	K467k	457	(R)AA|PGAEFA/P/Nk/R(R)	448.2354	1228.643	114.0484	4	54231.9	Q15233	Non-POU domain-containing octamer-binding protein	LLnL		40	2.8E-03		Y
234	3	13.04	13.04	82.0	K1548k	1535	(R)TL\Q/SL/L/T/PQ/PPLLk/ALYTYESK(M)	873.4893	2504.401	114.0523	3.6	227921.8	Q92621	Nuclear pore complex protein Nup205	LLnL	3.13E-13			-1.9	
235	3	16.97	10.15	78.8	K302k	293	(K)AE\V\V/DE/I/A/A/k/LGL/R(K)	533.305	1483.848	114.0526	6	68120.6	Q8TAT6	Nuclear protein localization protein 4 homolog	LLnL	5.17E-09	53	2.0E-04	-2.9	
236	3	16.36	16.36	86.2	K55k	50	(K)AAI|V\E\k/L/S/SL/PF/QK(I)	548.9859	1530.889	114.0541	6.8	14478.6	P61970	Nuclear transport factor 2	LLnL	9.21E-07			-2.9	
237	4	14.95	7.09	82.1	K56k	50	(K)EH\Y\VD\L/k/D/RPFFA/GL/V/K(Y)	537.7859	2034.081	114.041	-0.9	17148.8	P15531	Nucleoside diphosphate kinase A	LLnL	3.10E-07			-2.6	Y
238	3	15.26	15.26	85.3	K105k	105	(R)kYA\V\L|YQ/PL/F/D/K(R)	533.6264	1484.815	114.0499	4.3	45374.4	P55209	Nucleosome assembly protein 1-like 1	LLnL	1.17E-10	32	3.3E-02	-3.1	
239	3	9.96	9.96	62.9	K24k	24	(R)kVL\GSS\T\SA/T/N/S/T/S/V/SSR(K)	628.323	1768.903	114.0509	4.2	11986.6	Q15004	PCNA-associated factor	Vehicle	4.96E-20	32	3.2E-02		
240	2	13.33	13.33	76.6	K48k	42	(K)LL|N\L|I|S/kL/F/CSGT(-)	790.4299	1465.808	114.0442	0.8	6030.1	Q13794	Phorbol-12-myristate-13-acetate-induced protein 1	LLnL	3.34E-27	33	2.3E-02	-2.2	
241	4	21.02	16.23	87.5	K86k	74	(R)MI|A|P/E/GSLVFHEkA/W/N/A/Y/PYCR(T)	689.0832	2639.253	114.0576	5.3	31540.2	P48739	Phosphatidylinositol transfer protein beta isoform	LLnL	2.60E-06			-6	
242	4	13.89	6.64	72.4	K103k	87	(K)GAI\QL\GITHTVGSL/S/T/k/PE/R(D)	545.5577	2065.14	114.0689	11.9	62633.7	Q99755	Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha	Vehicle		39	4.8E-03	-2.6	
243	4	10.72	10.72	69.7	K27k	17	(K)LPH\SVL\LEIQ/k/ELL/D/YK(G)	538.8097	2038.158	114.0587	7.3	40422.9	Q9Y617	Phosphoserine aminotransferase	LLnL	7.24E-08				
244	3	22.94	12.97	97.4	K323k	320	(R)FL|D/kAL/E|L/N/M/L/SL/K(G)	583.6673	1634.919	114.0688	14.8	40422.9	Q9Y617	Phosphoserine aminotransferase	Both	7.65E-13	55	9.9E-05	-7.9	Y
245	3	19.26	19.26	88.5	K51k	46	(R)S/S\D\F\AkI/I/N/N/T/E/NLV/R(E)	645.6729	1820.95	114.054	5.7	40422.9	Q9Y617	Phosphoserine aminotransferase	LLnL	1.14E-28	60	5.5E-05	-10.7	Y
246	4	11.16	11.16	62.4	K207k	205	(K)ICkPLHEL\I\MQ\LL/E/E/T/PE/EK(Q)	641.8327	2450.267	114.042	-0.4	25569.4	P68402	Platelet-activating factor acetylhydrolase IB subunit beta	LLnL				-3.1	
247	3	13.81	13.81	55.3	K165k	157	(R)WYH|PG\CF/V/k/N/R(E)	526.5885	1463.7	114.0508	5	113084.4	P09874	Poly [ADP-ribose] polymerase 1	Vehicle	8.78E-06			-4	
248	3	21.65	11.47	93.4	K269k	263	(K)EL\L|I/F/NkQQ|V/P/SGE/SAILD/R(V)	791.0942	2257.219	114.0494	2.7	113084.4	P09874	Poly [ADP-ribose] polymerase 1	Vehicle	2.58E-11			-4	
249	3	15.68	8.04	78.9	K278k	268	(K)AL\N\MA/I/PGG/Pk/F/E/P\LVR(D)	642.0245	1810.004	114.0546	6	273601.9	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	LLnL				-1.3	
250	3	15.85	15.85	74.2	K727k	722	(K)AN\I/PWk/V/PGL|PT/PI/ENMI/L/R(Y)	791.7799	2259.268	114.0569	5.9	273601.9	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	LLnL				-2.5	
251	3	10.96	10.96	58.1	K24k	10	(K)DA\E\A\E/GLSGTTL/L/Pk/L/I/PSGAGR(E)	789.7652	2253.209	114.0725	12.5	20648.1	Q9UI14	Prenylated Rab acceptor protein 1	Both				-1.5	
252	3	14.92	14.92	75.6	K456k	453	(R)EL\I/kVLEE/AN/Q/A/I/N|PK(L)	641.6926	1809.012	114.0516	4.5	72371.8	Q92841	Probable ATP-dependent RNA helicase DDX17	LLnL	2.57E-12				
253	3	16.76	16.76	81.1	K470k	462	(R)EANQA/I/N/Pk/L/L/Q/L/VEDR(G)	689.0399	1951.061	114.0444	0.7	69148.5	P17844	Probable ATP-dependent RNA helicase DDX5	LLnL	8.49E-05			-3.9	
254	3	11.50	5.98	69.5	K54k	39	(K)TF|VNI/TPAE/V/GV|L/V/GkDR(S)	677.0397	1915.065	114.0398	-1.5	15054.3	P07737	Profilin-1	Vehicle				-3.3	
255	3	19.32	13.78	87.2	K707k	703	(R)DE|L|L/k/D/L/Q/Q/SI/A/R(E)	548.3017	1528.833	114.0576	8.9	96023.6	Q8WUM4	Programmed cell death 6-interacting protein	LLnL	1.97E-22	32	3.4E-02	-1.8	
256	4	20.68	20.68	94.4	K164k	150	(R)DLSH\IGD\A\V\V/I/S/C/A/kD/GV/K(F)	525.2778	1984.017	114.0726	14.1	28769	P12004	Proliferating cell nuclear antigen	Both	1.53E-18	38	8.9E-03	-3.5	
257	2	12.36	12.36	79.8	K254k	249	(K)YY|L|A|Pk\IEDEEG/S(-)	814.3819	1513.706	114.0508	4.9	28769	P12004	Proliferating cell nuclear antigen	LLnL	1.11E-18			-2.7	Y
258	3	10.97	10.97	60.6	K21k	17	(R)GA\SNk/Y|L/V/E/F/R(A)	466.5789	1283.674	114.0479	3.5	42153.5	Q16186	Proteasomal ubiquitin receptor ADRM1	LLnL	2.80E-13			-2.5	Y
259	3	16.38	11.61	79.9	K34k	31	(K)MS|L/k/GT/T/VT/PD/K(R)	464.5815	1277.677	114.053	7.2	42438.8	Q16186	Proteasomal ubiquitin receptor ADRM1	LLnL		46	1.4E-03	-3.9	
260	2	13.17	5.79	83.6	K239k	232	(K)EE\L\EEV|I|k/D/I(-)	665.846	1216.631	114.054	8.3	26582.3	P28066	Proteasome subunit alpha type-5	LLnL	4.41E-10	31	4.7E-02	-2	
261	3	18.83	18.83	85.9	K201k	197	(R)EV|LEkQ/P/V/L/S/Q/TE/A/R(D)	614.3363	1726.933	114.061	9.8	29204.4	P28070	Proteasome subunit beta type-4	LLnL	1.49E-11			-1.2	
262	4	13.29	13.29	67.4	K377k	372	(R)WENHNkSLQLE|A/QT/Y/Q/R(I)	565.5385	2145.047	114.085	18.6	57819.3	O95376	Protein ariadne-2 homolog	LLnL	1.34E-11				
263	4	12.66	12.66	53.2	K153k	140	(R)DM\LL/AN/PH/EL/SL/L/k/E/R(N)	499.024	1879.011	114.0636	10.4	44522.8	Q5TDH0	Protein DDI1 homolog 2	LLnL		42	3.3E-03	-3.8	
264	3	21.92	21.92	83.3	K170k	156	(R)N/P|PL/AEAL|L/S/GDL/E/k/FS/R(V)	691.0422	1957.039	114.0731	14.6	44522.8	Q5TDH0	Protein DDI1 homolog 2	LLnL	1.06E-07	40	6.2E-03	-8.1	
265	4	10.29	10.29	66.3	K325k	307	(R)GGRPNEI\E|PP/PPEM/P/PWQkR(Q)	607.314	2312.16	114.0737	12.7	55401	Q8NCA5	Protein FAM98A	LLnL	7.87E-05				
266	3	12.54	12.54	60.0	K377k	375	(R)LV\k\L/F/D/F/P/G/R(G)	435.9186	1191.689	114.0528	7.6	56084.8	Q9P258	Protein RCC2	LLnL	4.39E-10	33	1.8E-02		Y
267	4	23.86	11.23	94.7	K37k	33	(R)VL|ME/k/E/F|P/GFLENQKD/PL/A/V/DK(I)	666.1013	2547.316	114.067	9.1	11203.2	P60903	Protein S100-A10	Vehicle	6.17E-10			-1.7	Y
268	4	19.39	11.34	87.1	K37k K47k	33	(R)VL|MEkE\F/P/GFLENQk/D/PL/A/V/D/K(I)	694.6115	2547.316	228.1078	7.9	11203.2	P60903	Protein S100-A10	LLnL	1.74E-08				Y (K37)
269	3	13.11	7.73	77.1	K47k	38	(K)EF/PGF/LENQk/D/PL/AVDK(I)	687.6861	1946.986	114.0579	7.3	11203.2	P60903	Protein S100-A10	LLnL	4.94E-05				
270	3	19.55	19.55	84.9	K27k	24	(K)Y/A|Gk/DG\Y/N/Y/T/L/S/K(T)	531.9242	1479.711	114.0466	2.3	11740.5	P31949	Protein S100-A11	Both	9.96E-09	44	9.3E-04	-4.8	
271	3	14.12	14.12	74.4	K150k	150	(K)kAE\A\G\A\G\SA/T/E/F/Q/F/R(G)	561.9454	1569.766	114.0561	7.8	20120.4	Q9NQ39	Putative 40S ribosomal protein S10-like protein	LLnL	5.60E-10	57	5.7E-05	-4.3	
272	3	11.40	11.40	68.8	K12k	10	(K)VQk\VMV|Q/P/I/N/LIF/R(Y)	600.3518	1684.993	114.0478	2.7	10678.4	Q5VYJ4	Putative small nuclear ribonucleoprotein polypeptide E-like protein 1	Vehicle	4.57E-05			-1.4	
273	3	13.63	6.88	71.8	K305k	295	(R)GDL/G\IEI/PAEk/VFLAQ/K(M)	648.0334	1828.022	114.0642	10.9	57937.2	P14618	Pyruvate kinase isozymes M1/M2	LLnL				-1.3	Y
274	3	21.58	21.58	87.1	K209k	194	(K)IA\QDL/E/MY/GV/N/Y/F/E/I/k/NK(K)	763.717	2175.079	114.0574	6.3	68564.2	P35241	Radixin	LLnL	2.02E-12	36	1.2E-02	-1.6	
275	3	10.38	10.38	67.2	K526k	526	(K)kQ\LQA\L/S/S/E|L/AQ/A/R(D)	552.9752	1542.86	114.0512	5	68564.2	P35241	Radixin	LLnL	8.98E-08			-2.6	
276	4	11.57	11.57	62.8	K556k	539	(R)IL\AIGLI\NEALDEGDAQkTL/Q/A/L/Q/I/PA/AK(L)	783.6923	3017.688	114.0592	5.2	189252.9	P46940	Ras GTPase-activating-like protein IQGAP1	LLnL	3.23E-10			-3.5	
277	3	24.24	15.98	94.3	K147k	134	(K)LT|P|I/T/Y/PQGLA/M/A/k/EI/GAV/K(Y)	739.0838	2101.173	114.0643	9.6	21450.2	P63000	Ras-related C3 botulinum toxin substrate 1	Both	3.54E-10	43	2.2E-03	-8.5	
278	3	15.80	10.34	80.8	K165k	152	(K)TA|SN\V|E/EAFI/NTA/kEI/YE/K(I)	757.7162	2157.071	114.063	8.9	23545.7	P61019	Ras-related protein Rab-2A	LLnL				-1.5	
279	3	19.33	12.22	88.6	K410k	390	(R)SL|SV|L/SSSTII/A/N/PDI/PEAYkLR(G)	863.4742	2474.35	114.058	5.8	68138.6	P27694	Replication protein A 70 kDa DNA-binding subunit	LLnL	9.06E-17			-3.4	
280	3	13.12	13.12	69.0	K141k	139	(K)IDkTDY|M|V/G/S/Y/GP/R(A)	572.6094	1601.763	114.0508	4.6	23207.2	P52565	Rho GDP-dissociation inhibitor 1	LLnL	1.04E-13			-3.4	Y
281	4	15.83	15.83	78.7	K157k	142	(K)CS\V\C\PDY/D\L/CS/V/CE/GkGLH/R(G)	632.2764	2412.02	114.0638	8.3	47687.5	Q13501	Sequestosome-1	LLnL	4.47E-09				
282	3	22.12	18.42	91.7	K435k	421	(K)NY|D|I/G/A/A/LDTI/Q/Y/Sk/H/P/PPL(-)	776.4021	2213.124	114.068	10.8	47687.5	Q13501	Sequestosome-1	Both	1.71E-13	38	1.0E-02		
283	3	16.54	16.54	83.3	K456k	452	(R)LA\GD/kY/Q/A/A/V/QAL/R(E)	539.9647	1503.828	114.0517	5.4	53082.9	P34896	Serine hydroxymethyltransferase, cytosolic	LLnL	1.65E-09			-2.5	
284	3	10.48	10.48	69.2	K237k	234	(R)IQTkEPL/P/TL/PL/GR(S)	559.6587	1562.927	114.0351	-4.7	48841.1	O43464	Serine protease HTRA2, mitochondrial	LLnL	1.34E-06	40	2.6E-03	-1.6	
285	3	20.59	20.59	89.6	K306k	292	(K)F/P|ASV|PTGAQ/D|L/I/S/k/LL/R(H)	676.3806	1913.085	114.0418	-0.6	39280.7	Q96GD4	Serine/threonine-protein kinase 12	LLnL	3.94E-20				
286	2	11.47	3.22	65.3	K533k	526	(K)LL|F|LRYH/k/EK(E)	730.9128	1346.794	114.024	-13	410263.6	Q96Q15	Serine/threonine-protein kinase SMG1	LLnL				-7.1	
287	4	16.07	16.07	80.6	K374k	359	(K)DN\TIEHL\L|PL/F/L/AQ\L/k/DEC/PEV/R(L)	716.8758	2750.418	114.0632	7.1	65309	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	LLnL				-1.9	
288	4	20.01	20.01	89.8	K546k	543	(K)SL\Q/kI|G/PI/L/D/N/ST/LQ/SEV/K/PILEK(L)	691.8988	2650.503	114.0708	10.1	65309	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	LLnL	2.87E-06	36	4.3E-03	-10	
289	3	18.58	14.78	84.8	K41k	37	(K)EIL/T/k/E/S/N/V/Q/E/V/R(C)	553.631	1544.828	114.0506	4.6	35594.4	P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	LLnL	2.14E-06	36	1.4E-02	-2.6	
290	3	19.65	19.65	83.4	K391k	384	(K)I/S\Q/GN\I|S/k/A/C/L/I/L/R(S)	562.9842	1572.889	114.049	3.6	74606.6	O76094	Signal recognition particle 72 kDa protein	LLnL	4.55E-16	55	1.5E-04		
291	3	15.16	7.90	76.9	K162k	155	(K)AS/PA/LV/AkD/P/GTVA/NK(K)	551.6374	1538.854	114.044	0.6	59179.9	Q92783	Signal transducing adapter molecule 1	LLnL	1.08E-08				
292	4	19.59	19.59	87.7	K81k	67	(R)SGDSE\V\Y/Q/L/GD/V/SQ/k/TT/W/HR(I)	602.5423	2293.084	114.063	8.3	17259.8	Q04837	Single-stranded DNA-binding protein, mitochondrial	Vehicle	1.60E-13			-5.8	
293	3	17.50	17.50	80.9	K137k	132	(R)AA|A|Y/SkLGNY/A/GA/VQ/D/CE/R(A)	720.0063	2043.955	114.0491	2.9	34063.3	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	LLnL	1.87E-12	38	3.8E-03		Y
294	3	14.16	14.16	68.9	K160k	151	(R)AI\CID/PA/Y/Sk/AYG/R(M)	566.9489	1584.784	114.0483	3.1	34063.3	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	LLnL	9.55E-06			-8.6	
295	4	15.55	15.55	81.3	K419k	397	(K)ASKPLP\PA|PA|P\DEYL\VS/PI/TGEkI/PASK(M)	747.6616	2873.566	114.0587	5.3	88886.6	Q15459	Splicing factor 3 subunit 1	Vehicle				-3.3	
296	3	19.56	19.56	82.5	K38k	31	(K)DI|ED\V/F/Y/k/Y/GAI/R(D)	568.2901	1588.801	114.0552	7.2	27744.7	Q07955	Splicing factor, arginine/serine-rich 1	Both	1.58E-17	32	3.5E-02	-4.2	Y
297	3	15.16	15.16	83.5	K330k	320	(K)YG\E/PGE\V|F/I/N/kGK(G)	517.9362	1437.737	114.0568	8.9	76149.8	P23246	Splicing factor, proline- and glutamine-rich	LLnL	8.11E-17			-2.8	Y
298	4	17.06	17.06	60.4	K154k	139	(R)EA\LL/SS/A/VD/H/GSDE/V/k/F/R(Q)	519.2662	1959.977	114.0659	11.1	57488.5	P78371	T-complex protein 1 subunit beta	LLnL				-3.8	Y
299	3	15.58	8.39	78.2	K275k	266	(K)L/D|VTSV/E/DY/k/ALQ/K(Y)	574.9763	1608.848	114.0664	13.6	59671.4	P48643	T-complex protein 1 subunit epsilon	LLnL	3.67E-07	37	1.0E-02	-3.3	
300	3	12.32	12.32	72.9	K249k	238	(R)IV|LL/DSSL/E/Y/K/k(G)	507.9604	1407.809	114.0573	9.4	60534.3	P49368	T-complex protein 1 subunit gamma	LLnL		44	1.2E-03	-1.2	
301	3	19.07	19.07	82.0	K507k	503	(K)LQ|T\Yk/TA/V/E/T/A/V/L/L/L/R(I)	645.0453	1819.069	114.0526	5	60534.3	P49368	T-complex protein 1 subunit gamma	LLnL	1.89E-11	61	1.5E-05	-6.6	
302	3	21.34	17.37	94.7	K260k	255	(K)GTV|L|I/k/TA/E/E/L/M/NF/SK(G)	632.3417	1780.951	114.0592	8.6	59620.9	P50990	T-complex protein 1 subunit theta	LLnL	1.59E-23	59	5.8E-05	-3.4	
303	3	13.15	13.15	68.2	K341k	333	(R)SL\D\L/L/GLE/k/L/D/CGR(F)	568.3059	1588.836	114.0668	14	40929.8	O95551	TRAF and TNF receptor-associated protein	LLnL	8.93E-11	34	2.7E-02		
304	4	19.36	19.36	90.5	K43k	34	(R)EH\A\LTSGTI\k\AM\L\S\GPGQ\FAE/N/E/T/N/E/V/N/F/R(E)	841.4176	3248.564	114.0845	12.4	12473.2	Q15369	Transcription elongation factor B polypeptide 1	LLnL	6.55E-16	54	2.1E-04	-16.7	
305	3	17.25	17.25	92.4	K109k	96	(R)LGD\V|ISI/Q/PC/PDVk/YGK(R)	668.3483	1888.984	114.0466	1.9	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	4.27E-13	30	5.1E-02	-6.8	
306	3	11.61	11.61	72.4	K217k	212	(K)QLAQIkE/M/V|E/L/PLR(H)	594.6742	1667.951	114.0568	7.8	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	7.91E-13			-3.3	
307	3	12.42	12.42	71.2	K251k	240	(R)GI\L\L/Y/GP/PGT/Gk/TL/IAR(A)	614.362	1727.021	114.05	3.9	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	8.77E-07			-1.8	
308	3	14.16	14.16	69.8	K312k	296	(K)NA/PAIIFID/EL/D/A/I/A/Pk/R(E)	694.3877	1967.096	114.0525	4.6	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	1.06E-09	38	6.3E-03	-1.9	
309	3	19.33	19.33	84.7	K336k	324	(R)IV|SQ|L\L/T/L/M/D/GL/k/Q/R(A)	610.3558	1714.988	114.0644	11.8	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	3.25E-25	54	1.2E-04	-8.6	
310	3	11.42	11.42	67.9	K486k	466	(R)ETVV/E|V/PQVTWE/DI/GGLEDVkR(E)	871.4531	2498.277	114.0674	9.4	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	1.41E-11			-1.3	
311	4	15.02	15.02	80.2	K502k	488	(R)EL\Q\ELVQ/Y/PVEH/PD/kFL/K(F)	582.3112	2212.165	114.0581	6.5	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LLnL	1.39E-05			-3.6	

<table>
<tr><td>312</td><td>3</td><td>11.09</td><td>11.09</td><td>60.8</td><td>K524k</td><td>513</td><td>(K)GV\L\F|Y/GP/PGCGkTLL/AK(A)</td><td>631.346</td><td>1777.967</td><td>114.0565</td><td>7.2</td><td>89322.3</td><td>P55072</td><td>Transitional endoplasmic reticulum ATPase</td><td>LLnL</td><td></td><td></td><td></td><td>-3</td><td></td></tr>
<tr><td>313</td><td>3</td><td>12.14</td><td>12.14</td><td>71.5</td><td>K651k</td><td>639</td><td>(R)LD\Q\L\I\Y\I|PL/PDEkS/R(V)</td><td>638.6839</td><td>1799.99</td><td>114.047</td><td>2.1</td><td>89322.3</td><td>P55072</td><td>Transitional endoplasmic reticulum ATPase</td><td>LLnL</td><td>5.38E-15</td><td>35</td><td>1.8E-02</td><td>-4.4</td><td></td></tr>
<tr><td>314</td><td>3</td><td>11.60</td><td>11.60</td><td>61.0</td><td>K658k</td><td>654</td><td>(R)VA\I/L/k/A/N/L/R(K)</td><td>371.2373</td><td>997.652</td><td>114.0457</td><td>2.5</td><td>89322.3</td><td>P55072</td><td>Transitional endoplasmic reticulum ATPase</td><td>LLnL</td><td>7.77E-07</td><td>42</td><td>5.7E-04</td><td>-1.8</td><td></td></tr>
<tr><td>315</td><td>3</td><td>14.08</td><td>14.08</td><td>80.3</td><td>K668k</td><td>664</td><td>(K)SP\VA\kDV/D/L/E/FL/A/K(M)</td><td>549.3025</td><td>1531.837</td><td>114.0563</td><td>8.1</td><td>89322.3</td><td>P55072</td><td>Transitional endoplasmic reticulum ATPase</td><td>LLnL</td><td>4.03E-10</td><td>36</td><td>1.4E-02</td><td>-4.6</td><td></td></tr>
<tr><td>316</td><td>3</td><td>19.18</td><td>19.18</td><td>83.3</td><td>K73k</td><td>61</td><td>(R)VQ|N|M/AL/Y/AD/V/GGk/Q/F/PVTR(G)</td><td>736.7183</td><td>2094.08</td><td>114.0603</td><td>7.9</td><td>18998.7</td><td>P51571</td><td>Translocon-associated protein subunit delta</td><td>LLnL</td><td>7.87E-10</td><td>31</td><td>4.9E-02</td><td></td><td></td></tr>
<tr><td>317</td><td>4</td><td>17.24</td><td>17.24</td><td>81.5</td><td>K116k</td><td>113</td><td>(R)VVAkLPFT/PL/SYI/QGL/SH/R(N)</td><td>560.8251</td><td>2126.212</td><td>114.0665</td><td>10.5</td><td>21175.1</td><td>Q9UM00</td><td>Transmembrane and coiled-coil domain-containing protein 1</td><td>LLnL</td><td>4.58E-06</td><td>37</td><td>4.8E-03</td><td>-3</td><td></td></tr>
<tr><td>318</td><td>3</td><td>14.18</td><td>6.75</td><td>78.1</td><td>K68k</td><td>63</td><td>(R)LI|Q|V|Pk/GPVE/GYEEN/EEFLR(T)</td><td>820.7571</td><td>2346.198</td><td>114.0591</td><td>6.6</td><td>14199.5</td><td>Q9UI30</td><td>TRM112-like protein</td><td>LLnL</td><td>3.84E-11</td><td></td><td></td><td>-1.2</td><td></td></tr>
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<tr><td>320</td><td>3</td><td>17.78</td><td>11.20</td><td>84.6</td><td>K326k</td><td>321</td><td>(R)GD\V|V/Pk/DVNA/A/I/A/TI/K(T)</td><td>575.6588</td><td>1610.911</td><td>114.0506</td><td>4.5</td><td>50135.9</td><td>Q71U36</td><td>Tubulin alpha-1A chain</td><td>Both</td><td>2.41E-13</td><td>42</td><td>2.5E-03</td><td>-2.4</td><td>Y</td></tr>
<tr><td>321</td><td>4</td><td>10.52</td><td>10.52</td><td>64.6</td><td>K326k K336k</td><td>321</td><td>(R)GD\V\VPkDVNAAI/A/T/I/k/T/K(R)</td><td>517.7957</td><td>1840.054</td><td>228.1071</td><td>10.3</td><td>50135.9</td><td>Q71U36</td><td>Tubulin alpha-1A chain</td><td>Both</td><td>4.69E-05</td><td></td><td></td><td>-1.1</td><td>Y (K326)</td></tr>
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<tr><td>323</td><td>3</td><td>20.07</td><td>16.36</td><td>97.3</td><td>K370k</td><td>353</td><td>(K)VGINY\Q|PPT\V|V|P/GGD/L/A/k/VQR(A)</td><td>774.7622</td><td>2208.213</td><td>114.0585</td><td>6.7</td><td>50135.9</td><td>Q71U36</td><td>Tubulin alpha-1A chain</td><td>Both</td><td>4.16E-22</td><td>54</td><td>1.6E-04</td><td>-9</td><td>Y</td></tr>
<tr><td>324</td><td>4</td><td>24.96</td><td>24.96</td><td>94.5</td><td>K60k</td><td>41</td><td>(K)TI\G\GGDDSF/N/T/F/F/S/E/T/GA/Gk/H/V/P/R(A)</td><td>653.5588</td><td>2497.174</td><td>114.0391</td><td>-1.5</td><td>50135.9</td><td>Q71U36</td><td>Tubulin alpha-1A chain</td><td>Both</td><td>3.88E-05</td><td>41</td><td>2.1E-03</td><td>-9.7</td><td>Y</td></tr>
<tr><td>325</td><td>4</td><td>19.93</td><td>19.93</td><td>93.1</td><td>K96k</td><td>85</td><td>(R)QLFHPEQ\LI/T/Gk/E/D/AA/N/N/YA/R(G)</td><td>633.0715</td><td>2415.205</td><td>114.059</td><td>6.4</td><td>50135.9</td><td>Q71U36</td><td>Tubulin alpha-1A chain</td><td>Both</td><td>2.30E-11</td><td></td><td></td><td>-7.8</td><td></td></tr>
<tr><td>326</td><td>3</td><td>17.30</td><td>9.58</td><td>88.0</td><td>K297k</td><td>283</td><td>(R)AL|T|V|PELTQQVFDAkNM/M/A/ACD/PR(H)</td><td>940.7958</td><td>2706.305</td><td>114.068</td><td>8.9</td><td>49671.1</td><td>P07437</td><td>Tubulin beta chain</td><td>LLnL</td><td>1.60E-05</td><td></td><td></td><td></td><td></td></tr>
<tr><td>327</td><td>3</td><td>24.42</td><td>24.42</td><td>93.1</td><td>K58k</td><td>47</td><td>(R)I/S|V/Y/Y/NE/A/T/G/Gk/Y/V/PR(A)</td><td>644.3292</td><td>1816.923</td><td>114.0502</td><td>3.8</td><td>49671.1</td><td>P07437</td><td>Tubulin beta chain</td><td>Both</td><td>1.24E-24</td><td>72</td><td>3.6E-06</td><td>-10.5</td><td>Y</td></tr>
<tr><td>328</td><td>3</td><td>9.61</td><td>5.17</td><td>60.6</td><td>K252k</td><td>252</td><td>(R)kLAV\N\M\V/PF/P/R(L)</td><td>462.5983</td><td>1271.729</td><td>114.0511</td><td>5.9</td><td>50327.2</td><td>Q9H4B7</td><td>Tubulin beta-1 chain</td><td>Both</td><td>2.09E-10</td><td></td><td></td><td>-3.9</td><td></td></tr>
<tr><td>329</td><td>3</td><td>17.30</td><td>17.30</td><td>92.2</td><td>K324k</td><td>321</td><td>(R)M/S\MkEVD\EQ|M|L/N/V/Q/NK(N)</td><td>679.9929</td><td>1923.897</td><td>114.0669</td><td>11.7</td><td>49907.3</td><td>Q13885</td><td>Tubulin beta-2A chain</td><td>LLnL</td><td>3.77E-13</td><td>40</td><td>3.0E-03</td><td>-2</td><td></td></tr>
<tr><td>330</td><td>3</td><td>17.09</td><td>17.09</td><td>72.6</td><td>K58k</td><td>47</td><td>(R)IN\V\Y/YNE/A/T/G/Gk/Y/V/PR(A)</td><td>653.334</td><td>1843.934</td><td>114.0537</td><td>5.5</td><td>49831.3</td><td>P68371</td><td>Tubulin beta-2C chain</td><td>Both</td><td>1.92E-05</td><td>30</td><td>5.1E-02</td><td>-4.2</td><td>Y</td></tr>
<tr><td>331</td><td>3</td><td>15.81</td><td>9.62</td><td>82.2</td><td>K412k</td><td>401</td><td>(R)TV|V/S/GLVQF/V/PkEE/LQD/R(L)</td><td>720.0587</td><td>2044.107</td><td>114.0542</td><td>5.2</td><td>59143.8</td><td>P54577</td><td>Tyrosyl-tRNA synthetase, cytoplasmic</td><td>LLnL</td><td></td><td></td><td></td><td>-3.7</td><td></td></tr>
<tr><td>332</td><td>3</td><td>12.10</td><td>12.10</td><td>72.3</td><td>K513k</td><td>507</td><td>(K)QTNFMTk/L/G/S/I/S/C/K(S)</td><td>576.9535</td><td>1614.798</td><td>114.0481</td><td>3</td><td>59143.8</td><td>P54577</td><td>Tyrosyl-tRNA synthetase, cytoplasmic</td><td>LLnL</td><td>6.39E-16</td><td>47</td><td>6.2E-04</td><td>-2.2</td><td></td></tr>
<tr><td>333</td><td>4</td><td>17.08</td><td>13.70</td><td>72.9</td><td>K329k</td><td>319</td><td>(K)VL\Y\V/YDML/AGk/L/I/PV/HQV/R(G)</td><td>582.8332</td><td>2214.247</td><td>114.0642</td><td>9.1</td><td>62003.9</td><td>Q9Y5J1</td><td>U3 small nucleolar RNA-associated protein 18 homolog</td><td>Both</td><td></td><td>28</td><td>4.8E-02</td><td></td><td></td></tr>
<tr><td>334</td><td>2</td><td>25.09</td><td>25.09</td><td>97.6</td><td>K11k</td><td>7</td><td>(K)TL/T/Gk|T|I|T/L|E|V|E|PSD/TI/E/NV\K(A)</td><td>1201.6458</td><td>2288.223</td><td>114.0612</td><td>7.6</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>Both</td><td>4.88E-19</td><td>53</td><td>2.7E-04</td><td>-11.5</td><td>Y</td></tr>
<tr><td>335</td><td>4</td><td>13.45</td><td>9.13</td><td>68.3</td><td>K11k K27k</td><td>7</td><td>(K)TL\TGkTITLE/V/E/PSDTIENV/k/A/K(I)</td><td>679.6212</td><td>2487.355</td><td>228.1077</td><td>8.1</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td></td><td></td><td></td><td>-1.6</td><td>Y (K11)</td></tr>
<tr><td>336</td><td>3</td><td>23.06</td><td>11.27</td><td>96.9</td><td>K27k</td><td>12</td><td>(K)TI|T\L/E/VE/PSDT/I/E/NV/k/A/K(I)</td><td>701.0411</td><td>1987.059</td><td>114.0494</td><td>3.1</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>Both</td><td>7.40E-17</td><td>48</td><td>9.6E-04</td><td>-1.9</td><td></td></tr>
<tr><td>337</td><td>4</td><td>17.15</td><td>8.26</td><td>91.6</td><td>K27k K29k</td><td>12</td><td>(K)T\I\TLEVE/PSD/TIENV/k/Ak/IQD/K(E)</td><td>675.6143</td><td>2471.324</td><td>228.1114</td><td>9.5</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td>1.49E-14</td><td></td><td></td><td>-3.9</td><td></td></tr>
<tr><td>338</td><td>3</td><td>14.69</td><td>8.56</td><td>84.2</td><td>K29k</td><td>28</td><td>(K)AkIQD/KEG\I/P/P/D/QQR(L)</td><td>612.9837</td><td>1722.913</td><td>114.0232</td><td>-10.7</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td>7.92E-11</td><td></td><td></td><td>-1.1</td><td></td></tr>
<tr><td>339</td><td>4</td><td>10.01</td><td>2.43</td><td>62.4</td><td>K29k K33k</td><td>28</td><td>(K)Ak\IQDkEGI|P/PD/QQ/R(L)</td><td>488.5043</td><td>1722.913</td><td>228.082</td><td>-2</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td>9.83E-08</td><td></td><td></td><td>-2.6</td><td></td></tr>
<tr><td>340</td><td>3</td><td>12.50</td><td>4.99</td><td>83.3</td><td>K33k</td><td>30</td><td>(K)IQ\DkEG\I/P/PD/QQR(L)</td><td>546.6133</td><td>1523.781</td><td>114.0441</td><td>0.7</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td>2.35E-06</td><td></td><td></td><td>-1.5</td><td></td></tr>
<tr><td>341</td><td>2</td><td>24.82</td><td>15.45</td><td>96.6</td><td>K48k</td><td>43</td><td>(R)L/I|F|A|G/k|Q/L/E/D/GR(T)</td><td>730.8999</td><td>1346.743</td><td>114.0498</td><td>4.7</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>Both</td><td>1.39E-09</td><td>55</td><td>1.7E-04</td><td>-6.2</td><td>Y</td></tr>
<tr><td>342</td><td>3</td><td>28.38</td><td>15.15</td><td>97.9</td><td>K63k</td><td>55</td><td>(R)T/L|S/D/Y/N/I/Q/k/E/STL/H/L/VL/R(L)</td><td>748.7436</td><td>2130.155</td><td>114.0609</td><td>8</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>Both</td><td>1.00E-21</td><td>59</td><td>6.1E-05</td><td>-9.4</td><td></td></tr>
<tr><td>343</td><td>3</td><td>20.80</td><td>20.80</td><td>93.0</td><td>K6k</td><td>1</td><td>(-)MQ|I|F/V|k/T/L/T/G/K(T)</td><td>460.5952</td><td>1265.729</td><td>114.0424</td><td>-0.4</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>Both</td><td>5.12E-10</td><td>54</td><td>1.2E-04</td><td>-2.9</td><td>Y</td></tr>
<tr><td>344</td><td>4</td><td>9.89</td><td>6.49</td><td>68.3</td><td>K6k K11k</td><td>1</td><td>(-)MQ\I\FVk\TLTGkTITLEVE/PSD/T/IENVK(A)</td><td>816.4424</td><td>3034.638</td><td>228.1097</td><td>7.3</td><td>8564.9</td><td>P62988</td><td>Ubiquitin</td><td>LLnL</td><td></td><td></td><td></td><td>-2.5</td><td>Y (K6)</td></tr>
<tr><td>345</td><td>3</td><td>11.92</td><td>8.21</td><td>79.0</td><td>K421k</td><td>413</td><td>(K)LI|EDST/L/Sk/SV/K(N)</td><td>478.6021</td><td>1319.742</td><td>114.0501</td><td>5</td><td>294366.9</td><td>Q9UPU5</td><td>Ubiquitin carboxyl-terminal hydrolase 24</td><td>LLnL</td><td>2.22E-05</td><td></td><td></td><td></td><td></td></tr>
<tr><td>346</td><td>3</td><td>20.66</td><td>20.66</td><td>92.2</td><td>K360k</td><td>358</td><td>(K)LE/k\I\FQ\N/A|PTD/PT/QD/FSTQV/A/K(L)</td><td>864.7743</td><td>2478.251</td><td>114.0573</td><td>5.5</td><td>95786.8</td><td>P45974</td><td>Ubiquitin carboxyl-terminal hydrolase 5</td><td>LLnL</td><td>1.35E-12</td><td>31</td><td>4.8E-02</td><td>-3.1</td><td></td></tr>
<tr><td>347</td><td>3</td><td>16.07</td><td>6.67</td><td>81.0</td><td>K793k</td><td>779</td><td>(R)SA|AD\SISESV/P/V/G/PkV/R(D)</td><td>604.9907</td><td>1698.902</td><td>114.0555</td><td>6.9</td><td>95786.8</td><td>P45974</td><td>Ubiquitin carboxyl-terminal hydrolase 5</td><td>LLnL</td><td>1.79E-06</td><td></td><td></td><td>-2</td><td></td></tr>
<tr><td>348</td><td>3</td><td>12.68</td><td>12.68</td><td>66.6</td><td>K115k</td><td>106</td><td>(K)LG/FED/GSVL/k/Q/F/L/SE/TEK(M)</td><td>714.3708</td><td>2027.033</td><td>114.0647</td><td>10.2</td><td>24824.5</td><td>P09936</td><td>Ubiquitin carboxyl-terminal hydrolase isozyme L1</td><td>LLnL</td><td>1.28E-11</td><td></td><td></td><td>-1.5</td><td></td></tr>
<tr><td>349</td><td>4</td><td>15.84</td><td>15.84</td><td>88.5</td><td>K210k</td><td>187</td><td>(R)K\PFPINHGETSD\E\T\L\L\E/D\A|I/E/V/C/k/K(F)</td><td>746.8753</td><td>2870.424</td><td>114.0553</td><td>4.2</td><td>26182.7</td><td>P15374</td><td>Ubiquitin carboxyl-terminal hydrolase isozyme L3</td><td>LLnL</td><td>7.36E-07</td><td>31</td><td>4.5E-02</td><td>-3.7</td><td></td></tr>
<tr><td>350</td><td>2</td><td>16.90</td><td>16.90</td><td>85.1</td><td>K529k</td><td>524</td><td>(K)DT\V/L|G\k/W/Q|Y|F(-)</td><td>685.8454</td><td>1256.631</td><td>114.0525</td><td>7</td><td>57295.2</td><td>O14562</td><td>Ubiquitin domain-containing protein UBFD1</td><td>Both</td><td>1.15E-17</td><td>28</td><td>5.2E-02</td><td>-4.4</td><td></td></tr>
<tr><td>351</td><td>4</td><td>18.93</td><td>18.93</td><td>83.2</td><td>K109k</td><td>95</td><td>(R)AF|GFSHLEALL/D/D/Sk/E/L/Q/R(F)</td><td>573.2983</td><td>2176.103</td><td>114.0681</td><td>11</td><td>31284.2</td><td>Q96FW1</td><td>Ubiquitin thioesterase OTUB1</td><td>LLnL</td><td>2.20E-07</td><td>42</td><td>3.9E-03</td><td>-6.6</td><td></td></tr>
<tr><td>352</td><td>3</td><td>11.77</td><td>11.77</td><td>76.9</td><td>K178k</td><td>166</td><td>(K)L/L\ALN\PDAV/E/LF/k/K(A)</td><td>562.3305</td><td>1570.92</td><td>114.0566</td><td>8.1</td><td>45338.7</td><td>Q9BSL1</td><td>Ubiquitin-associated domain-containing protein 1</td><td>LLnL</td><td>5.77E-07</td><td></td><td></td><td></td><td></td></tr>
<tr><td>353</td><td>4</td><td>19.21</td><td>10.83</td><td>85.8</td><td>K119k</td><td>98</td><td>(K)FL|T|PCYHPNVDTQGNI/C/L/DI/L/kE/K(W)</td><td>748.1233</td><td>2875.412</td><td>114.0597</td><td>5.6</td><td>19652.4</td><td>O00762</td><td>Ubiquitin-conjugating enzyme E2 C</td><td>LLnL</td><td></td><td>41</td><td>4.2E-03</td><td>-5.1</td><td></td></tr>
<tr><td>354</td><td>4</td><td>18.97</td><td>11.37</td><td>84.3</td><td>K121k</td><td>98</td><td>(K)FL|T|PCYHPNVDTQGN/I/C/L/DI/L/KE|k(W)</td><td>748.1275</td><td>2875.412</td><td>114.0765</td><td>11.2</td><td>19652.4</td><td>O00762</td><td>Ubiquitin-conjugating enzyme E2 C</td><td>LLnL</td><td></td><td>39</td><td>6.0E-03</td><td>-5.7</td><td></td></tr>
<tr><td>355</td><td>4</td><td>23.83</td><td>23.83</td><td>95.5</td><td>K136k</td><td>119</td><td>(R)IYHCNI\N\SQ/G\V|I/C/L/DIL/k/DNW/S/PAL/TI/SK(V)</td><td>872.4521</td><td>3372.708</td><td>114.0787</td><td>10.3</td><td>21404.3</td><td>P51965</td><td>Ubiquitin-conjugating enzyme E2 E1</td><td>LLnL</td><td>3.81E-16</td><td>37</td><td>1.1E-02</td><td>-8.3</td><td></td></tr>
<tr><td>356</td><td>3</td><td>15.87</td><td>15.87</td><td>81.4</td><td>K72k</td><td>62</td><td>(K)IPETY\PF/N/P/PkVR(F)</td><td>557.9703</td><td>1557.842</td><td>114.054</td><td>6.6</td><td>22406.8</td><td>P61086</td><td>Ubiquitin-conjugating enzyme E2 K</td><td>LLnL</td><td>5.17E-09</td><td></td><td></td><td></td><td></td></tr>
<tr><td>357</td><td>4</td><td>22.40</td><td>15.01</td><td>100.0</td><td>K67k</td><td>53</td><td>(R)IE\INF\PA/E/Y/PF/K/PPk/I/T/F/K(T)</td><td>599.0789</td><td>2279.247</td><td>114.0463</td><td>1.4</td><td>17861.7</td><td>P68036</td><td>Ubiquitin-conjugating enzyme E2 L3</td><td>LLnL</td><td>6.01E-06</td><td></td><td></td><td></td><td></td></tr>
<tr><td>358</td><td>4</td><td>22.40</td><td>15.01</td><td>100.0</td><td>K71k</td><td>53</td><td>(R)IE\INF\PA/E/Y/PF/K/PPKITF/k(T)</td><td>599.0789</td><td>2279.247</td><td>114.0463</td><td>1.4</td><td>17861.7</td><td>P68036</td><td>Ubiquitin-conjugating enzyme E2 L3</td><td>LLnL</td><td>4.99E-06</td><td></td><td></td><td></td><td></td></tr>
<tr><td>359</td><td>2</td><td>16.81</td><td>8.84</td><td>84.5</td><td>K92k</td><td>86</td><td>(R)I/C|L|D|IL/k/DK(W)</td><td>616.3424</td><td>1117.629</td><td>114.049</td><td>4.9</td><td>17137.9</td><td>P61088</td><td>Ubiquitin-conjugating enzyme E2 N</td><td>Both</td><td>2.11E-07</td><td>37</td><td>1.3E-02</td><td>-4.6</td><td></td></tr>
<tr><td>360</td><td>4</td><td>13.22</td><td>13.22</td><td>70.6</td><td>K132k</td><td>124</td><td>(R)VQ\W\YPE/GVkQ/HV/K(E)</td><td>428.7308</td><td>1597.849</td><td>114.0528</td><td>5.8</td><td>141294.2</td><td>Q9C0C9</td><td>Ubiquitin-conjugating enzyme E2 O</td><td>LLnL</td><td>9.26E-06</td><td></td><td></td><td></td><td></td></tr>
<tr><td>361</td><td>4</td><td>20.86</td><td>20.86</td><td>87.6</td><td>K825k</td><td>820</td><td>(K)IL\ES\LkNMTVE/Q|L|L/T/G/S/PT/S/PTVE/PEK/PTR(E)</td><td>853.2092</td><td>3295.745</td><td>114.0696</td><td>7.8</td><td>141294.2</td><td>Q9C0C9</td><td>Ubiquitin-conjugating enzyme E2 O</td><td>LLnL</td><td></td><td></td><td></td><td>-2</td><td></td></tr>
<tr><td>362</td><td>3</td><td>16.49</td><td>16.49</td><td>83.4</td><td>K63k</td><td>62</td><td>(R)Lk\FPID\Y|P/Y/S/P/PAF/R(F)</td><td>642.3386</td><td>1810.953</td><td>114.0486</td><td>2.9</td><td>26736.9</td><td>P49427</td><td>Ubiquitin-conjugating enzyme E2 R1</td><td>LLnL</td><td>8.51E-06</td><td>32</td><td>2.7E-02</td><td>-4.4</td><td></td></tr>
<tr><td>363</td><td>3</td><td>22.21</td><td>22.21</td><td>81.5</td><td>K197k</td><td>170</td><td>(R)AL|A|S|G/TE/A/S/STD/PGA|PG/G/PGGAE/GPMAk/K(H)</td><td>895.1029</td><td>2569.22</td><td>114.0743</td><td>11.7</td><td>23845.4</td><td>Q16763</td><td>Ubiquitin-conjugating enzyme E2 S</td><td>Vehicle</td><td>1.49E-15</td><td>34</td><td>1.6E-02</td><td>-6.8</td><td></td></tr>
<tr><td>364</td><td>2</td><td>20.22</td><td>15.17</td><td>93.3</td><td>K91k</td><td>85</td><td>(R)I/C|L/D|V|L\k|L|P/PK(G)</td><td>705.4186</td><td>1295.776</td><td>114.0544</td><td>8.1</td><td>22521</td><td>Q9NPD8</td><td>Ubiquitin-conjugating enzyme E2 T</td><td>Both</td><td>1.06E-15</td><td>70</td><td>1.6E-06</td><td></td><td></td></tr>
<tr><td>365</td><td>4</td><td>15.85</td><td>15.85</td><td>85.1</td><td>K627k</td><td>605</td><td>(K)GN\VQV\V|I|PFLTES/Y/SS/SQD/PPEkSI/PICTLK(N)</td><td>887.7112</td><td>3433.756</td><td>114.067</td><td>6.8</td><td>117849.6</td><td>P22314</td><td>Ubiquitin-like modifier-activating enzyme 1</td><td>LLnL</td><td></td><td></td><td></td><td>-6.4</td><td></td></tr>
<tr><td>366</td><td>3</td><td>26.90</td><td>15.06</td><td>98.9</td><td>K635k</td><td>628</td><td>(K)SI|P/I/C/T/L/k/N/F/PNAI/E/HTLQWAR(D)</td><td>908.4736</td><td>2609.366</td><td>114.0406</td><td>-0.9</td><td>117849.6</td><td>P22314</td><td>Ubiquitin-like modifier-activating enzyme 1</td><td>Both</td><td></td><td>29</td><td>8.2E-02</td><td></td><td></td></tr>
<tr><td>367</td><td>4</td><td>19.59</td><td>19.59</td><td>86.7</td><td>K746k</td><td>724</td><td>(R)QLLHNF\PPDQ\L|TS|SGA/PF/W/S/G/Pk/R(C)</td><td>699.3648</td><td>2680.363</td><td>114.0743</td><td>11.2</td><td>117849.6</td><td>P22314</td><td>Ubiquitin-like modifier-activating enzyme 1</td><td>LLnL</td><td></td><td>34</td><td>2.5E-02</td><td></td><td></td></tr>
<tr><td>368</td><td>4</td><td>20.80</td><td>15.41</td><td>91.2</td><td>K628k</td><td>616</td><td>(R)D/P|PE/EE/I|PFCTL/kS/F/PAAIEHTIQWAR(D)</td><td>824.9209</td><td>3182.561</td><td>114.1002</td><td>17.4</td><td>117970.6</td><td>A0AVT1</td><td>Ubiquitin-like modifier-activating enzyme 6</td><td>LLnL</td><td>4.48E-06</td><td></td><td></td><td>-4.5</td><td></td></tr>
<tr><td>369</td><td>4</td><td>12.83</td><td>12.83</td><td>67.2</td><td>K739k</td><td>730</td><td>(K)DG\SL/F/W/Q/S/PkRPPSPI/K(F)</td><td>514.285</td><td>1940.039</td><td>114.0793</td><td>17.7</td><td>117970.6</td><td>A0AVT1</td><td>Ubiquitin-like modifier-activating enzyme 6</td><td>LLnL</td><td></td><td></td><td></td><td>-1.9</td><td></td></tr>
<tr><td>370</td><td>3</td><td>14.47</td><td>14.47</td><td>72.2</td><td>K71k</td><td>63</td><td>(R)MD/NNA\A/A/I/k/ALE/L/Y/K(I)</td><td>593.6451</td><td>1664.868</td><td>114.0531</td><td>5.7</td><td>100688.2</td><td>Q05086</td><td>Ubiquitin-protein ligase E3A</td><td>LLnL</td><td>6.72E-13</td><td></td><td></td><td></td><td></td></tr>
<tr><td>371</td><td>4</td><td>17.49</td><td>17.49</td><td>81.7</td><td>K67k</td><td>56</td><td>(R)GGG\VGGFL|PAMkQI\GNV/A/A/L/P/GIV/H/R(S)</td><td>658.3662</td><td>2516.392</td><td>114.0511</td><td>3.1</td><td>55210.6</td><td>Q9Y3I0</td><td>UPF0027 protein C22orf28</td><td>LLnL</td><td>3.11E-08</td><td></td><td></td><td>-1.9</td><td></td></tr>
<tr><td>372</td><td>3</td><td>18.73</td><td>18.73</td><td>81.4</td><td>K65k</td><td>50</td><td>(R)LC|E|Q/GI|N|PEAL/S/SV/I/kEL/R(K)</td><td>757.4015</td><td>2156.138</td><td>114.052</td><td>4</td><td>8478.8</td><td>Q08AG7</td><td>UPF0582 protein C13orf37</td><td>LLnL</td><td>8.20E-09</td><td>70</td><td>5.5E-06</td><td></td><td></td></tr>
<tr><td>373</td><td>3</td><td>23.43</td><td>13.09</td><td>92.3</td><td>K53k</td><td>48</td><td>(K)LI|Y/A/Gk|I/L/S/D/D/V/PI/R(D)</td><td>596.3444</td><td>1672.963</td><td>114.0554</td><td>7</td><td>39609.4</td><td>P54725</td><td>UV excision repair protein RAD23 homolog A</td><td>Both</td><td>8.79E-14</td><td></td><td></td><td>-6.3</td><td></td></tr>
<tr><td>374</td><td>3</td><td>17.05</td><td>17.05</td><td>81.8</td><td>K24k</td><td>15</td><td>(K)ID\ID|P/E/E/TV/kAL/K(E)</td><td>528.9566</td><td>1470.805</td><td>114.0502</td><td>4.6</td><td>43171.4</td><td>P54727</td><td>UV excision repair protein RAD23 homolog B</td><td>LLnL</td><td>2.98E-11</td><td></td><td></td><td>-1.6</td><td></td></tr>
<tr><td>375</td><td>3</td><td>25.30</td><td>13.18</td><td>94.4</td><td>K51k</td><td>46</td><td>(K)L/I|Y/A/G/k|I/L/N/D/D/TA/L/K(E)</td><td>587.9992</td><td>1647.932</td><td>114.0514</td><td>4.8</td><td>43171.4</td><td>P54727</td><td>UV excision repair protein RAD23 homolog B</td><td>Both</td><td>7.69E-10</td><td>69</td><td>3.9E-06</td><td>-4.9</td><td></td></tr>
<tr><td>376</td><td>3</td><td>10.04</td><td>10.04</td><td>71.3</td><td>K76k</td><td>68</td><td>(K)NF\V\VV/MV/Tk/P/K(A)</td><td>459.2645</td><td>1261.734</td><td>114.0453</td><td>1.7</td><td>43171.4</td><td>P54727</td><td>UV excision repair protein RAD23 homolog B</td><td>Both</td><td>7.89E-05</td><td>43</td><td>2.2E-03</td><td></td><td></td></tr>
<tr><td>377</td><td>3</td><td>11.11</td><td>11.11</td><td>71.5</td><td>K129k</td><td>123</td><td>(R)FL\EQQNk/I|L/L/A/E/LEQLK(G)</td><td>724.4134</td><td>2057.164</td><td>114.0615</td><td>8.6</td><td>53651.9</td><td>P08670</td><td>Vimentin</td><td>LLnL</td><td>1.09E-11</td><td></td><td></td><td>-1.3</td><td></td></tr>
<tr><td>378</td><td>3</td><td>21.82</td><td>9.24</td><td>94.0</td><td>K139k</td><td>130</td><td>(K)IL|L/AE/L/E/Q/L/k/GQ/GK(S)</td><td>551.9945</td><td>1539.911</td><td>114.0585</td><td>9.4</td><td>53651.9</td><td>P08670</td><td>Vimentin</td><td>LLnL</td><td>7.16E-10</td><td>34</td><td>9.6E-03</td><td>-3.5</td><td>Y</td></tr>
<tr><td>379</td><td>4</td><td>24.97</td><td>24.97</td><td>94.9</td><td>K396k</td><td>393</td><td>(K)IL\Tk\LL\E|V/S/D/D/PQ/V/L/AV/AA/H/D/VGEYVR(H)</td><td>766.9212</td><td>2950.588</td><td>114.0746</td><td>10.3</td><td>55883.4</td><td>Q9UI12</td><td>V-type proton ATPase subunit H</td><td>LLnL</td><td>5.50E-07</td><td>37</td><td>7.8E-03</td><td></td><td></td></tr>
<tr><td>380</td><td>3</td><td>12.31</td><td>12.31</td><td>63.9</td><td>K116k</td><td>112</td><td>(K)IG\LTkAL/T/Q/M/E/E/AQ/R(K)</td><td>601.653</td><td>1688.9</td><td>114.0445</td><td>0.9</td><td>31293.6</td><td>O95229</td><td>ZW10 interactor</td><td>LLnL</td><td>3.01E-17</td><td>62</td><td>3.5E-05</td><td></td><td></td></tr>
</table>

* The lysine acetylation sites are obtained from the following publications and the Swiss-Prot database for the ubiquitinated proteins identified in our experiments.

1. Choudhary, C. et al. Lysine acetylation targets protein complexes and co-regulates major cellular functions. Science 325, 834-840 (2009).
2. Gnad, F. et al. PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. Genome Biol 8, R250 (2007).
3. Kim, S.C. et al. Substrate and functional diversity of lysine acetylation revealed by a proteomics survey. Mol Cell 23, 607-618 (2006).
4. Zhao, S. et al. Regulation of cellular metabolism by protein lysine acetylation. Science 327, 1000-1004.

** Peptides 76, 92, 144 have slightly lower Phenyx p value, and Peptide 177 has slightly low Mascot score and expectation value. These peptides are included in the list because they have high Spectrum Mill score and good MS/MS spectra.

Supplementary Table 2 The PDB codes of the crystal structures used for the analysis of secondary structures and solvent-accessible areas for the ubiquitinated lysines and all lysines in the crystal structures.

1A31	1MH1	1Z0A	2OB4
1A4P	1NTG	1Z7G	2PBD
1ALD	1OGW	1ZR3	2Q12
1B3U	1OQY	2AGA	2RIQ
1BJ4	1P4R	2AXN	2VYI
1C4Z	1Q02	2BR9	2ZFY
1E5W	1Q8G	2C23	2ZKR
1G73	1QGR	2CS2	3BOR
1GH2	1SYW	2CV5	3BQC
1GK7	1U7B	2DGV	3BYH
1GY5	1U8F	2DZM	3BZH
1I0Z	1UCN	2E8A	3CPF
1I10	1UEL	2EC4	3E46
1I7K	1US0	2ETL	3E77
1INZ	1UW5	2F3Y	3EI3
1J7D	1VYH	2G9N	3FEY
1JDH	1W7J	2HDE	3GJ0
1JEY	1WH9	2HR0	3GR4
1JMC	1WTB	2IE4	3I33
1KMT	1X4A	2JKV	3ULL
1KMV	1X4B	2KG4	
1LCY	1XD3	2O28	
1LM8	1YH2	2OB0	

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1. Garcia-Saez, I., Parraga, A., Phillips, M.F., Mantle, T.J. & Coll, M. Molecular structure at 1.8 A of mouse liver class pi glutathione S-transferase complexed with S-(p-nitrobenzyl)glutathione and other inhibitors. *J Mol Biol* **237**, 298-314 (1994).
2. Lorick, K.L. et al. RING fingers mediate ubiquitin-conjugating enzyme (E2)-dependent ubiquitination. *Proc Natl Acad Sci U S A* **96**, 11364-11369 (1999).
3. Denis, N.J., Vasilescu, J., Lambert, J.P., Smith, J.C. & Figeys, D. Tryptic digestion of ubiquitin standards reveals an improved strategy for identifying ubiquitinated proteins by mass spectrometry. *Proteomics* **7**, 868-874 (2007).
4. Schwartz, D. & Gygi, S.P. An iterative statistical approach to the identification of protein phosphorylation motifs from large-scale data sets. *Nat Biotechnol* **23**, 1391-1398 (2005).
5. Schneider, T.D. & Stephens, R.M. Sequence Logos - a New Way to Display Consensus Sequences. *Nucleic Acids Research* **18**, 6097-6100 (1990).
6. Crooks, G.E., Hon, G., Chandonia, J.M. & Brenner, S.E. WebLogo: A sequence logo generator. *Genome Research* **14**, 1188-1190 (2004).
7. Peng, J. et al. A proteomics approach to understanding protein ubiquitination. *Nat Biotechnol* **21**, 921-926 (2003).
8. DeLano, W.L. DeLano Scientific, Palo Alto, CA, USA. http://www.pymol.org, 2002).