Fig. S1. Mechanism of Edman degradation and *in silico* analysis of N-CLAP peptides derived from the N termini of human proteins.

(*A*) Schematic of the chemoselective reactions in Edman degradation. Amine groups in proteins are modified by PITC, resulting in the incorporation of PITC at the N terminus and ε-amines of lysines. The residues in the peptide from the second amino acid are denoted as X2 × 3···Xn. TFA treatment of the PITC-modified peptide results in an intramolecular cyclization in which the thiourea of the PITC adduct reacts with the carbonyl component of the first peptide bond. This cyclization releases PITC conjugated to the first amino acid, forming a new N-terminal amine while maintaining ε-amines blocked.

(*B*) Theoretical distribution of the length of predicted human N-CLAP peptides after *in silico* trypsin digestion. Trypsin cleaves only after arginine in PITC-modified proteins, since this treatment modifies the charge and size of the lysine side chain. Thus, digestion of proteins processed through the N-CLAP protocol provides a digestion pattern that is identical to Arg-C. To assess the size distribution of potential N-CLAP peptides, the human protein database and its annotation of N-terminal signal peptides were downloaded from Swiss-Prot database (v55.6, July 1, 2008). Redundant sequences were removed by an in-house computer code. The signal peptides were also removed according to the annotation in Swiss-Prot database before performing *in silico* analysis of the N-CLAP peptides. The starting N-terminal amino acid of the proteins was further removed, because the N-terminal amino acid is cleaved during the N-CLAP procedure. Shown is the frequency of peptides generated after a virtual N-CLAP protocol of the indicated length. As can be seen, a significant fraction of virtual N-CLAP peptides are five amino acids or longer.

(*C*) Cumulative fraction of N-CLAP peptides for the human proteome. The results in *A* are presented to show the cumulative fraction of peptides of the indicated length or smaller. Peptides that are between five and 40 aa in length are shown in the shaded area. A significant portion (65%) of N-CLAP peptides could be a suitable size for MS/MS analysis.

(*D*) The fraction of unique N-CLAP peptides as a function of peptide length in the human proteome. For peptides of each indicated length, we determined how many of them can be assigned to a single protein. This is indicated as the fraction of unique N-CLAP peptides. As shown, for peptides that are four amino acids, 36% can be assigned to a unique protein. For peptides that are five amino acids or longer, 68.2% are unique (denoted by the dashed line). Most of the peptides that match to more than one protein are matched to highly similar members of a protein family. The high uniqueness of the N-terminal peptides in different organisms was also discussed by Wilkin and coworkers when a small database was used [Wilkins MR, et al. (1998) *J Mol Biol* 278:599-608]. These results support the hypothesis that the N-CLAP peptides could be used for protein identification in a high-throughput fashion. However, due to the nonuniqueness of some N-CLAP peptides, biochemical validation would be needed in some cases to confirm that a specific protein corresponds to a given N-CLAP peptide.

(*E*) The theoretical percentage of N-terminal peptides with less than five amino acids when different enzymes are used for theoretical digestion of proteins in the human proteome. When peptides are smaller than five amino acids, they typically have too many potential matches to be useful for parent protein identification. When a virtual trypsin digestion is performed on a lysate, which is not modified on lysines, 26.6% are shorter than five amino acids. However, the fraction decreases when either Arg-C, or Glu-C, which cleaves after Glu, is used. However, if the datasets of a Arg-C experiment and a Glu-C experiment are combined (Arg-C∩Glu-C), then only a small fraction of proteins (3.3%) provide N-CLAP peptides that are shorter than five amino acids under both conditions. These data suggest that combining datasets could be used to improve the coverage of N-terminally derived peptides.

(*F*) The percentage of N-CLAP peptides with unique mass as a function of the mass accuracy for three organisms, *Homo sapiens*, *Saccharomyces cerevisiae*, and *Mycoplasma genitalium*. Theoretical N-CLAP peptides were obtained according to the method described in *A* using trypsin as a protease to conduct *in silico* protein digestion. Indicated in parentheses are the numbers of full length protein sequences downloaded from Swiss-Prot database for each proteome. As the mass accuracy increases, the percentage of N-CLAP peptides that are found to match mass that uniquely identifies the parent protein increases. For example, in the human proteome, when the mass accuracy is 1 ppm, >31% N-CLAP peptides have unique masses. However, when the mass accuracy decreases to 20 ppm, only 10% N-CLAP peptides have unique masses. The size of the proteome is another major factor which affects the percentage of N-CLAP peptides with unique mass. Using a mass accuracy of 10 ppm, which can be readily achieved by Q-TOF as an example, the human proteome, which contains more than 50,000 unique proteins, has about 17% N-CLAP peptides with unique masses. When the size of the proteome is reduced to 7,000 (the yeast proteome), the percentage of N-CLAP peptides with unique masses increases to 62%. The percentage of N-CLAP peptides with unique mass for the *M. genitalium* proteome, a bacterial proteome that comprises about 500 proteins, is >90%. The same trend holds true for the uniqueness of the N-CLAP peptide sequences. For the human proteome, only 68% N-CLAP peptide sequences are unique while for the yeast and bacterium proteomes, the percentages of unique N-CLAP peptide sequences are increased to 86% and 100%, respectively, when the N-CLAP peptides with a length of no less than five amino acids are analyzed. These results indicate that the N-CLAP peptides can almost completely unambiguously identify proteins for small proteomes solely based on the accurate masses of the N-CLAP peptides.

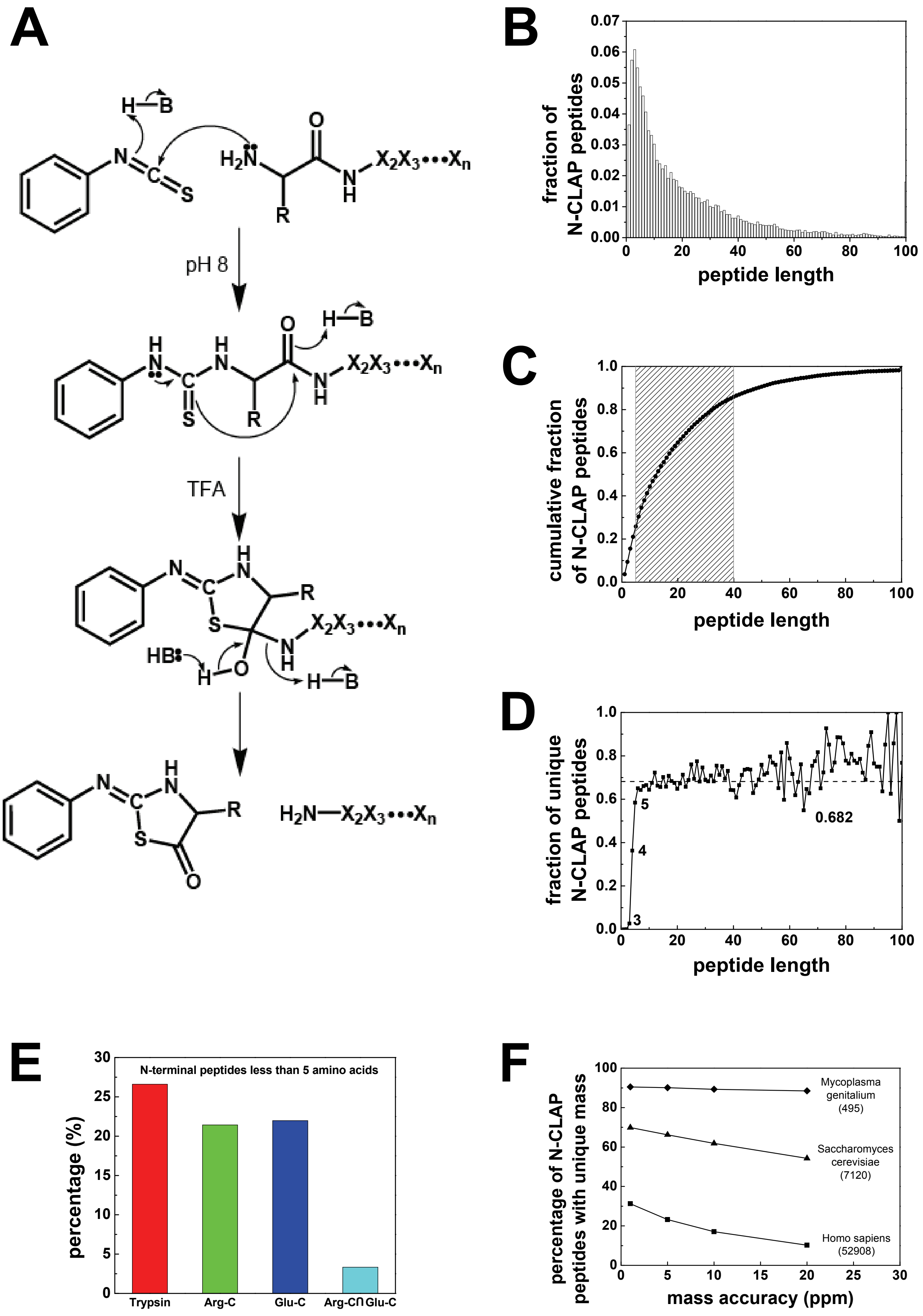

A
H—B
H₂N
O
N
H
X₂X₃•••Xₙ
C
S
R
pH 8
TFA
HB:
H—B
H₂N—X₂X₃•••Xₙ
B
fraction of N-CLAP peptides
peptide length
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
0
20
40
60
80
100
C
cumulative fraction of N-CLAP peptides
peptide length
1.0
0.8
0.6
0.4
0.2
0.0
D
fraction of unique N-CLAP peptides
peptide length
5
4
3
0.682
E
N-terminal peptides less than 5 amino acids
percentage (%)
30
25
20
15
10
5
0
Trypsin
Arg-C
Glu-C
Arg-C∩Glu-C
F
percentage of N-CLAP peptides with unique mass
mass accuracy (ppm)
Mycoplasma genitalium (495)
Saccharomyces cerevisiae (7120)
Homo sapiens (52908)
100
80
60
40
20
0
5
10
15
20
25
30

Fig. S2. Chemical modifications of peptides at different stages of the N-CLAP procedure. (*A*–*F*) N-CLAP was performed using a peptide derived from β-catenin after caspase cleavage at Asp-115 residue, which was discovered by Mahrus S, et al. (1). (*G*–*K*) Experiments using the c-Myc peptide, which has one internal lysine residue.

(*A*) MALDI-TOF-MS of the β-catenin peptide AAHPTNVQR (amino acids 116-124) results in a major peptide ion at 993.74 Da. β-catenin is known to be cleaved by caspases (1), and produces this internal tryptic peptide.

(*B*) PITC-treated β-catenin peptide results in a major ion reflecting the expected thiocarbamoyl PITC modification.

(*C*) TFA treatment of PITC-modified β-catenin results in a single prominent peptide ion with a mass corresponding to the β-catenin peptide missing the first N-terminal residue (Ala).

(*D*) The deblocked β-catenin peptide was reacted with EZ-Link Sulfo NHS-SS-biotin. MALDITOF-MS revealed a single major peak corresponding to the modified peptide.

(*E*) TCEP-reduced sample results in a 1,010.77 Da peptide ion, corresponding to the β-catenin peptide without the N-terminal Ala and with a remnant from the cleavable biotin tag.

(*F*) MS/MS spectrum of the β-catenin peptide (116-124) after N-CLAP. The peptide was detected using ESI-Q-TOF analysis with a score of 16.89 and an SPI of 88.8% by Spectrum Mill database searching. The MS/MS spectrum (*i*) demonstrates that the peptide contains the remnant of the cleaved N-terminal EZ-Link Sulfo NHS-SS-biotin adduct and (*ii*) confirms the loss of the N-terminal Ala.

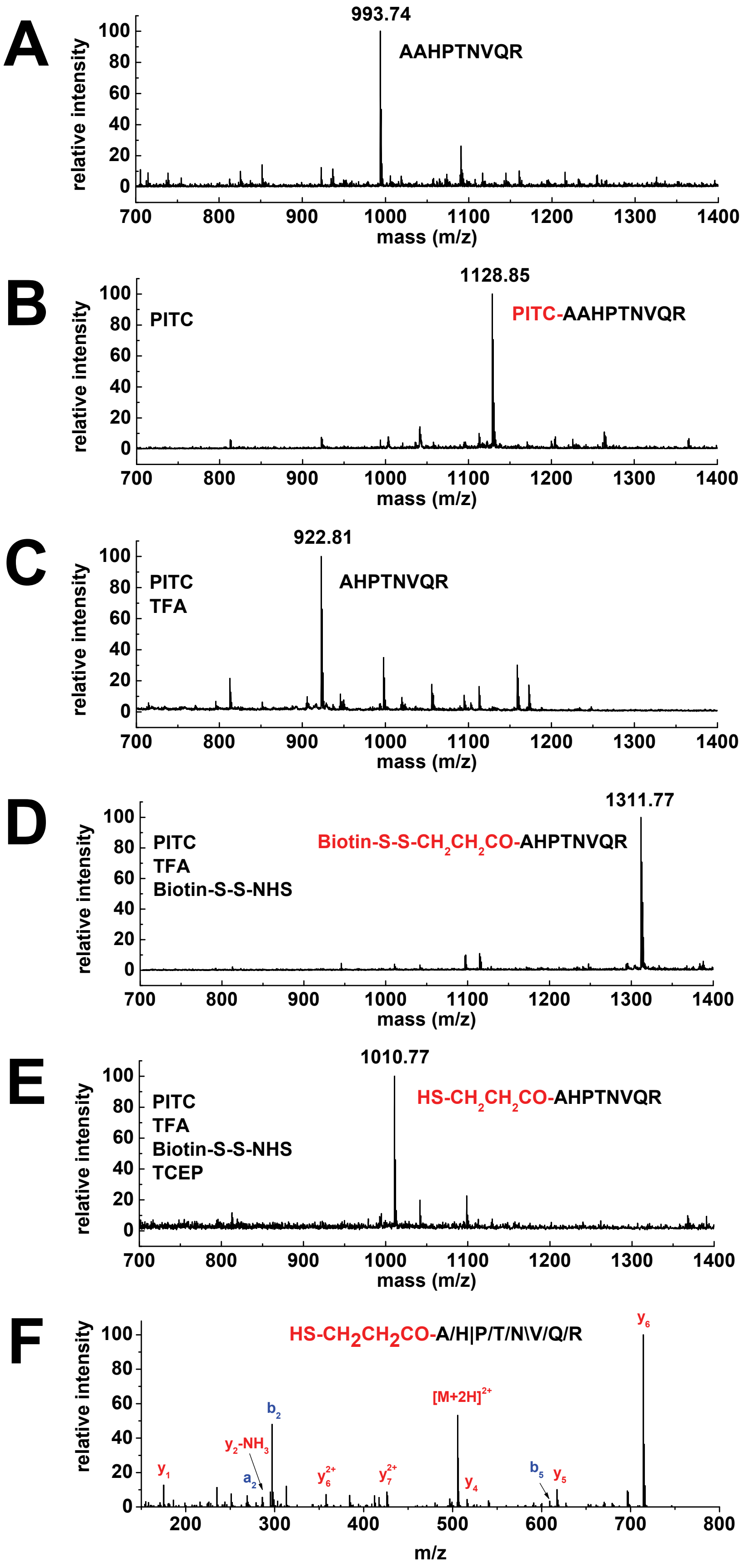
(*G*) MS/MS spectra of the unmodified c-Myc peptide.

(*H*) PITC-treated c-Myc peptide. The MS/MS spectrum is consistent with two PITC modifications, with one PITC adduct on the N-terminal amine, while the other adduct is on the ε-amine of the lysine in the c-Myc peptide.

(*I*) PITC- and TFA-treated c-Myc peptide. The MS/MS spectrum indicates a loss of the N-terminal residue, which is consistent with the TFA-mediated intramolecular cyclization that releases the first residue. The PITC adduct on the lysine remains on the peptide.

(*J*) PITC-, TFA- and EZ-Link-Sulfo-NHS-SS-biotin-treated c-Myc peptide. The MS/MS spectrum exhibits a shift in the *b*-ion series consistent with the N-terminal modification by the biotinylation reagent and the PITC-modified lysine. (*K*) PITC-, TFA-, EZ-Link-Sulfo-NHS-SS-biotin-, and TCEP-treated c-Myc peptide. The MS/MS spectrum indicates the expected cleavage of the disulfide in the biotinylation reagent. The PITC adduct on the ε-amine of the lysine residue results in an uncharged amino acid adduct. Because PITC-modified lysine is not charged, complex MS/MS spectra due to the presence of internal unmodified basic residues in peptides are avoided. Additionally, the PITC modification did not impair peptide fragmentation, indicating that MS/MS spectra obtained from PITC-modified peptides can be used for peptide identification. N-terminal modifications are shown in red text and the PITC modification on lysine is indicated by an asterisk. The symbols \, /, and | represent *b* -ions, *y*-ions, and both *b*-ions and *y*-ions, respectively. The peptide sequence and modification is shown in the spectra and the *b*-ions and *y*-ions are labeled.

1. Mahrus S, et al. (2008) Global sequencing of proteolytic cleavage sites in apoptosis by specific labeling of protein N termini. *Cell* 134:866-876.


A
993.74
AAHPTNVQR
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80
60
40
20
0
700
800
900
1000
1100
1200
1300
1400
mass (m/z)
B
1128.85
PITC
PITC-AAHPTNVQR
C
922.81
PITC
TFA
AHPTNVQR
D
1311.77
PITC
TFA
Biotin-S-S-NHS
Biotin-S-S-CH2CH2CO-AHPTNVQR
E
1010.77
PITC
TFA
Biotin-S-S-NHS
TCEP
HS-CH2CH2CO-AHPTNVQR
F
HS-CH2CH2CO-A/H|P/T/N\V/Q/R
y6
[M+2H]2+
b2
y2-NH3
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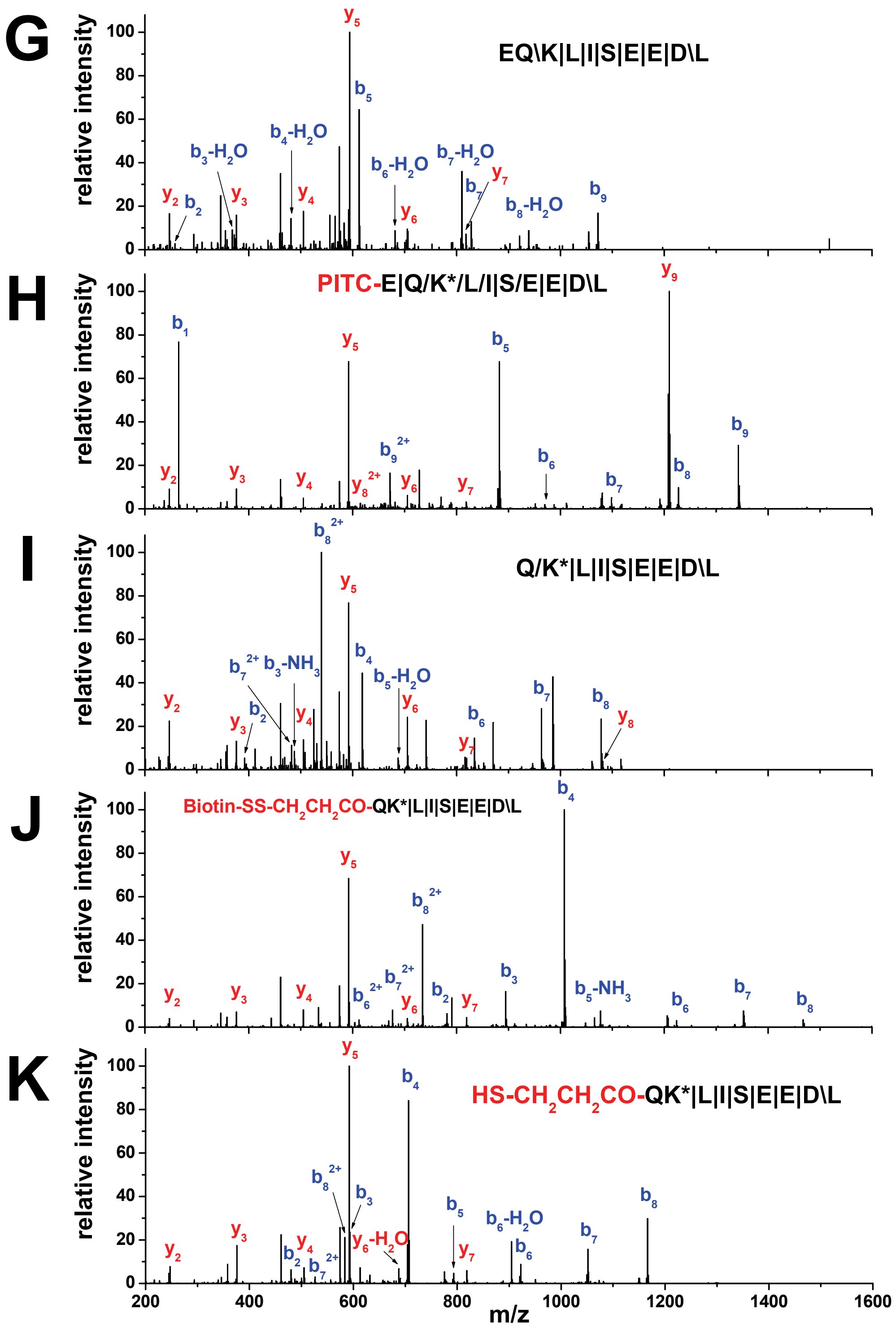
500
600
700
800
m/z


G
relative intensity
EQ\K|L|I|S|E|E|D\L
y_5
b_5
b_3-H_2O
b_4-H_2O
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b_7-H_2O
y_2
b_2
y_3
y_4
y_6
b_7
y_7
b_8-H_2O
b_9
H
PITC-E|Q/K*/L/I/S/E|E|D\L
y_9
b_1
y_5
b_5
b_9^{2+}
b_9
b_6
b_8
b_7
y_2
y_3
y_4
y_8^{2+}
y_6
y_7
I
Q/K*|L|I|S|E|E|D\L
b_8^{2+}
y_5
b_4
b_7^{2+}
b_3-NH_3
b_5-H_2O
y_2
y_3
b_2
y_4
y_6
b_6
y_7
b_7
b_8
y_8
J
Biotin-SS-CH_2CH_2CO-QK*|L|I|S|E|E|D\L
b_4
y_5
b_8^{2+}
b_7^{2+}
b_6^{2+}
y_2
y_3
y_4
y_6
b_2
y_7
b_3
b_5-NH_3
b_6
b_7
b_8
K
$HS-CH_2CH_2CO$-QK*|L|I|S|E|E|D\L
y_5
b_4
b_8^{2+}
b_3
b_5
b_6-H_2O
b_8
y_2
y_3
y_4
b_2
b_7^{2+}
y_6-H_2O
y_7
b_6
b_7
0
20
40
60
80
100
200
400
600
800
1000
1200
1400
1600
m/z

Fig. S3. MS/MS spectrum of neutravidin-purified and TCEP-eluted N-terminal peptide from RNase A obtained using N-CLAP.

The fragmentation pattern established the identity of the peptide and confirmed the N-terminal and lysine modification. The N-terminal modification is shown in red text and the PITC modification on lysine is indicated by an asterisk. The symbols \, /, and | represent *b*-ions, *y*-ions, and both *b*-ions and *y*-ions, respectively. The peptide sequence and modification is shown in the spectra and the *b*-ions and *y*-ions are labeled.

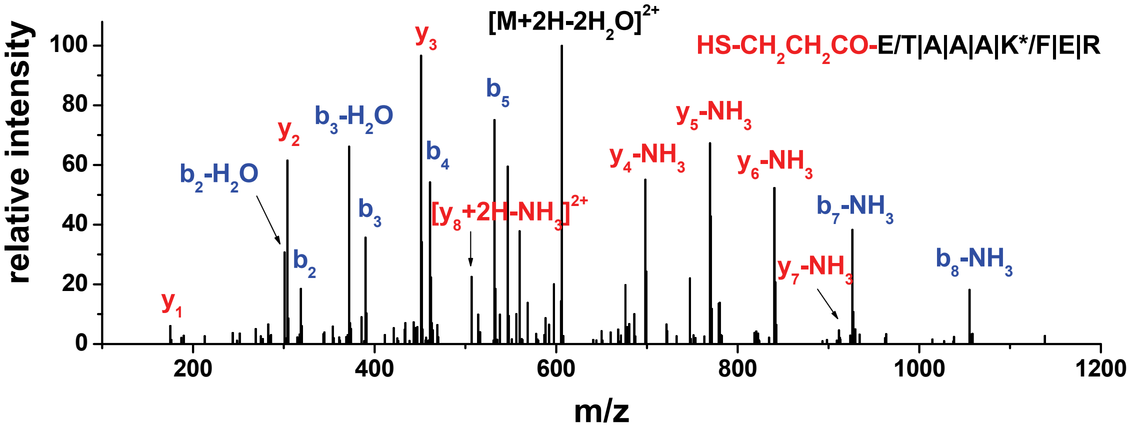

relative intensity
m/z
0
20
40
60
80
100
200
400
600
800
1000
1200
$[M+2H-2H_2O]^{2+}$
$HS-CH_2CH_2CO-$E/T|A|A|A|K*/F|E|R
y_1
b_2-H_2O
b_2
y_2
b_3-H_2O
b_3
y_3
b_4
$[y_8+2H-NH_3]^{2+}$
b_5
y_4-NH_3
y_5-NH_3
y_6-NH_3
y_7-NH_3
b_7-NH_3
b_8-NH_3

Fig. S4. MS/MS spectra of N-CLAP peptides identified in Jurkat T-cells.

The peptide rank, score, the percentage of assigned spectrum intensity of total spectrum intensity (SPI), sequence map, mass of precursor ion (MH^+), precursor ion mass error (MH^+ error), protein molecular weight (MW), Swiss-Prot accession number, and protein name are listed above the table. The symbols \, /, and | represent *b*-ions, *y*-ions, and both *b*-ions and *y*-ions, respectively.

The table shows the experimental MS/MS fragments and the matched theoretical MS/MS fragments as well as the peak intensity, score of each fragment, matched ions, and delta mass of the fragment deviating from its theoretical mass.

In the 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 of the 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 can be obtained from the table of mass fragments.

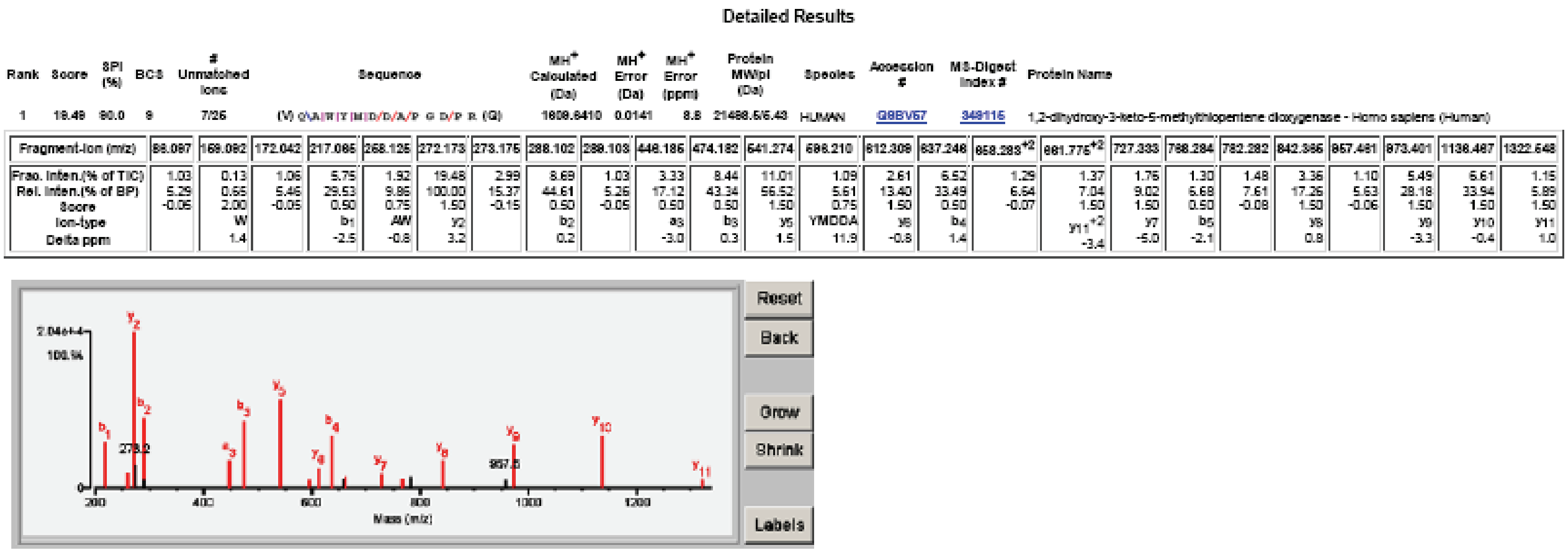
In total, 278 N-CLAP peptides have been identified. Among them, 80 peptides are derived from the predicted protein N-termini (denoted by “N” at the beginning of the number of the spectra). These peptides comprise N-terminal peptides from proteins that exhibited either no or moderate trimming of the N terminus (e.g., up to three amino acids).

Thirty-eight (38) N-CLAP peptides are obtained from N-termini of proteins with removed signal peptides or transit peptides (denoted by “S” at the beginning of the number of the spectra).

Twenty-three (23) N-CLAP peptides are derived from caspase cleavages in Jurkat T-cells after cisplatin treatment (denoted by “C” at the beginning of the number of the spectra).

Another 137 N-CLAP peptides are identified from protein internal cleavages (denoted by “I” at the beginning of the number of the spectra). The number at the left upper corner of each spectrum corresponds to the number in Tables S1, S2, S3, and S4, respectively.

N1



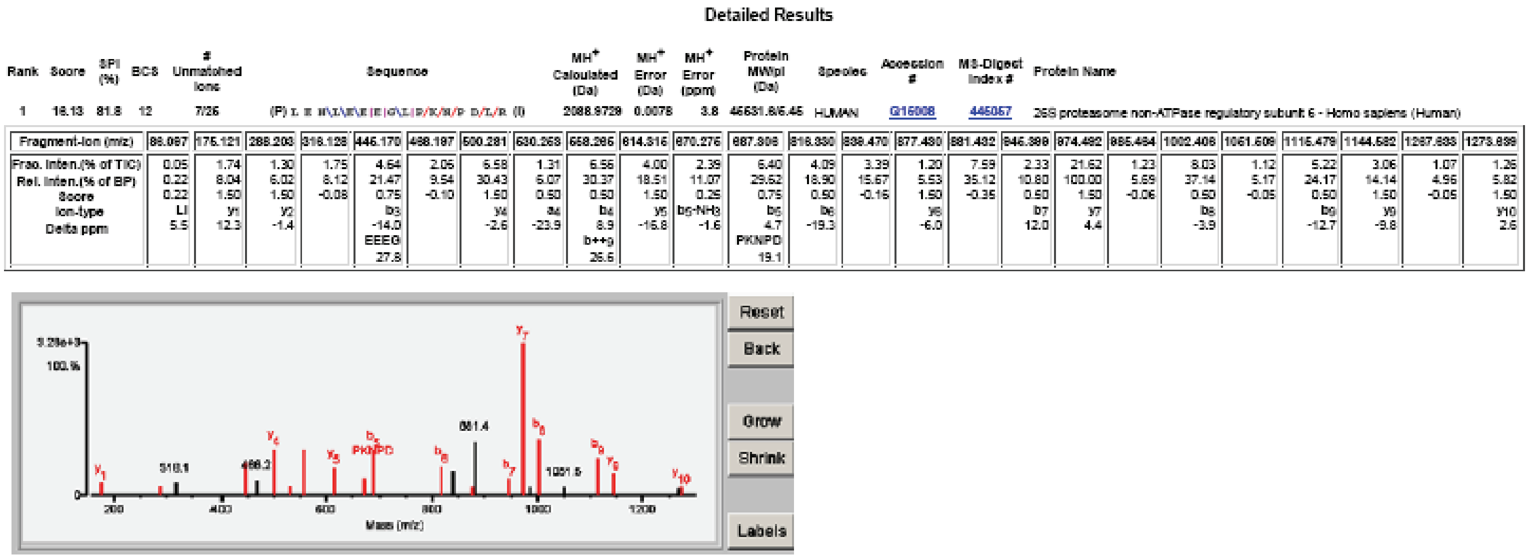
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.49	90.0	9	7/26	(V) Q\A|W|Y|M|D/D/A/P G D/P R (Q)	1809.8410	0.0141	8.8	21498.5/6.43	HUMAN	Q9BV57	349115	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	169.092	172.042	217.086	268.125	272.173	273.176	288.102	289.103	446.186	474.182	541.274	596.210
Frac. Inten.(% of TIC)	1.03	0.13	1.06	5.75	1.92	19.48	2.99	8.69	1.03	3.33	8.44	11.01	1.09
Rel. Inten.(% of BP)	5.29	0.65	5.46	29.53	9.86	100.00	15.37	44.61	5.26	17.12	43.34	56.52	5.61
Score	-0.05	2.00	-0.05	0.50	0.75	1.50	-0.15	0.50	-0.05	0.50	0.50	1.50	0.75
Ion-type		W		b_1	AW	y_2		b_2		a_3	b_3	y_5	YMDDA
Delta ppm		1.4		-2.5	-0.8	3.2		0.2		-3.0	0.3	1.5	11.9

Fragment-Ion (m/z)	612.309	637.246	658.283^{+2}	661.776^{+2}	727.333	768.284	782.282	842.366	957.461	973.401	1138.467	1322.648
Frac. Inten.(% of TIC)	2.61	6.52	1.29	1.37	1.76	1.30	1.48	3.36	1.10	5.49	6.61	1.15
Rel. Inten.(% of BP)	13.40	33.49	6.64	7.04	9.02	6.68	7.61	17.26	5.63	28.18	33.94	5.89
Score	1.50	0.50	-0.07	1.50	1.50	0.50	-0.08	1.50	-0.06	1.50	1.50	1.50
Ion-type	y_6	b_4		y_{11}^{+2}	y_7	b_5		y_8		y_9	y_{10}	y_{11}
Delta ppm	-0.8	1.4		-3.4	-5.0	-2.1		0.8		-3.3	-0.4	1.0

N2



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.13	81.8	12	7/26	(P) L E H\I\E\E|E|G\L|P/K/N/P D/L/R (I)	2088.9729	0.0078	3.8	46631.6/6.45	HUMAN	Q15008	446057	26S proteasome non-ATPase regulatory subunit 6 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	175.121	288.203	316.128	446.170	466.197	500.281	530.263	558.286	614.316	670.276	687.306
Frac. Inten.(% of TIC)	0.05	1.74	1.30	1.75	4.64	2.06	6.58	1.31	6.56	4.00	2.39	6.40
Rel. Inten.(% of BP)	0.22	8.04	6.02	8.12	21.47	9.54	30.43	6.07	30.37	18.51	11.07	29.62
Score	0.22	1.50	1.50	-0.08	0.75	-0.10	1.50	0.50	0.50	1.50	0.25	0.75
Ion-type	LI	y_1	y_2		b_3		y_4	a_4	b_4	y_5	b_5-NH_3	b_5
Delta ppm	5.5	12.3	-1.4		-14.0		-2.6	-23.9	8.9	-16.8	-1.6	4.7
					EEEG				b++g			PKNPD
					27.8				26.6			19.1

Fragment-Ion (m/z)	816.330	838.470	877.430	881.432	946.399	974.492	985.484	1002.406	1051.609	1116.479	1144.582	1267.893	1273.899
Frac. Inten.(% of TIC)	4.09	3.39	1.20	7.59	2.33	21.62	1.23	8.03	1.12	5.22	3.06	1.07	1.26
Rel. Inten.(% of BP)	18.90	15.67	5.53	35.12	10.80	100.00	5.69	37.14	5.17	24.17	14.14	4.96	5.82
Score	0.50	-0.16	1.50	-0.35	0.50	1.50	-0.06	0.50	-0.05	0.50	1.50	-0.05	1.50
Ion-type	b_6		y_6		b_7	y_7		b_8		b_9	y_9		y_{10}
Delta ppm	-19.3		-6.0		12.0	4.4		-3.9		-12.7	-9.8		2.6

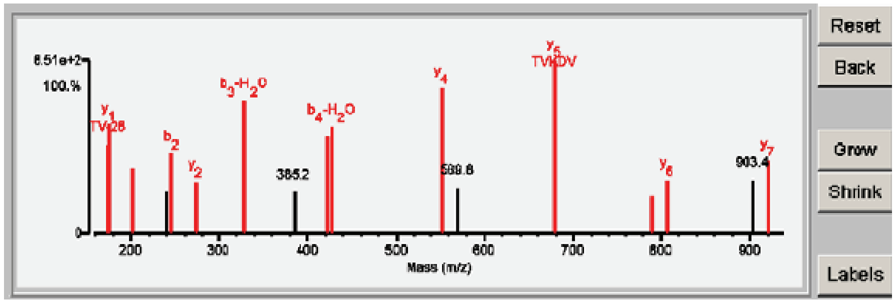
N3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.29	71.4	8	8/25	(P) G V\T V K D V/N/Q/Q/E/F/V/R (A)	1841.8673	0.0069	3.8	16060.6/10.31	HUMAN	P39019	559683	40S ribosomal protein S19 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	84.081	86.096	94.065	110.071	120.081	129.102	173.125	175.115	201.121	241.074	245.093
Frac. Inten.(% of TIC)	0.00	0.90	4.02	7.02	4.22	2.69	0.09	0.07	5.20	6.27	3.77	2.41	4.64
Rel. Inten.(% of BP)	0.04	8.97	40.15	70.21	42.15	26.87	0.90	0.74	52.02	62.65	37.66	24.10	46.40
Score	0.20	0.50	-0.40	-0.70	-0.42	-0.27	1.00	0.20	0.50	1.50	0.75	-0.24	0.50
Ion-type	PR	V					F	RKQ	TV-28	y1	TV		b2
Delta ppm	-7.5	7.3					-2.3	-2.6	-25.7	-21.4	-19.2		-14.0

Fragment-ion (m/z)	274.183	328.130	385.154	421.252	427.207	550.292	569.848	678.351	789.373	806.418	903.386	920.444
Frac. Inten.(% of TIC)	3.04	7.63	2.42	5.59	6.22	8.43	2.72	10.00	2.21	3.14	3.09	4.23
Rel. Inten.(% of BP)	30.37	76.29	24.23	55.94	62.20	84.28	27.16	100.00	22.07	31.41	30.86	42.27
Score	1.50	0.25	-0.24	1.50	0.25	1.50	-0.27	1.50	0.50	1.50	-0.31	1.50
Ion-type	y2	b3-H_2O		y3	b4-H_2O	y4		y5 TVKDV	y6-NH_3	y6		y7
Delta ppm	-16.7	-12.3		-8.7	12.3	-11.0		-8.0 33.1	-19.9	3.1		-15.7



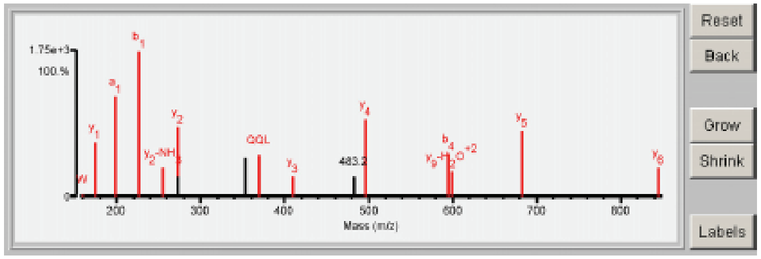
N4

Detailed Results

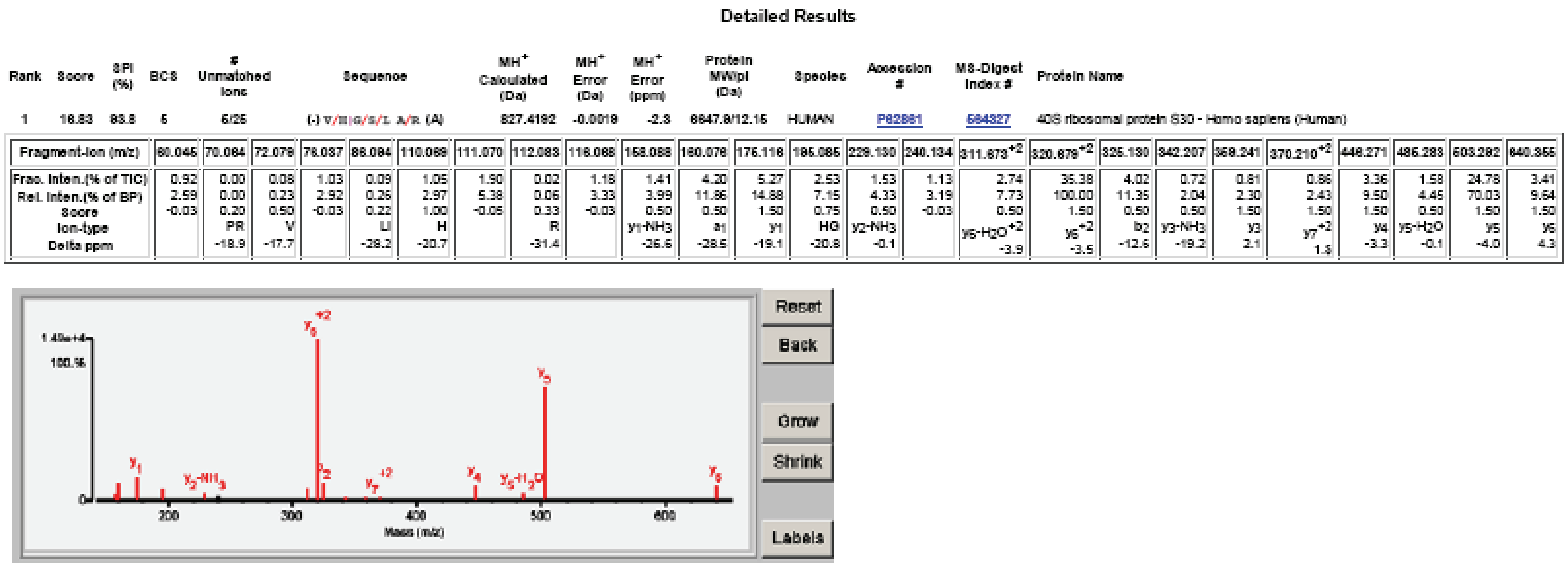
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.20	76.8	7	7/25	(G) H\Q Q L|Y/W/S/H/P/R (K)	1439.6837	0.0089	6.2	6676.8/10.16	HUMAN	P62273	683267	40S ribosomal protein S29 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	84.043	86.097	110.071	127.031	128.084	130.064	132.077	136.074	159.090	175.121	198.087	226.084
Frac. Inten.(% of TIC)	0.00	2.76	0.36	0.32	6.65	2.59	0.13	2.40	0.35	0.31	5.82	10.62	15.70
Rel. Inten.(% of BP)	0.02	17.56	2.30	2.05	42.38	16.50	0.80	15.31	2.21	1.95	37.05	67.62	100.00
Score	0.20	-0.18	0.22	1.00	-0.42	-0.16		-0.15	1.00	2.00	1.50	0.50	0.50
Ion-type	PR		LI	H			W		Y	W	y_1	a_1	b_1
Delta ppm	1.1		5.5	-7.0					-11.0	-8.6	10.0	-19.5	-5.2

Fragment-ion (m/z)	255.146	272.174	273.178	363.183	370.209	409.234	483.194	496.267	595.268	598.808+2	682.342	845.408
Frac. Inten.(% of TIC)	3.21	7.50	2.23	4.29	4.43	2.28	2.24	8.25	4.63	2.78	7.00	3.15
Rel. Inten.(% of BP)	20.46	47.75	14.19	27.32	28.24	14.52	14.28	52.56	29.47	17.72	44.60	20.04
Score	0.50	1.50	-0.14	-0.27	0.75	1.50	-0.14	1.50	0.50	0.50	1.50	1.50
Ion-type	y_2-NH_3	y_2			QGL	y_3		y_4	b_4	y_9-H_2O^{+2}	y_5	y_6
Delta ppm	-1.4	8.0			-1.9	9.2		-10.6	-1.5	7.7	0.2	1.2



N5

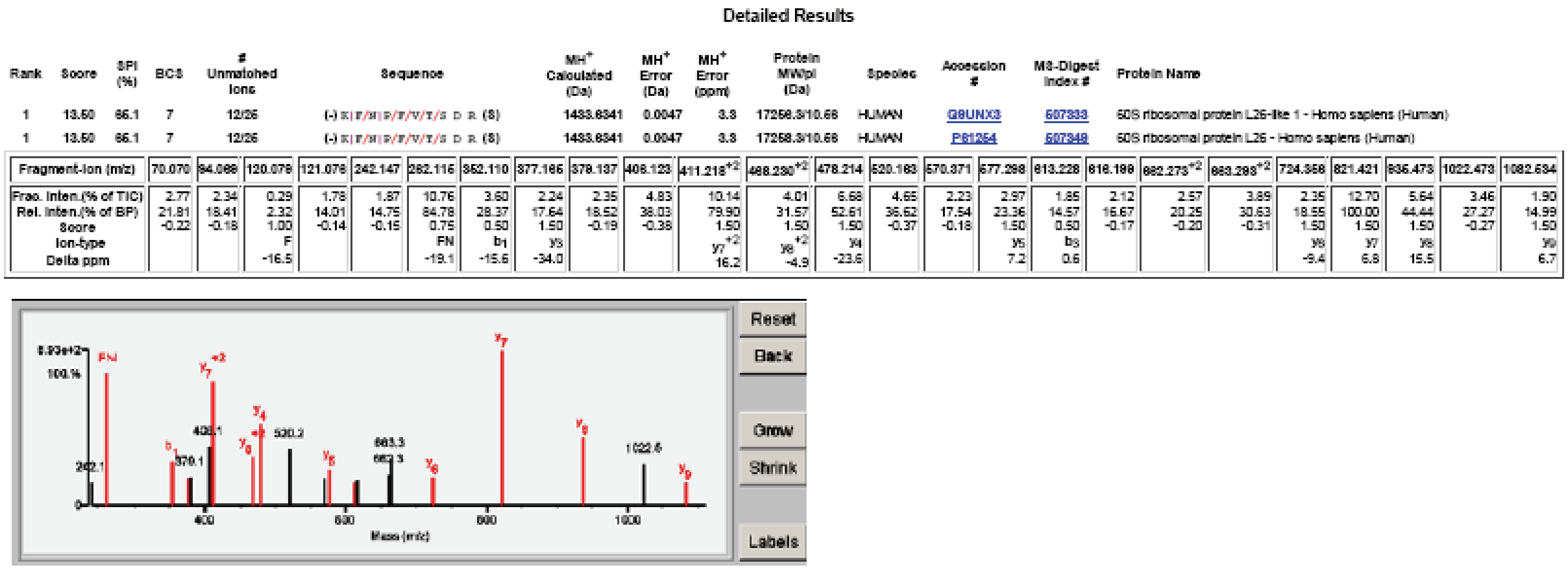


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.83	83.8	5	6/26	(-) V/H|G/S/L A/R (A)	827.4192	-0.0019	-2.3	6647.8/12.15	HUMAN	P62861	584327	40S ribosomal protein S30 - Homo sapiens (Human)

Fragment-Ion (m/z)	60.045	70.084	72.079	76.037	86.094	110.069	111.070	112.083	116.088	158.088	160.076	176.116	186.085	229.130	240.134	311.673^{+2}	320.679^{+2}	326.130	342.207	369.241	370.210^{+2}	446.271	486.283	503.282	640.355
Frac. Inten.(% of TIC)	0.92	0.00	0.08	1.03	0.09	1.05	1.90	0.02	1.18	1.41	4.20	5.27	2.53	1.53	1.13	2.74	35.38	4.02	0.72	0.81	0.86	3.36	1.58	24.78	3.41
Rel. Inten.(% of BP)	2.59	0.00	0.23	2.92	0.26	2.97	5.38	0.06	3.33	3.99	11.86	14.88	7.15	4.33	3.19	7.73	100.00	11.35	2.04	2.30	2.43	9.50	4.45	70.03	9.64
Score	-0.03	0.20	0.50	-0.03	0.22	1.00	-0.05	0.33	-0.03	0.50	0.50	1.50	0.75	0.50	-0.03	0.50	1.50	0.50	0.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type		PR	V		LI	H		R		y_1-NH_3	a_1	y_1	HG	y_2-NH_3		y_6-H_2O^{+2}	y_6^{+2}	b_2	y_3-NH_3	y_3	y_7^{+2}	y_4	y_5-H_2O	y_5	y_6
Delta ppm		-18.9	-17.7		-28.2	-20.7		-31.4		-26.6	-28.5	-19.1	-20.8	-0.1		-3.9	-3.5	-12.6	-19.2	2.1	1.5	-3.3	-0.1	-4.0	4.3

N6



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.60	66.1	7	12/26	(-) K|F/N|P/F/V/T/S D R (S)	1433.6341	0.0047	3.3	17258.3/10.66	HUMAN	Q9UNX3	607333	60S ribosomal protein L26-like 1 - Homo sapiens (Human)
1	13.60	66.1	7	12/26	(-) K|F/N|P/F/V/T/S D R (S)	1433.6341	0.0047	3.3	17258.3/10.66	HUMAN	P61254	607349	60S ribosomal protein L26 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.070	84.069	120.079	121.076	242.147	262.116	352.110	377.166	378.137	408.123	411.218^{+2}	468.230^{+2}	478.214	520.163	570.371	677.298	613.228	616.199	662.273^{+2}	663.293^{+2}	724.358	821.421	936.473	1022.473	1082.634
Frac. Inten.(% of TIC)	2.77	2.34	0.29	1.78	1.87	10.76	3.60	2.24	2.35	4.83	10.14	4.01	6.68	4.65	2.23	2.97	1.85	2.12	2.57	3.89	2.35	12.70	5.64	3.46	1.90
Rel. Inten.(% of BP)	21.81	18.41	2.32	14.01	14.75	84.78	28.37	17.64	18.52	38.03	79.90	31.57	52.61	36.62	17.54	23.36	14.57	16.67	20.25	30.63	18.55	100.00	44.44	27.27	14.99
Score	-0.22	-0.18	1.00	-0.14	-0.15	0.75	0.50	1.50	-0.19	-0.38	1.50	1.50	1.50	-0.37	-0.18	1.50	0.50	-0.17	-0.20	-0.31	1.50	1.50	1.50	-0.27	1.50
Ion-type			F			FN	b_1	y_3			y_7^{+2}	y_8^{+2}	y_4			y_5	b_3				y_6	y_7	y_8		y_9
Delta ppm			-16.5			-19.1	-15.6	-34.0			16.2	-4.9	-23.6			7.2	0.6				-9.4	6.8	15.5		6.7

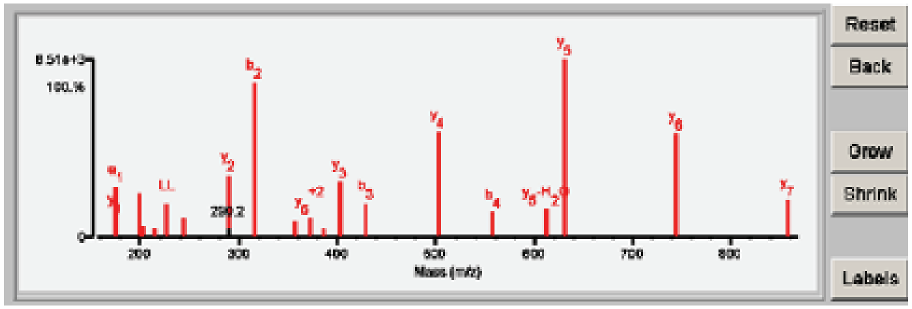
N7

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.81	87.4	7	2/25	(-) I|L|L|E|V/N/N/R (I)	1068.5883	0.0034	3.2	34333.2/6.84	HUMAN	O15144	35681	Actin-related protein 2/3 complex subunit 2 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	86.096	87.101	174.088	176.118	199.180	202.092	216.140	227.176	243.138	289.164	290.188	316.174
Frac. Inten.(% of TIC)	0.02	0.83	1.80	4.73	1.82	4.07	1.04	0.75	3.07	1.77	5.82	0.82	14.28
Rel. Inten.(% of BP)	0.14	5.10	11.06	29.04	11.20	25.01	6.37	4.63	18.88	10.88	35.74	5.03	87.72
Score	0.50	0.22	-0.11	0.50	1.50	0.50	0.50	0.50	0.75	0.75	1.50	-0.05	0.50
Ion-type	V	LI		a_1	y_1	LL-28	b_1	LE-28	LL	LE	y_2		b_2
Delta ppm	-14.9	17.1		2.8	-6.0	-9.5	6.3	-1.5	-0.4	5.6	7.3		-3.1

Fragment-Ion (m/z)	368.214	372.702^{+2}	388.183	403.209	428.267	429.261^{+2}	502.274	557.313	613.298	631.314	744.399	867.485
Frac. Inten.(% of TIC)	1.67	1.70	0.76	5.12	3.13	2.89	9.70	2.34	2.64	16.28	9.52	3.41
Rel. Inten.(% of BP)	10.23	10.46	4.70	31.42	19.25	17.77	59.58	14.39	16.19	100.00	58.48	20.94
Score	0.75	1.50	0.50	1.50	0.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	LLE	y_6^{+2}	y_3-NH_3	y_3	b_3	y_7^{+2}	y_4	b_4	y_5-H_2O	y_5	y_6	y_7
Delta ppm	-14.6	-4.5	12.0	11.1	-5.0	12.1	1.0	20.4	-11.7	-3.3	-1.7	1.4



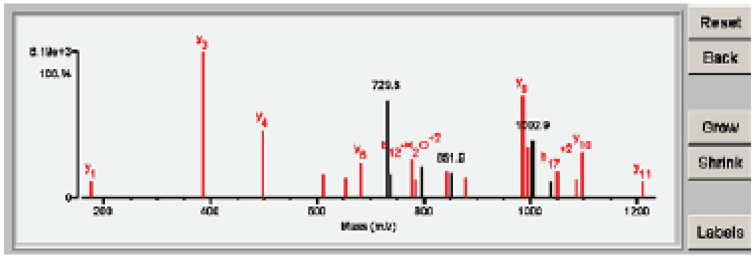
N8

Detailed Results

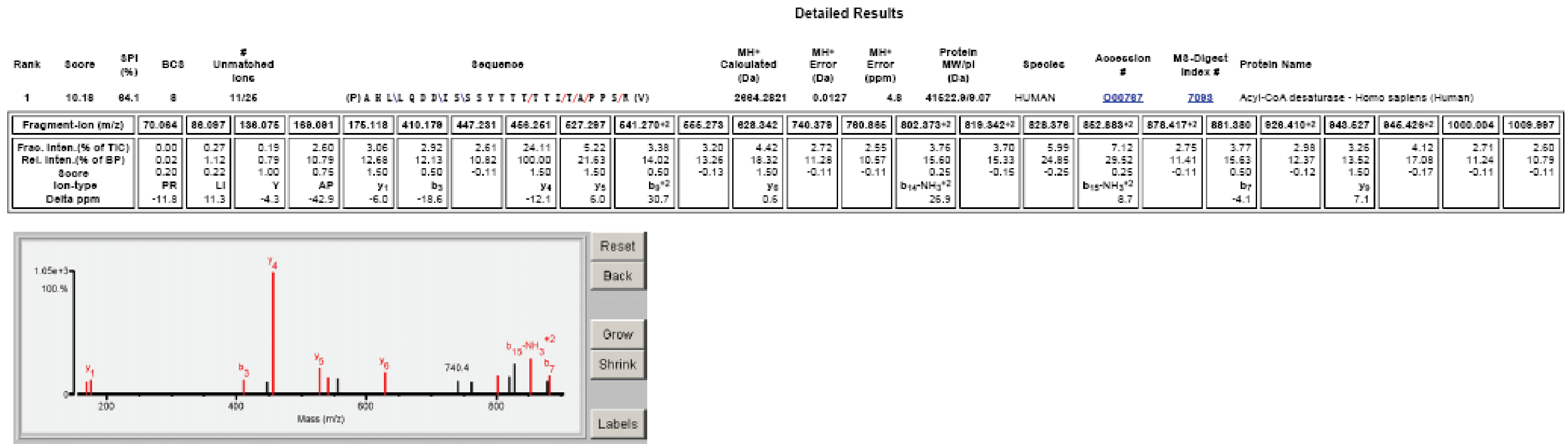
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.11	71.4	11	7/25	(P) A Y H S S L M\D\P D T\K|L|I/G N M|A|L/L/P I/R (S)	2779.3438	-0.0035	-1.3	20546.8/8.77	HUMAN	O15145	35809	Actin-related protein 2/3 complex subunit 3 - Homo sapiens (Human)

Fragment-Ion (m/z)	84.081	86.096	136.075	175.118	385.255	498.337	611.418	653.761^{+2}	682.458	729.774^{+2}	738.786^{+2}	776.308^{+2}	785.314
Frac. Inten.(% of TIC)	1.67	0.21	0.08	1.80	15.40	7.15	2.56	2.11	3.76	10.36	2.55	3.99	1.88
Rel. Inten.(% of BP)	12.13	1.38	0.37	11.67	100.00	46.43	16.61	13.71	24.39	67.27	16.57	25.94	12.19
Score	-0.12	0.22	1.00	1.50	1.50	1.50	1.50	0.50	1.50	-0.67	-0.17	0.25	0.50
Ion-type		LI	Y	y_1	y_3	y_4	y_5	b_{11}^{+2}	y_6			b_{12}-H_2O^{+2}	b^{++}_{12}
Delta ppm		-6.1	-5.1	-3.7	-1.2	-4.9	-9.7	4.6	-3.8			0.2	2.0

Fragment-Ion (m/z)	795.324^{+2}	841.840^{+2}	851.885^{+2}	878.367	984.561	993.372	1002.917^{+2}	1038.461^{+2}	1049.442^{+2}	1084.958^{+2}	1097.650	1210.748
Frac. Inten.(% of TIC)	3.33	2.80	2.67	2.19	10.75	5.47	6.11	1.75	2.79	1.91	4.80	1.75
Rel. Inten.(% of BP)	21.62	18.21	17.31	14.20	69.82	35.49	39.70	11.34	18.11	12.41	31.17	11.35
Score	-0.22	0.50	-0.17	0.50	1.50	0.50	-0.40	-0.11	0.50	0.50	1.50	1.50
Ion-type		b_{13}^{+2}		b_7	y_9	b_8			b_{17}^{+2}	b_{18}^{+2}	y_{10}	y_{11}
Delta ppm		-18.0		14.7	-5.3	-9.7			-8.8	-9.0	0.4	11.4



N9



Detailed Results

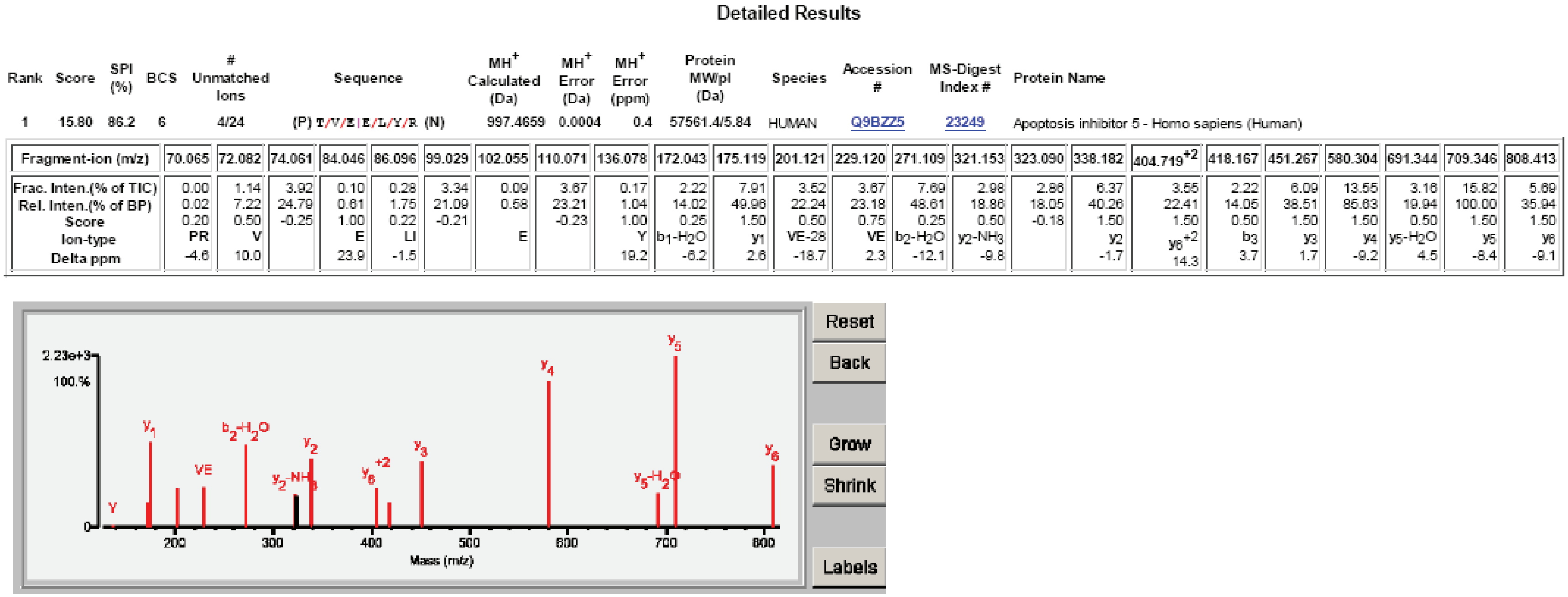
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.18	84.1	8	11/26	(P) A H L\L Q D D\I S\S S Y T T T/T T I/T/A/P P S/R (V)	2684.2821	0.0127	4.8	41522.9/9.07	HUMAN	O00767	7083	Acyl-CoA desaturase - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	86.097	136.075	168.081	175.118	410.178	447.231	456.261	527.287
Frac. Inten.(% of TIC)	0.00	0.27	0.19	2.60	3.06	2.92	2.61	24.11	5.22
Rel. Inten.(% of BP)	0.02	1.12	0.79	10.79	12.68	12.13	10.82	100.00	21.63
Score	0.20	0.22	1.00	0.75	1.50	0.50	-0.11	1.50	1.50
Ion-type	PR	LI	Y	AP	y_1	b_3		y_4	y_5
Delta ppm	-11.8	11.3	-4.3	-42.9	-6.0	-18.6		-12.1	6.0

Fragment-ion (m/z)	541.270^{+2}	555.273	628.342	740.379	780.866	802.373^{+2}	819.342^{+2}	828.376	852.883^{+2}
Frac. Inten.(% of TIC)	3.38	3.20	4.42	2.72	2.55	3.76	3.70	5.99	7.12
Rel. Inten.(% of BP)	14.02	13.26	18.32	11.28	10.57	15.60	15.33	24.85	29.52
Score	0.50	-0.13	1.50	-0.11	-0.11	0.25	-0.15	-0.25	0.25
Ion-type	b_9^{+2}		y_6			$b_{14}\text{-}NH_3^{+2}$			$b_{15}\text{-}NH_3^{+2}$
Delta ppm	30.7		0.6			26.9			8.7

Fragment-ion (m/z)	878.417^{+2}	881.380	926.410^{+2}	943.527	946.426^{+2}	1000.004	1009.997
Frac. Inten.(% of TIC)	2.75	3.77	2.98	3.26	4.12	2.71	2.60
Rel. Inten.(% of BP)	11.41	15.63	12.37	13.52	17.08	11.24	10.79
Score	-0.11	0.50	-0.12	1.50	-0.17	-0.11	-0.11
Ion-type		b_7		y_8			
Delta ppm		-4.1		7.1			

N10



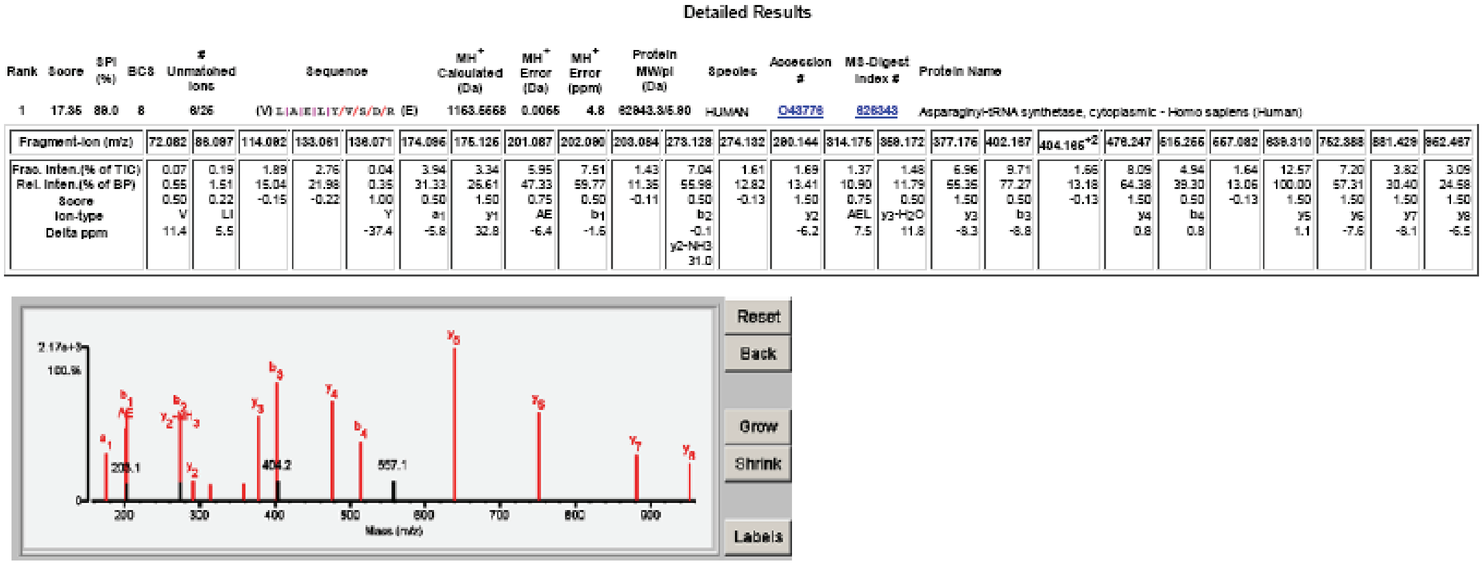
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.80	86.2	6	4/24	(P) T/V/E|E/L/Y/R (N)	997.4659	0.0004	0.4	57561.4/5.84	HUMAN	Q9BZZ5	23249	Apoptosis inhibitor 5 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.082	74.061	84.046	86.096	99.029	102.055	110.071	136.078	172.043	175.119	201.121
Frac. Inten.(% of TIC)	0.00	1.14	3.92	0.10	0.28	3.34	0.09	3.67	0.17	2.22	7.91	3.52
Rel. Inten.(% of BP)	0.02	7.22	24.79	0.61	1.75	21.09	0.58	23.21	1.04	14.02	49.96	22.24
Score	0.20	0.50	-0.25	1.00	0.22	-0.21		-0.23	1.00	0.25	1.50	0.50
Ion-type	PR	V		E	LI		E		Y	$b_1\text{-}H_2O$	y_1	VE-28
Delta ppm	-4.6	10.0		23.9	-1.5				19.2	-6.2	2.6	-18.7

Fragment-ion (m/z)	229.120	271.109	321.153	323.090	338.182	404.719^{+2}	418.167	451.267	580.304	691.344	709.346	808.413
Frac. Inten.(% of TIC)	3.67	7.69	2.98	2.86	6.37	3.55	2.22	6.09	13.55	3.16	15.82	5.69
Rel. Inten.(% of BP)	23.18	48.61	18.86	18.05	40.26	22.41	14.05	38.51	85.63	19.94	100.00	35.94
Score	0.75	0.25	0.50	-0.18	1.50	1.50	0.50	1.50	1.50	0.50	1.50	1.50
Ion-type	VE	$b_2\text{-}H_2O$	$y_2\text{-}NH_3$		y_2	y_6^{+2}	b_3	y_3	y_4	$y_5\text{-}H_2O$	y_5	y_6
Delta ppm	2.3	-12.1	-9.8		-1.7	14.3	3.7	1.7	-9.2	4.5	-8.4	-9.1

N11



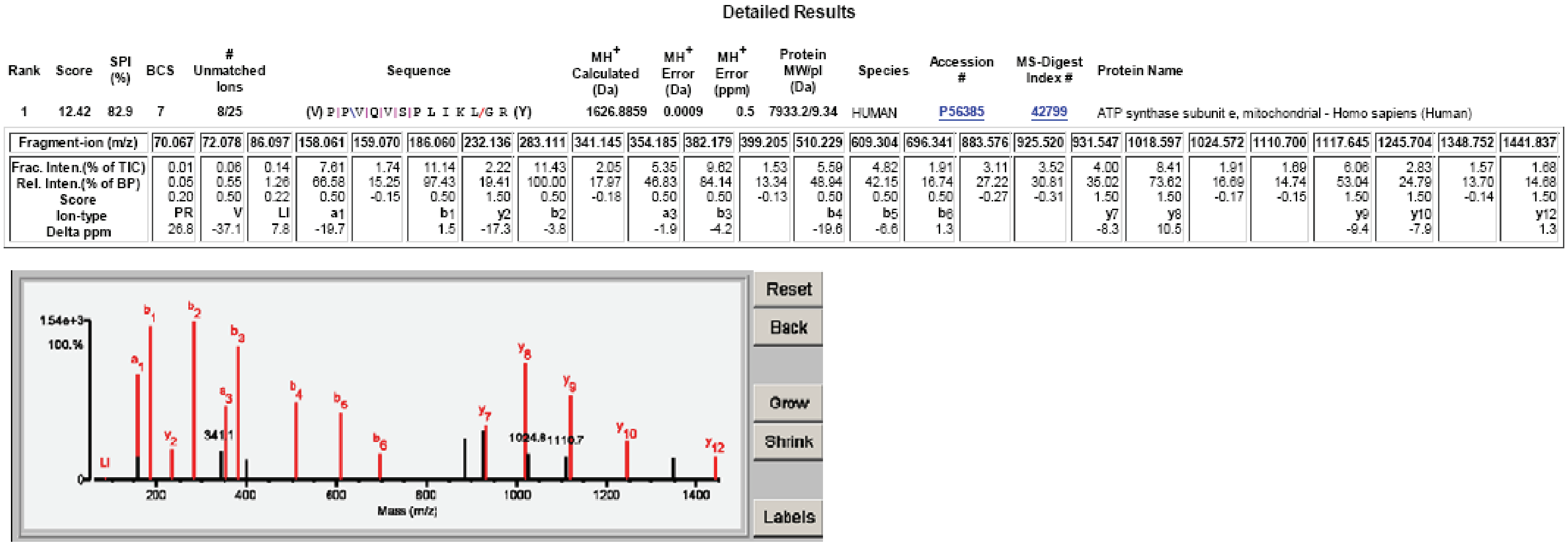
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.35	88.0	8	6/26	(V) L|A|E|L|Y/V/S/D/R (E)	1163.5668	0.0065	4.8	62943.3/5.80	HUMAN	O43776	826343	Asparaginyl-tRNA synthetase, cytoplasmic - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.097	114.082	133.061	136.071	174.096	175.126	201.087	202.080	203.084	273.128	274.132
Frac. Inten.(% of TIC)	0.07	0.19	1.89	2.76	0.04	3.94	3.34	5.95	7.51	1.43	7.04	1.61
Rel. Inten.(% of BP)	0.55	1.51	15.04	21.98	0.35	31.33	26.61	47.33	59.77	11.35	55.98	12.82
Score	0.50	0.22	-0.15	-0.22	1.00	0.50	1.50	0.75	0.50	-0.11	0.50	-0.13
Ion-type	V	LI			Y	a1	y1	AE	b1		b2 y2-NH3	
Delta ppm	11.4	5.5			-37.4	-5.8	32.8	-6.4	-1.6		-0.1 31.0	

Fragment-ion (m/z)	280.144	314.175	359.172	377.176	402.167	404.186^{+2}	478.247	516.266	667.082	638.310	752.388	881.429	962.467
Frac. Inten.(% of TIC)	1.69	1.37	1.48	6.96	9.71	1.66	8.09	4.94	1.64	12.57	7.20	3.82	3.09
Rel. Inten.(% of BP)	13.41	10.90	11.79	55.35	77.27	13.18	64.38	39.30	13.06	100.00	57.31	30.40	24.58
Score	1.50	0.75	0.50	1.50	0.50	-0.13	1.50	0.50	-0.13	1.50	1.50	1.50	1.50
Ion-type	y2	AEL	y3-H2O	y3	b3		y4	b4		y5	y6	y7	y8
Delta ppm	-6.2	7.5	11.8	-8.3	-8.8		0.8	0.8		1.1	-7.6	-8.1	-6.5

N12



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.42	82.9	7	8/25	(V) P|P\V|Q|V|S|P L I K L/G R (Y)	1626.8859	0.0009	0.5	7933.2/9.34	HUMAN	P56385	42799	ATP synthase subunit e, mitochondrial - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.078	86.097	158.061	159.070	186.060	232.136	283.111	341.145	354.185	382.179	399.205
Frac. Inten.(% of TIC)	0.01	0.06	0.14	7.61	1.74	11.14	2.22	11.43	2.05	5.35	9.62	1.53
Rel. Inten.(% of BP)	0.05	0.55	1.26	66.58	15.25	97.43	19.41	100.00	17.97	46.83	84.14	13.34
Score	0.20	0.50	0.22	0.50	-0.15	0.50	1.50	0.50	-0.18	0.50	0.50	-0.13
Ion-type	PR	V	LI	a1		b1	y2	b2		a3	b3	
Delta ppm	26.8	-37.1	7.8	-19.7		1.5	-17.3	-3.8		-1.9	-4.2	

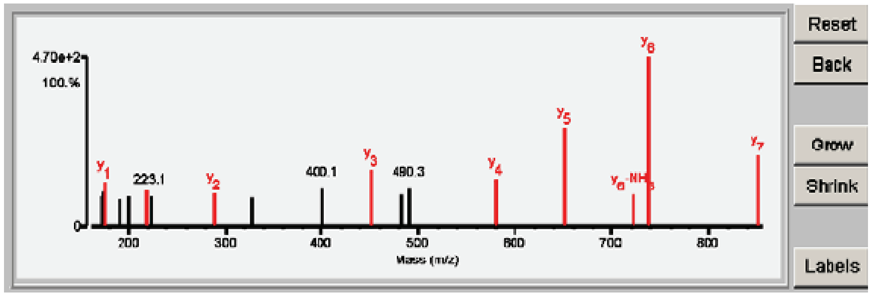
Fragment-ion (m/z)	510.229	609.304	696.341	883.576	925.520	931.547	1018.597	1024.572	1110.700	1117.645	1245.704	1348.752	1441.837
Frac. Inten.(% of TIC)	5.59	4.82	1.91	3.11	3.52	4.00	8.41	1.91	1.69	6.06	2.83	1.57	1.68
Rel. Inten.(% of BP)	48.94	42.15	16.74	27.22	30.81	35.02	73.62	16.69	14.74	53.04	24.79	13.70	14.68
Score	0.50	0.50	0.50	-0.27	-0.31	1.50	1.50	-0.17	-0.15	1.50	1.50	-0.14	1.50
Ion-type	b4	b5	b6			y7	y8			y9	y10		y12
Delta ppm	-19.6	-6.6	1.3			-8.3	10.5			-9.4	-7.9		1.3

N13

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.81	64.7	7	10/25	(-) E|L/S/A/E/Y/L/R (E)	1068.5030	0.0025	2.3	10116.6/6.07	HUMAN	Q9H3K6	56707	BolA-like protein 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.079	86.097	102.054	129.107	136.076	172.041	173.124	175.117	190.069	201.114	218.041	223.104	288.114	288.198	328.134	400.135	451.268	482.196	490.257	580.304	651.339	721.362	738.383	851.473
Frac. Inten.(% of TIC)	0.01	5.23	1.26	0.13	0.09	0.17	3.20	3.56	4.57	2.80	3.17	3.72	3.20	3.21	3.43	2.98	3.92	5.79	3.30	3.90	4.92	9.97	3.25	17.07	7.15
Rel. Inten.(% of BP)	0.04	30.66	7.39	0.77	0.51	1.00	18.74	20.87	26.79	16.40	18.57	21.79	18.72	18.79	20.09	17.45	22.98	33.89	19.36	22.85	28.83	58.40	19.06	100.00	41.89
Score	0.20	-0.31	0.22	1.00	0.20	1.00	-0.19	-0.21	1.50	-0.16	-0.19	0.50	-0.19	0.75	1.50	-0.17	-0.23	1.50	-0.19	-0.23	1.50	1.50	0.50	1.50	1.50
Ion-type	PR		LI	E	RKQ	Y			y1			b1		SAE	y2			y3			y4	y5	y6-NH3	y6	y7
Delta ppm	11.1		10.2	-13.3	37.6	3.7			-9.4			-36.5		-21.9	-16.7			3.2			-7.6	-10.8	14.8	7.2	12.3

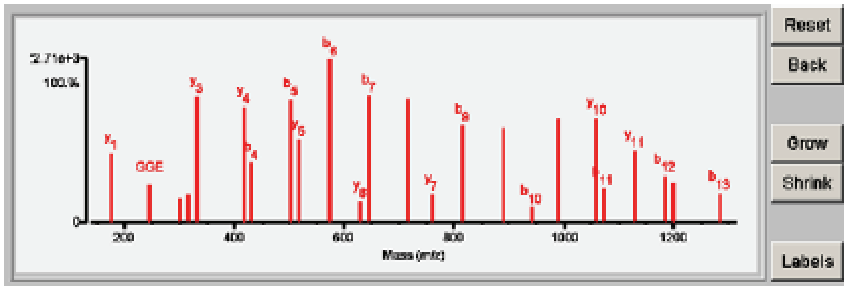


N14

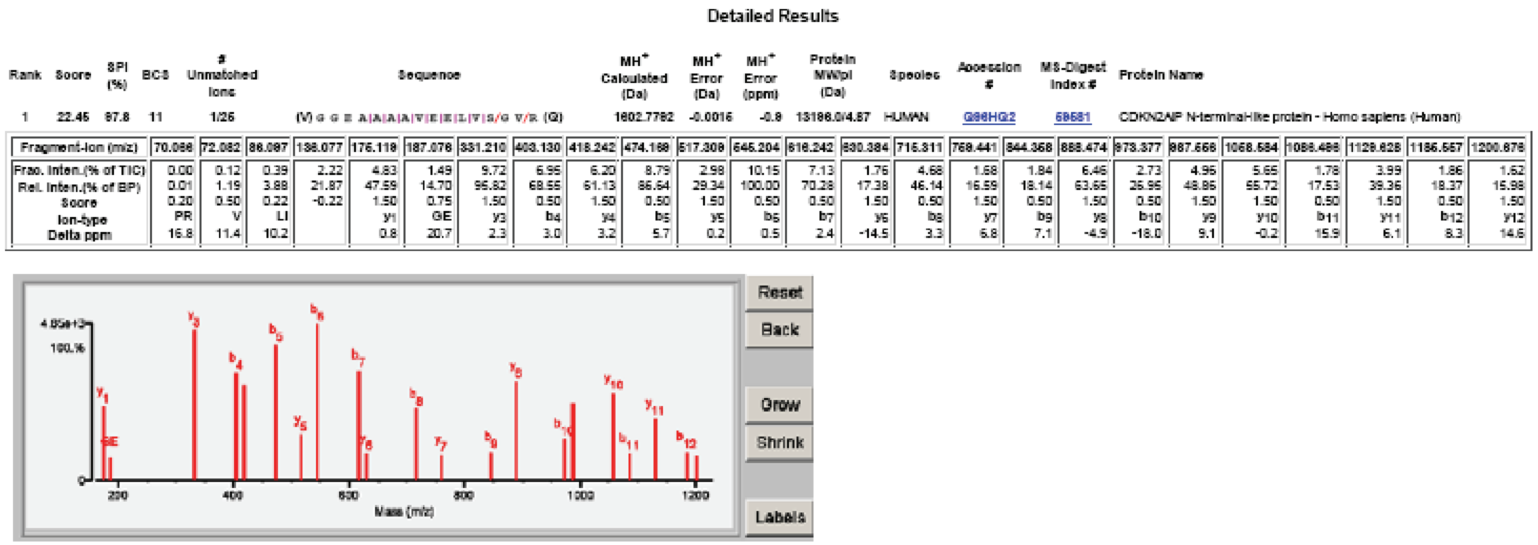
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.72	100.0	13	0/26	(-) V G G\E\A|A|A|A|V|E|E|L|V|S/G V/R (Q)	1701.8478	0.0009	0.6	13186.0/4.87	HUMAN	Q96HQ2	69681	CDKN2AIP N-terminal-like protein - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	175.118	244.093	302.118	316.129	331.208	418.238	431.164	502.186	517.304	573.233	630.384	644.271	715.307	759.438	814.368	888.476	943.418	987.541	1058.578	1072.444	1129.617	1185.531	1200.648	1284.605
Frac. Inten.(% of TIC)	0.07	3.92	2.17	1.38	1.64	7.03	6.53	3.39	6.90	4.73	9.23	1.23	7.15	6.98	1.58	5.48	5.29	0.94	5.87	5.90	1.97	4.05	2.61	2.25	1.72
Rel. Inten.(% of BP)	0.75	42.42	23.49	14.98	17.81	76.11	70.77	36.72	74.78	51.25	100.00	13.28	77.44	75.64	17.11	59.31	57.30	10.15	63.60	63.92	21.30	43.82	28.25	24.32	18.60
Score	0.22	1.50	0.75	0.50	0.75	1.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50
Ion-type	LI	y1	GGE	b3	GGEA	y3	y4	b4	b5	y5	b6	y6	b7	b8	y7	b9	y8	b10	y9	y10	b11	y11	b12	y12	b13
Delta ppm	-4.9	-6.0	7.0	1.7	-5.7	0.2	-5.6	-16.0	-3.8	-9.4	-2.8	0.9	-0.8	-3.0	3.1	-11.5	-2.6	-1.0	-5.6	-5.2	-17.0	-3.3	-13.3	-8.1	-7.9



N15

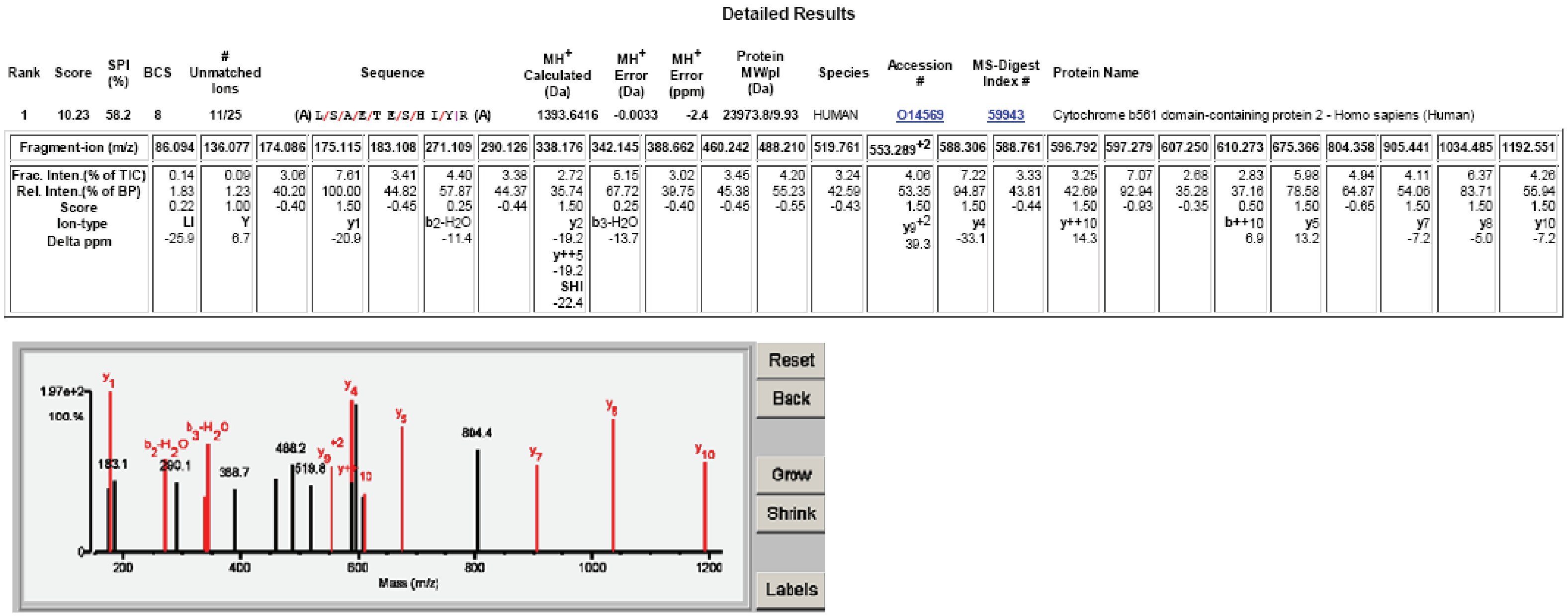


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^{+} Calculated (Da)	MH^{+} Error (Da)	MH^{+} Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.45	97.8	11	1/26	(V) G G E A|A|A|A|V|E|E|L|V|S/G V/R (Q)	1602.7792	-0.0016	-0.8	13186.0/4.87	HUMAN	Q96HQ2	68681	CDKN2AIP N-terminal-like protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	86.097	136.077	176.118	187.076	331.210	403.130	418.242	474.168	517.308	645.204	616.242	630.384	715.311	769.441	844.368	888.474	973.377	987.566	1068.584	1086.486	1129.628	1186.567	1200.876
Frac. Inten.(% of TIC)	0.00	0.12	0.39	2.22	4.83	1.49	9.72	6.95	6.20	8.79	2.98	10.15	7.13	1.76	4.68	1.68	1.84	6.46	2.73	4.96	5.65	1.78	3.99	1.86	1.62
Rel. Inten.(% of BP)	0.01	1.19	3.88	21.87	47.59	14.70	95.82	68.55	61.13	86.64	29.34	100.00	70.28	17.38	46.14	16.59	18.14	63.65	26.95	48.86	55.72	17.53	39.36	18.37	15.98
Score	0.20	0.50	0.22	-0.22	1.50	0.75	1.50	0.50	1.50	0.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type	PR	V	LI		y1	GE	y3	b4	y4	b5	y5	b6	b7	y6	b8	y7	b9	y8	b10	y9	y10	b11	y11	b12	y12
Delta ppm	16.8	11.4	10.2		0.8	20.7	2.3	3.0	3.2	5.7	0.2	0.5	2.4	-14.5	3.3	6.8	7.1	-4.9	-18.0	9.1	-0.2	15.9	6.1	8.3	14.6

N16



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^{+} Calculated (Da)	MH^{+} Error (Da)	MH^{+} Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.23	58.2	8	11/25	(A) L/S/A/E/T E/S/H I/Y|R (A)	1393.6416	-0.0033	-2.4	23973.8/9.93	HUMAN	O14569	59943	Cytochrome b561 domain-containing protein 2 - Homo sapiens (Human)

Fragment-ion (m/z)	86.094	136.077	174.086	175.115	183.108	271.109	290.126	338.176	342.145	388.662	460.242	488.210	519.761	553.289^{+2}	588.306	588.761	596.792	597.279	607.250	610.273	675.366	804.358	905.441	1034.485	1192.551
Frac. Inten.(% of TIC)	0.14	0.09	3.06	7.61	3.41	4.40	3.38	2.72	5.15	3.02	3.45	4.20	3.24	4.06	7.22	3.33	3.25	7.07	2.68	2.83	5.98	4.94	4.11	6.37	4.26
Rel. Inten.(% of BP)	1.83	1.23	40.20	100.00	44.82	57.87	44.37	35.74	67.72	39.75	45.38	55.23	42.59	53.35	94.87	43.81	42.69	92.94	35.28	37.16	78.58	64.87	54.06	83.71	55.94
Score	0.22	1.00	-0.40	1.50	-0.45	0.25	-0.44	1.50	0.25	-0.40	-0.45	-0.55	-0.43	1.50	1.50	-0.44	1.50	-0.93	-0.35	0.50	1.50	-0.65	1.50	1.50	1.50
Ion-type	LI	Y		y1		b2-H2O		y2 y++5 SHI	b3-H2O					y9^{+2}	y4		y++10			b++10	y5		y7	y8	y10
Delta ppm	-25.9	6.7		-20.9		-11.4		-19.2 -19.2 -22.4	-13.7					39.3	-33.1		14.3			6.9	13.2		-7.2	-5.0	-7.2

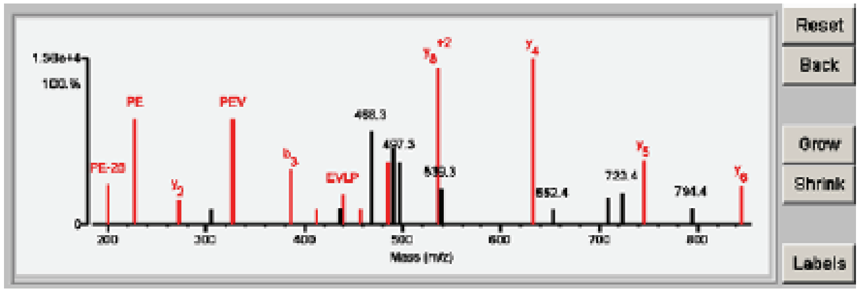
N17

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.33	69.3	6	10/26	(-) A/P E|V|L/P K/P R (M)	1229.6169	0.0004	0.3	8781.6/10.39	HUMAN	P09669	101669	Cytochrome c oxidase polypeptide Vic precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	86.096	199.107	227.102	272.170	305.131	326.170	386.139	411.259	436.138	439.266	457.212	468.291^{+2}
Frac. Inten.(% of TIC)	0.01	0.04	3.16	8.38	1.94	1.15	8.31	4.31	1.12	1.31	2.35	1.18	7.27
Rel. Inten.(% of BP)	0.04	0.32	24.17	64.06	14.82	8.79	63.54	32.93	8.58	9.99	18.00	9.05	55.57
Score	0.20	0.22	0.50	0.75	1.50	-0.09	0.75	0.50	0.50	-0.10	0.75	0.50	-0.56
Ion-type	PR	LI	PE-28	PE	y2		PEV	b3	EVLP-28		EVLP	a4	
Delta ppm	6.8	-4.9	-10.1	-8.9	-6.7		-6.0	0.4	-6.6		-2.1	-1.8	

Fragment-Ion (m/z)	485.208	489.285^{+2}	497.318	535.796^{+2}	538.274	632.332	652.383	709.468	723.382	745.414	784.402	844.485
Frac. Inten.(% of TIC)	5.02	6.05	5.00	12.31	2.82	13.08	1.21	2.04	2.49	5.03	1.31	3.08
Rel. Inten.(% of BP)	38.36	46.26	38.25	94.08	21.57	100.00	9.25	15.60	19.07	38.47	10.01	23.56
Score	0.50	-0.46	-0.38	1.50	-0.22	1.50	-0.09	-0.16	-0.19	1.50	-0.10	1.50
Ion-type	b4			y8^{+2}		y4				y5		y6
Delta ppm	-3.0			1.5		-2.9				-5.7		-1.3



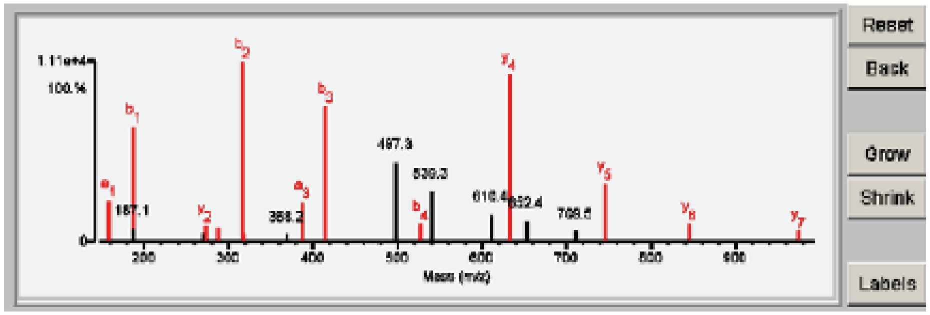
N18

Detailed Results

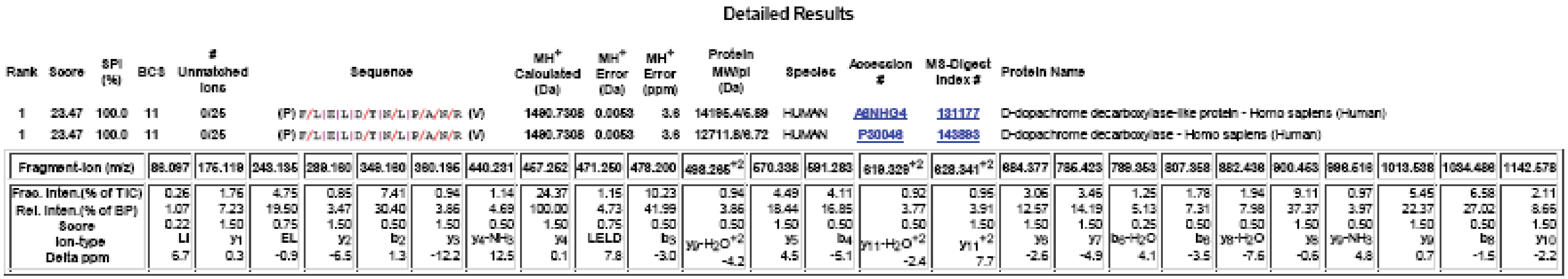
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.16	78.2	6	9/26	(A) P|E|V|L|P K/P R (M)	1168.6798	0.0031	2.7	8781.6/10.39	HUMAN	P09669	101669	Cytochrome c oxidase polypeptide Vic precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.064	72.081	86.097	94.066	168.094	186.068	187.061	270.142	272.171	287.107	315.100	318.670	368.188
Frac. Inten.(% of TIC)	0.00	0.04	0.04	1.16	3.91	10.93	1.26	0.81	1.54	1.42	17.19	0.73	0.63
Rel. Inten.(% of BP)	0.01	0.23	0.24	6.72	22.74	63.57	7.30	4.74	8.94	8.24	100.00	4.27	3.65
Score	0.20	0.50	0.22	-0.07	0.50	0.50	-0.07	-0.05	1.50	0.50	0.50	1.50	-0.04
Ion-type	PR	V	LI		a1	b1			y2	a2	b2	y++4	
Delta ppm	-10.4	8.7	3.2		-5.1	-9.3			-1.9	0.3	-7.0	-1.9	

Fragment-Ion (m/z)	388.174	414.188	497.314	527.249	538.269	610.404	632.333	652.362	709.468	746.421	844.477	973.507
Frac. Inten.(% of TIC)	3.72	12.81	7.63	1.71	4.76	2.60	15.97	1.95	1.03	5.51	1.74	0.92
Rel. Inten.(% of BP)	21.61	74.48	44.36	9.92	27.71	15.10	92.90	11.37	5.97	32.06	10.12	5.33
Score	0.50	0.50	-0.44	0.50	-0.28	-0.15	1.50	-0.11	-0.06	1.50	1.50	1.50
Ion-type	a3	b3		b4			y4			y5	y6	y7
Delta ppm	-4.2	-5.9		-9.7			-0.8			4.7	-10.4	-22.6



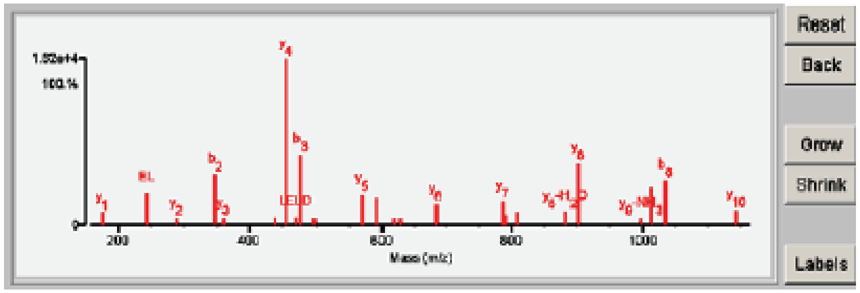
N19



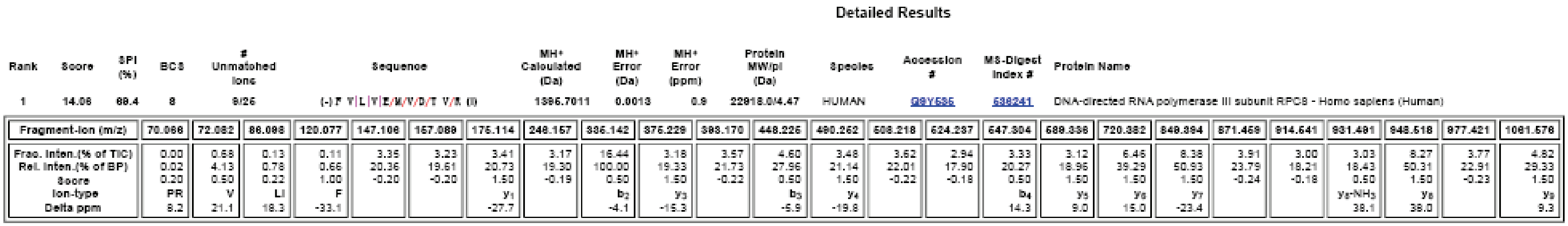
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	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	(P) F/L|E|L|D/T|N/L|P/A/N/R (V)	1480.7308	0.0053	3.6	14195.4/6.89	HUMAN	A6NHG4	131177	D-dopachrome decarboxylase-like protein - Homo sapiens (Human)
1	23.47	100.0	11	0/25	(P) F/L|E|L|D/T|N/L|P/A/N/R (V)	1480.7308	0.0053	3.6	12711.8/6.72	HUMAN	P30046	143883	D-dopachrome decarboxylase - Homo sapiens (Human)

Fragment-Ion (m/z)	88.097	176.119	243.135	289.160	348.160	360.196	440.231	467.262	471.250	478.200	498.265^{+2}	570.338	591.283	618.329^{+2}	628.341^{+2}	684.377	786.423	789.353	807.358	882.438	900.463	998.516	1013.538	1034.488	1142.578
Frac. Inten.(% of TIC)	0.26	1.76	4.75	0.85	7.41	0.94	1.14	24.37	1.15	10.23	0.94	4.49	4.11	0.92	0.95	3.06	3.46	1.25	1.78	1.94	9.11	0.97	5.45	6.58	2.11
Rel. Inten.(% of BP)	1.07	7.23	19.50	3.47	30.40	3.86	4.69	100.00	4.73	41.99	3.86	18.44	16.85	3.77	3.91	12.57	14.19	5.13	7.31	7.98	37.37	3.97	22.37	27.02	8.66
Score	0.22	1.50	0.75	1.50	0.50	1.50	0.50	1.50	0.75	0.50	0.50	1.50	0.50	0.50	1.50	1.50	1.50	0.25	0.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	LI	y_1	EL	y_2	b_2	y_3	y_4-NH_3	y_4	LELD	b_3	y_9-H_2O^{+2}	y_5	b_4	y_{11}-H_2O^{+2}	y_{11}^{+2}	y_6	y_7	b_6-H_2O	b_6	y_8-H_2O	y_8	y_9-NH_3	y_9	b_8	y_{10}
Delta ppm	6.7	0.3	-0.9	-6.5	1.3	-12.2	12.5	0.1	7.8	-3.0	-4.2	4.5	-5.1	-2.4	7.7	-2.6	-4.9	4.1	-3.5	-7.6	-0.6	4.8	0.7	-1.5	-2.2



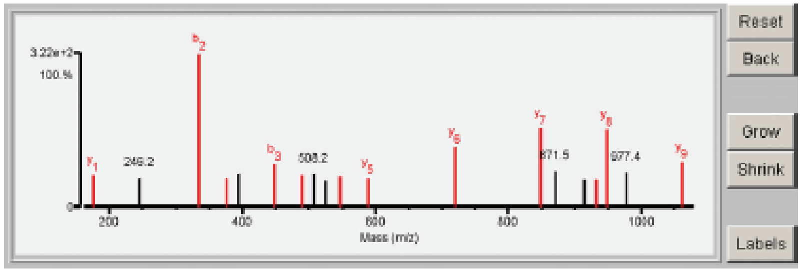
N20



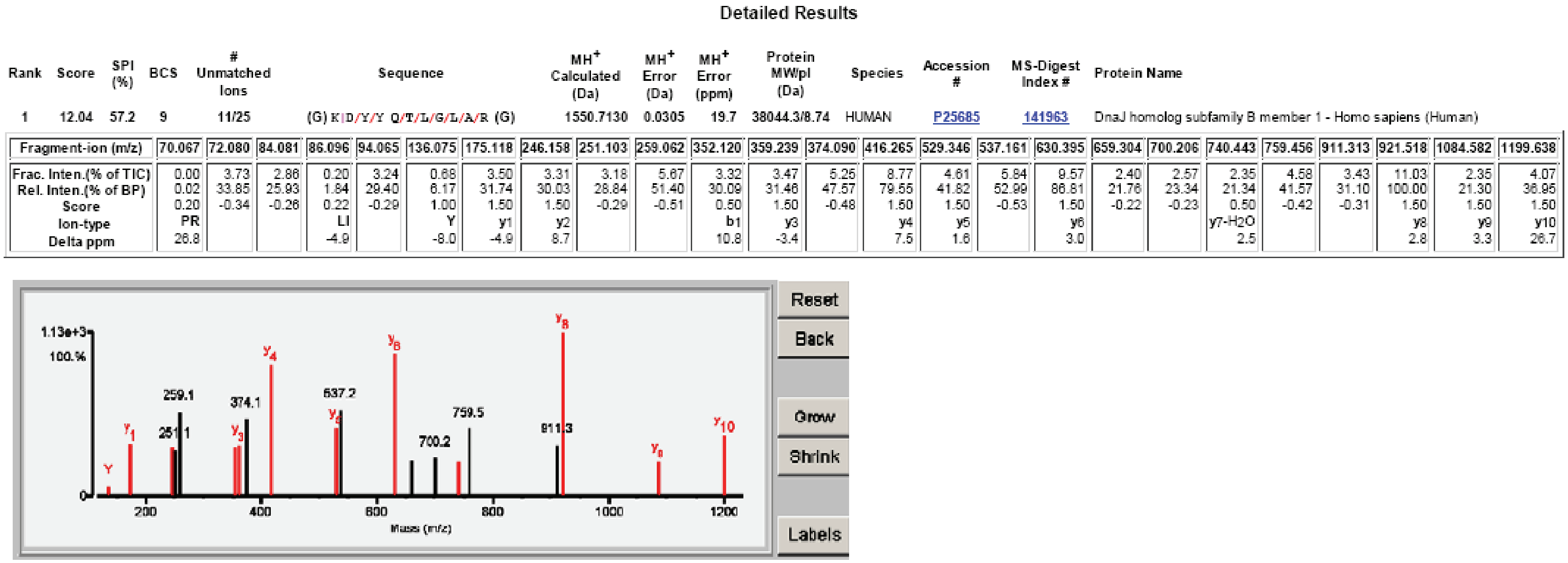
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.06	68.4	8	9/26	(-) F V|L|V|E/M/V/D/T V/K (I)	1396.7011	0.0013	0.9	22918.0/4.47	HUMAN	Q9Y535	538241	DNA-directed RNA polymerase III subunit RPC8 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.082	86.098	120.077	147.106	157.089	176.114	246.157	336.142	376.229	393.170	448.226	490.262	508.218	624.287	647.304	689.336	720.382	849.394	871.469	914.641	931.491	948.518	977.421	1061.578
Frac. Inten.(% of TIC)	0.00	0.68	0.13	0.11	3.35	3.23	3.41	3.17	16.44	3.18	3.57	4.60	3.48	3.62	2.94	3.33	3.12	6.46	8.38	3.91	3.00	3.03	8.27	3.77	4.82
Rel. Inten.(% of BP)	0.02	4.13	0.78	0.66	20.36	19.61	20.73	19.30	100.00	19.33	21.73	27.96	21.14	22.01	17.90	20.27	18.96	39.29	50.93	23.79	18.21	18.43	50.31	22.91	29.33
Score	0.20	0.50	0.22	1.00	-0.20	-0.20	1.50	-0.19	0.50	1.50	-0.22	0.50	1.50	-0.22	-0.18	0.50	1.50	1.50	1.50	-0.24	-0.18	0.50	1.50	-0.23	1.50
Ion-type	PR	V	LI	F			y_1		b_2	y_3		b_3	y_4			b_4	y_5	y_6	y_7			y_8-NH_3	y_8		y_9
Delta ppm	8.2	21.1	18.3	-33.1			-27.7		-4.1	-15.3		-5.9	-19.8			14.3	9.0	15.0	-23.4			38.1	38.0		9.3



N21



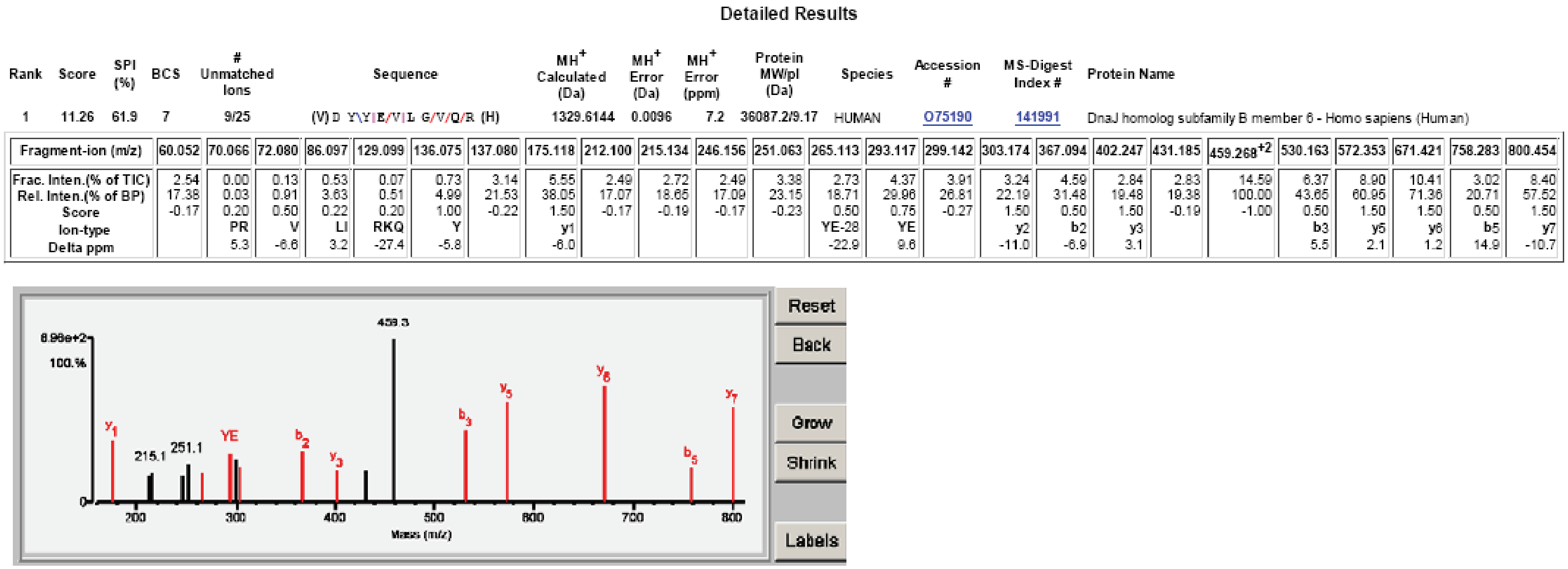
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.04	57.2	9	11/25	(G) K|D/Y/Y Q/T/L/G/L/A/R (G)	1550.7130	0.0305	19.7	38044.3/8.74	HUMAN	P25685	141963	DnaJ homolog subfamily B member 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.080	84.081	86.096	94.065	136.075	175.118	246.158	251.103	259.062	352.120	359.239
Frac. Inten.(% of TIC)	0.00	3.73	2.86	0.20	3.24	0.68	3.50	3.31	3.18	5.67	3.32	3.47
Rel. Inten.(% of BP)	0.02	33.85	25.93	1.84	29.40	6.17	31.74	30.03	28.84	51.40	30.09	31.46
Score	0.20	-0.34	-0.26	0.22	-0.29	1.00	1.50	1.50	-0.29	-0.51	0.50	1.50
Ion-type	PR			LI		Y	y1	y2			b1	y3
Delta ppm	26.8			-4.9		-8.0	-4.9	8.7			10.8	-3.4

Fragment-ion (m/z)	374.090	416.265	529.346	537.161	630.395	659.304	700.206	740.443	759.456	911.313	921.518	1084.582	1199.638
Frac. Inten.(% of TIC)	5.25	8.77	4.61	5.84	9.57	2.40	2.57	2.35	4.58	3.43	11.03	2.35	4.07
Rel. Inten.(% of BP)	47.57	79.55	41.82	52.99	86.81	21.76	23.34	21.34	41.57	31.10	100.00	21.30	36.95
Score	-0.48	1.50	1.50	-0.53	1.50	-0.22	-0.23	0.50	-0.42	-0.31	1.50	1.50	1.50
Ion-type		y4	y5		y6			y7-H2O			y8	y9	y10
Delta ppm		7.5	1.6		3.0			2.5			2.8	3.3	26.7

N22



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.26	61.9	7	9/25	(V) D Y\Y|E/V|L G/V/Q/R (H)	1329.6144	0.0096	7.2	36087.2/9.17	HUMAN	O75190	141991	DnaJ homolog subfamily B member 6 - Homo sapiens (Human)

Fragment-ion (m/z)	60.052	70.066	72.080	86.097	129.099	136.075	137.080	175.118	212.100	215.134	246.156	251.063
Frac. Inten.(% of TIC)	2.54	0.00	0.13	0.53	0.07	0.73	3.14	5.55	2.49	2.72	2.49	3.38
Rel. Inten.(% of BP)	17.38	0.03	0.91	3.63	0.51	4.99	21.53	38.05	17.07	18.65	17.09	23.15
Score	-0.17	0.20	0.50	0.22	0.20	1.00	-0.22	1.50	-0.17	-0.19	-0.17	-0.23
Ion-type		PR	V	LI	RKQ	Y		y1				
Delta ppm		5.3	-6.6	3.2	-27.4	-5.8		-6.0				

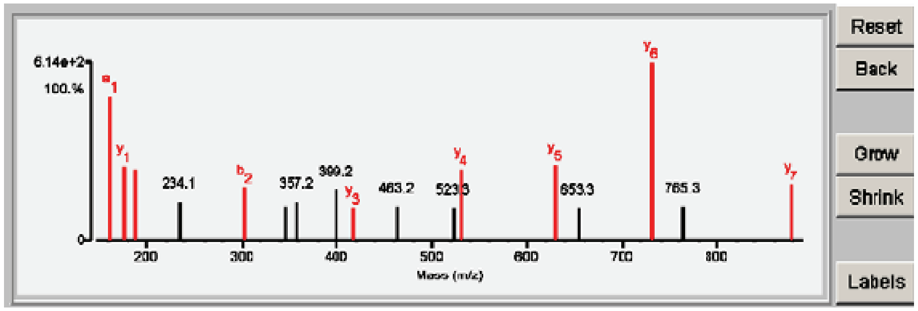
Fragment-ion (m/z)	265.113	293.117	299.142	303.174	367.094	402.247	431.185	459.268^{+2}	530.163	572.353	671.421	758.283	800.454
Frac. Inten.(% of TIC)	2.73	4.37	3.91	3.24	4.59	2.84	2.83	14.59	6.37	8.90	10.41	3.02	8.40
Rel. Inten.(% of BP)	18.71	29.96	26.81	22.19	31.48	19.48	19.38	100.00	43.65	60.95	71.36	20.71	57.52
Score	0.50	0.75	-0.27	1.50	0.50	1.50	-0.19	-1.00	0.50	1.50	1.50	0.50	1.50
Ion-type	YE-28	YE		y2	b2	y3			b3	y5	y6	b5	y7
Delta ppm	-22.9	9.6		-11.0	-6.9	3.1			5.5	2.1	1.2	14.9	-10.7

N23

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.02	61.2	7	11/25	(-) V\H|F/T/V/D/Q I/R (A)	1179.5827	0.0001	0.0	95338.7/6.41	HUMAN	P13639	154511	Elongation factor 2 - Homo sapiens (Human)

Fragment-ion (m/z)	60.044	70.067	72.081	84.043	86.096	87.055	110.071	120.079	160.078	175.114	188.076	234.118	302.113	345.156	357.203	399.218	416.264	463.249^{+2}	523.289	531.286	630.350	653.305	731.406	765.307	878.464
Frac. Inten.(% of TIC)	3.62	0.01	0.25	8.68	0.49	0.19	2.76	0.20	11.44	5.92	5.59	3.05	4.25	2.79	3.09	4.11	2.56	2.76	2.60	5.61	6.05	2.64	14.20	2.70	4.44
Rel. Inten.(% of BP)	25.47	0.06	1.77	61.15	3.42	1.36	19.43	1.41	80.52	41.70	39.36	21.45	29.92	19.67	21.79	28.91	18.04	19.46	18.29	39.50	42.58	18.60	100.00	18.99	31.29
Score	-0.25	0.20	0.50	-0.61	0.22	0.33	-0.19	1.00	0.50	1.50	0.50	-0.21	0.50	-0.20	-0.22	-0.29	1.50	-0.19	-0.18	1.50	1.50	-0.19	1.50	-0.19	1.50
Ion-type		PR	V		LI	NR		F	a1	y1	b1		b2				y3			y4	y5		y6		y7
Delta ppm		19.6	3.1		-0.3	-4.5		-13.1	-15.4	-28.3	6.0		-18.2				5.5			-5.3	-10.6		1.7		-10.0

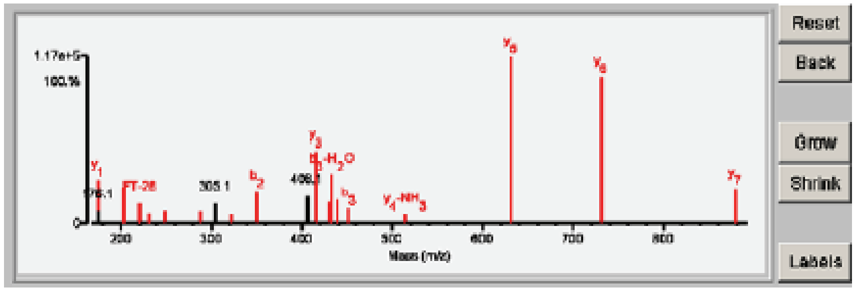


N24

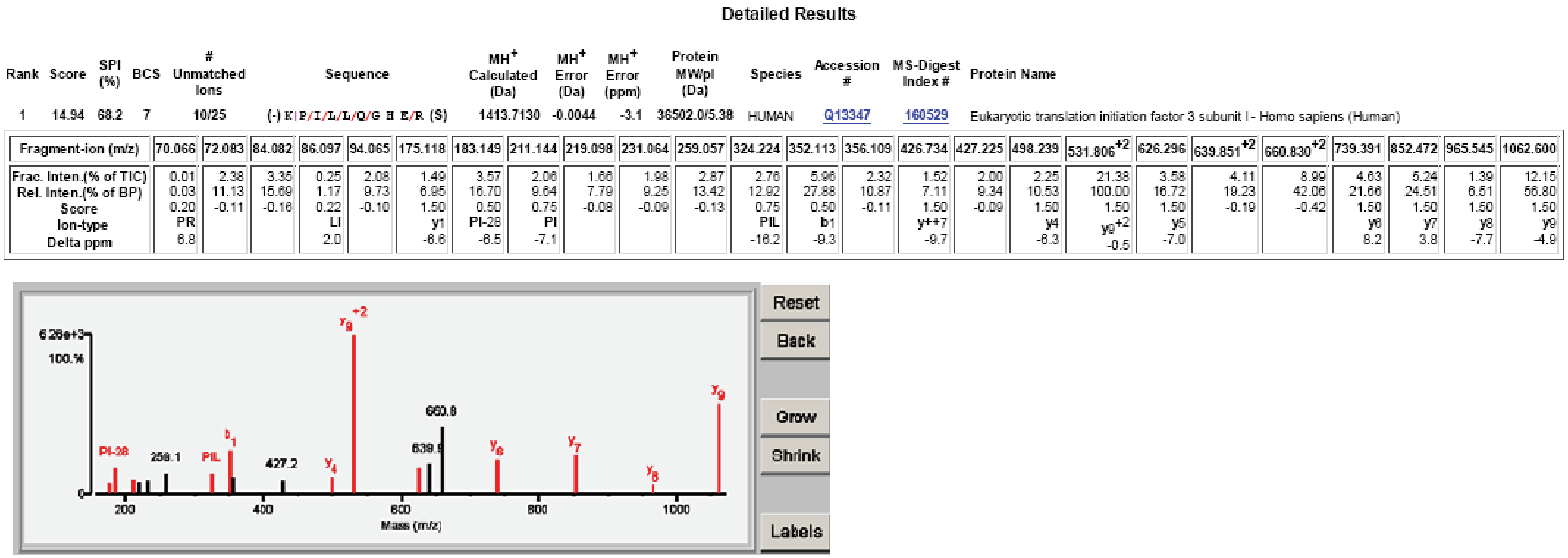
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.18	84.2	6	6/25	(V) H|F|T|V D/Q/I/R (A)	1080.5143	0.0067	6.2	95338.7/6.41	HUMAN	P13639	154511	Elongation factor 2 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	115.050	120.081	121.083	158.027	175.118	178.109	203.048	221.128	231.114	249.124	288.202	305.086	322.123	350.117	406.143	416.261	430.738^{+2}	433.154	439.740^{+2}	451.166	614.268	630.357	731.404	878.473
Frac. Inten.(% of TIC)	0.04	3.88	0.74	2.11	2.69	5.09	1.57	4.25	2.35	1.32	1.53	1.47	2.43	1.02	3.67	3.16	8.38	2.60	5.70	2.85	1.81	1.01	19.32	16.92	4.10
Rel. Inten.(% of BP)	0.21	20.07	3.83	10.92	13.91	26.35	8.15	22.02	12.15	6.84	7.93	7.59	12.57	5.28	19.00	16.38	43.37	13.48	29.50	14.75	9.36	5.25	100.00	87.59	21.21
Score	0.50	-0.20	1.00	-0.11	-0.14	1.50	-0.08	0.50	0.50	0.50	0.75	1.50	-0.13	0.50	0.50	-0.16	1.50	0.50	0.25	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	V		F			y_1		b_1	FT-28	FT-H_2O	FT	y_2		a_2	b_2		y_3	y_7-H_2O^{+2}	b_3-H_2O	y_7^{+2}	b_3	y_4-NH_3	y_5	y_6	y_7
Delta ppm	7.3		-2.3			-4.9		-6.3	-5.2	-1.3	-2.7	-1.8		-0.6	-3.1		-1.4	1.7	-2.1	-0.8	-2.2	-6.2	-0.6	-1.0	-0.4



N25



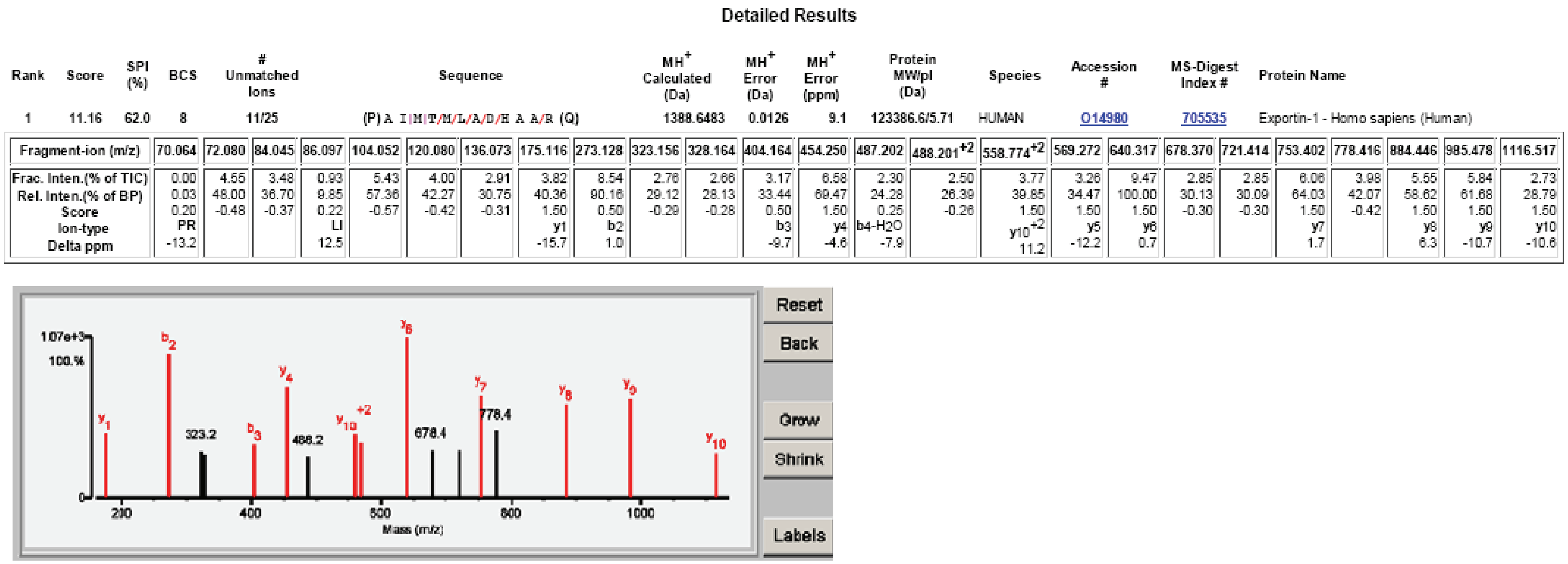
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.94	68.2	7	10/25	(-) K|P/I/L/L/Q/G H E/R (S)	1413.7130	-0.0044	-3.1	36502.0/5.38	HUMAN	Q13347	160529	Eukaryotic translation initiation factor 3 subunit I - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.083	84.082	86.097	94.065	175.118	183.149	211.144	219.098	231.064	259.057	324.224
Frac. Inten.(% of TIC)	0.01	2.38	3.35	0.25	2.08	1.49	3.57	2.06	1.66	1.98	2.87	2.76
Rel. Inten.(% of BP)	0.03	11.13	15.69	1.17	9.73	6.95	16.70	9.64	7.79	9.25	13.42	12.92
Score	0.20	-0.11	-0.16	0.22	-0.10	1.50	0.50	0.75	-0.08	-0.09	-0.13	0.75
Ion-type	PR			LI		y1	PI-28	PI				PIL
Delta ppm	6.8			2.0		-6.6	-6.5	-7.1				-16.2

Fragment-ion (m/z)	352.113	356.109	426.734	427.225	498.239	531.806^{+2}	626.296	639.851^{+2}	660.830^{+2}	739.391	852.472	965.545	1062.600
Frac. Inten.(% of TIC)	5.96	2.32	1.52	2.00	2.25	21.38	3.58	4.11	8.99	4.63	5.24	1.39	12.15
Rel. Inten.(% of BP)	27.88	10.87	7.11	9.34	10.53	100.00	16.72	19.23	42.06	21.66	24.51	6.51	56.80
Score	0.50	-0.11	1.50	-0.09	1.50	1.50	1.50	-0.19	-0.42	1.50	1.50	1.50	1.50
Ion-type	b1		y++7		y4	y9^{+2}	y5			y6	y7	y8	y9
Delta ppm	-9.3		-9.7		-6.3	-0.5	-7.0			8.2	3.8	-7.7	-4.9

N26



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.16	62.0	8	11/25	(P) A I|M|T/M/L/A/D/H A A/R (Q)	1388.6483	0.0126	9.1	123386.6/5.71	HUMAN	O14980	705535	Exportin-1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.080	84.045	86.097	104.052	120.080	136.073	175.116	273.128	323.156	328.164	404.164
Frac. Inten.(% of TIC)	0.00	4.55	3.48	0.93	5.43	4.00	2.91	3.82	8.54	2.76	2.66	3.17
Rel. Inten.(% of BP)	0.03	48.00	36.70	9.85	57.36	42.27	30.75	40.36	90.16	29.12	28.13	33.44
Score	0.20	-0.48	-0.37	0.22	-0.57	-0.42	-0.31	1.50	0.50	-0.29	-0.28	0.50
Ion-type	PR			LI				y1	b2			b3
Delta ppm	-13.2			12.5				-15.7	1.0			-9.7

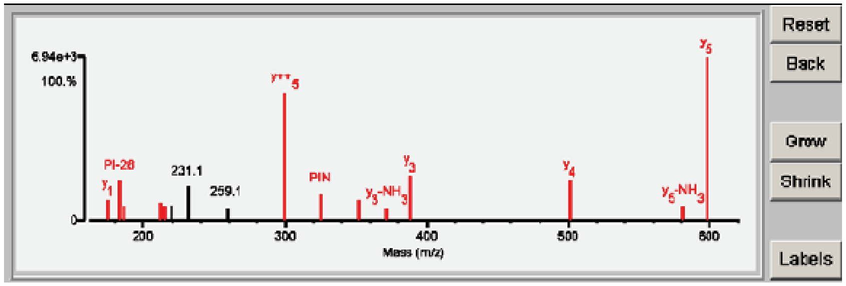
Fragment-ion (m/z)	454.250	487.202	488.201^{+2}	558.774^{+2}	569.272	640.317	678.370	721.414	753.402	778.416	884.446	985.478	1116.517
Frac. Inten.(% of TIC)	6.58	2.30	2.50	3.77	3.26	9.47	2.85	2.85	6.06	3.98	5.55	5.84	2.73
Rel. Inten.(% of BP)	69.47	24.28	26.39	39.85	34.47	100.00	30.13	30.09	64.03	42.07	58.62	61.68	28.79
Score	1.50	0.25	-0.26	1.50	1.50	1.50	-0.30	-0.30	1.50	-0.42	1.50	1.50	1.50
Ion-type	y4	b4-H2O		y10^{+2}	y5	y6			y7		y8	y9	y10
Delta ppm	-4.6	-7.9		11.2	-12.2	0.7			1.7		6.3	-10.7	-10.6

N27

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.34	62.9	4	8/25	(V) K|P/I/N V/R (S)	949.4746	0.0025	2.6	191615.7/5.48	HUMAN	RQ00610	87338	REVERSE Clathrin heavy chain 1 - Homo sapiens (Human)
1	11.34	62.9	4	8/25	(V) K|P/I/N V/R (S)	949.4746	0.0025	2.6	187031.0/5.57	HUMAN	RP53675	87344	REVERSE Clathrin heavy chain 2 - Homo sapiens (Human)
1	11.34	62.9	4	8/25	(P) K|P/I/N V/R (V)	949.4746	0.0025	2.6	69413.2/5.94	HUMAN	P15311	172147	Ezrin - Homo sapiens (Human)
1	11.34	62.9	4	8/25	(P) K|P/I/N V/R (V)	949.4746	0.0025	2.6	68564.2/6.03	HUMAN	P35241	466757	Radixin - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.080	84.081	86.096	94.066	116.054	129.099	160.025	175.116	183.149	186.122	211.144	214.116	219.095	231.060	259.057	299.688	325.184	352.116	371.201	388.230	501.312	581.337	598.367	856.410
Frac. Inten.(% of TIC)	0.01	0.04	8.56	0.05	12.73	3.01	0.04	1.16	2.47	4.48	1.56	2.02	1.65	1.79	3.79	1.48	14.30	3.05	2.40	1.46	5.01	4.52	1.70	18.20	4.54
Rel. Inten.(% of BP)	0.06	0.21	47.03	0.26	69.94	16.53	0.22	6.37	13.58	24.60	8.55	11.12	9.07	9.84	20.85	8.12	78.56	16.76	13.18	8.04	27.50	24.81	9.36	100.00	24.95
Score	0.20	0.50	-0.47	0.22	-0.70	-0.17	0.20	-0.06	1.50	0.50	0.50	0.75	0.75	-0.10	-0.21	-0.08	1.50	0.75	0.50	0.50	1.50	1.50	0.50	1.50	-0.25
Ion-type	PR	V		LI			RKQ		y_1	PI-28	NV-28	PI	NV				y^{++}_5	PIN	b_1	y_3-NH$_3$	y_3	y_4	y_5-NH$_3$	y_5	
Delta ppm	3.9	-12.1		-3.8			-25.1		-18.0	-5.4	-16.1	-5.2	-15.9				1.0	-12.4	0.3	-7.7	-1.5	-4.3	-8.3	-0.2	

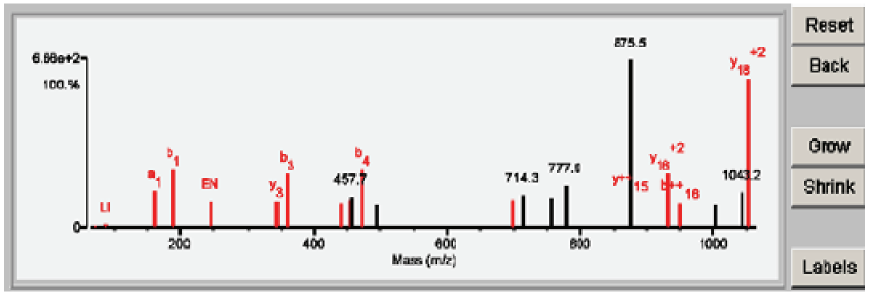


N28

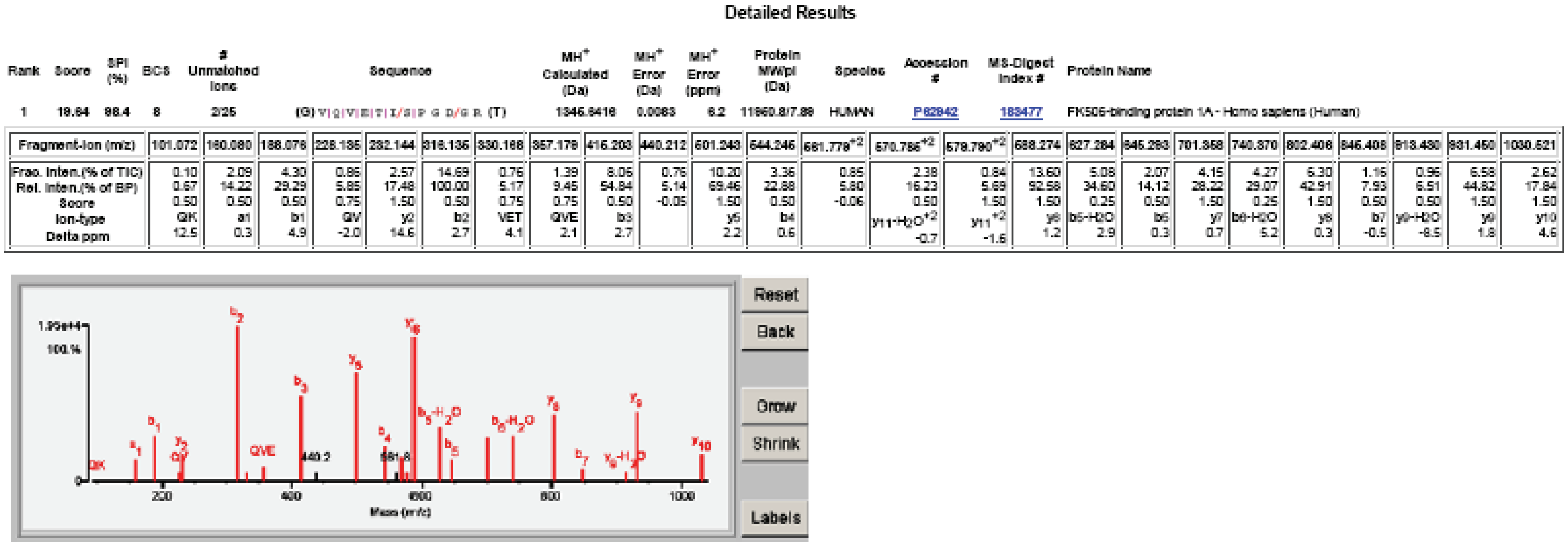
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.70	60.1	8	9/25	(A) V\G N\I|N E/L/P E N I L L E L F\T H/V/P A R (Q)	2576.3541	0.0014	0.6	29746.9/5.52	HUMAN	Q9H4M3	179237	F-box only protein 44 - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.096	160.079	188.073	244.095	341.145	343.204	359.137	442.280	454.217	457.686^{+2}	472.217	495.234	698.291	714.307	756.727	777.937	874.982	875.496^{+2}	931.530^{+2}	948.979	1003.071	1043.236	1053.060^{+2}	1110.133
Frac. Inten.(% of TIC)	0.18	0.37	3.51	5.52	2.57	2.52	2.52	5.13	2.43	2.70	2.85	5.55	2.20	2.65	3.08	2.79	4.03	2.99	15.85	5.05	2.37	2.29	3.27	14.04	3.53
Rel. Inten.(% of BP)	1.14	2.33	22.16	34.81	16.19	15.89	15.91	32.37	15.34	17.02	17.98	35.04	13.90	16.74	19.42	17.60	25.43	18.88	100.00	31.88	14.95	14.46	20.65	88.58	22.30
Score	0.50	0.22	0.50	0.50	0.75	0.75	1.50	0.50	1.50	0.75	-0.18	0.50	-0.14	0.25	-0.19	-0.18	-0.25	1.50	-1.00	1.50	0.50	-0.14	-0.21	1.50	-0.22
Ion-type	V	LI	a_1	b_1	EN	PEN	y_3	b_3	y_4	PENI		b_4		b_6-NH$_3$				y^{++}_{15}		y_{16}^{+2}	b^{++}_{16}			y_{18}^{+2}	
Delta ppm	-13.5	-6.1	-6.6	-8.9	4.1	-6.0	-13.5	-6.6	6.9	-30.0		-13.2		12.7				-7.5		-0.3	-14.9			-12.8	



N29

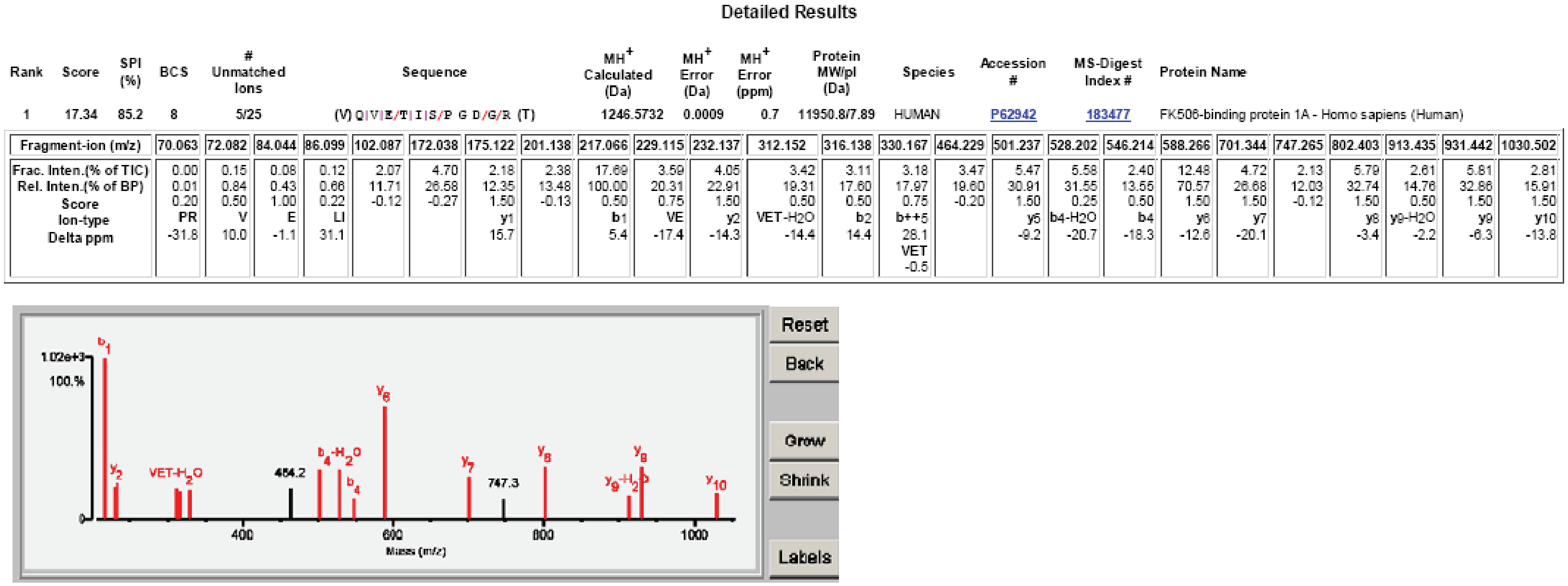


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.64	98.4	8	2/25	(G) V|Q|V|E|T|I/S|P G D/G R (T)	1345.6416	0.0083	6.2	11950.8/7.89	HUMAN	P62942	183477	FK506-binding protein 1A - Homo sapiens (Human)

Fragment-ion (m/z)	101.072	160.080	188.076	228.135	232.144	316.136	330.168	357.179	416.203	440.212	501.243	544.246	561.779^{+2}	570.786^{+2}	579.790^{+2}	588.274	627.284	645.293	701.358	740.370	802.406	846.408	913.430	931.450	1030.521
Frac. Inten.(% of TIC)	0.10	2.09	4.30	0.86	2.57	14.69	0.76	1.39	8.06	0.76	10.20	3.36	0.85	2.38	0.84	13.60	5.08	2.07	4.15	4.27	6.30	1.16	0.96	6.58	2.62
Rel. Inten.(% of BP)	0.67	14.22	29.29	5.85	17.48	100.00	5.17	9.45	54.84	5.14	69.46	22.88	5.80	16.23	5.69	92.58	34.60	14.12	28.22	29.07	42.91	7.93	6.51	44.82	17.84
Score	0.50	0.50	0.50	0.75	1.50	0.50	0.75	0.75	0.50	-0.05	1.50	0.50	-0.06	0.50	1.50	1.50	0.25	0.50	1.50	0.25	1.50	0.50	0.50	1.50	1.50
Ion-type	QK	a1	b1	QV	y2	b2	VET	QVE	b3		y5	b4		y11-H_2O^{+2}	y11^{+2}	y6	b5-H_2O	b5	y7	b6-H_2O	y8	b7	y9-H_2O	y9	y10
Delta ppm	12.5	0.3	4.9	-2.0	14.6	2.7	4.1	2.1	2.7		2.2	0.6		-0.7	-1.6	1.2	2.9	0.3	0.7	5.2	0.3	-0.5	-8.5	1.8	4.6

N30



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.34	85.2	8	5/25	(V) Q|V|E/T|I|S/P G D/G/R (T)	1246.5732	0.0009	0.7	11950.8/7.89	HUMAN	P62942	183477	FK506-binding protein 1A - Homo sapiens (Human)

Fragment-ion (m/z)	70.063	72.082	84.044	86.099	102.087	172.038	175.122	201.138	217.066	229.115	232.137	312.152	316.138	330.167	464.229	501.237	528.202	546.214	588.266	701.344	747.265	802.403	913.435	931.442	1030.502
Frac. Inten.(% of TIC)	0.00	0.15	0.08	0.12	2.07	4.70	2.18	2.38	17.69	3.59	4.05	3.42	3.11	3.18	3.47	5.47	5.58	2.40	12.48	4.72	2.13	5.79	2.61	5.81	2.81
Rel. Inten.(% of BP)	0.01	0.84	0.43	0.66	11.71	26.58	12.35	13.48	100.00	20.31	22.91	19.31	17.60	17.97	19.60	30.91	31.55	13.55	70.57	26.68	12.03	32.74	14.76	32.86	15.91
Score	0.20	0.50	1.00	0.22	-0.12	-0.27	1.50	-0.13	0.50	0.75	1.50	0.50	0.50	0.75	-0.20	1.50	0.25	0.50	1.50	1.50	-0.12	1.50	0.50	1.50	1.50
Ion-type	PR	V	E	LI			y1		b1	VE	y2	VET-H_2O	b2	b++5 VET		y5	b4-H_2O	b4	y6	y7		y8	y9-H_2O	y9	y10
Delta ppm	-31.8	10.0	-1.1	31.1			15.7		5.4	-17.4	-14.3	-14.4	14.4	28.1 -0.5		-9.2	-20.7	-18.3	-12.6	-20.1		-3.4	-2.2	-6.3	-13.8

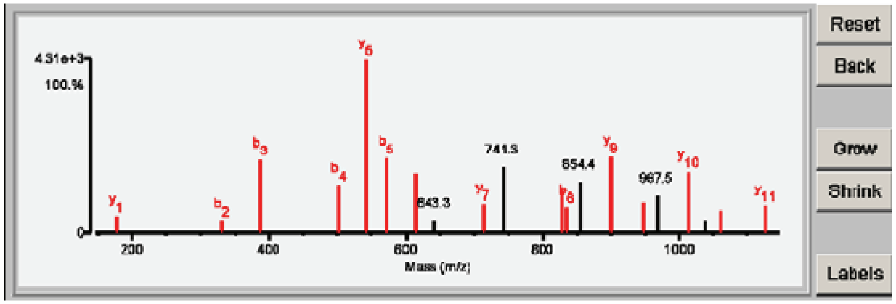
N31

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.54	79.2	12	7/25	(G) I Q\G\L\A\K|L|I|A/D/V/A/P S A I/R (E)	1959.0554	0.0095	4.8	42593.2/8.80	HUMAN	P39748	180389	Flap endonuclease 1 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.098	101.068	175.119	330.153	387.171	500.252	543.324	571.289	614.361	643.251	713.423	741.346
Frac. Inten.(% of TIC)	0.03	0.04	0.04	1.72	1.35	7.38	4.89	17.59	7.64	6.10	1.34	2.87	6.76
Rel. Inten.(% of BP)	0.17	0.25	0.22	9.80	7.68	41.94	27.78	100.00	43.46	34.66	7.62	16.31	38.45
Score	0.50	0.22	0.50	1.50	0.50	0.50	0.50	1.50	0.50	1.50	-0.08	1.50	-0.38
Ion-type	V	LI	QK	y1	b2	b3	b4	y5	b5	y6		y7	
Delta ppm	-3.8	14.8	-32.0	2.0	10.9	-0.7	-6.5	-1.0	-4.6	-1.8		-11.0	

Fragment-ion (m/z)	828.452	834.404	854.417	899.491	947.485	967.507	1012.574	1038.539	1060.558	1125.659	1295.699	1366.734
Frac. Inten.(% of TIC)	4.63	2.62	5.17	7.72	3.10	3.79	6.31	1.25	2.34	2.85	1.11	1.35
Rel. Inten.(% of BP)	26.34	14.87	29.42	43.88	17.64	21.53	35.86	7.12	13.31	16.20	6.29	7.67
Score	1.50	0.50	-0.29	1.50	0.50	-0.22	1.50	-0.07	0.50	1.50	-0.06	-0.08
Ion-type	y8	b6		y9	b7		y10		b8	y11		
Delta ppm	-6.4	3.4		-3.9	-0.4		-4.2		-10.4	-2.9		



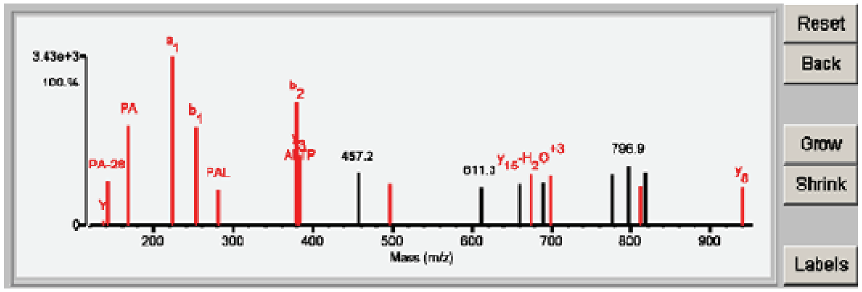
N32

Detailed Results

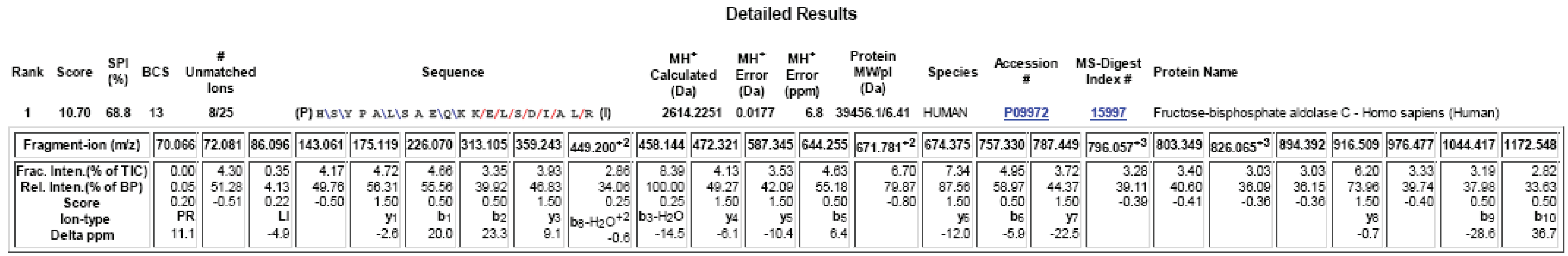
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.19	69.9	7	8/25	(P) Y\Q\Y P A L T P E Q K K/E/L/S D/I/A H R (I)	2745.2622	0.0160	5.8	39420.2/8.30	HUMAN	P04075	15959	Fructose-bisphosphate aldolase A - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	84.044	86.097	94.066	101.071	136.075	141.103	169.097	224.075	252.069	282.182	380.124	383.221
Frac. Inten.(% of TIC)	0.01	0.15	0.23	3.00	0.27	0.28	3.50	7.97	13.49	7.92	2.86	9.90	5.69
Rel. Inten.(% of BP)	0.10	1.15	1.72	22.24	1.98	2.08	25.98	59.06	100.00	58.74	21.22	73.40	42.20
Score	0.20	1.00	0.22	-0.22	0.50	1.00	0.50	0.75	0.50	0.50	0.75	0.50	1.50
Ion-type	PR	E	LI		QK	Y	PA-28	PA	a_1	b_1	PAL	b_2	y_3 ALTP
Delta ppm	2.5	-8.2	10.2		1.6	-2.1	0.4	-9.2	-1.7	-3.9	-1.5	-12.3	17.0 -22.2

Fragment-ion (m/z)	457.242^{+2}	496.297	611.335^{+2}	659.001^{+3}	672.993^{+3}	690.019^{+3}	698.345	775.924^{+2}	796.895^{+2}	811.432	817.881^{+2}	940.488
Frac. Inten.(% of TIC)	4.20	3.33	3.08	3.31	4.10	3.37	4.01	4.09	4.83	3.23	4.18	3.00
Rel. Inten.(% of BP)	31.17	24.66	22.82	24.56	30.38	24.98	29.72	30.30	35.79	23.92	30.96	22.24
Score	-0.31	1.50	-0.23	-0.25	0.50	-0.25	1.50	-0.30	-0.36	1.50	-0.31	1.50
Ion-type		y_4			y_{15}-H_2O^{+3}		y_6			y_7		y_8
Delta ppm		-4.3			-6.8		-18.8			-12.5		3.6



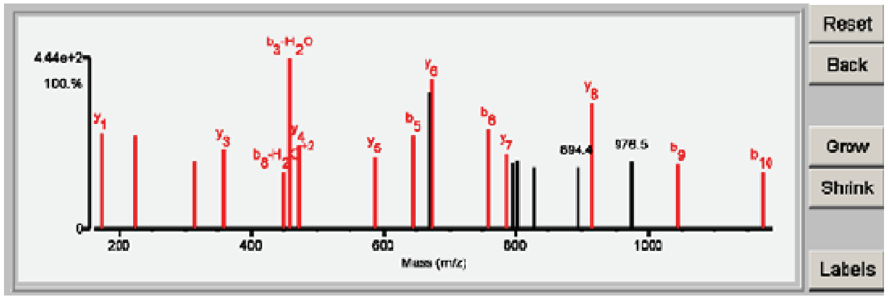
N33



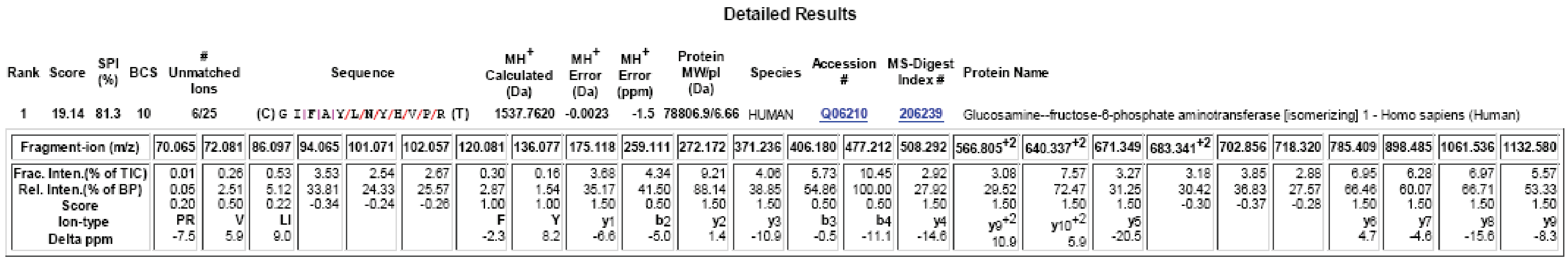
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.70	68.8	13	8/25	(P) H\S\Y P A\L\S A E\Q\K K/E/L/S/D/I/A L/R (I)	2614.2251	0.0177	6.8	39456.1/6.41	HUMAN	P09972	15997	Fructose-bisphosphate aldolase C - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	86.096	143.061	175.119	226.070	313.105	359.243	449.200^{+2}	458.144	472.321	587.345	644.255	671.781^{+2}	674.375	757.330	787.449	796.057^{+3}	803.349	826.065^{+3}	894.392	916.509	976.477	1044.417	1172.548
Frac. Inten.(% of TIC)	0.00	4.30	0.35	4.17	4.72	4.66	3.35	3.93	2.86	8.39	4.13	3.53	4.63	6.70	7.34	4.95	3.72	3.28	3.40	3.03	3.03	6.20	3.33	3.19	2.82
Rel. Inten.(% of BP)	0.05	51.28	4.13	49.76	56.31	55.56	39.92	46.83	34.06	100.00	49.27	42.09	55.18	79.87	87.56	58.97	44.37	39.11	40.60	36.09	36.15	73.96	39.74	37.98	33.63
Score	0.20	-0.51	0.22	-0.50	1.50	0.50	0.50	1.50	0.25	0.25	1.50	1.50	0.50	-0.80	1.50	0.50	1.50	-0.39	-0.41	-0.36	-0.36	1.50	-0.40	0.50	0.50
Ion-type	PR		LI		y_1	b_1	b_2	y_3	$b_8\text{-}H_2O^{+2}$	$b_3\text{-}H_2O$	y_4	y_5	b_5		y_6	b_6	y_7					y_8		b_9	b_{10}
Delta ppm	11.1		-4.9		-2.6	20.0	23.3	9.1	-0.6	-14.5	-6.1	-10.4	6.4		-12.0	-5.9	-22.5					-0.7		-28.6	36.7



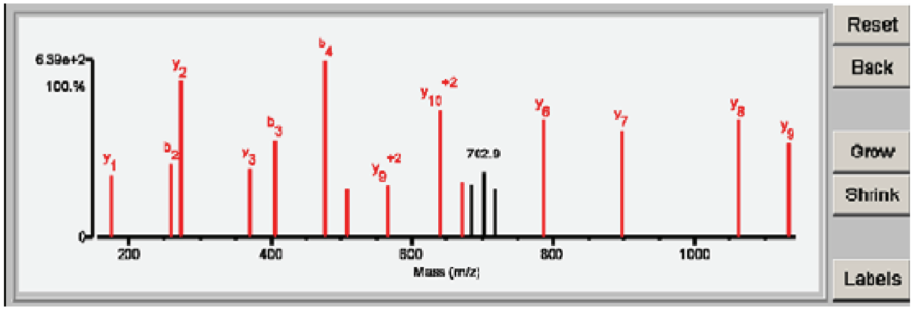
N34



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.14	81.3	10	6/25	(C) G I|F|A|Y/L/N/Y/E/V/P/R (T)	1537.7620	-0.0023	-1.5	78806.9/6.66	HUMAN	Q06210	206239	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.097	94.065	101.071	102.057	120.081	136.077	175.118	259.111	272.172	371.236	406.180	477.212	508.292	566.805^{+2}	640.337^{+2}	671.349	683.341^{+2}	702.856	718.320	785.409	898.485	1061.536	1132.580
Frac. Inten.(% of TIC)	0.01	0.26	0.53	3.53	2.54	2.67	0.30	0.16	3.68	4.34	9.21	4.06	5.73	10.45	2.92	3.08	7.57	3.27	3.18	3.85	2.88	6.95	6.28	6.97	5.57
Rel. Inten.(% of BP)	0.05	2.51	5.12	33.81	24.33	25.57	2.87	1.54	35.17	41.50	88.14	38.85	54.86	100.00	27.92	29.52	72.47	31.25	30.42	36.83	27.57	66.46	60.07	66.71	53.33
Score	0.20	0.50	0.22	-0.34	-0.24	-0.26	1.00	1.00	1.50	0.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50	1.50	-0.30	-0.37	-0.28	1.50	1.50	1.50	1.50
Ion-type	PR	V	LI				F	Y	y_1	b_2	y_2	y_3	b_3	b_4	y_4	y_9^{+2}	y_{10}^{+2}	y_5				y_6	y_7	y_8	y_9
Delta ppm	-7.5	5.9	9.0				-2.3	8.2	-6.6	-5.0	1.4	-10.9	-0.5	-11.1	-14.6	10.9	5.9	-20.5				4.7	-4.6	-15.6	-8.3



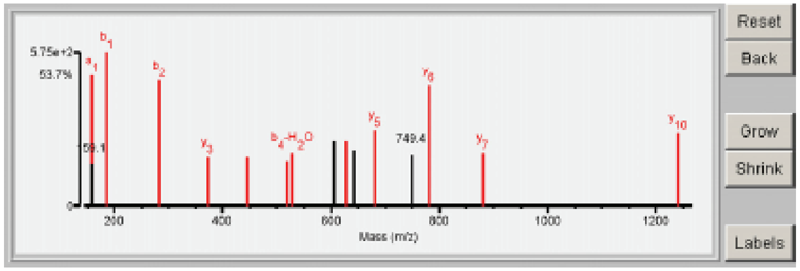
N35

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.84	68.7	8	8/24	(-) P|P\Y\T/V/V/Y/F/P V R (G)	1426.7236	0.0076	6.3	23356.0/5.43	HUMAN	P09211	227826	Glutathione S-transferase P - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.080	86.097	87.100	102.067	110.070	120.080	136.075	168.064	169.072	186.062	283.113
Frac. Inten.(% of TIC)	0.01	0.20	17.05	3.28	2.95	4.16	0.20	0.15	7.81	2.57	9.16	7.51
Rel. Inten.(% of BP)	0.04	1.19	100.00	19.23	17.33	24.41	1.15	0.89	45.82	15.09	53.75	44.07
Score	0.20	0.50	-1.00	-0.19	-0.17	-0.24	1.00	1.00	0.50	-0.15	0.50	0.50
Ion-type	PR	V					F	Y	a_1		b_1	b_2
Delta ppm	5.3	-6.6					-3.1	-7.3	-0.7		12.2	3.9

Fragment-Ion (m/z)	371.236	446.181	618.307	629.228	606.293^{+2}	628.276	641.339	681.357	749.402	780.446	879.478	1240.684
Frac. Inten.(% of TIC)	2.93	2.92	2.71	3.14	3.86	3.90	3.30	4.48	3.10	7.14	3.14	4.32
Rel. Inten.(% of BP)	17.20	17.15	15.91	18.41	22.63	22.85	19.35	26.29	18.16	41.89	18.42	25.34
Score	1.50	0.50	1.50	0.25	-0.23	0.25	-0.19	1.50	-0.18	1.50	1.50	1.50
Ion-type	y_3	b_3	y_4	b_4-H_2O		b_5-H_2O		y_5		y_6	y_7	y_{10}
Delta ppm	-14.4	12.3	-2.8	29.0		-9.9		-22.3		5.9	-34.8	17.4



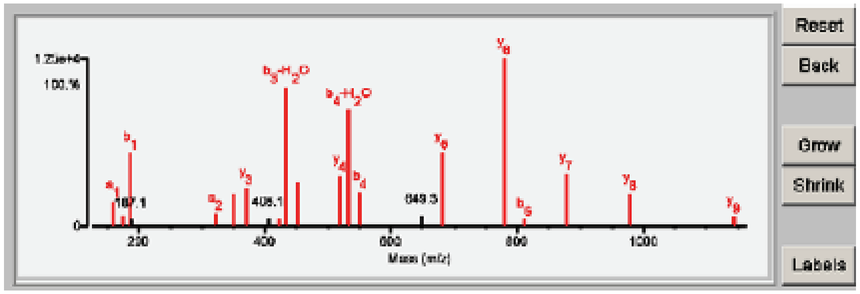
N36

Detailed Results

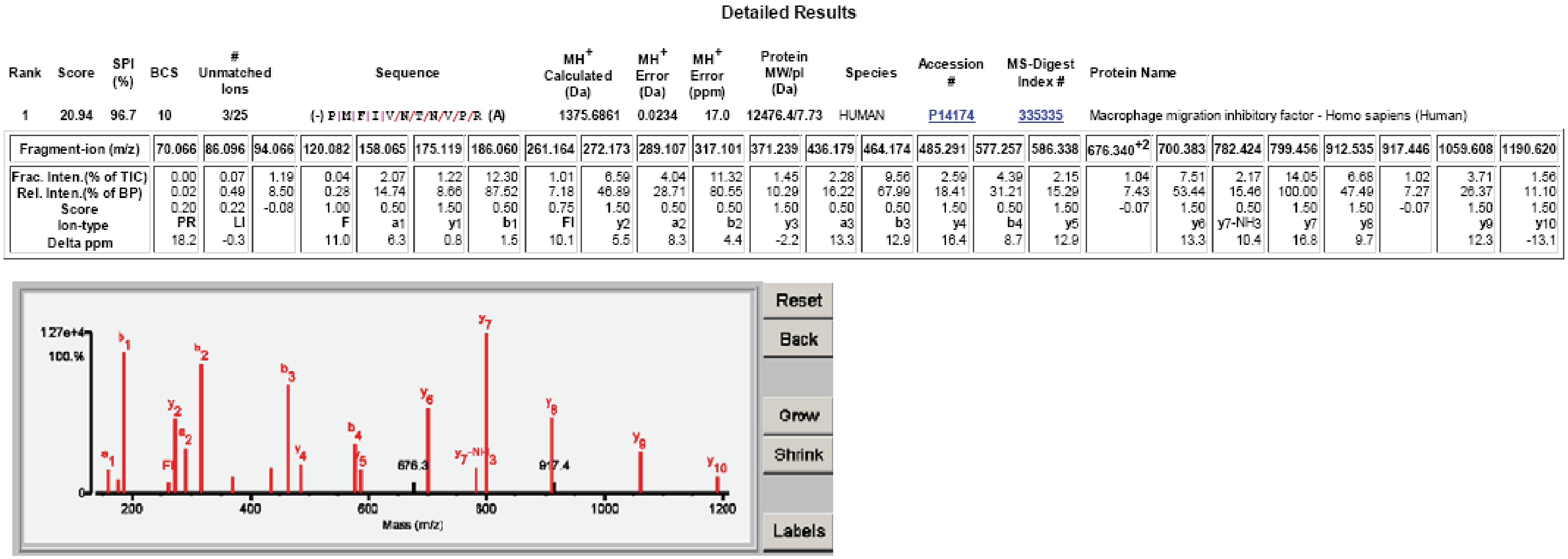
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.46	96.7	8	6/25	(P) P|Y|T|V|V/Y|F/P V/R (G)	1328.6708	0.0040	3.0	23356.0/5.43	HUMAN	P09211	227826	Glutathione S-transferase P - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	86.095	136.077	168.082	175.118	186.068	187.081	321.128	348.121	371.240	404.163	406.138	422.178
Frac. Inten.(% of TIC)	0.00	1.00	0.02	2.63	1.16	7.62	0.68	1.29	3.38	3.88	0.71	0.77	0.70
Rel. Inten.(% of BP)	0.01	5.78	0.12	15.22	6.69	44.05	3.95	7.48	19.56	22.40	4.10	4.44	4.05
Score	0.20	-0.06	1.00	0.50	1.50	0.50	-0.04	0.50	0.50	1.50	-0.04	-0.04	0.50
Ion-type	PR		Y	a_1	y_1	b_1		a_2	b_2	y_3			a_3
Delta ppm	13.9		8.2	-13.3	-4.9	-6.6		-6.3	-5.9	0.2			1.1

Fragment-Ion (m/z)	432.159	450.167	518.306	531.228	549.237	649.305	681.369	780.438	811.387	879.606	980.665	1143.812
Frac. Inten.(% of TIC)	14.43	4.53	5.21	12.06	3.47	1.16	7.65	17.30	0.74	5.35	3.27	0.98
Rel. Inten.(% of BP)	83.38	26.20	30.14	69.69	20.05	6.70	44.20	100.00	4.25	30.94	18.93	5.64
Score	0.25	0.50	1.50	0.25	0.50	-0.07	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	b_3-H_2O	b_3	y_4	b_4-H_2O	b_4		y_5	y_6	b_6	y_7	y_8	y_9
Delta ppm	-2.9	-7.4	-7.0	-0.9	-2.8		-4.8	-2.3	-4.4	-2.8	-1.1	-7.2



N37



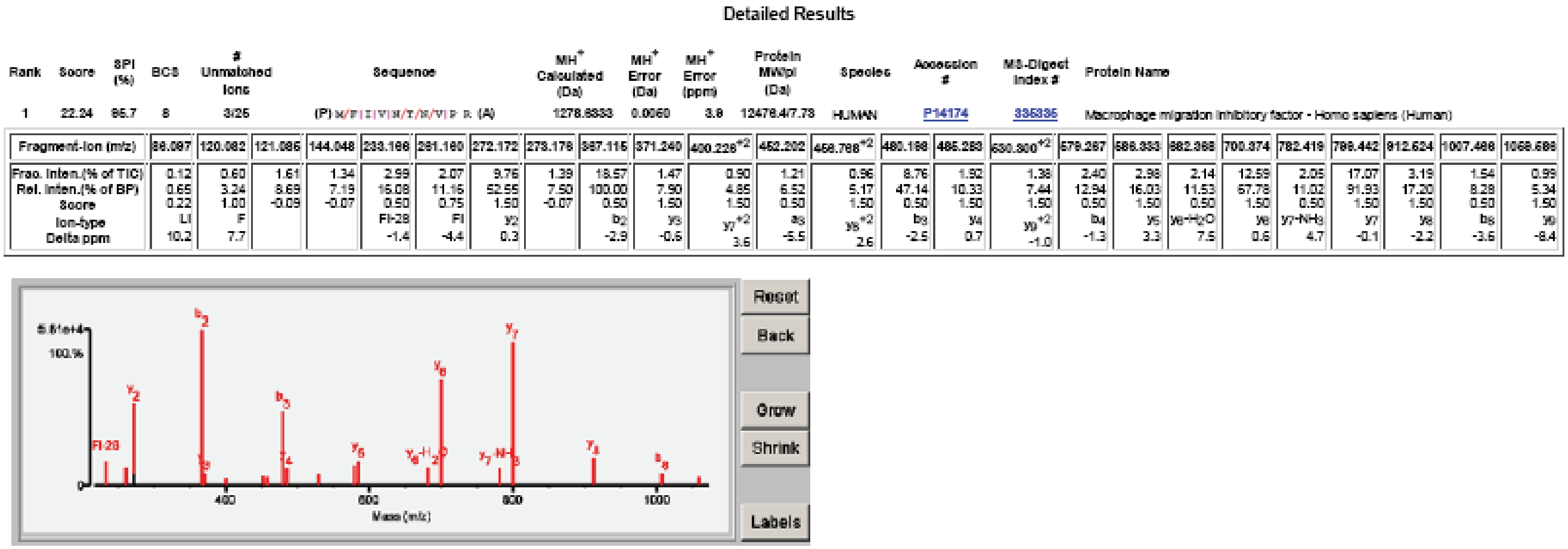
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.94	96.7	10	3/25	(-) P|M|F|I|V/N/T/N/V/P/R (A)	1375.6861	0.0234	17.0	12476.4/7.73	HUMAN	P14174	335335	Macrophage migration inhibitory factor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	86.096	94.066	120.082	158.065	175.119	186.060	261.164	272.173	289.107	317.101	371.239
Frac. Inten.(% of TIC)	0.00	0.07	1.19	0.04	2.07	1.22	12.30	1.01	6.59	4.04	11.32	1.45
Rel. Inten.(% of BP)	0.02	0.49	8.50	0.28	14.74	8.66	87.52	7.18	46.89	28.71	80.55	10.29
Score	0.20	0.22	-0.08	1.00	0.50	1.50	0.50	0.75	1.50	0.50	0.50	1.50
Ion-type	PR	LI		F	a1	y1	b1	FI	y2	a2	b2	y3
Delta ppm	18.2	-0.3		11.0	6.3	0.8	1.5	10.1	5.5	8.3	4.4	-2.2

Fragment-ion (m/z)	436.179	464.174	485.291	577.257	586.338	676.340^{+2}	700.383	782.424	799.456	912.535	917.446	1059.608	1190.620
Frac. Inten.(% of TIC)	2.28	9.56	2.59	4.39	2.15	1.04	7.51	2.17	14.05	6.68	1.02	3.71	1.56
Rel. Inten.(% of BP)	16.22	67.99	18.41	31.21	15.29	7.43	53.44	15.46	100.00	47.49	7.27	26.37	11.10
Score	0.50	0.50	1.50	0.50	1.50	-0.07	1.50	0.50	1.50	1.50	-0.07	1.50	1.50
Ion-type	a3	b3	y4	b4	y5		y6	y7-NH3	y7	y8		y9	y10
Delta ppm	13.3	12.9	16.4	8.7	12.9		13.3	10.4	16.8	9.7		12.3	-13.1

N38



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.24	95.7	8	3/25	(P) M/F|I|V|N/T/N/V|P R (A)	1278.6333	0.0050	3.8	12476.4/7.73	HUMAN	P14174	335335	Macrophage migration inhibitory factor - Homo sapiens (Human)

Fragment-ion (m/z)	86.097	120.082	121.086	144.048	233.166	261.160	272.172	273.176	367.115	371.240	400.226^{+2}	452.202
Frac. Inten.(% of TIC)	0.12	0.60	1.61	1.34	2.99	2.07	9.76	1.39	18.57	1.47	0.90	1.21
Rel. Inten.(% of BP)	0.65	3.24	8.69	7.19	16.08	11.16	52.55	7.50	100.00	7.90	4.85	6.52
Score	0.22	1.00	-0.09	-0.07	0.50	0.75	1.50	-0.07	0.50	1.50	1.50	0.50
Ion-type	LI	F			FI-28	FI	y_2		b_2	y_3	y_7^{+2}	a_3
Delta ppm	10.2	7.7			-1.4	-4.4	0.3		-2.9	-0.6	3.6	-5.5

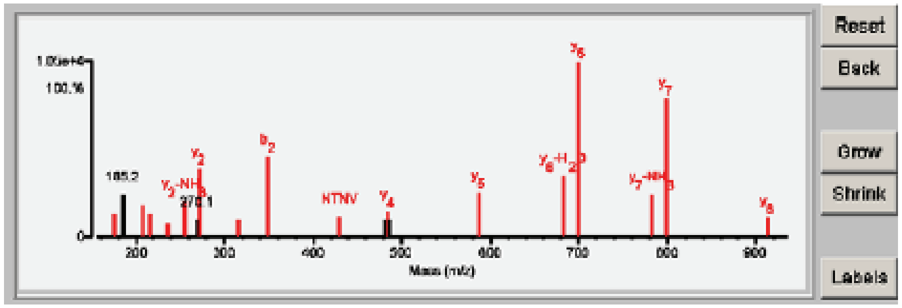
Fragment-ion (m/z)	456.766^{+2}	480.198	485.283	630.300^{+2}	579.267	586.333	682.368	700.374	782.419	799.442	912.524	1007.486	1068.686
Frac. Inten.(% of TIC)	0.96	8.76	1.92	1.38	2.40	2.98	2.14	12.59	2.05	17.07	3.19	1.54	0.99
Rel. Inten.(% of BP)	5.17	47.14	10.33	7.44	12.94	16.03	11.53	67.78	11.02	91.93	17.20	8.28	5.34
Score	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	0.50	1.50
Ion-type	y_8^{+2}	b_3	y_4	y_9^{+2}	b_4	y_5	y_6-H_2O	y_6	y_7-NH_3	y_7	y_8	b_8	y_9
Delta ppm	2.6	-2.5	0.7	-1.0	-1.3	3.3	7.5	0.6	4.7	-0.1	-2.2	-3.6	-8.4

N39

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.01	87.7	7	6/26	(M) F|I|V/N/T/N V/P/R (A)	1147.6828	0.0076	6.6	12476.4/7.73	HUMAN	P14174	335336	Macrophage migration inhibitory factor - Homo sapiens (Human)

Fragment-ion (m/z)	70.084	72.081	86.096	110.069	120.077	176.118	186.161	208.078	216.097	238.082	256.140	270.072	272.172	316.161	349.160	429.198	481.168	486.281	488.786^{+2}	586.334	682.353	700.374	782.411	799.447	912.621
Frac. Inten.(% of TIC)	0.00	0.20	1.41	2.25	0.16	2.51	4.56	3.41	2.49	1.52	3.69	1.84	7.16	1.80	8.40	2.10	1.82	2.53	1.80	4.70	6.42	18.43	4.53	14.39	1.90
Rel. Inten.(% of BP)	0.01	1.09	7.65	12.22	0.86	13.61	24.74	18.49	13.51	8.23	20.05	10.01	38.84	9.79	45.60	11.37	9.85	13.72	9.75	25.49	34.81	100.00	24.57	78.07	10.28
Score	0.20	0.50	0.22	-0.12	1.00	1.50	-0.25	0.50	0.75	0.50	0.50	-0.10	1.50	0.75	0.50	0.75	-0.10	1.50	-0.10	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	PR	V	LI		F	y_1		a_1	TN	b_1	y_2-NH_3		y_2	TNV	b_2	NTNV		y_4		y_5	y_6-H_2O	y_6	y_7-NH_3	y_7	y_8
Delta ppm	-8.9	7.3	-6.1		-28.9	-7.7		-8.5	-9.2	28.5	-19.1		2.1	-20.3	1.6	-28.7		-5.3		5.7	-14.2	0.3	-5.9	6.0	-5.4

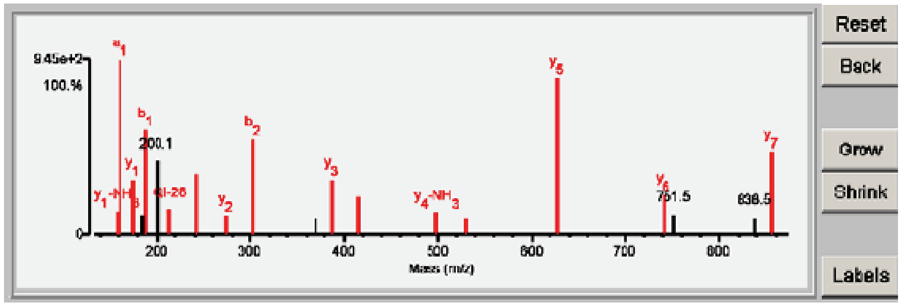


N40

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.72	83.6	7	7/25	(-) V|N|L|L\Q/I/V/R (D)	1042.6078	0.0012	1.1	6961.2/9.03	HUMAN	O75438	368007	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	84.083	86.097	87.054	158.088	160.078	175.119	185.167	188.072	200.140	214.153	242.145	274.188	302.118	370.171	387.207^{+2}	387.274	415.196	498.305	528.288	628.416	741.508	751.465	838.477	855.537
Frac. Inten.(% of TIC)	0.23	1.38	0.33	0.19	1.95	15.03	4.72	1.67	8.94	6.32	2.13	5.26	1.58	8.21	1.51	2.30	4.73	3.23	1.90	1.44	13.37	3.35	1.71	1.47	7.07
Rel. Inten.(% of BP)	1.51	9.18	2.19	1.29	12.98	100.00	31.39	11.13	59.51	42.08	14.19	34.99	10.51	54.66	10.06	15.31	31.45	21.50	12.62	9.55	88.99	22.29	11.37	9.75	47.06
Score	0.50	-0.09	0.22	0.33	0.50	0.50	1.50	-0.11	0.50	-0.42	0.50	0.75	1.50	0.50	-0.10	-0.15	1.50	0.50	0.50	0.50	1.50	1.50	-0.11	-0.10	1.50
Ion-type	V		LI	NR	y_1-NH_3	a_1	y_1		b_1		QI-28	QI	y_2	b_2			y_3	b_3	y_4-NH_3	b_4	y_5	y_6			y_7
Delta ppm	3.1		3.2	-14.8	-28.5	-12.9	0.8		-13.7		-14.9	-25.7	2.7	1.7			6.4	-13.9	3.7	2.8	3.5	13.0			-5.3



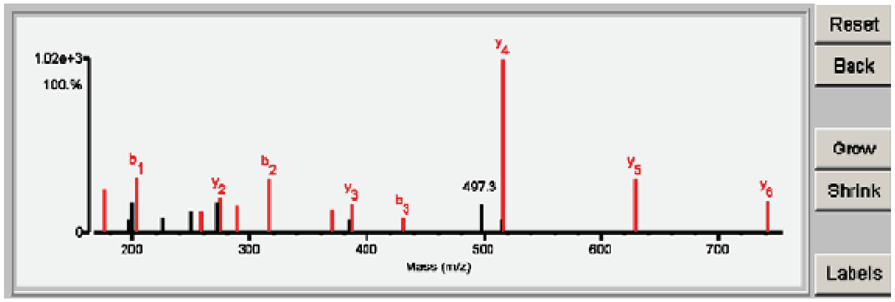
N41

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.40	71.5	6	11/25	(V) N|L|L|Q/I/V/R (D)	943.5393	0.0126	13.3	6961.2/9.03	HUMAN	O75438	368007	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.097	87.100	115.047	142.095	175.116	197.140	199.178	203.050	224.139	249.157	257.162	271.118
Frac. Inten.(% of TIC)	0.05	0.80	2.62	3.02	1.69	5.47	1.73	3.78	7.01	1.93	2.60	2.59	3.87
Rel. Inten.(% of BP)	0.23	3.71	12.09	13.95	7.83	25.26	7.98	17.48	32.36	8.89	12.02	11.98	17.89
Score	0.50	0.22	-0.12	-0.14	-0.08	1.50	-0.08	-0.17	0.50	-0.09	-0.12	0.50	-0.18
Ion-type	V	LI				y_1			b_1			y_2-NH_3	
Delta ppm	-16.3	6.7				-15.7			2.0			3.8	

Fragment-ion (m/z)	274.191	288.137	316.130	370.246	384.194	387.267	429.226	497.334	514.578	515.330	628.420	741.504
Frac. Inten.(% of TIC)	4.32	3.37	6.82	2.94	1.83	3.66	1.90	3.64	1.82	21.65	6.83	4.05
Rel. Inten.(% of BP)	19.95	15.58	31.50	13.58	8.45	16.91	8.77	16.82	8.39	100.00	31.56	18.71
Score	1.50	0.50	0.50	0.50	-0.08	1.50	0.50	-0.17	-0.08	1.50	1.50	1.50
Ion-type	y_2	a_2	b_2	y_3-NH_3		y_3	b_3			y_4	y_5	y_6
Delta ppm	13.6	-7.1	-10.0	1.9		-10.9	18.8			0.6	9.9	8.2



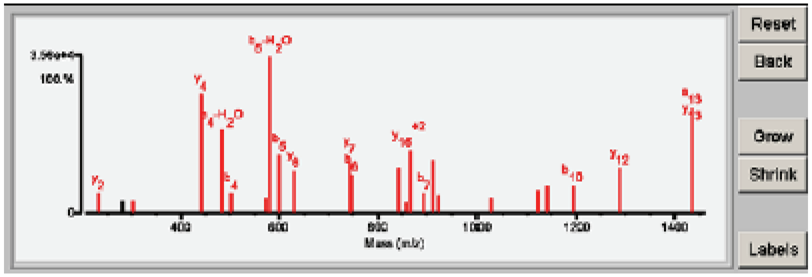
N42

Detailed Results

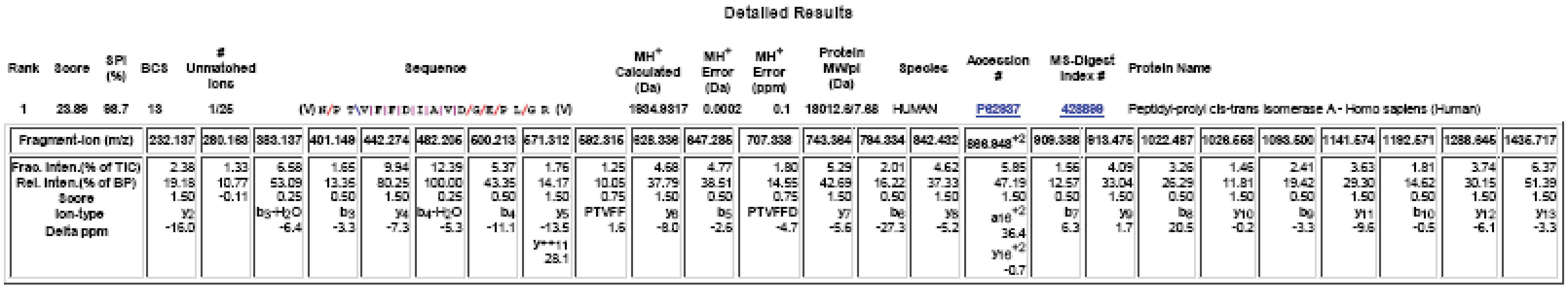
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.15	88.9	14	1/25	(-) V/N|P T\V|F|F|D/I|A|V/D/G/E/P L/G R (V)	2084.0001	0.0012	0.6	18012.6/7.68	HUMAN	P62937	428889	Peptidyl-prolyl cis-trans isomerase A - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	232.138	280.164	302.118	442.276	482.203	500.218	571.313	581.273	599.284	628.338	743.364	748.361
Frac. Inten.(% of TIC)	0.03	1.82	1.05	1.04	10.97	7.62	1.86	1.35	14.52	5.44	3.87	5.18	3.56
Rel. Inten.(% of BP)	0.18	12.55	7.33	7.18	75.53	52.47	12.78	9.34	100.00	37.48	26.67	35.64	24.54
Score	0.22	1.50	-0.07	0.50	1.50	0.25	0.50	1.50	0.25	0.50	1.50	1.50	0.50
Ion-type	LI	y_2		b_2	y_4	b_4-H_2O	b_4	a_5 y_5 y^{++}_{11}	b_5-H_2O	b_5	y_6	y_7	b_6
Delta ppm	-11.9	-11.7		1.7	-4.2	-9.9	-1.7	37.7 -11.1 30.6	-6.4	-4.4	-4.5	-5.3	-5.6

Fragment-ion (m/z)	842.430	857.931^{+2}	868.949^{+2}	883.430	913.469	923.988^{+2}	1028.538	1121.531	1141.577	1192.566	1288.646	1436.710
Frac. Inten.(% of TIC)	4.12	0.93	5.77	1.79	4.90	1.73	1.26	2.03	2.57	2.60	4.22	9.74
Rel. Inten.(% of BP)	28.40	6.39	39.76	12.33	33.74	11.94	8.71	13.99	17.72	17.91	29.06	67.09
Score	1.50	0.50	1.50	0.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y_8	y_{16}-H_2O^{+2}	y_{16}^{+2}	b_7	y_9	y_{17}^{+2}	y_{10}	b_9	y_{11}	b_{10}	y_{12}	a_{13} y_{13}
Delta ppm	-8.1	-14.3	0.3	7.3	-5.3	-4.9	-18.6	-3.4	-6.6	-4.4	-5.8	11.1 -8.3



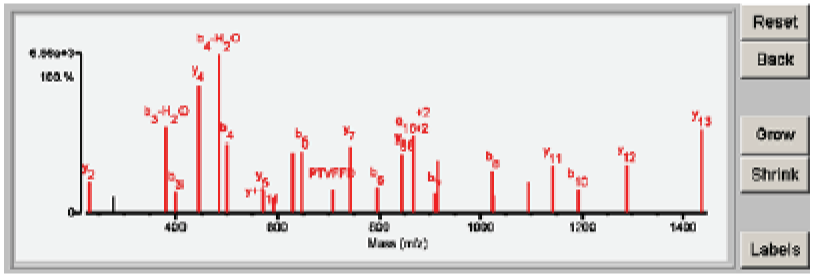
N43



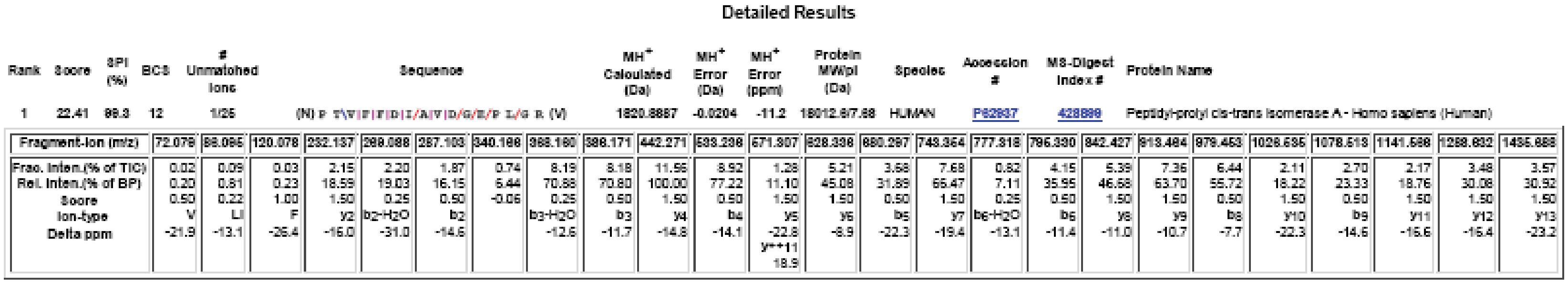
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.89	98.7	13	1/25	(V) N/P T\V|F|F|D|I|A|V|D/G/E/P L/G R (V)	1934.9317	0.0002	0.1	18012.6/7.68	HUMAN	P62937	428889	Peptidyl-prolyl cis-trans isomerase A - Homo sapiens (Human)

Fragment-Ion (m/z)	232.137	280.163	383.137	401.149	442.274	482.206	600.213	671.312	682.316	628.338	647.285	707.338	743.384	794.334	842.432	886.948^{+2}	909.388	913.475	1022.487	1026.668	1093.600	1141.674	1192.671	1288.845	1436.717
Frac. Inten.(% of TIC)	2.38	1.33	6.58	1.65	9.94	12.39	5.37	1.76	1.25	4.68	4.77	1.80	5.29	2.01	4.62	5.85	1.56	4.09	3.26	1.46	2.41	3.63	1.81	3.74	6.37
Rel. Inten.(% of BP)	19.18	10.77	53.09	13.35	80.25	100.00	43.35	14.17	10.05	37.79	38.51	14.55	42.69	16.22	37.33	47.19	12.57	33.04	26.29	11.81	19.42	29.30	14.62	30.15	51.39
Score	1.50	-0.11	0.25	0.50	1.50	0.25	0.50	1.50	0.75	1.50	0.50	0.75	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y_2		b_3-H_2O	b_3	y_4	b_4-H_2O	b_4	y_5 y++11	PTVFF	y_6	b_5	PTVFFD	y_7	b_6	y_8	a_{16}^{+2} y_{16}^{+2}	b_7	y_9	b_8	y_{10}	b_9	y_{11}	b_{10}	y_{12}	y_{13}
Delta ppm	-16.0		-6.4	-3.3	-7.3	-5.3	-11.1	-13.5 28.1	1.6	-8.0	-2.6	-4.7	-5.6	-27.3	-5.2	36.4 -0.7	6.3	1.7	20.5	-0.2	-3.3	-9.6	-0.5	-6.1	-3.3



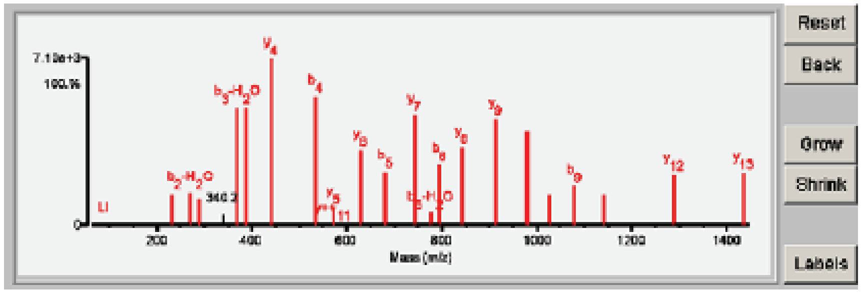
N44



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.41	99.3	12	1/25	(N) P T\V|F|F|D|I/A|V|D/G/E/P L/G R (V)	1820.8887	-0.0204	-11.2	18012.6/7.68	HUMAN	P62937	428889	Peptidyl-prolyl cis-trans isomerase A - Homo sapiens (Human)

Fragment-Ion (m/z)	72.079	86.096	120.078	232.137	269.088	287.103	340.166	368.160	386.171	442.271	533.238	571.307	628.338	680.297	743.364	777.318	796.330	842.427	913.464	979.453	1026.635	1078.513	1141.598	1288.632	1435.688
Frac. Inten.(% of TIC)	0.02	0.09	0.03	2.15	2.20	1.87	0.74	8.19	8.18	11.56	8.92	1.28	5.21	3.68	7.68	0.82	4.15	5.39	7.36	6.44	2.11	2.70	2.17	3.48	3.57
Rel. Inten.(% of BP)	0.20	0.81	0.23	18.59	19.03	16.15	6.44	70.88	70.80	100.00	77.22	11.10	45.08	31.89	66.47	7.11	35.95	46.68	63.70	55.72	18.22	23.33	18.76	30.08	30.92
Score	0.50	0.22	1.00	1.50	0.25	0.50	-0.06	0.25	0.50	1.50	0.50	1.50	1.50	0.50	1.50	0.25	0.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	V	LI	F	y_2	b_2-H_2O	b_2		b_3-H_2O	b_3	y_4	b_4	y_5 y++11	y_6	b_5	y_7	b_6-H_2O	b_6	y_8	y_9	b_8	y_{10}	b_9	y_{11}	y_{12}	y_{13}
Delta ppm	-21.9	-13.1	-26.4	-16.0	-31.0	-14.6		-12.6	-11.7	-14.8	-14.1	-22.8 18.9	-8.9	-22.3	-19.4	-13.1	-11.4	-11.0	-10.7	-7.7	-22.3	-14.6	-16.6	-16.4	-23.2



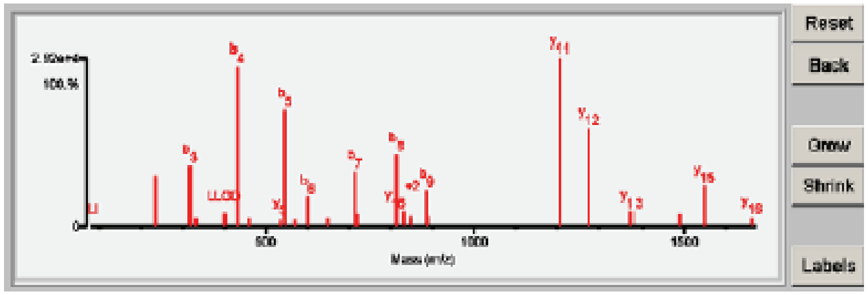
N45

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	28.87	100.0	13	0/25	(P) G G L|L|L|G|D|V|A|P N F/E/A/N/T T/V/G R (I)	2089.0383	0.0019	0.8	25035.1/6.00	HUMAN	P30041	431821	Peroxiredoxin-6 - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	232.141	316.131	331.207	399.221	429.217	456.245	533.302	542.299	569.328	599.321	647.342	714.347
Frac. Inten.(% of TIC)	0.03	4.88	5.95	0.94	1.35	15.48	0.91	0.75	11.38	0.71	2.82	0.92	5.38
Rel. Inten.(% of BP)	0.16	29.98	36.56	5.75	8.28	95.08	5.62	4.60	69.90	4.39	17.34	5.67	33.06
Score	0.22	1.50	0.50	1.50	0.75	0.50	0.75	1.50	0.50	0.75	0.50	1.50	0.50
Ion-type	LI	y_2	b_3	y_3	LLGD	b_4	LGDVA	y_5	b_5	LLGDVA	b_6	y_6	b_7
Delta ppm	-4.9	0.4	-8.7	-4.0	-10.0	-2.8	-3.9	-3.7	-4.4	-7.8	-4.4	-7.4	-5.0

Fragment-ion (m/z)	718.378	813.416	830.917^{+2}	847.418	884.464	887.468^{+2}	1205.588	1276.626	1375.693	1490.708	1547.742	1660.832
Frac. Inten.(% of TIC)	1.15	7.05	1.48	1.07	3.58	1.05	16.28	9.53	1.40	1.13	3.92	0.85
Rel. Inten.(% of BP)	7.09	43.30	9.09	6.57	22.01	6.47	100.00	58.51	8.62	6.95	24.11	5.19
Score	1.50	0.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_7	b_8	y_{16}^{+2}	y_8	b_9	y_{17}^{+2}	y_{11}	y_{12}	y_{13}	y_{14}	y_{15}	y_{16}
Delta ppm	-9.2	-3.3	-1.2	-9.6	-2.2	-2.1	-2.6	-2.5	-2.2	-10.3	-1.8	1.9



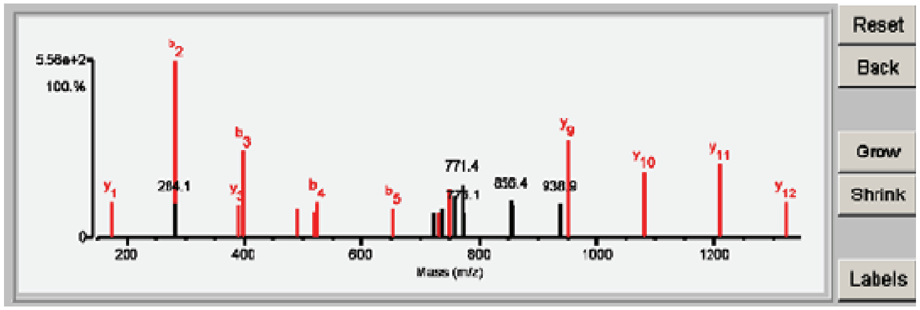
N46

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.71	72.0	9	9/25	(P) G/H|L|Q|E|G F/G C V/V/T N/R (F)	1604.7308	0.0039	2.4	44965.6/8.66	HUMAN	Q8NC51	399931	Plasminogen activator inhibitor 1 RNA-binding protein - Homo sapiens (Human)

Fragment-ion (m/z)	86.095	110.067	175.120	283.084	284.089	390.200	396.168	489.280	519.240	524.227	653.253	724.408	730.338^{+2}
Frac. Inten.(% of TIC)	0.07	0.16	3.18	15.90	3.04	2.94	7.85	2.65	2.32	3.16	2.64	2.27	2.23
Rel. Inten.(% of BP)	0.42	0.98	20.03	100.00	19.15	18.52	49.37	16.68	14.59	19.90	16.59	14.28	14.01
Score	0.22	1.00	1.50	0.50	-0.19	1.50	0.50	1.50	0.75	0.50	0.50	-0.14	1.50
Ion-type	LI	H	y_1	b_2		y_3	b_3	y_4	QEGFG	b_4	b_5		y_{13}^{+2}
Delta ppm	-21.2	-36.1	4.3	-12.5		-23.5	-6.6	3.3	37.0	-4.9	-30.0		-28.5

Fragment-ion (m/z)	737.341^{+2}	748.366	755.812^{+2}	771.368	775.087	856.383	857.879	938.898	952.449	1081.501	1209.558	1322.644
Frac. Inten.(% of TIC)	2.68	4.43	3.76	4.79	2.22	3.27	2.90	3.05	8.73	5.89	6.62	3.24
Rel. Inten.(% of BP)	16.86	27.88	23.67	30.12	13.98	20.57	18.23	19.18	54.94	37.03	41.66	20.35
Score	-0.17	1.50	-0.24	-0.30	-0.14	-0.21	-0.18	-0.19	1.50	1.50	1.50	1.50
Ion-type		y_7							y_9	y_{10}	y_{11}	y_{12}
Delta ppm		-14.3							-18.6	-7.7	-8.3	-6.5



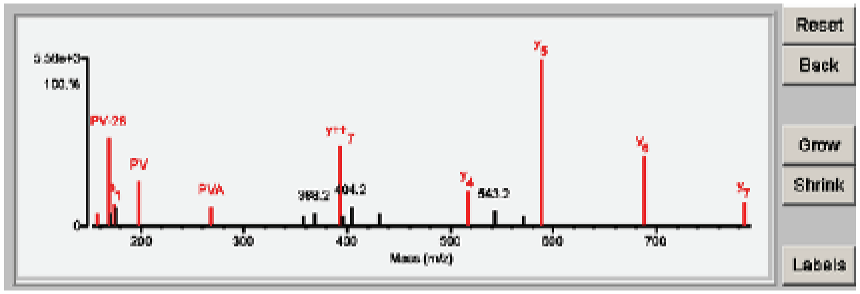
N47

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.33	75.8	4	12/25	(P) L/P/V/A/L Q T R (L)	985.5499	0.0058	5.9	30472.4/5.82	HUMAN	O60828	431011	Polyglutamine-binding protein 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.085	72.080	86.096	120.079	130.048	136.076	168.093	169.133	170.139	174.093	176.110	197.128	268.168
Frac. Inten.(% of TIC)	0.02	0.05	0.39	4.07	1.53	2.12	1.55	11.83	1.75	2.94	2.35	6.12	2.60
Rel. Inten.(% of BP)	0.10	0.22	1.73	18.16	6.83	9.45	6.92	52.79	7.80	13.11	10.50	27.32	11.60
Score	0.20	0.50	0.22	-0.18	-0.07	-0.09	0.50	0.50	-0.08	0.50	-0.10	0.75	0.75
Ion-type	PR	V	LI				y$_1$-NH$_3$	PV-28		a$_1$		PV	PVA
Delta ppm	-1.8	-14.9	-10.8				0.6	-9.7		-14.4		-20.0	3.1

Fragment-Ion (m/z)	357.152	368.221	392.738	395.235	404.228^{+2}	432.167	517.311	543.223	570.287	588.350	687.413	784.476
Frac. Inten.(% of TIC)	1.50	1.76	10.66	1.51	2.63	1.70	4.65	2.03	1.48	22.40	9.30	3.08
Rel. Inten.(% of BP)	6.68	7.85	47.59	6.73	11.72	7.58	20.74	9.05	6.61	100.00	41.53	13.76
Score	-0.07	-0.08	1.50	-0.07	-0.12	-0.08	1.50	-0.09	-0.07	1.50	1.50	1.50
Ion-type			y^{++}7				y$_4$			y$_5$	y$_6$	y$_7$
Delta ppm			1.0				3.7			5.6	-2.3	9.6



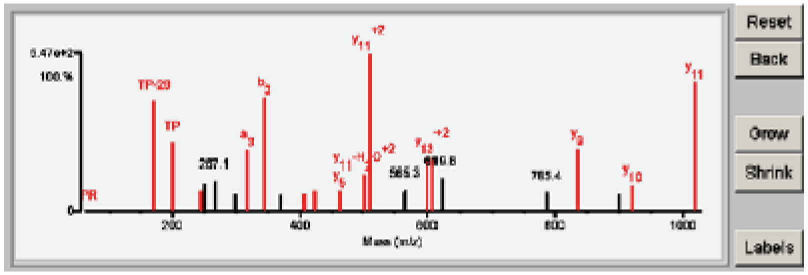
N48

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.38	82.1	7	8/25	(P) G/P\T|P/S/G T N V/G/S S G R (S)	1381.6114	0.0016	1.1	9974.6/11.57	HUMAN	P60468	686058	Protein transport protein Sec61 subunit beta - Homo sapiens (Human)

Fragment-Ion (m/z)	70.088	171.110	189.104	243.078	249.054	287.067	288.117	316.129	344.132	369.842	406.202	423.158	483.210
Frac. Inten.(% of TIC)	0.00	9.57	5.86	1.79	2.35	2.62	1.62	5.17	9.77	1.49	1.59	1.77	1.85
Rel. Inten.(% of BP)	0.02	70.06	42.90	13.12	17.17	19.18	11.88	37.87	71.47	10.93	11.64	12.98	13.54
Score	0.20	0.50	0.75	0.50	-0.17	-0.19	-0.12	0.50	0.50	-0.11	1.50	0.25	1.50
Ion-type	PR	TP-28	TP	b$_2$				a$_3$	b$_3$		y$_4$	b$_4$-H$_2$O	y$_5$
Delta ppm	35.3	-22.8	-23.2	-12.7				-13.8	10.9		-7.3	-33.9	-34.6

Fragment-Ion (m/z)	500.738^{+2}	509.743^{+2}	583.348	586.288^{+2}	589.776^{+2}	608.814^{+2}	619.808	786.383	834.385	900.038	921.422	1018.507
Frac. Inten.(% of TIC)	3.16	13.67	1.66	1.98	4.51	4.62	2.90	1.70	5.30	1.61	2.27	11.15
Rel. Inten.(% of BP)	23.15	100.00	12.13	14.49	33.00	33.80	21.23	12.45	38.78	11.77	16.64	81.61
Score	0.50	1.50	-0.12	-0.14	0.50	1.50	-0.21	-0.12	1.50	-0.12	1.50	1.50
Ion-type	y$_{11}$-H$_2$O^{+2}	y$_{11}$$^{+2}$			y$_{13}$-H$_2$O^{+2}	y$_{13}$$^{+2}$			y$_9$		y$_{10}$	y$_{11}$
Delta ppm	-11.1	-11.3			-30.3	23.9			-13.3		-18.1	15.6

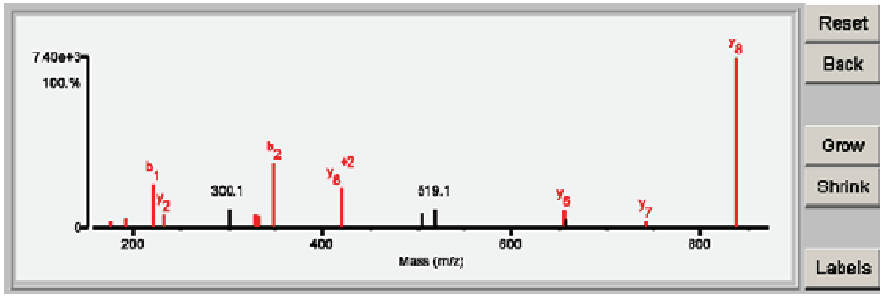


N49

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.47	71.5	8	10/25	(V) M\E\K/P/S/P L L/V/G/R (E)	1449.7051	0.0080	5.5	52164.5/5.37	HUMAN	Q13283	194989	Ras GTPase-activating protein-binding protein 1 - Homo sapiens (Human)
1	14.47	71.5	8	10/25	(V) M\E\K/P/S/P L L/V/G/R (E)	1449.7051	0.0080	5.5	54121.4/5.41	HUMAN	Q9UN86	194995	Ras GTPase-activating protein-binding protein 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.081	86.096	94.067	102.055	136.074	143.062	144.048	175.121	192.051	220.048	232.144	300.098	327.716	331.207	349.089	419.766^{+2}	504.793^{+2}	519.138	654.429	656.371^{+2}	741.452	838.517	1008.569
Frac. Inten.(% of TIC)	0.00	0.05	5.38	0.13	2.25	0.13	1.54	1.51	3.73	1.53	2.00	7.88	2.32	3.53	2.38	2.21	11.50	6.99	2.70	3.56	3.12	1.76	1.31	30.00	2.48
Rel. Inten.(% of BP)	0.01	0.16	17.94	0.44	7.50	0.44	5.15	5.03	12.43	5.10	6.67	26.25	7.73	11.76	7.95	7.36	38.33	23.29	8.99	11.88	10.39	5.88	4.35	100.00	8.28
Score	0.20	0.50	-0.18	0.22	-0.07	1.00	-0.05	-0.05	-0.12	1.50	0.50	0.50	1.50	-0.12	1.50	1.50	0.50	1.50	-0.09	-0.12	1.50	-0.06	1.50	1.50	-0.08
Ion-type	PR	V		LI		E				y1	a1	b1	y2		y++6	y3	b2	y8^{+2}			y6		y7	y8	
Delta ppm	12.5	-1.0		-3.8		-0.5				12.3	-4.8	4.8	14.6		-6.4	-5.5	-3.0	11.5			-1.3		-12.6	3.4	

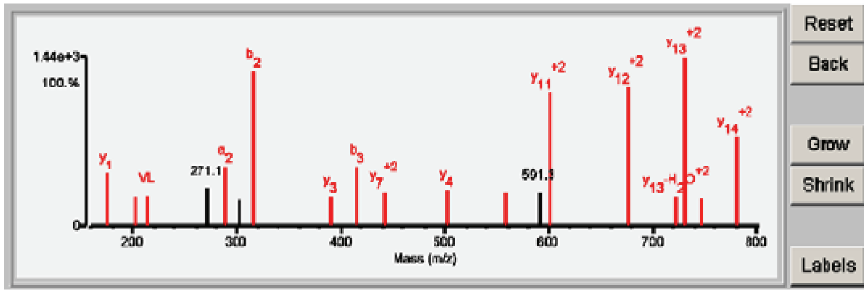


N50

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.08	91.9	11	3/25	(P) M\I|V|L/F/S/G S S/H/Q D/L/S Q/R (V)	1875.9018	0.0126	6.7	34769.3/6.15	HUMAN	P11908	436229	Ribose-phosphate pyrophosphokinase 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.080	86.097	101.070	110.071	120.080	175.117	203.048	213.156	271.110	288.140	302.182	316.135	390.209	415.199	442.228^{+2}	503.293	557.777	591.277	601.287^{+2}	674.817^{+2}	722.350^{+2}	731.362^{+2}	746.371	780.898^{+2}
Frac. Inten.(% of TIC)	0.00	0.14	0.81	0.07	0.17	0.19	4.27	2.46	2.51	3.14	4.94	2.21	12.65	2.40	4.84	2.80	2.88	2.73	2.77	10.90	11.40	2.37	13.78	2.35	7.21
Rel. Inten.(% of BP)	0.02	1.02	5.90	0.48	1.23	1.35	30.95	17.86	18.24	22.77	35.84	16.04	91.79	17.43	35.09	20.32	20.91	19.82	20.13	79.09	82.71	17.18	100.00	17.05	52.30
Score	0.20	0.50	0.22	0.50	1.00	1.00	1.50	0.50	0.75	-0.23	0.50	-0.16	0.50	1.50	0.50	1.50	1.50	1.50	-0.20	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	PR	V	LI	QK	H	F	y1	b1	VL		a2		b2	y3	b3	y7^{+2}	y4	y++10		y11^{+2}	y12^{+2}	y13-H$_2$O^{+2}	y13^{+2}	y6	y14^{+2}
Delta ppm	-20.3	-8.0	4.3	-5.3	-6.1	-6.5	-11.1	-9.8	-20.9		3.3		5.5	-2.7	-8.1	11.9	-2.0	20.9		9.1	1.6	-3.5	6.2	-11.4	7.7



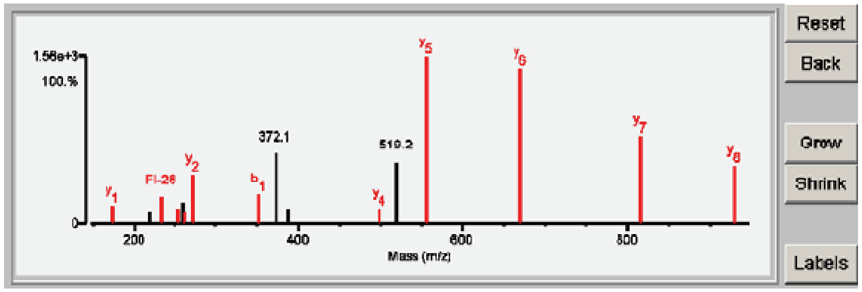
N51

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.25	66.7	7	11/25	(V) K|L/F/I/G/N L/P/R (E)	1280.6642	0.0045	3.5	40149.8/6.28	HUMAN	Q9BQ04	470753	RNA-binding protein 4B - Homo sapiens (Human)
1	12.25	66.7	7	11/25	(V) K|L/F/I/G/N L/P/R (E)	1280.6642	0.0045	3.5	40314.1/6.61	HUMAN	Q9BWF3	470765	RNA-binding protein 4 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	84.080	86.097	87.101	94.064	95.068	120.080	175.120	219.093	233.164	255.147	259.056
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -6.1	2.73 15.78 -0.16	0.60 3.48 0.22 LI 12.5	1.53 8.82 -0.09	5.60 32.34 -0.32	1.21 6.97 -0.07	0.13 0.75 1.00 F -9.8	1.92 11.08 1.50 y1 6.6	1.47 8.48 -0.08	2.94 16.99 0.50 FI-28 -10.5	1.62 9.34 0.50 y2-NH$_3$ 6.8	2.29 13.22 -0.13

Fragment-ion (m/z)	260.055	261.163	272.171	352.115	372.138	388.107	499.285	519.214	556.320	669.403	816.465	929.562	1187.643
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.21 6.99 -0.07	1.46 8.45 0.75 FI 6.7	5.11 29.54 1.50 y2 -4.1	2.98 17.19 0.50 b1 -2.5	7.39 42.71 -0.43	1.57 9.06 -0.09	1.50 8.66 1.50 y4 -28.3	6.40 36.96 -0.37	17.31 100.00 1.50 y5 0.2	16.01 92.47 1.50 y6 -2.6	9.06 52.31 1.50 y7 -9.4	6.02 34.78 1.50 y8 5.9	1.95 11.27 -0.11



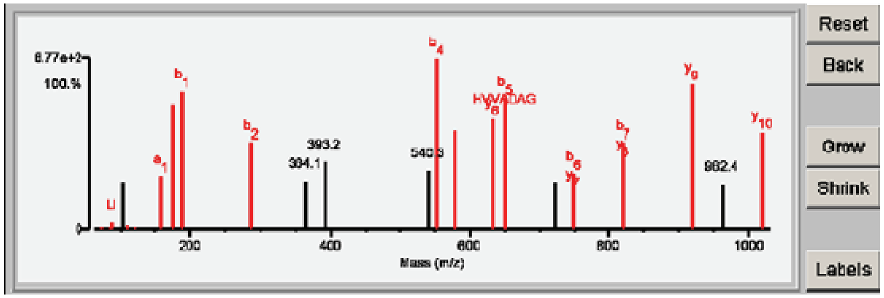
N52

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.32	80.7	9	6/25	(A) P\V\E/H|V|V|A|D/A G A F L/R (H)	1568.7890	0.0055	3.5	46675.2/6.72	HUMAN	Q9ULX3	374303	RNA-binding protein NOB1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.079	84.044	86.096	102.053	104.058	110.071	120.080	158.063	175.116	186.057	285.132
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.01 0.09 0.20 PR -10.4	0.14 1.34 0.50 V -26.0	0.15 1.39 1.00 E -2.3	0.52 4.94 0.22 LI -1.5	0.09 0.82 E	2.88 27.58 -0.28	0.25 2.42 1.00 H -6.1	0.10 0.94 1.00 F -6.5	3.28 31.43 0.50 a1 -9.5	7.65 73.31 1.50 y1 -16.9	8.47 81.18 0.50 b1 -13.0	5.28 50.65 0.50 b2 12.8

Fragment-ion (m/z)	364.112	393.203	540.262	551.231	578.317^{+2}	634.363	650.306	723.350^{+2}	749.384	820.413	919.496	962.431	1018.554
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.99 28.64 -0.29	4.12 39.54 -0.40	3.63 34.82 -0.35	10.43 100.00 0.50 b4 2.3	6.00 57.54 1.50 y11^{+2} -0.9	6.73 64.53 1.50 y6 -6.8	8.01 76.74 0.75 b5 13.0 HVVADAG -31.6	2.88 27.62 -0.28	3.46 33.16 1.50 b6 23.5 y7 -13.7	5.28 50.59 1.50 b7 12.0 y8 -22.0	8.86 84.88 1.50 y9 -4.1	2.84 27.24 -0.27	5.97 57.20 1.50 y10 -13.4

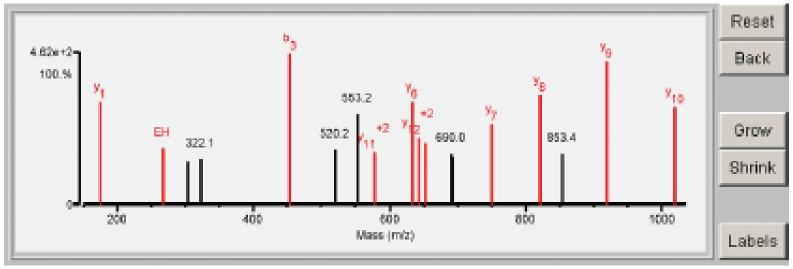


N53

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.43	67.9	8	9/25	(P) Y/E/H|V/V|A/D/A G A F L/R (H)	1471.7362	0.0067	3.9	46876.2/6.72	HUMAN	Q9ULX3	374303	RNA-binding protein NOB1 - Homo sapiens (Human)

Fragment-ion (m/z)	60.043	70.064	72.078	86.096	94.066	110.072	120.079	176.122	287.111	304.130	322.136	464.178	520.248+2	553.238+2	578.323+2	634.369	642.830+2	662.323	690.040	692.889	749.393	820.441	853.380	919.482	1018.558
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.78 38.18 -0.38	0.00 0.04 0.20 PR -17.5	0.22 2.19 0.50 V -37.1	0.58 5.88 0.22 LI -4.9	3.22 32.57 -0.33	0.43 4.35 1.00 H 8.4	0.09 0.89 1.00 F -16.5	6.69 67.58 1.50 y_1 19.7	3.70 37.42 0.75 EH 2.3	2.86 28.91 -0.29	3.05 30.79 -0.31	9.89 100.00 0.50 b_3 4.5	3.56 35.97 -0.36	5.86 59.26 -0.59	3.44 34.80 1.50 y_{11}^{+2} 11.1	6.64 67.15 1.50 y_6 3.4	4.34 43.84 1.50 y_{12}^{+2} -12.9	4.03 40.78 0.50 b_5 14.9	3.32 33.59 -0.34	3.08 31.18 -0.31	5.21 52.65 1.50 y_7 -1.3	7.08 71.55 1.50 y_8 11.4	3.33 33.65 -0.34	9.32 94.24 1.50 y_9 -8.3	6.28 63.49 1.50 y_{10} -8.7

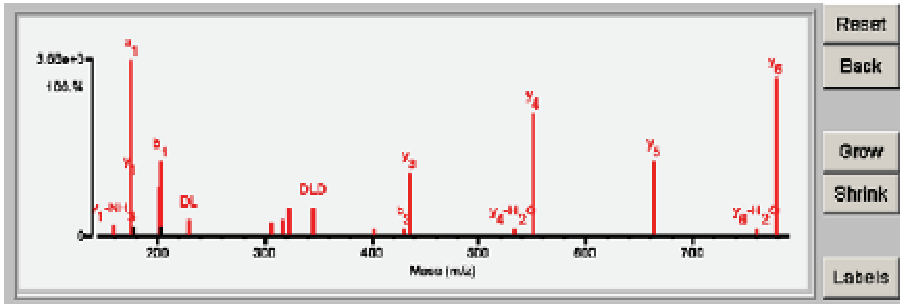


N54

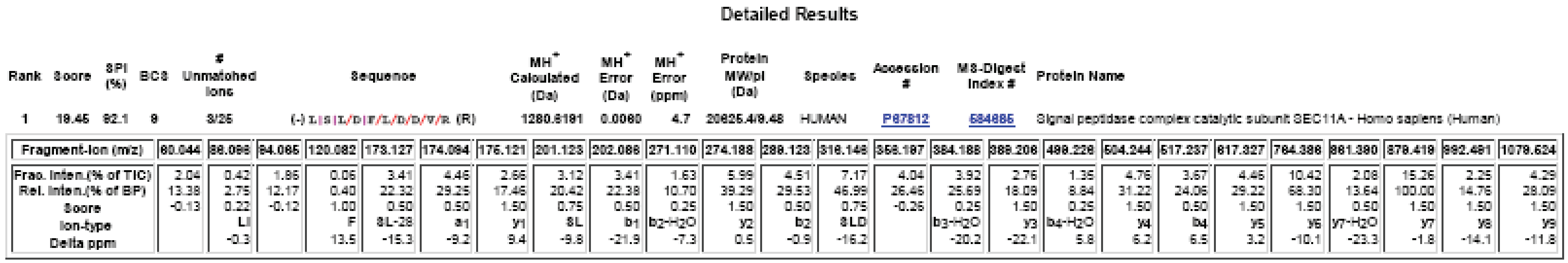
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.44	94.9	6	6/25	(V) L|D|L|D/L/F/R (V)	879.4917	0.0022	2.2	58777.6/6.05	HUMAN	P49591	629417	Seryl-tRNA synthetase, cytoplasmic - Homo sapiens (Human)

Fragment-ion (m/z)	86.097	88.039	94.063	120.081	132.103	168.094	174.095	175.118	177.046	201.123	202.088	203.098	229.115	305.162	317.108	322.185	344.147	402.196	430.204	435.287	532.287	560.297	663.387	780.380	778.409
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.69 3.86 0.22 LI 9.0	1.02 5.75 -0.06	1.13 6.37 -0.06	0.05 0.29 1.00 F 4.4	1.02 5.72 -0.06	1.20 6.71 0.50 y_1-NH_3 6.9	17.81 100.00 0.50 a_1 -5.2	5.82 32.71 1.50 y_1 -4.9	0.92 5.15 -0.05	4.93 27.70 0.50 DL-28 -6.8	7.72 43.37 0.50 b_1 -6.1	1.00 5.60 -0.06	1.68 9.46 0.75 DL -20.4	1.43 8.04 0.50 y_2-NH_3 4.5	1.77 9.92 0.50 b_2 -29.2	2.90 16.28 1.50 y_2 -6.4	3.02 16.98 0.75 DLD 3.4	0.78 4.36 0.50 a_3 -29.9	0.82 4.59 0.50 b_3 4.6	6.46 36.26 1.50 y_3 -9.7	0.83 4.68 0.50 y_4-H_2O -1.0	12.53 70.40 1.50 y_4 -2.7	7.70 43.22 1.50 y_5 7.5	0.80 4.47 0.50 y_6-H_2O -25.0	15.98 89.73 1.50 y_6 -0.6



N55

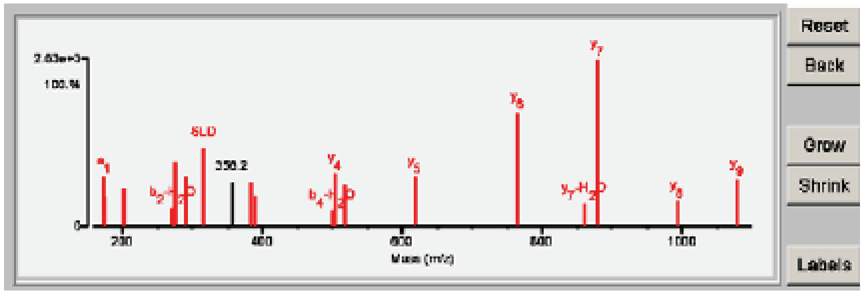


Detailed Results

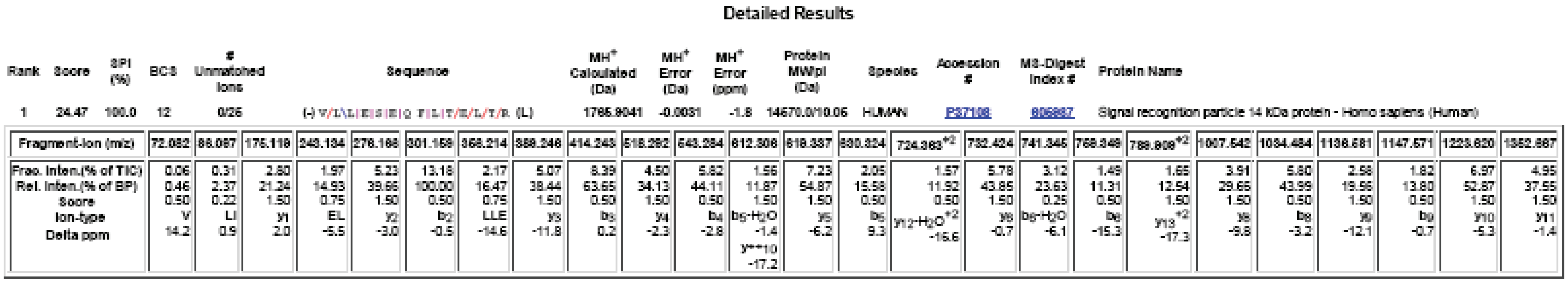
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.45	92.1	9	3/26	(-) L|S|L/D|F/L/D/D/V/R (R)	1280.6191	0.0060	4.7	20625.4/9.48	HUMAN	P67812	684685	Signal peptidase complex catalytic subunit SEC11A - Homo sapiens (Human)

Fragment-Ion (m/z)	60.044	86.096	94.065	120.082	173.127	174.094	175.121	201.123	202.086	271.110	274.188	288.123	316.146
Frac. Inten.(% of TIC)	2.04	0.42	1.86	0.06	3.41	4.46	2.66	3.12	3.41	1.63	5.99	4.51	7.17
Rel. Inten.(% of BP)	13.38	2.75	12.17	0.40	22.32	29.25	17.46	20.42	22.38	10.70	39.29	29.53	46.99
Score	-0.13	0.22	-0.12	1.00	0.50	0.50	1.50	0.75	0.50	0.25	1.50	0.50	0.75
Ion-type		LI		F	SL-28	a_1	y_1	SL	b_1	b_2-H_2O	y_2	b_2	SLD
Delta ppm		-0.3		13.5	-15.3	-9.2	9.4	-9.8	-21.9	-7.3	0.5	-0.9	-16.2

Fragment-Ion (m/z)	356.187	384.188	389.206	499.226	504.244	517.237	617.327	764.386	861.380	879.419	992.491	1079.524
Frac. Inten.(% of TIC)	4.04	3.92	2.76	1.35	4.76	3.67	4.46	10.42	2.08	15.26	2.25	4.29
Rel. Inten.(% of BP)	26.46	25.69	18.09	8.84	31.22	24.06	29.22	68.30	13.64	100.00	14.76	28.09
Score	-0.26	0.25	1.50	0.25	1.50	0.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type		b_3-H_2O	y_3	b_4-H_2O	y_4	b_4	y_5	y_6	y_7-H_2O	y_7	y_8	y_9
Delta ppm		-20.2	-22.1	5.8	6.2	6.5	3.2	-10.1	-23.3	-1.8	-14.1	-11.8



N56

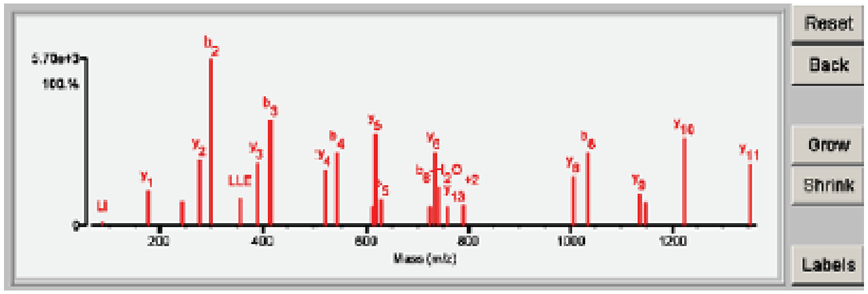


Detailed Results

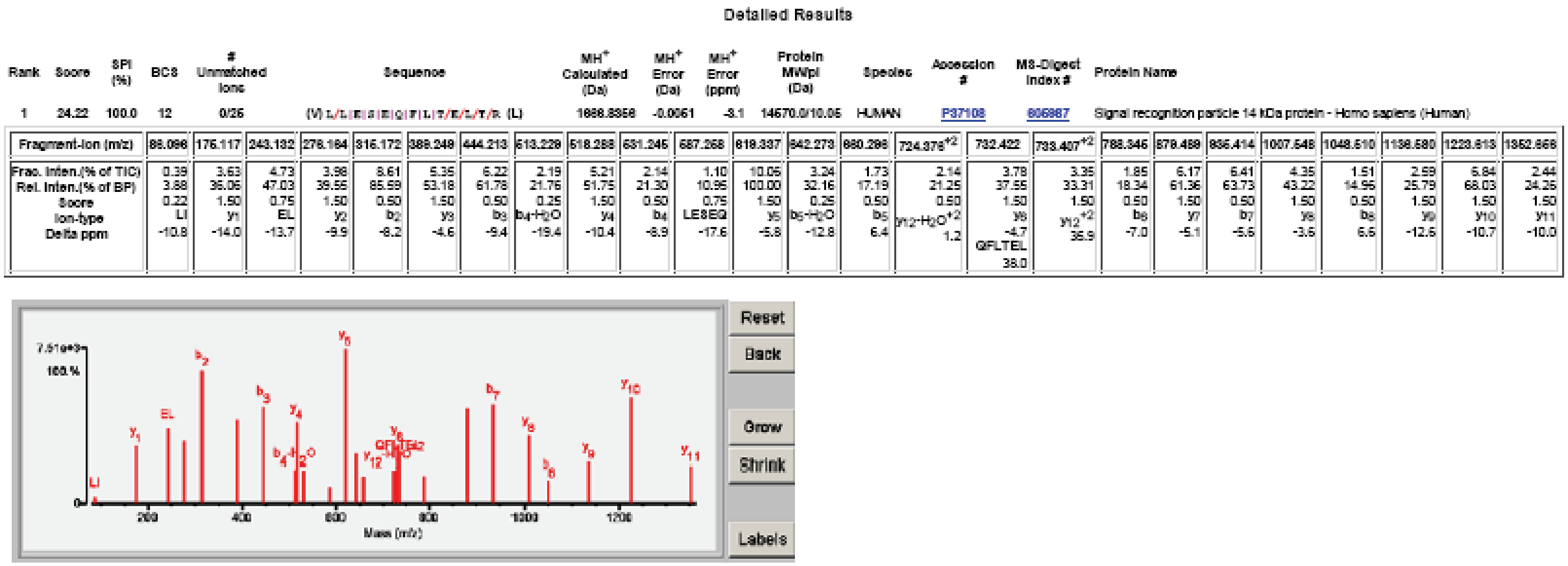
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.47	100.0	12	0/26	(-) V/L\L|E|S|E|Q F|L|T/E/L/T/R (L)	1765.9041	-0.0031	-1.8	14570.0/10.06	HUMAN	P37108	606867	Signal recognition particle 14 kDa protein - Homo sapiens (Human)

Fragment-Ion (m/z)	72.082	86.097	175.118	243.134	276.166	301.159	356.214	389.246	414.243	518.292	543.284	612.308	619.337
Frac. Inten.(% of TIC)	0.06	0.31	2.80	1.97	5.23	13.18	2.17	5.07	8.39	4.50	5.82	1.56	7.23
Rel. Inten.(% of BP)	0.46	2.37	21.24	14.93	39.66	100.00	16.47	38.44	63.65	34.13	44.11	11.87	54.87
Score	0.50	0.22	1.50	0.75	1.50	0.50	0.75	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	V	LI	y_1	EL	y_2	b_2	LLE	y_3	b_3	y_4	b_4	b_5-H_2O	y_5
Delta ppm	14.2	0.9	2.0	-5.5	-3.0	-0.5	-14.6	-11.8	0.2	-2.3	-2.8	-1.4 y**10 -17.2	-6.2

Fragment-Ion (m/z)	630.324	724.383^{+2}	732.424	741.345	759.349	789.909^{+2}	1007.542	1034.484	1136.581	1147.571	1223.620	1352.667
Frac. Inten.(% of TIC)	2.05	1.57	5.78	3.12	1.49	1.65	3.91	5.80	2.58	1.82	6.97	4.95
Rel. Inten.(% of BP)	15.58	11.92	43.85	23.63	11.31	12.54	29.65	43.99	19.56	13.80	52.87	37.55
Score	0.50	0.50	1.50	0.25	0.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	b_5	y_{12}-H_2O^{+2}	y_6	b_6-H_2O	b_6	y_{13}^{+2}	y_8	b_8	y_9	b_9	y_{10}	y_{11}
Delta ppm	9.3	-16.6	-0.7	-6.1	-15.3	-17.3	-9.8	-3.2	-12.1	-0.7	-5.3	-1.4



N57



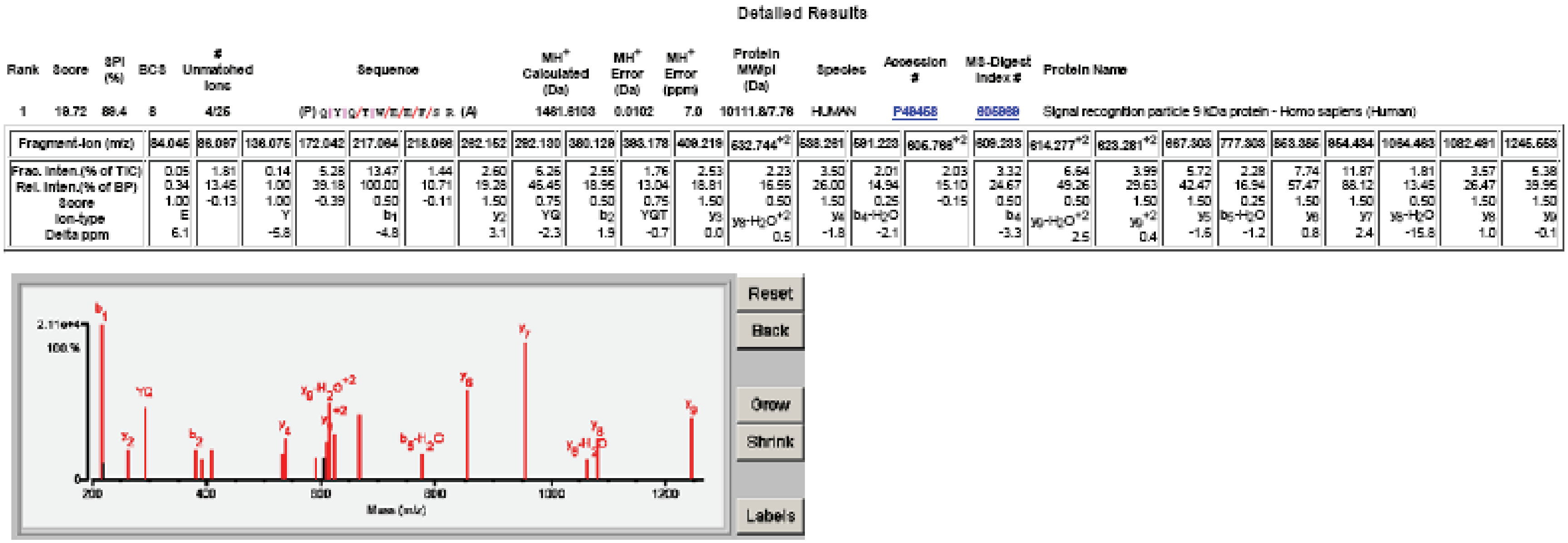
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.22	100.0	12	0/26	(V) L/L|E|S|E|Q|F|L|T/E/L/T/R (L)	1666.8358	-0.0061	-3.1	14570.0/10.05	HUMAN	P37108	606987	Signal recognition particle 14 kDa protein - Homo sapiens (Human)

Fragment-Ion (m/z)	88.096	176.117	243.132	276.164	316.172	389.249	444.213	513.229	518.288	531.245	587.268	619.337	642.273
Frac. Inten.(% of TIC)	0.39	3.63	4.73	3.98	8.61	5.35	6.22	2.19	5.21	2.14	1.10	10.06	3.24
Rel. Inten.(% of BP)	3.88	36.06	47.03	39.55	85.59	53.18	61.78	21.76	51.75	21.30	10.95	100.00	32.16
Score	0.22	1.50	0.75	1.50	0.50	1.50	0.50	0.25	1.50	0.50	0.75	1.50	0.25
Ion-type	LI	y_1	EL	y_2	b_2	y_3	b_3	b_4-H_2O	y_4	b_4	LESEQ	y_5	b_5-H_2O
Delta ppm	-10.8	-14.0	-13.7	-9.9	-8.2	-4.6	-9.4	-19.4	-10.4	-8.9	-17.6	-5.8	-12.8

Fragment-Ion (m/z)	660.286	724.376^{+2}	732.422	733.407^{+2}	788.346	879.459	936.414	1007.548	1048.510	1136.580	1223.613	1352.656
Frac. Inten.(% of TIC)	1.73	2.14	3.78	3.35	1.85	6.17	6.41	4.35	1.51	2.59	6.84	2.44
Rel. Inten.(% of BP)	17.19	21.25	37.55	33.31	18.34	61.36	63.73	43.22	14.95	25.79	68.03	24.26
Score	0.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	b_5	y_{12}-H_2O^{+2}	y_6	y_{12}^{+2}	b_6	y_7	b_7	y_8	b_8	y_9	y_{10}	y_{11}
Delta ppm	6.4	1.2	-4.7 QFLTEL 38.0	35.9	-7.0	-5.1	-5.6	-3.6	6.6	-12.6	-10.7	-10.0

N58



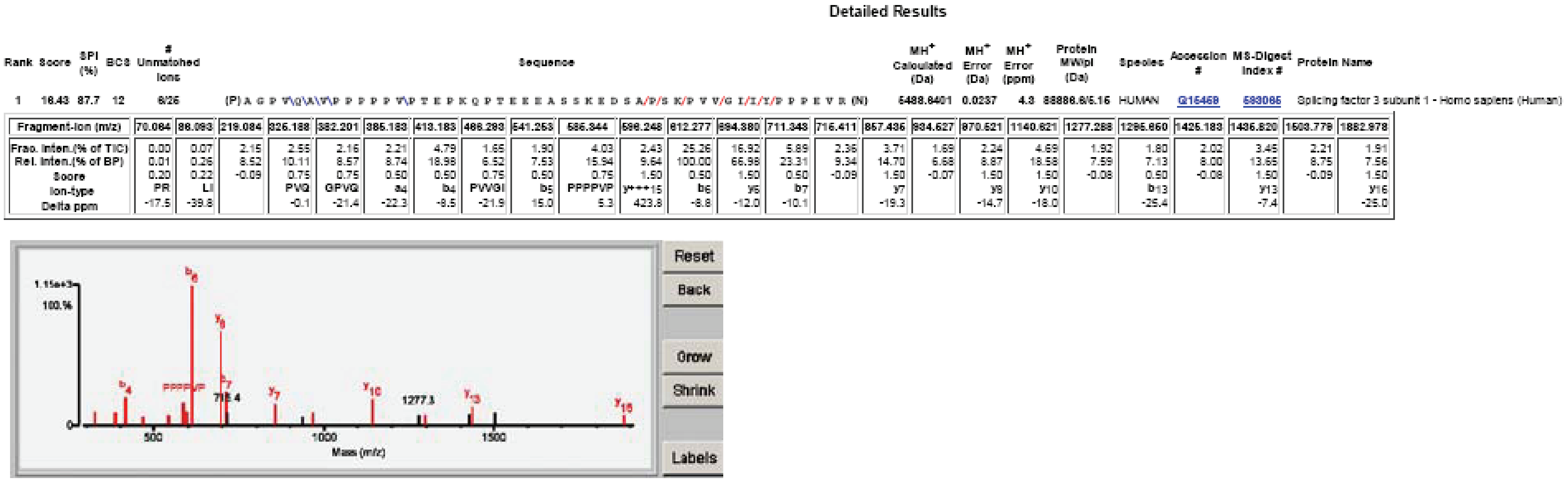
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.72	88.4	8	4/26	(P) Q|Y|Q/T|W/E/E/F/S R (A)	1461.6103	0.0102	7.0	10111.8/7.76	HUMAN	P49458	606989	Signal recognition particle 9 kDa protein - Homo sapiens (Human)

Fragment-Ion (m/z)	84.045	86.097	136.076	172.042	217.084	218.068	262.152	292.130	380.128	393.178	409.219	532.744^{+2}	538.261
Frac. Inten.(% of TIC)	0.05	1.81	0.14	5.28	13.47	1.44	2.60	6.26	2.55	1.76	2.53	2.23	3.50
Rel. Inten.(% of BP)	0.34	13.45	1.00	39.18	100.00	10.71	19.28	46.45	18.95	13.04	18.81	16.55	26.00
Score	1.00	-0.13	1.00	-0.39	0.50	-0.11	1.50	0.75	0.50	0.75	1.50	0.50	1.50
Ion-type	E		Y		b_1		y_2	YQ	b_2	YQT	y_3	y_8-H_2O^{+2}	y_4
Delta ppm	6.1		-5.8		-4.8		3.1	-2.3	1.9	-0.7	0.0	0.5	-1.8

Fragment-Ion (m/z)	591.223	606.766^{+2}	609.233	614.277^{+2}	623.281^{+2}	667.308	777.308	863.386	964.434	1064.463	1082.491	1245.553
Frac. Inten.(% of TIC)	2.01	2.03	3.32	6.64	3.99	5.72	2.28	7.74	11.87	1.81	3.57	5.38
Rel. Inten.(% of BP)	14.94	15.10	24.67	49.26	29.63	42.47	16.94	57.47	88.12	13.45	26.47	39.95
Score	0.25	-0.15	0.50	0.50	1.50	1.50	0.25	1.50	1.50	0.50	1.50	1.50
Ion-type	b_4-H_2O		b_4	y_9-H_2O^{+2}	y_9^{+2}	y_5	b_5-H_2O	y_6	y_7	y_8-H_2O	y_8	y_9
Delta ppm	-2.1		-3.3	2.5	0.4	-1.6	-1.2	0.8	2.4	-15.8	1.0	-0.1

N59



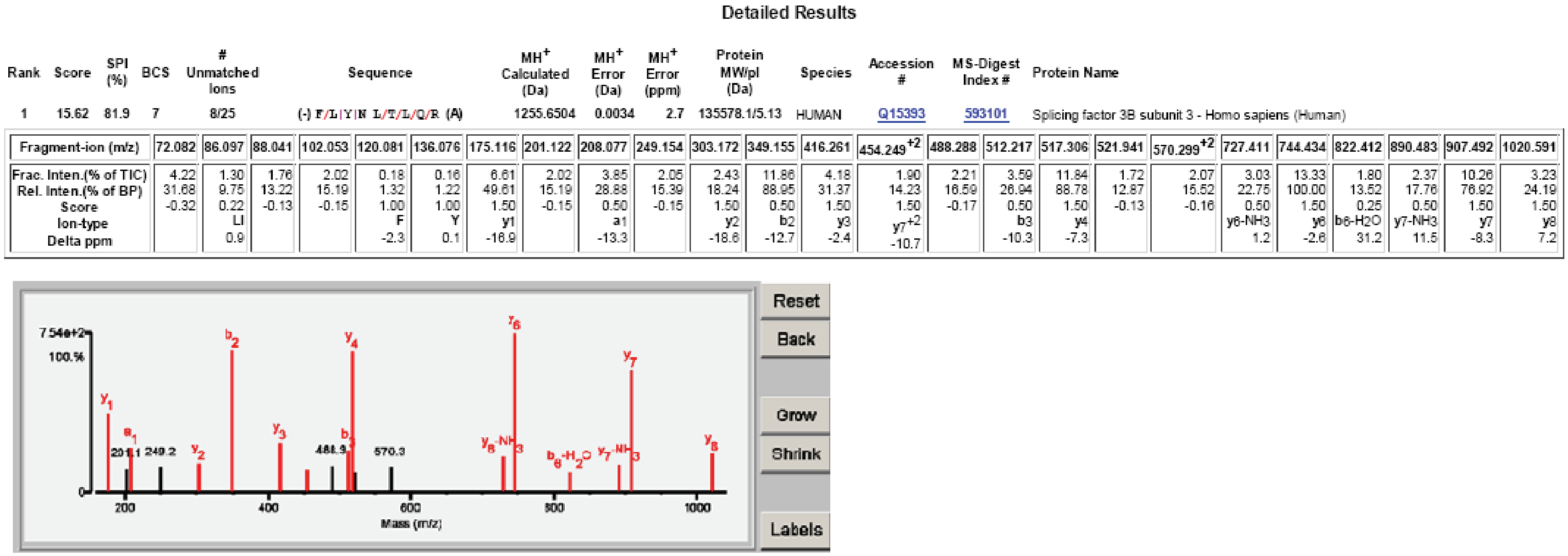
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.43	87.7	12	6/26	(P) A G P V\Q\A\V\P P P P P V\P T E P K Q P T E E E A S S K E D S A/P/S K/P V V/G I/I/Y/P P P E V R (N)	5488.8401	0.0237	4.3	88886.6/5.16	HUMAN	Q15459	593085	Splicing factor 3 subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.084	86.093	219.084	326.188	382.201	385.183	413.183	486.283	541.253	586.344	598.248	612.277	694.380
Frac. Inten.(% of TIC)	0.00	0.07	2.15	2.55	2.16	2.21	4.79	1.65	1.90	4.03	2.43	25.26	16.92
Rel. Inten.(% of BP)	0.01	0.26	8.52	10.11	8.57	8.74	18.98	6.52	7.53	15.94	9.64	100.00	66.98
Score	0.20	0.22	-0.09	0.75	0.75	0.50	0.50	0.75	0.50	0.75	1.50	0.50	1.50
Ion-type	PR	LI		PVQ	GPVQ	a_4	b_4	PVVGI	b_5	PPPPVP	y^{+++}_{15}	b_6	y_6
Delta ppm	-17.5	-39.8		-0.1	-21.4	-22.3	-8.5	-21.9	15.0	5.3	423.8	-8.8	-12.0

Fragment-ion (m/z)	711.343	716.411	857.436	934.627	970.521	1140.621	1277.288	1295.860	1425.183	1436.820	1503.779	1882.978
Frac. Inten.(% of TIC)	5.89	2.36	3.71	1.69	2.24	4.69	1.92	1.80	2.02	3.45	2.21	1.91
Rel. Inten.(% of BP)	23.31	9.34	14.70	6.68	8.87	18.58	7.59	7.13	8.00	13.65	8.75	7.56
Score	0.50	-0.09	1.50	-0.07	1.50	1.50	-0.08	0.50	-0.08	1.50	-0.09	1.50
Ion-type	b_7		y_7		y_8	y_{10}		b_{13}		y_{13}		y_{16}
Delta ppm	-10.1		-19.3		-14.7	-18.0		-25.4		-7.4		-25.0

N60



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.62	81.9	7	8/25	(-) F/L|Y|N L/T/L/Q/R (A)	1255.6504	0.0034	2.7	135578.1/5.13	HUMAN	Q15393	593101	Splicing factor 3B subunit 3 - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.097	88.041	102.053	120.081	136.076	175.116	201.122	208.077	249.154	303.172	349.155	416.261
Frac. Inten.(% of TIC)	4.22	1.30	1.76	2.02	0.18	0.16	6.61	2.02	3.85	2.05	2.43	11.86	4.18
Rel. Inten.(% of BP)	31.68	9.75	13.22	15.19	1.32	1.22	49.61	15.19	28.88	15.39	18.24	88.95	31.37
Score	-0.32	0.22	-0.13	-0.15	1.00	1.00	1.50	-0.15	0.50	-0.15	1.50	0.50	1.50
Ion-type		LI			F	Y	y1		a1		y2	b2	y3
Delta ppm		0.9			-2.3	0.1	-16.9		-13.3		-18.6	-12.7	-2.4

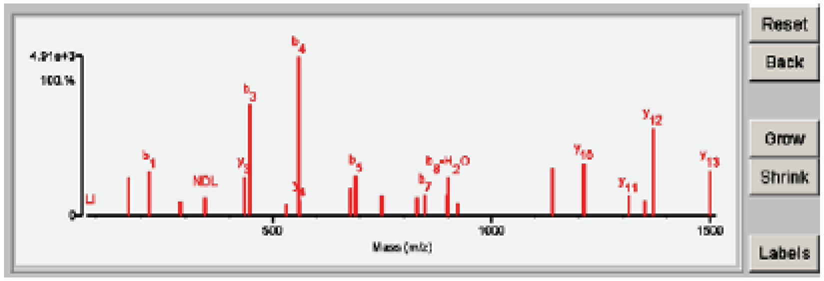
Fragment-ion (m/z)	454.249^{+2}	488.288	512.217	517.306	521.941	570.299^{+2}	727.411	744.434	822.412	890.483	907.492	1020.591
Frac. Inten.(% of TIC)	1.90	2.21	3.59	11.84	1.72	2.07	3.03	13.33	1.80	2.37	10.26	3.23
Rel. Inten.(% of BP)	14.23	16.59	26.94	88.78	12.87	15.52	22.75	100.00	13.52	17.76	76.92	24.19
Score	1.50	-0.17	0.50	1.50	-0.13	-0.16	0.50	1.50	0.25	0.50	1.50	1.50
Ion-type	$y7^{+2}$		b3	y4			y6-NH3	y6	b6-H2O	y7-NH3	y7	y8
Delta ppm	-10.7		-10.3	-7.3			1.2	-2.6	31.2	11.5	-8.3	7.2

N61

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	26.22	100.0	14	0/25	(G) Q|N D\L|M|G|T|A/E D/F/A/D/Q/F/L/R (V)	2068.8898	0.0042	2.0	30384.2/7.64	HUMAN	O15260	614211	Surfeit locus protein 4 - Homo sapiens (Human)

Fragment-ion (m/z)	86.097	175.119	217.086	288.188	343.160	435.267	446.132	531.215	559.217	563.324	678.365	690.256	747.251	749.393	830.308	848.319	896.455	901.341	821.931^{+2}	1140.529	1211.556	1312.588	1351.606	1369.633	1500.689
Frac. Inten.(% of TIC)	0.04	4.15	4.69	1.56	1.92	4.13	11.78	1.29	17.00	1.68	2.93	4.30	1.41	2.14	1.99	2.32	2.32	4.07	1.33	5.21	5.63	2.15	1.66	9.39	4.91
Rel. Inten.(% of BP)	0.22	24.41	27.57	9.20	11.30	24.28	69.29	7.58	100.00	9.85	17.22	25.28	8.29	12.59	11.70	13.64	13.61	23.96	7.81	30.65	33.10	12.62	9.78	55.23	28.89
Score	0.22	1.50	0.50	1.50	0.75	1.50	0.50	0.75	0.50	1.50	1.50	0.50	0.50	1.50	0.25	0.50	1.50	0.25	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	LI	y_1	b_1	y_2	NDL	y_3	b_3	a_4	b_4	y_4	y_5	b_5	b_6	y_6	b_7-H_2O	b_7	y_7	b_8-H_2O	y_{16}^{+2}	y_9	y_{10}	y_{11}	y_{12}-H_2O	y_{12}	y_{13}
Delta ppm	12.5	-1.4	2.1	-17.8	-5.9	-9.7	-7.9	-17.8 NDLMG -17.8	-4.2	-9.8	-2.9	-5.0	-39.8	-1.8	-12.7	-11.3	-8.7	-15.6	11.5	-2.7	-11.6	-14.4	-16.1	-4.1	13.2

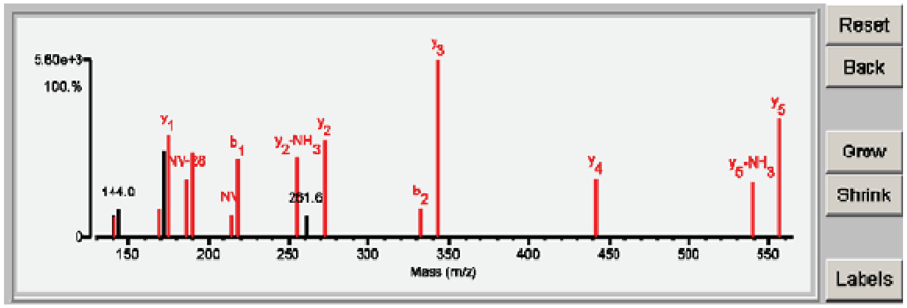


N62

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.04	79.5	5	6/25	(P) E|N|V/A/P/R (S)	773.3610	0.0023	2.9	57924.6/7.96	HUMAN	P50991	639723	T-complex protein 1 subunit delta - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.045	85.030	87.055	102.053	106.033	140.081	141.100	144.048	169.095	172.043	175.120	186.123	190.054	214.118	218.048	255.143	261.635	272.172	332.094	343.208	442.277	539.291	556.318
Frac. Inten.(% of TIC)	0.01	0.19	0.12	2.99	0.21	0.08	5.11	1.79	1.73	2.16	2.14	6.71	7.91	4.52	6.64	1.85	6.03	6.22	1.71	7.54	2.27	13.76	4.65	4.37	9.29
Rel. Inten.(% of BP)	0.04	1.38	0.88	21.74	1.54	0.60	37.17	13.00	12.55	15.71	15.55	48.78	57.47	32.85	48.28	13.44	43.80	45.19	12.46	54.82	16.46	100.00	33.77	31.79	67.52
Score	0.20	0.50	1.00	-0.22	0.33		-0.37	-0.13	0.50	-0.16	0.75	-0.49	1.50	0.50	0.50	0.75	0.50	0.50	-0.12	1.50	0.50	1.50	1.50	0.50	1.50
Ion-type	PR	V	E		NR	E			AP-28		AP		y_1	NV-28	a_1	NV	b_1	y_2-NH_3		y_2	b_2	y_3	y_4	y_5-NH_3	y_5
Delta ppm	5.3	-1.0	7.3		1.3				-21.5		-17.5		3.7	-11.8	-3.4	-8.5	-3.9	-10.1		-0.4	5.8	-2.1	-1.5	-4.7	-3.5



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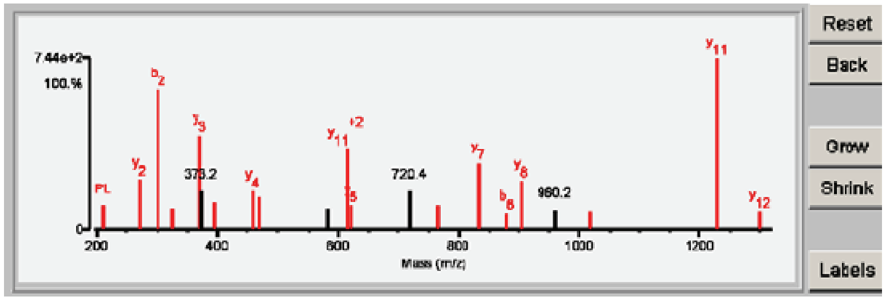
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.17	86.9	11	5/25	(A) V L|A/P\L/I/A|L\V/Y/S/V/P R (L)	1598.9338	0.0043	2.7	34037.8/8.90	HUMAN	Q9Y320	671473	Thioredoxin domain-containing protein 14 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	74.064	86.096	136.074	211.146	272.168	301.157	324.219	371.243	373.201^{+2}	395.274	458.271
Frac. Inten.(% of TIC)	0.09	1.65	0.52	0.05	2.33	4.77	13.39	2.08	9.04	3.70	2.61	3.65
Rel. Inten.(% of BP)	0.56	10.09	3.16	0.33	14.21	29.10	81.74	12.67	55.18	22.59	15.92	22.27
Score	0.50	-0.10	0.22	1.00	0.75	1.50	0.50	0.75	1.50	-0.23	0.75	1.50
Ion-type	V		LI	Y	PL	y2	b2	PLI	y3		PLIA	y4
Delta ppm	23.9		-2.6	-11.0	4.3	-14.0	-6.8	-32.3	8.8		20.5	-2.7

Fragment-ion (m/z)	469.243	583.332	614.387^{+2}	621.331	720.393^{+2}	766.451	833.489	879.525	904.527	960.155	1017.628	1227.736	1298.791
Frac. Inten.(% of TIC)	3.14	2.09	7.75	2.33	3.76	2.38	6.37	1.65	4.74	1.90	1.81	16.39	1.81
Rel. Inten.(% of BP)	19.17	12.73	47.31	14.25	22.95	14.55	38.89	10.08	28.90	11.61	11.02	100.00	11.02
Score	0.50	-0.13	1.50	1.50	-0.23	0.50	1.50	0.50	1.50	-0.12	1.50	1.50	1.50
Ion-type	b4		$y11^{+2}$	y5		b7	y7	b8	y8		y9	y11	y12
Delta ppm	-13.9		17.4	-7.4		-4.4	0.9	-15.3	2.2		18.6	-8.2	5.7



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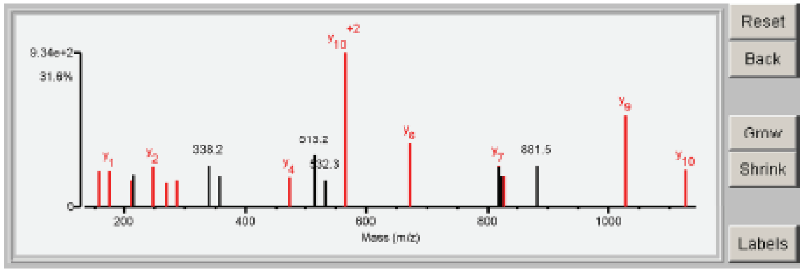
Detailed Results

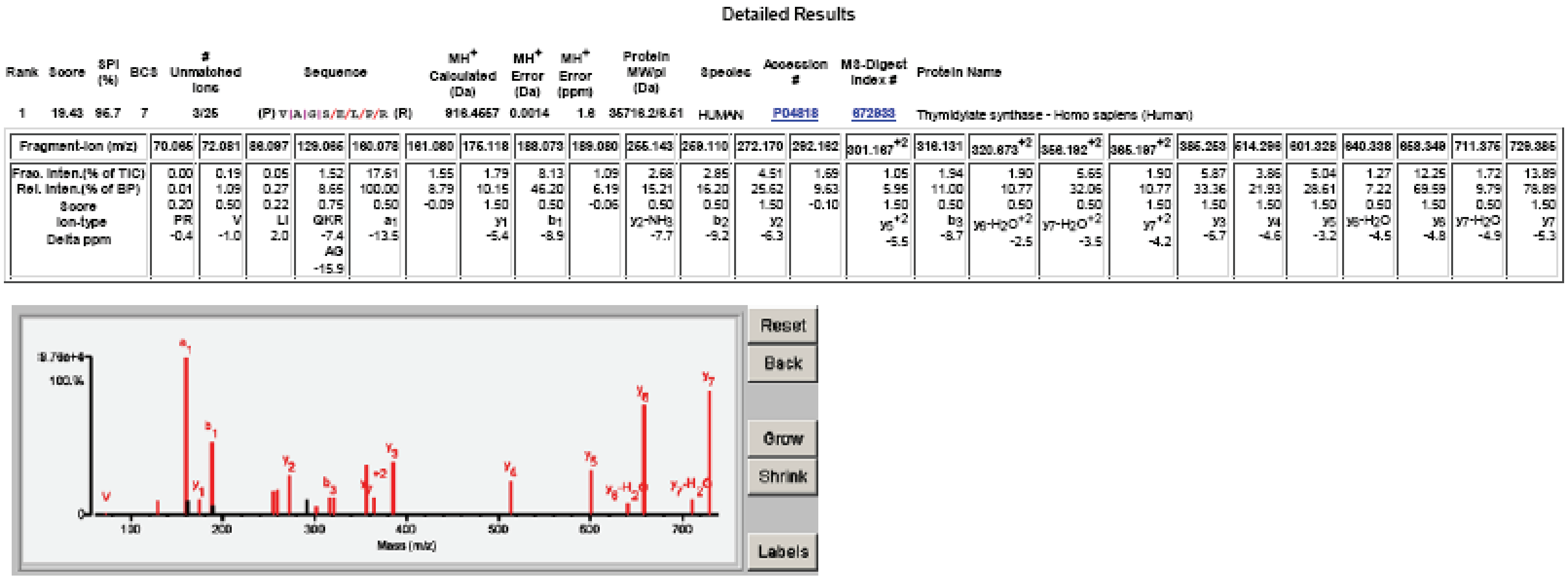
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.26	75.3	8	9/25	(S) P T|P/P L/F/S\L/P E/A/R (T)	1412.7242	-0.0045	-3.2	75666.7/4.92	HUMAN	Q96FV9	647051	THO complex subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.079	86.096	120.081	158.062	175.115	211.140	215.140	246.156	269.100	287.103	338.154
Frac. Inten.(% of TIC)	0.01	2.12	0.25	0.07	2.75	2.77	2.10	2.47	3.12	1.90	2.10	3.16
Rel. Inten.(% of BP)	0.04	5.65	0.66	0.17	7.35	7.40	5.60	6.59	8.34	5.08	5.60	8.44
Score	0.20	-0.06	0.22	1.00	0.50	1.50	0.75	-0.07	1.50	0.25	0.50	-0.08
Ion-type	PR		LI	F	a_1	y_1	LP		y_2	b_2-H_2O	b_2	
Delta ppm	5.3		-1.5	-1.5	-14.0	-22.6	-24.2		-0.7	12.5	-14.3	

Fragment-ion (m/z)	356.206	472.250	513.199	532.280	563.820^{+2}	672.373	819.431	819.520	823.902	828.366	881.482	1029.576	1126.615
Frac. Inten.(% of TIC)	2.33	2.26	3.99	2.08	37.45	4.95	3.15	3.04	2.39	2.40	3.16	7.12	2.85
Rel. Inten.(% of BP)	6.22	6.05	10.66	5.55	100.00	13.23	8.42	8.12	6.39	6.40	8.44	19.02	7.60
Score	-0.06	1.50	-0.11	-0.06	1.50	1.50	1.50	-0.08	-0.06	0.50	-0.08	1.50	1.50
Ion-type		y_4			y_{10}^{+2}	y_6	y_7			b_7		y_9	y_{10}
Delta ppm		-2.0			6.6	8.2	-6.5			-37.7		3.3	-9.2



N65



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.43	96.7	7	3/25	(P) V|A|G|S/E/L/P/R (R)	916.4657	0.0014	1.8	35716.2/6.61	HUMAN	P04818	872833	Thymidylate synthase - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.097	129.066	160.078	161.080	176.118	188.073	189.080	265.143	269.110	272.170	292.162
Frac. Inten.(% of TIC)	0.00	0.19	0.05	1.52	17.61	1.55	1.79	8.13	1.09	2.68	2.85	4.51	1.69
Rel. Inten.(% of BP)	0.01	1.09	0.27	8.65	100.00	8.79	10.15	46.20	6.19	15.21	16.20	25.62	9.63
Score	0.20	0.50	0.22	0.75	0.50	-0.09	1.50	0.50	-0.06	0.50	0.50	1.50	-0.10
Ion-type	PR	V	LI	QKR AG	a_1		y_1	b_1		y_2-NH_3	b_2	y_2	
Delta ppm	-0.4	-1.0	2.0	-7.4 -15.9	-13.5		-5.4	-8.9		-7.7	-9.2	-6.3	

Fragment-ion (m/z)	301.167^{+2}	316.131	320.873^{+2}	358.192^{+2}	385.187^{+2}	386.253	514.296	601.328	640.338	658.349	711.376	729.385
Frac. Inten.(% of TIC)	1.05	1.94	1.90	5.65	1.90	5.87	3.86	5.04	1.27	12.25	1.72	13.89
Rel. Inten.(% of BP)	5.95	11.00	10.77	32.06	10.77	33.36	21.93	28.61	7.22	69.59	9.79	78.89
Score	1.50	0.50	0.50	0.50	1.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50
Ion-type	y_5^{+2}	b_3	$y_6-H_2O^{+2}$	$y_7-H_2O^{+2}$	y_7^{+2}	y_3	y_4	y_5	y_6-H_2O	y_6	y_7-H_2O	y_7
Delta ppm	-5.5	-8.7	-2.5	-3.5	-4.2	-6.7	-4.6	-3.2	-4.5	-4.8	-4.9	-5.3

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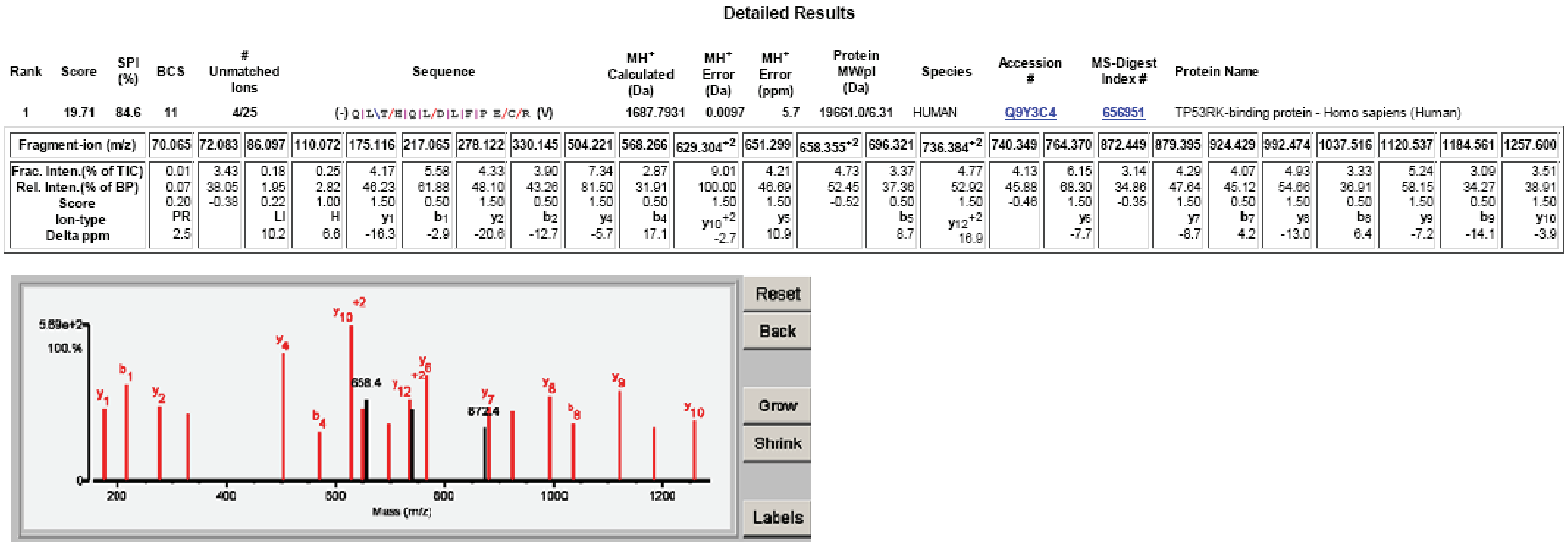

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.71	84.6	11	4/25	(-) Q|L\T/H|Q|L/D|L|F|P E/C/R (V)	1687.7931	0.0097	5.7	19661.0/6.31	HUMAN	Q9Y3C4	656951	TP53RK-binding protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.083	86.097	110.072	175.116	217.065	278.122	330.145	504.221	568.266	629.304^{+2}	651.299	658.355^{+2}
Frac. Inten.(% of TIC)	0.01	3.43	0.18	0.25	4.17	5.58	4.33	3.90	7.34	2.87	9.01	4.21	4.73
Rel. Inten.(% of BP)	0.07	38.05	1.95	2.82	46.23	61.88	48.10	43.26	81.50	31.91	100.00	46.69	52.45
Score	0.20	-0.38	0.22	1.00	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	-0.52
Ion-type	PR		LI	H	y_1	b_1	y_2	b_2	y_4	b_4	y_{10}^{+2}	y_5	
Delta ppm	2.5		10.2	6.6	-16.3	-2.9	-20.6	-12.7	-5.7	17.1	-2.7	10.9	

Fragment-ion (m/z)	696.321	736.384^{+2}	740.349	764.370	872.449	879.395	924.429	992.474	1037.516	1120.537	1184.561	1257.600
Frac. Inten.(% of TIC)	3.37	4.77	4.13	6.15	3.14	4.29	4.07	4.93	3.33	5.24	3.09	3.51
Rel. Inten.(% of BP)	37.36	52.92	45.88	68.30	34.86	47.64	45.12	54.66	36.91	58.15	34.27	38.91
Score	0.50	1.50	-0.46	1.50	-0.35	1.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	b_5	y_{12}^{+2}		y_6		y_7	b_7	y_8	b_8	y_9	b_9	y_{10}
Delta ppm	8.7	16.9		-7.7		-8.7	4.2	-13.0	6.4	-7.2	-14.1	-3.9

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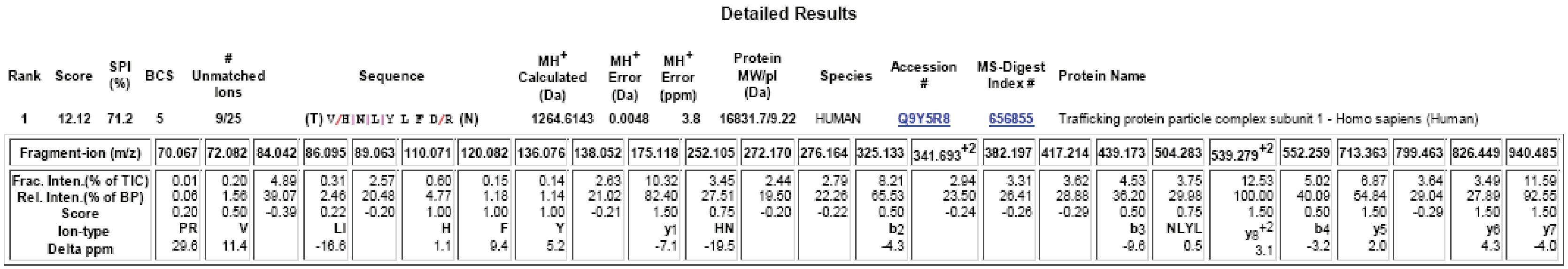
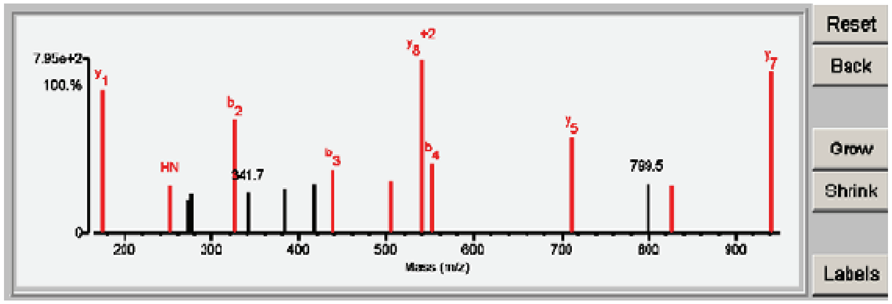


Detailed Results

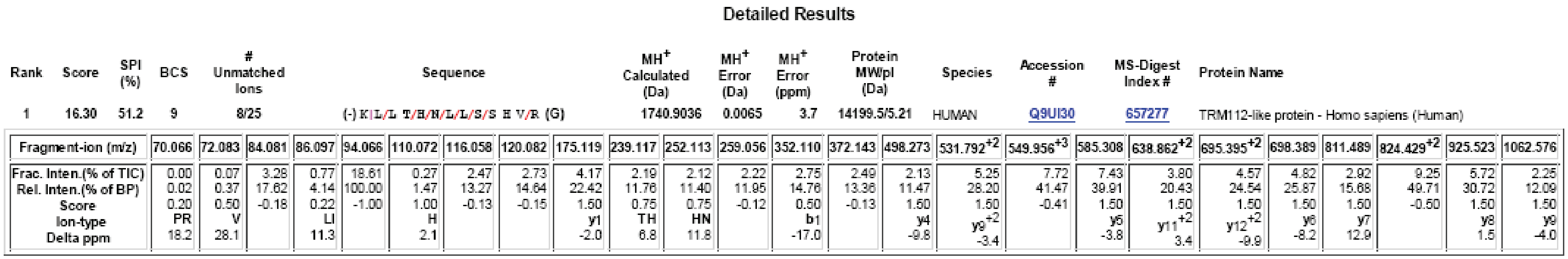
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.12	71.2	5	9/25	(T) V/H|N|L|Y L F D/R (N)	1264.6143	0.0048	3.8	16831.7/9.22	HUMAN	Q9Y5R8	656855	Trafficking protein particle complex subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.082	84.042	86.095	89.063	110.071	120.082	136.076	138.052	175.118	252.105	272.170	276.164
Frac. Inten.(% of TIC)	0.01	0.20	4.89	0.31	2.57	0.60	0.15	0.14	2.63	10.32	3.45	2.44	2.79
Rel. Inten.(% of BP)	0.06	1.56	39.07	2.46	20.48	4.77	1.18	1.14	21.02	82.40	27.51	19.50	22.26
Score	0.20	0.50	-0.39	0.22	-0.20	1.00	1.00	1.00	-0.21	1.50	0.75	-0.20	-0.22
Ion-type	PR	V		LI		H	F	Y		y1	HN		
Delta ppm	29.6	11.4		-16.6		1.1	9.4	5.2		-7.1	-19.5		

Fragment-ion (m/z)	325.133	341.693^{+2}	382.197	417.214	439.173	504.283	539.279^{+2}	552.259	713.363	799.463	826.449	940.485
Frac. Inten.(% of TIC)	8.21	2.94	3.31	3.62	4.53	3.75	12.53	5.02	6.87	3.64	3.49	11.59
Rel. Inten.(% of BP)	65.53	23.50	26.41	28.88	36.20	29.98	100.00	40.09	54.84	29.04	27.89	92.55
Score	0.50	-0.24	-0.26	-0.29	0.50	0.75	1.50	0.50	1.50	-0.29	1.50	1.50
Ion-type	b2				b3	NLYL	$y8^{+2}$	b4	y5		y6	y7
Delta ppm	-4.3				-9.6	0.5	3.1	-3.2	2.0		4.3	-4.0



N68

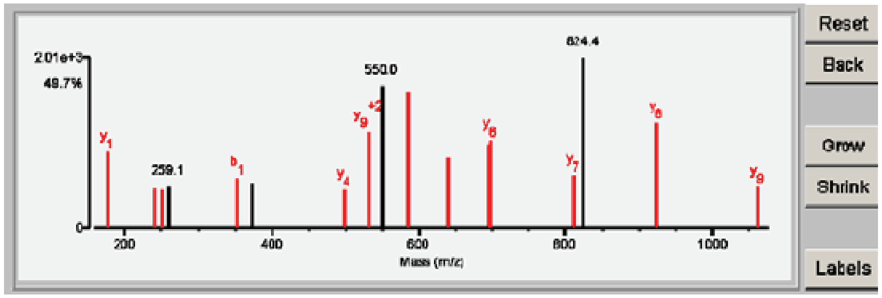


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.30	51.2	9	8/25	(-) K|L/L T/H/N/L/L/S/S H V/R (G)	1740.9036	0.0065	3.7	14199.5/5.21	HUMAN	Q9UI30	657277	TRM112-like protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.083	84.081	86.097	94.066	110.072	116.058	120.082	175.119	239.117	252.113	259.056	352.110
Frac. Inten.(% of TIC)	0.00	0.07	3.28	0.77	18.61	0.27	2.47	2.73	4.17	2.19	2.12	2.22	2.75
Rel. Inten.(% of BP)	0.02	0.37	17.62	4.14	100.00	1.47	13.27	14.64	22.42	11.76	11.40	11.95	14.76
Score	0.20	0.50	-0.18	0.22	-1.00	1.00	-0.13	-0.15	1.50	0.75	0.75	-0.12	0.50
Ion-type	PR	V		LI		H			y1	TH	HN		b1
Delta ppm	18.2	28.1		11.3		2.1			-2.0	6.8	11.8		-17.0

Fragment-ion (m/z)	372.143	498.273	531.792^{+2}	549.956^{+3}	585.308	638.862^{+2}	695.395^{+2}	698.389	811.489	824.429^{+2}	925.523	1062.576
Frac. Inten.(% of TIC)	2.49	2.13	5.25	7.72	7.43	3.80	4.57	4.82	2.92	9.25	5.72	2.25
Rel. Inten.(% of BP)	13.36	11.47	28.20	41.47	39.91	20.43	24.54	25.87	15.68	49.71	30.72	12.09
Score	-0.13	1.50	1.50	-0.41	1.50	1.50	1.50	1.50	1.50	-0.50	1.50	1.50
Ion-type		y4	$y9^{+2}$		y5	$y11^{+2}$	$y12^{+2}$	y6	y7		y8	y9
Delta ppm		-9.8	-3.4		-3.8	3.4	-9.9	-8.2	12.9		1.5	-4.0



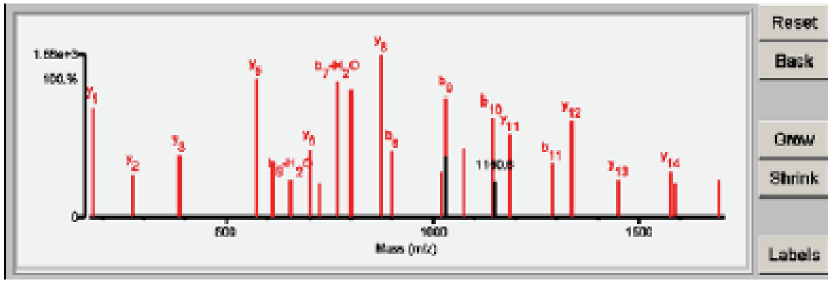
N69

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	24.39	94.8	13	2/25	(P) N S E P A S L/L|E|L|F|N/S I/A/T/Q/G E/L/V/R (S)	2476.2388	0.0099	4.0	53165.7/5.83	HUMAN	P23381	632343	Tryptophanyl-tRNA synthetase, cytoplasmic - Homo sapiens (Human)

Fragment-ion (m/z)	175.118	274.184	387.270	573.335	611.341	656.238	701.399	724.416	769.317	802.436	873.479	900.410	1020.551^{+2}
Frac. Inten.(% of TIC)	5.86	2.35	3.38	7.36	3.01	2.06	3.65	1.83	7.23	6.81	8.67	3.59	2.46
Rel. Inten.(% of BP)	67.54	27.13	38.99	84.86	34.70	23.80	42.14	21.07	83.38	78.51	100.00	41.36	28.36
Score	1.50	1.50	1.50	1.50	0.75	0.25	1.50	1.50	0.25	1.50	1.50	0.50	0.50
Ion-type	y_1	y_2	y_3	y_5	PASLLE	b_6-H_2O	y_6	y^{++}_{13} PASLLEL	b_7-H_2O	y_7	y_8	b_8	y_{13}-H_2O^{+2}
Delta ppm	-8.3	-13.7	-3.2	-0.5	0.5	3.3	6.8	23.9 -12.4	-3.7	-7.2	-0.4	-4.9	-8.7

Fragment-ion (m/z)	1029.493	1030.071	1073.591	1142.540	1150.559	1187.624	1289.607	1334.696	1447.787	1576.828	1585.777	1689.959
Frac. Inten.(% of TIC)	6.38	3.28	3.77	5.37	1.96	4.49	2.94	5.19	2.03	2.46	1.81	2.06
Rel. Inten.(% of BP)	73.63	37.88	43.51	61.93	22.63	51.74	33.87	59.91	23.39	28.37	20.93	23.74
Score	0.50	-0.38	1.50	0.50	-0.23	1.50	0.50	1.50	1.50	1.50	0.25	1.50
Ion-type	b_9		y_{10}	b_{10}		y_{11}	b_{11}	y_{12}	y_{13}	y_{14}	b_{14}-H_2O	y_{15}
Delta ppm	35.0		-3.5	-0.5		-11.7	-2.1	-7.7	-2.3	-2.9	11.9	25.1



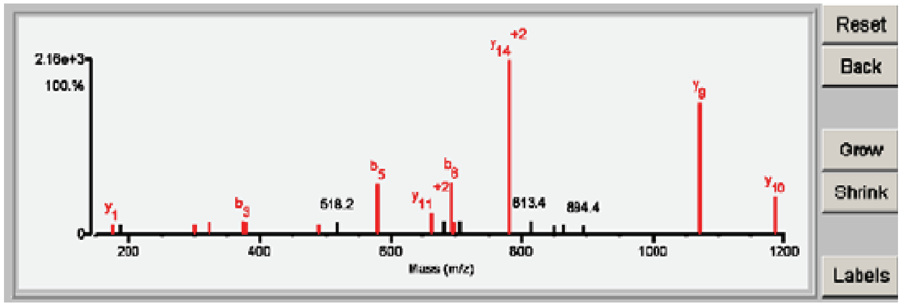
N70

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.02	83.1	7	9/25	(P) D/P\A|A/H|L|P F F Y G S I S/R (A)	1765.8367	0.0061	3.4	69872.7/7.79	HUMAN	P43403	777339	Tyrosine-protein kinase ZAP-70 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.081	86.096	110.073	175.113	185.166	301.089	322.190	372.119	377.194	490.277	518.248	580.211
Frac. Inten.(% of TIC)	0.00	2.31	0.15	0.11	1.72	1.56	1.57	1.79	2.17	1.89	1.56	1.87	7.73
Rel. Inten.(% of BP)	0.01	8.88	0.59	0.43	6.60	6.00	6.04	6.87	8.33	7.26	6.00	7.18	29.69
Score	0.20	-0.09	0.22	1.00	1.50	-0.06	0.50	0.75	0.50	0.75	0.75	-0.07	0.50
Ion-type	PR		LI	H	y_1		b_2	AHL	b_3	PAAH	AAHLP		b_5
Delta ppm	-13.2		-9.6	16.6	-35.1		9.7	6.0	-11.8	0.3	-2.5		-14.0

Fragment-ion (m/z)	662.352^{+2}	681.244	693.295	697.870^{+2}	706.430	781.910^{+2}	813.399	848.931	862.414^{+2}	894.380	1073.535	1186.630
Frac. Inten.(% of TIC)	3.31	2.04	7.94	1.82	2.19	26.03	2.22	1.51	1.60	1.56	19.61	5.73
Rel. Inten.(% of BP)	12.70	7.84	30.51	6.99	8.43	100.00	8.53	5.80	6.14	5.98	75.33	21.99
Score	1.50	-0.08	0.50	1.50	-0.08	1.50	-0.09	-0.06	-0.06	-0.06	1.50	1.50
Ion-type	y_{11}^{+2}		b_6	y_{12}^{+2}		y_{14}^{+2}					y_9	y_{10}
Delta ppm	8.7		-11.9	8.7		0.3					-6.0	3.7



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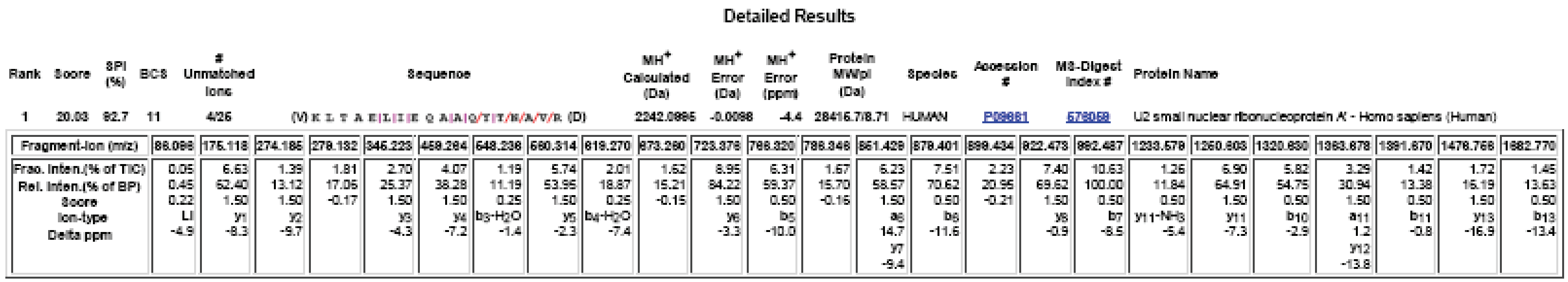
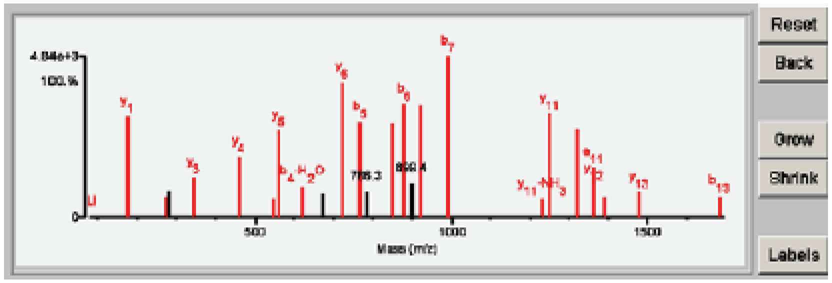


Detailed Results

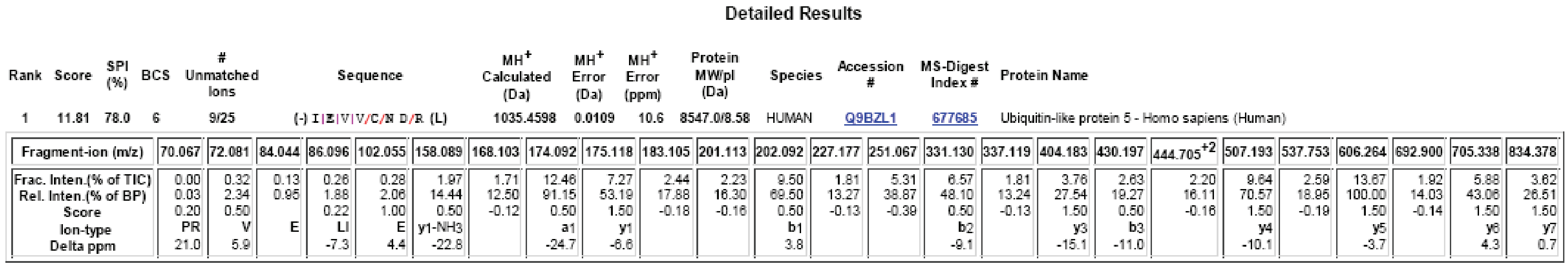
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.03	92.7	11	4/26	(V) K L T A E|L|I|E Q A|A|Q/T|T/H/A/V/R (D)	2242.0995	-0.0098	-4.4	28416.7/8.71	HUMAN	P09661	679059	U2 small nuclear ribonucleoprotein A' - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	175.118	274.186	278.132	346.223	459.284	648.238	680.314	819.270	873.260	723.376	786.320
Frac. Inten.(% of TIC)	0.05	6.63	1.39	1.81	2.70	4.07	1.19	5.74	2.01	1.62	8.95	6.31
Rel. Inten.(% of BP)	0.45	62.40	13.12	17.06	25.37	38.28	11.19	53.95	18.87	15.21	84.22	59.37
Score	0.22	1.50	1.50	-0.17	1.50	1.50	0.25	1.50	0.25	-0.15	1.50	0.50
Ion-type	LI	y_1	y_2		y_3	y_4	b_3-H_2O	y_5	b_4-H_2O		y_6	b_5
Delta ppm	-4.9	-8.3	-9.7		-4.3	-7.2	-1.4	-2.3	-7.4		-3.3	-10.0

Fragment-ion (m/z)	788.346	861.429	879.401	899.434	922.473	992.487	1233.578	1260.608	1320.630	1363.678	1391.670	1476.768	1682.770
Frac. Inten.(% of TIC)	1.67	6.23	7.51	2.23	7.40	10.63	1.26	6.90	5.82	3.29	1.42	1.72	1.45
Rel. Inten.(% of BP)	15.70	58.57	70.62	20.95	69.62	100.00	11.84	64.91	54.75	30.94	13.38	16.19	13.63
Score	-0.16	1.50	0.50	-0.21	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50
Ion-type		a_6 14.7 y_7	b_6		y_8	b_7	$y_{11}-NH_3$	y_{11}	b_{10}	a_{11} 1.2 y_{12}	b_{11}	y_{13}	b_{13}
Delta ppm		-9.4	-11.6		-0.9	-8.5	-5.4	-7.3	-2.9	-13.8	-0.8	-16.9	-13.4



N72

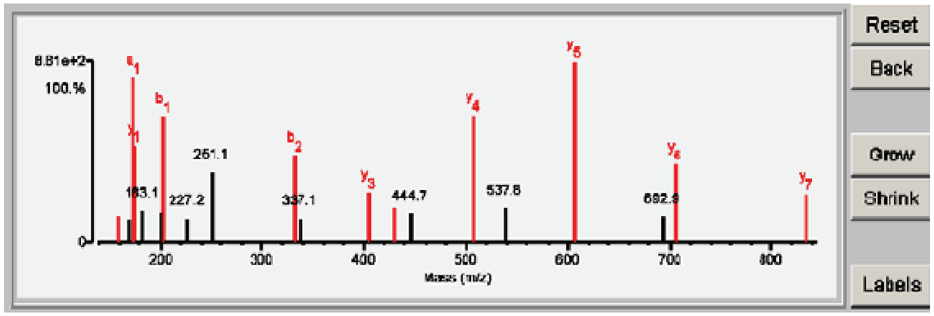


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.81	78.0	6	9/25	(-) I|E|V|V/C/N D/R (L)	1035.4598	0.0109	10.6	8547.0/8.58	HUMAN	Q9BZL1	677685	Ubiquitin-like protein 5 - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.081	84.044	86.096	102.055	158.089	168.103	174.092	175.118	183.105	201.113	202.092	227.177
Frac. Inten.(% of TIC)	0.00	0.32	0.13	0.26	0.28	1.97	1.71	12.46	7.27	2.44	2.23	9.50	1.81
Rel. Inten.(% of BP)	0.03	2.34	0.95	1.88	2.06	14.44	12.50	91.15	53.19	17.88	16.30	69.50	13.27
Score	0.20	0.50		0.22	1.00	0.50	-0.12	0.50	1.50	-0.18	-0.16	0.50	-0.13
Ion-type	PR	V	E	LI	E	y_1-NH_3		a_1	y_1			b_1	
Delta ppm	21.0	5.9		-7.3	4.4	-22.8		-24.7	-6.6			3.8	

Fragment-ion (m/z)	251.067	331.130	337.119	404.183	430.197	444.705^{+2}	507.193	537.753	606.264	692.900	705.338	834.378
Frac. Inten.(% of TIC)	5.31	6.57	1.81	3.76	2.63	2.20	9.64	2.59	13.67	1.92	5.88	3.62
Rel. Inten.(% of BP)	38.87	48.10	13.24	27.54	19.27	16.11	70.57	18.95	100.00	14.03	43.06	26.51
Score	-0.39	0.50	-0.13	1.50	0.50	-0.16	1.50	-0.19	1.50	-0.14	1.50	1.50
Ion-type		b_2		y_3	b_3		y_4		y_5		y_6	y_7
Delta ppm		-9.1		-15.1	-11.0		-10.1		-3.7		4.3	0.7

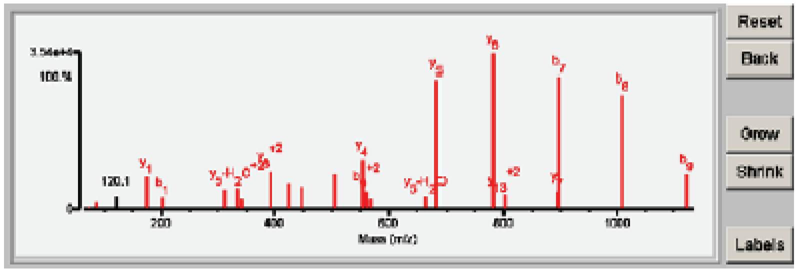


N73

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.98	86.7	10	1/26	(-) N|V/D H E V N\L|L|V/E/E/I/H/R (L)	1903.9331	0.0121	6.3	9056.5/5.86	HUMAN	Q9P1F3	76775	Uncharacterized protein C6orf115 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.096	87.056	110.069	120.081	175.119	208.048	312.178	333.173^{+2}	342.180^{+2}	391.710^{+2}	425.263	448.266^{+2}	505.223^{+2}	554.304	561.788^{+2}	587.983^{+3}	666.335	683.348	782.413	801.910^{+2}	896.487	898.357	1008.441	1122.627
Frac. Inten.(% of TIC)	0.22	0.83	0.08	0.04	1.30	3.49	1.19	2.09	2.18	1.04	4.14	2.81	2.33	3.79	5.35	1.97	1.04	1.35	13.97	16.76	1.58	2.00	14.25	12.38	3.83
Rel. Inten.(% of BP)	1.31	4.93	0.49	0.23	7.76	20.82	7.11	12.46	13.02	6.19	24.67	16.74	13.88	22.62	31.89	11.76	6.19	8.07	83.36	100.00	9.40	11.95	85.03	73.84	22.86
Score	0.50	0.22	0.33	1.00	-0.08	1.50	0.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	0.50	0.50
Ion-type	V	LI	NR	H		y_1	b_1	y_2	y_6-H_2O^{+2}	y_5^{+2}	y_6^{+2}	y_3	y_7^{+2}	b_8^{+2}	y_4	b_9^{+2}	a_{14}^{+3} 36.2 y_{14}^{+3}	y_5-H_2O	y_5	y_6	y_{13}^{+2}	y_7	b_7	b_8	b_9
Delta ppm	1.7	-1.5	-5.6	-17.9		-1.4	-2.9	0.1	1.8	9.1	-2.6	2.5	4.8	-2.7	-0.2	2.1	-1.6	-2.8	-1.9	-2.7	-6.2	-2.4	-1.0	-1.0	1.1

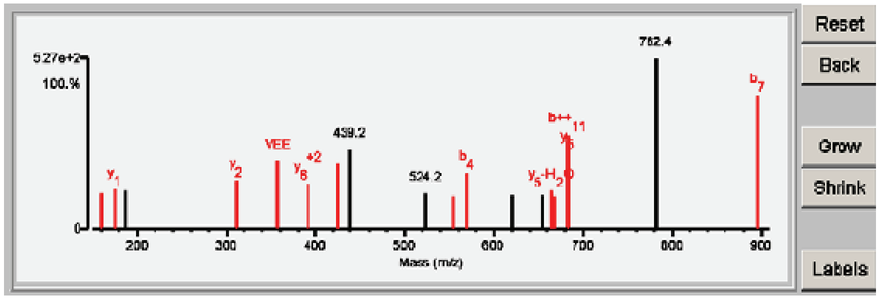


N74

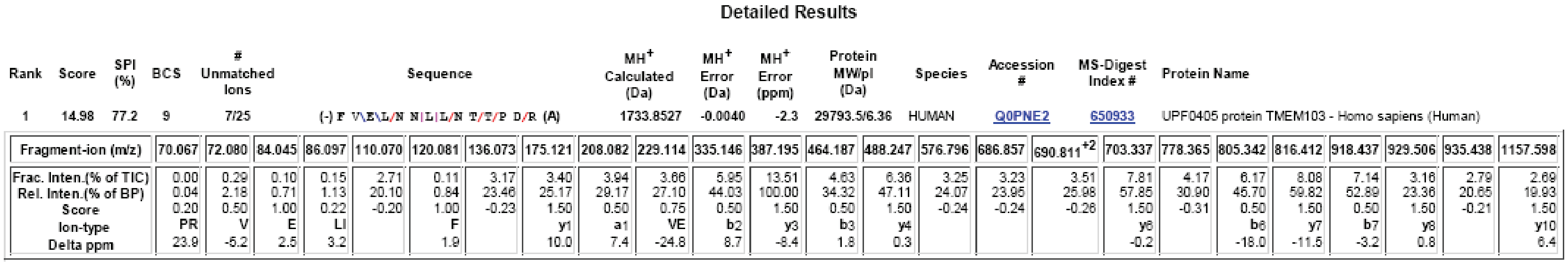
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.28	59.0	9	9/25	(N) V D H E\V\N L\L/V|E/E|I/H/R (L)	1789.8901	0.0064	3.6	9056.5/5.86	HUMAN	Q9P1F3	76775	Uncharacterized protein C6orf115 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.080	86.097	94.065	110.071	120.078	136.075	160.075	175.117	187.144	312.171	358.164	391.715^{+2}	425.258	439.217	524.160	554.300	569.195	621.359^{+2}	655.690	665.343	668.273	683.340	782.373	895.390
Frac. Inten.(% of TIC)	0.00	0.45	0.75	2.66	0.21	2.75	3.10	3.03	3.29	3.16	4.11	5.64	3.79	5.46	6.57	2.94	2.73	4.62	2.82	2.79	3.24	2.70	7.88	14.19	11.12
Rel. Inten.(% of BP)	0.03	3.20	5.27	18.74	1.48	19.36	21.81	21.32	23.20	22.29	28.97	39.71	26.71	38.50	46.30	20.75	19.25	32.56	19.86	19.67	22.85	19.00	55.52	100.00	78.34
Score	0.20	0.50	0.22	-0.19	1.00	-0.19	-0.22	0.50	1.50	-0.22	1.50	0.75	1.50	1.50	-0.46	-0.21	1.50	0.50	-0.20	-0.20	0.50	0.50	1.50	-1.00	0.50
Ion-type	PR	V	LI		H			a1	y1		y2	VEE	$y6^{+2}$	y3			b++9 38.0 y4	b4			y5-H2O	b5	b++11 25.7 y5		b7
Delta ppm	-0.4	-9.4	3.2		-1.6			-31.0	-13.4		-21.3	5.4	10.2	-9.2			-7.4	-15.3			9.5	1.7	-11.1		-9.6



N75

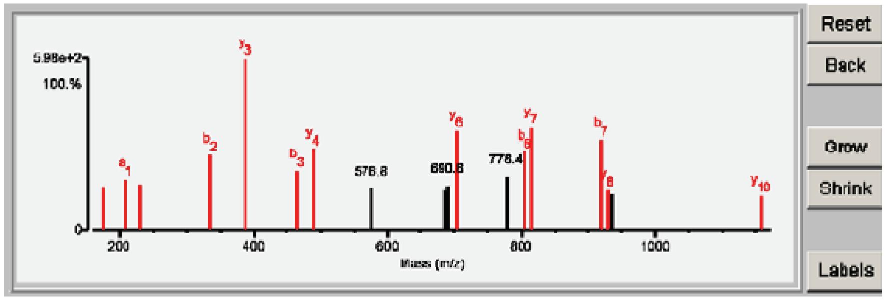


Detailed Results

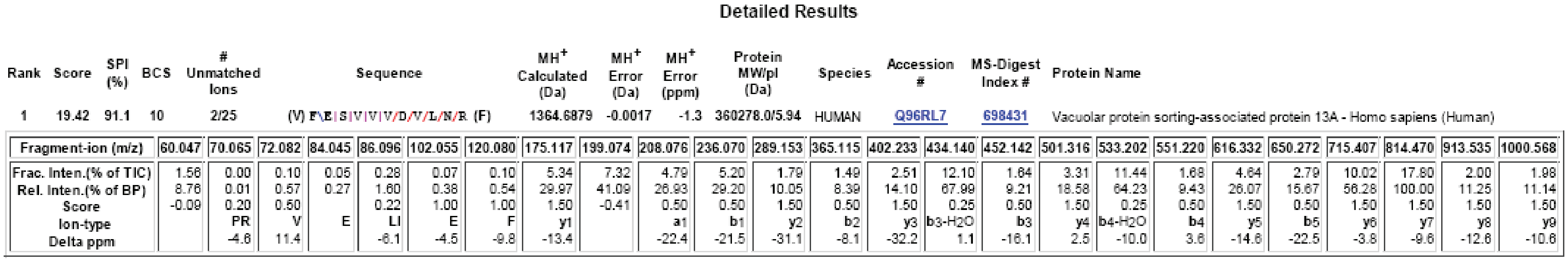
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.98	77.2	9	7/25	(-) F V\E\L/N N|L|L/N T/T/P D/R (A)	1733.8527	-0.0040	-2.3	29793.5/6.36	HUMAN	Q0PNE2	650933	UPF0405 protein TMEM103 - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.080	84.045	86.097	110.070	120.081	136.073	175.121	208.082	229.114	335.146	387.195	464.187
Frac. Inten.(% of TIC)	0.00	0.29	0.10	0.15	2.71	0.11	3.17	3.40	3.94	3.66	5.95	13.51	4.63
Rel. Inten.(% of BP)	0.04	2.18	0.71	1.13	20.10	0.84	23.46	25.17	29.17	27.10	44.03	100.00	34.32
Score	0.20	0.50	1.00	0.22	-0.20	1.00	-0.23	1.50	0.50	0.75	0.50	1.50	0.50
Ion-type	PR	V	E	LI		F		y1	a1	VE	b2	y3	b3
Delta ppm	23.9	-5.2	2.5	3.2		1.9		10.0	7.4	-24.8	8.7	-8.4	1.8

Fragment-ion (m/z)	488.247	576.796	686.857	690.811^{+2}	703.337	778.365	805.342	816.412	918.437	929.506	935.438	1157.598
Frac. Inten.(% of TIC)	6.36	3.25	3.23	3.51	7.81	4.17	6.17	8.08	7.14	3.16	2.79	2.69
Rel. Inten.(% of BP)	47.11	24.07	23.95	25.98	57.85	30.90	45.70	59.82	52.89	23.36	20.65	19.93
Score	1.50	-0.24	-0.24	-0.26	1.50	-0.31	0.50	1.50	0.50	1.50	-0.21	1.50
Ion-type	y4				y6		b6	y7	b7	y8		y10
Delta ppm	0.3				-0.2		-18.0	-11.5	-3.2	0.8		6.4



N76

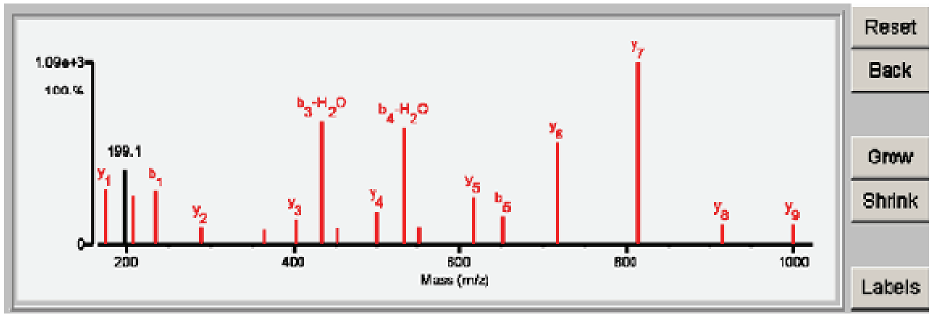


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.42	91.1	10	2/25	(V) F\E|S|V|V|V/D/V/L/N/R (F)	1364.6879	-0.0017	-1.3	360278.0/5.94	HUMAN	Q96RL7	698431	Vacuolar protein sorting-associated protein 13A - Homo sapiens (Human)

Fragment-ion (m/z)	60.047	70.065	72.082	84.045	86.096	102.055	120.080	175.117	199.074	208.076	236.070	289.153	365.115
Frac. Inten.(% of TIC)	1.56	0.00	0.10	0.05	0.28	0.07	0.10	5.34	7.32	4.79	5.20	1.79	1.49
Rel. Inten.(% of BP)	8.76	0.01	0.57	0.27	1.60	0.38	0.54	29.97	41.09	26.93	29.20	10.05	8.39
Score	-0.09	0.20	0.50		0.22	1.00	1.00	1.50	-0.41	0.50	0.50	1.50	0.50
Ion-type		PR	V	E	LI	E	F	y1		a1	b1	y2	b2
Delta ppm		-4.6	11.4		-6.1	-4.5	-9.8	-13.4		-22.4	-21.5	-31.1	-8.1

Fragment-ion (m/z)	402.233	434.140	452.142	501.316	533.202	551.220	616.332	650.272	715.407	814.470	913.535	1000.568
Frac. Inten.(% of TIC)	2.51	12.10	1.64	3.31	11.44	1.68	4.64	2.79	10.02	17.80	2.00	1.98
Rel. Inten.(% of BP)	14.10	67.99	9.21	18.58	64.23	9.43	26.07	15.67	56.28	100.00	11.25	11.14
Score	1.50	0.25	0.50	1.50	0.25	0.50	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	y3	b3-H2O	b3	y4	b4-H2O	b4	y5	b5	y6	y7	y8	y9
Delta ppm	-32.2	1.1	-16.1	2.5	-10.0	3.6	-14.6	-22.5	-3.8	-9.6	-12.6	-10.6



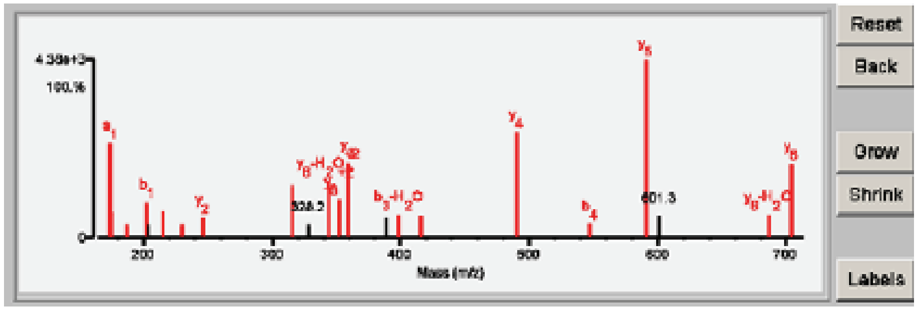
N77

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.84	89.8	6	6/25	(V) L | L | T | M | I/A/R (V)	906.4947	0.0044	4.9	24740.7/8.87	HUMAN	O75396	584763	Vesicle-trafficking protein SEC22b - Homo sapiens (Human)

Fragment-Ion (m/z)	86.098	87.102	167.100	174.086	176.120	187.142	202.090	203.177	215.145	228.130	246.168	316.174	328.188
Frac. Inten.(% of TIC)	1.16	1.97	1.47	9.45	2.43	1.32	3.50	1.27	2.70	1.33	2.10	5.26	1.29
Rel. Inten.(% of BP)	6.59	11.17	8.34	53.60	13.76	7.47	19.87	7.18	15.30	7.52	11.92	29.82	7.30
Score	0.22	-0.11	-0.08	0.50	1.50	0.50	0.50	-0.07	0.75	0.50	1.50	0.50	-0.07
Ion-type	LI			a_1	y_1	LT-28	b_1		LT	y_2-NH_3	y_2	b_2	
Delta ppm	16.0			-2.9	7.1	-17.6	-3.6		22.7	2.1	5.8	-1.5	

Fragment-Ion (m/z)	343.705^{+2}	362.711^{+2}	369.240	389.225	398.209	416.219	490.284	547.281	591.328	601.317	686.402	704.415
Frac. Inten.(% of TIC)	5.67	3.87	7.47	2.01	2.30	2.13	10.50	1.36	17.63	2.21	2.31	7.31
Rel. Inten.(% of BP)	32.17	21.96	42.38	11.41	13.05	12.06	59.59	7.74	100.00	12.52	13.09	41.47
Score	0.50	1.50	1.50	-0.11	0.25	0.50	1.50	0.50	1.50	-0.13	0.50	1.50
Ion-type	y_6-H_2O^{+2}	y_6^{+2}	y_3		b_3-H_2O	b_3	y_4	b_4	y_5		y_6-H_2O	y_6
Delta ppm	0.8	2.5	-1.2		-6.5	-7.8	5.9	33.5	-0.8		0.3	3.3



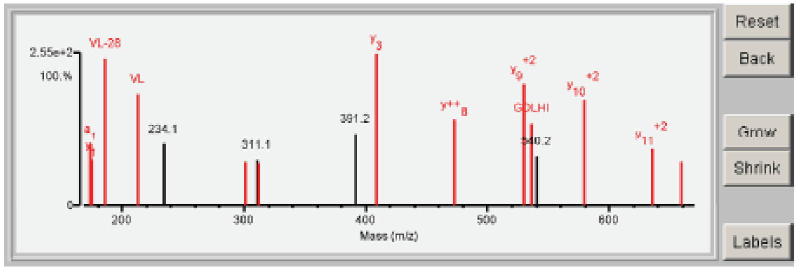
N78

Detailed Results

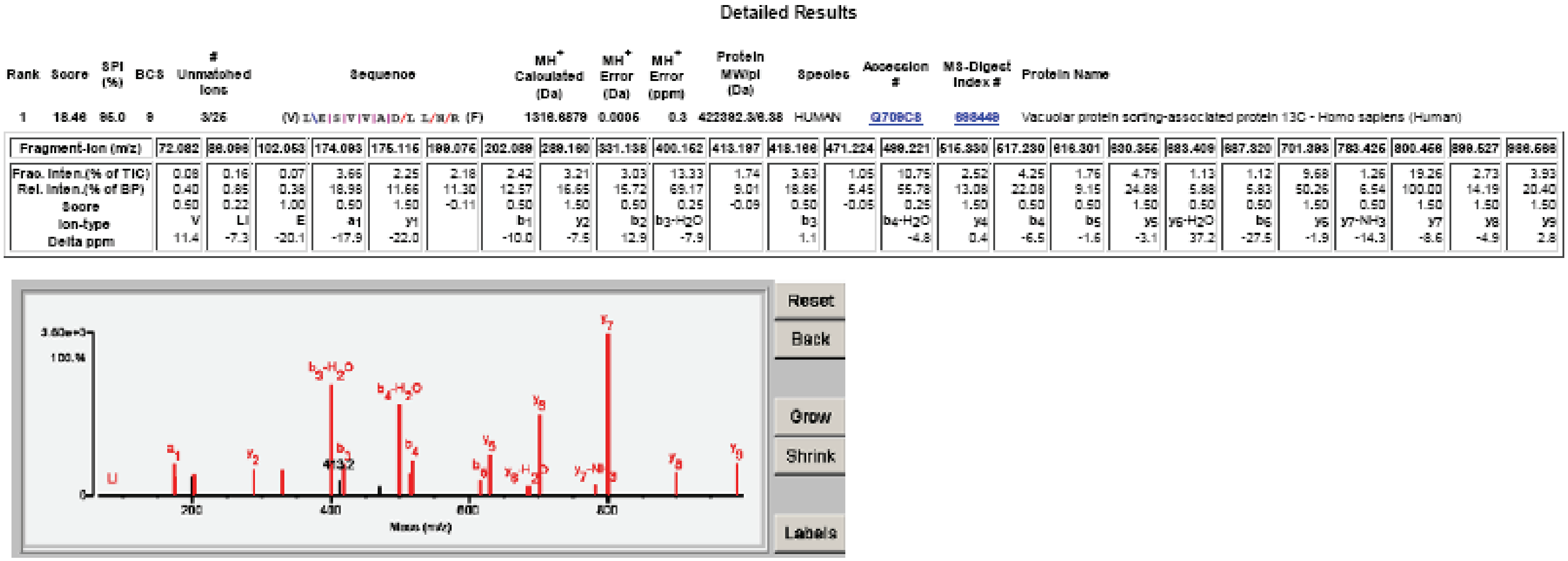
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.52	68.2	7	9/25	(-) L V | L/Y/L/G D L/H I/P H/R (C)	1569.8934	0.0219	13.9	20505.8/6.28	HUMAN	Q9UBQ0	700045	Vacuolar protein sorting-associated protein 29 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	73.080	86.094	102.062	106.064	110.073	156.074	160.040	174.095	175.115	185.170	213.162	234.126
Frac. Inten.(% of TIC)	0.83	2.89	0.38	2.93	4.59	0.15	2.80	4.81	3.78	2.74	8.91	6.77	3.72
Rel. Inten.(% of BP)	8.96	31.39	4.10	31.79	49.78	1.58	30.37	52.22	40.94	29.74	96.66	73.44	40.31
Score	0.50	-0.31	0.22	-0.32	-0.50	1.00	-0.30	-0.52	0.50	1.50	0.50	0.75	-0.40
Ion-type	V		LI			H			a_1	y_1	VL-28	VL	
Delta ppm	-5.2		-23.5			11.1			-2.9	-23.7	23.0	4.9	

Fragment-Ion (m/z)	301.152	311.112	312.235	391.231	409.232	472.769	529.287^{+2}	536.283	540.182	578.842^{+2}	635.368^{+2}	659.383
Frac. Inten.(% of TIC)	2.66	2.71	2.54	4.35	9.22	5.27	7.38	5.04	2.99	6.47	3.45	2.63
Rel. Inten.(% of BP)	28.88	29.43	27.50	47.15	100.00	57.13	80.04	54.62	32.46	70.18	37.37	28.53
Score	0.50	-0.29	0.75	-0.47	1.50	1.50	1.50	0.75	-0.32	1.50	1.50	1.50
Ion-type	b_2		VLV		y_3	$y{+}{+}_8$	y_9^{+2}	GDLHI		y_{10}^{+2}	y_{11}^{+2}	y_5
Delta ppm	-22.4		17.4		3.8	27.1	-21.6	-0.8		16.4	-11.3	13.6



N79



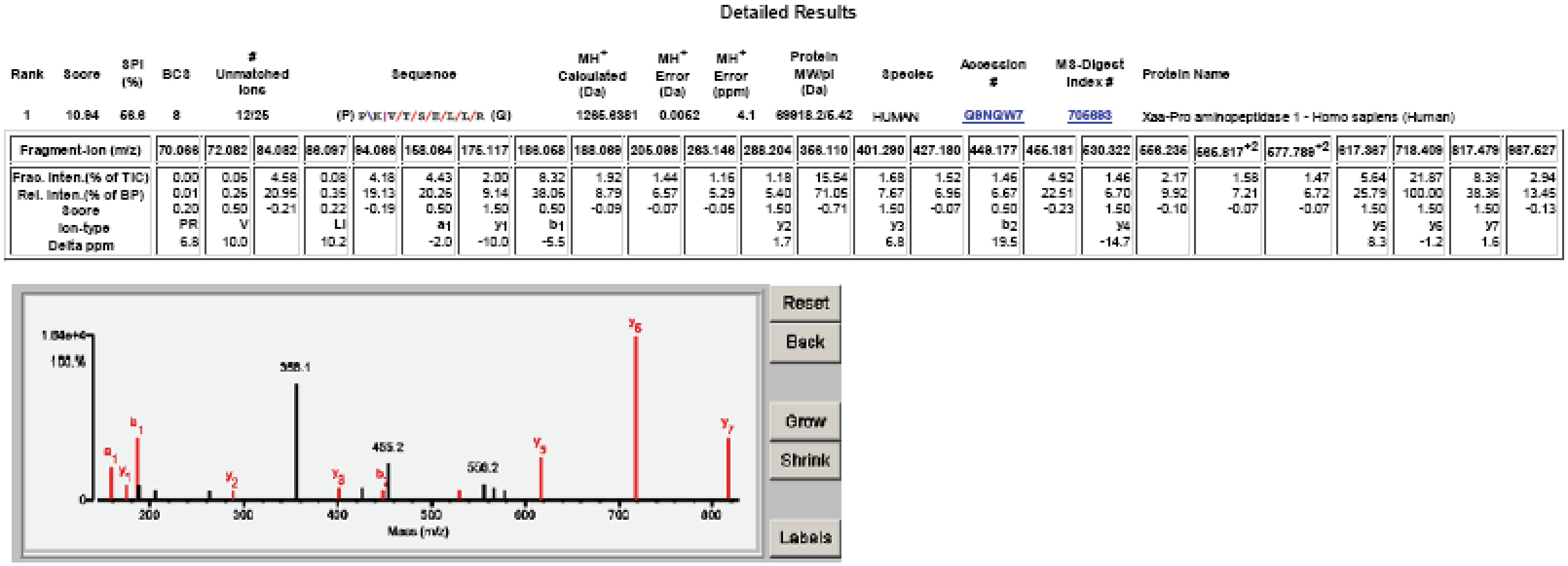
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.46	95.0	9	3/26	(V) I\E|S|V|V|A|D/L L/H/R (F)	1316.6879	0.0006	0.3	422382.3/6.38	HUMAN	Q709C8	698449	Vacuolar protein sorting-associated protein 13C - Homo sapiens (Human)

Fragment-Ion (m/z)	72.082	86.096	102.053	174.093	175.116	199.076	202.089	289.160	331.138	400.162	413.197	418.166	471.224
Frac. Inten.(% of TIC)	0.08	0.16	0.07	3.66	2.25	2.18	2.42	3.21	3.03	13.33	1.74	3.63	1.05
Rel. Inten.(% of BP)	0.40	0.85	0.38	18.98	11.66	11.30	12.57	16.65	15.72	69.17	9.01	18.86	5.45
Score	0.50	0.22	1.00	0.50	1.50	-0.11	0.50	1.50	0.50	0.25	-0.09	0.50	-0.05
Ion-type	V	LI	E	a_1	y_1		b_1	y_2	b_2	b_3-H_2O		b_3	
Delta ppm	11.4	-7.3	-20.1	-17.9	-22.0		-10.0	-7.5	12.9	-7.9		1.1	

Fragment-Ion (m/z)	499.221	516.330	617.230	618.301	630.356	683.409	687.320	701.393	783.426	800.468	899.527	988.688
Frac. Inten.(% of TIC)	10.75	2.52	4.25	1.76	4.79	1.13	1.12	9.68	1.26	19.26	2.73	3.93
Rel. Inten.(% of BP)	55.78	13.08	22.08	9.15	24.88	5.88	5.83	50.26	6.54	100.00	14.19	20.40
Score	0.25	1.50	0.50	0.50	1.50	0.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	b_4-H_2O	y_4	b_4	b_5	y_5	y_6-H_2O	b_6	y_6	y_7-NH_3	y_7	y_8	y_9
Delta ppm	-4.8	0.4	-6.5	-1.6	-3.1	37.2	-27.5	-1.9	-14.3	-8.6	-4.9	2.8

N80



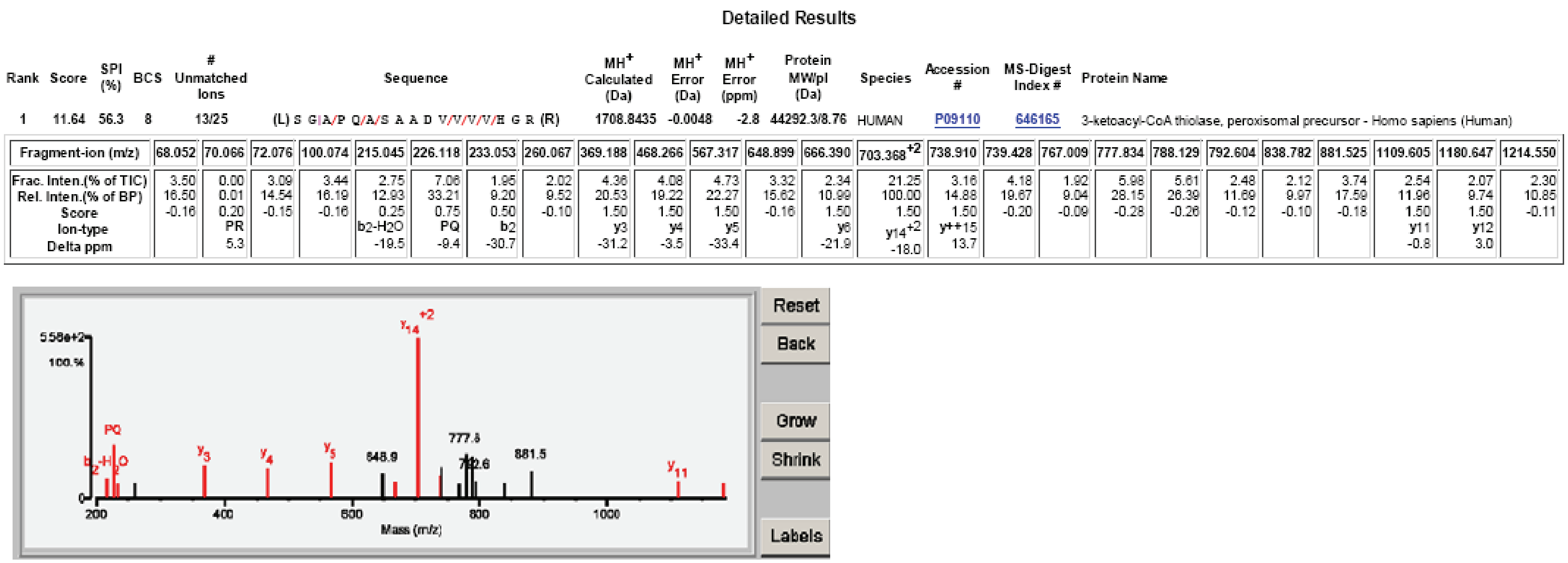
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.94	66.6	8	12/25	(P) F\K|V/T/S/E/L/L/R (G)	1266.6381	0.0062	4.1	69918.2/6.42	HUMAN	Q9NQW7	706893	Xaa-Pro aminopeptidase 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.082	84.082	86.097	94.066	158.084	175.117	186.068	188.069	205.088	263.148	288.204	368.110
Frac. Inten.(% of TIC)	0.00	0.06	4.58	0.08	4.18	4.43	2.00	8.32	1.92	1.44	1.16	1.18	15.54
Rel. Inten.(% of BP)	0.01	0.26	20.95	0.35	19.13	20.26	9.14	38.06	8.79	6.57	5.29	5.40	71.05
Score	0.20	0.50	-0.21	0.22	-0.19	0.50	1.50	0.50	-0.09	-0.07	-0.05	1.50	-0.71
Ion-type	PR	V		LI		a_1	y_1	b_1				y_2	
Delta ppm	6.8	10.0		10.2		-2.0	-10.0	-5.5				1.7	

Fragment-Ion (m/z)	401.290	427.180	449.177	466.181	530.322	568.236	586.817^{+2}	677.789^{+2}	617.367	718.409	817.479	987.627
Frac. Inten.(% of TIC)	1.68	1.52	1.46	4.92	1.46	2.17	1.58	1.47	5.64	21.87	8.39	2.94
Rel. Inten.(% of BP)	7.67	6.96	6.67	22.51	6.70	9.92	7.21	6.72	25.79	100.00	38.36	13.45
Score	1.50	-0.07	0.50	-0.23	1.50	-0.10	-0.07	-0.07	1.50	1.50	1.50	-0.13
Ion-type	y_3		b_2		y_4				y_5	y_6	y_7	
Delta ppm	6.8		19.5		-14.7				8.3	-1.2	1.6	

S1

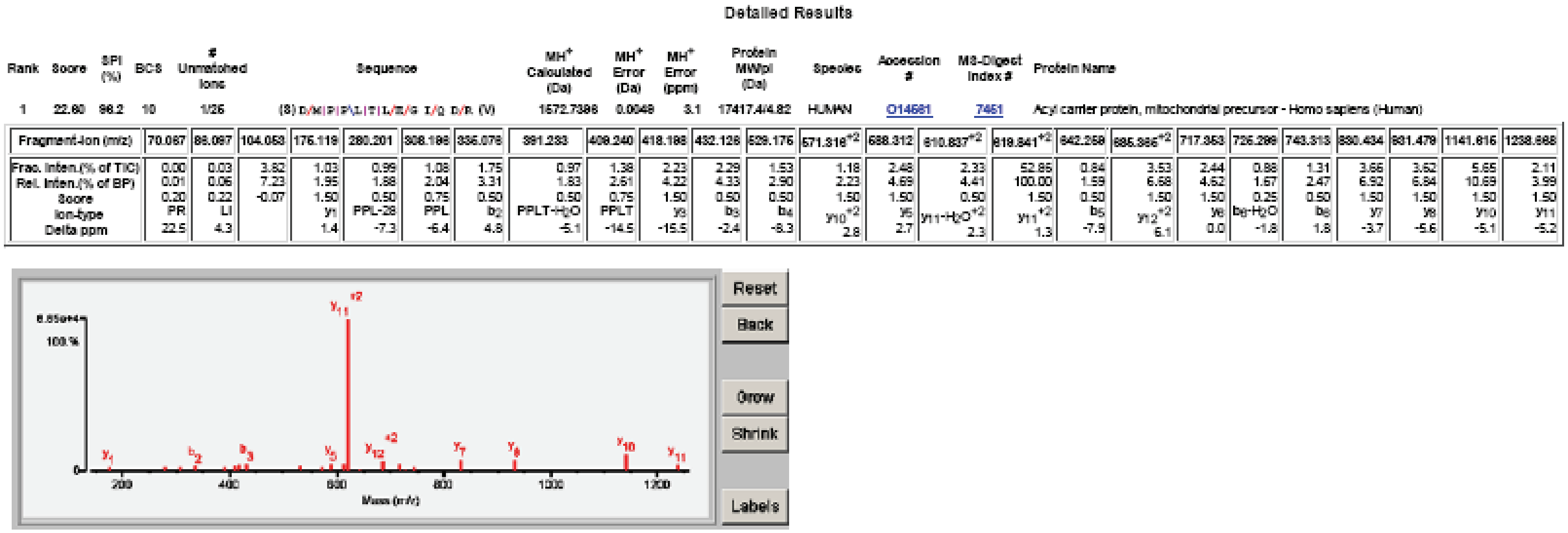


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.64	56.3	8	13/25	(L) S G|A/P Q/A/S A A D V/V/V/V/H G R (R)	1708.8435	-0.0048	-2.8	44292.3/8.76	HUMAN	P09110	646165	3-ketoacyl-CoA thiolase, peroxisomal precursor - Homo sapiens (Human)

Fragment-ion (m/z)	68.052	70.066	72.076	100.074	215.045	226.118	233.053	260.067	369.188	468.266	567.317	648.899	666.390	703.368^{+2}	738.910	739.428	767.009	777.834	788.129	792.604	838.782	881.525	1109.605	1180.647	1214.550
Frac. Inten.(% of TIC)	3.50	0.00	3.09	3.44	2.75	7.06	1.95	2.02	4.36	4.08	4.73	3.32	2.34	21.25	3.16	4.18	1.92	5.98	5.61	2.48	2.12	3.74	2.54	2.07	2.30
Rel. Inten.(% of BP)	16.50	0.01	14.54	16.19	12.93	33.21	9.20	9.52	20.53	19.22	22.27	15.62	10.99	100.00	14.88	19.67	9.04	28.15	26.39	11.69	9.97	17.59	11.96	9.74	10.85
Score	-0.16	0.20	-0.15	-0.16	0.25	0.75	0.50	-0.10	1.50	1.50	1.50	-0.16	1.50	1.50	1.50	-0.20	-0.09	-0.28	-0.26	-0.12	-0.10	-0.18	1.50	1.50	-0.11
Ion-type		PR			b_2-H_2O	PQ	b_2		y3	y4	y5		y6	y_{14}^{+2}	y++15								y11	y12	
Delta ppm		5.3			-19.5	-9.4	-30.7		-31.2	-3.5	-33.4		-21.9	-18.0	13.7								-0.8	3.0	

S2



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.80	96.2	10	1/26	(S) D/M|P|P\L|T|L/E/G I/Q D/R (V)	1572.7386	0.0048	3.1	17417.4/4.82	HUMAN	O14561	7451	Acyl carrier protein, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	86.097	104.053	176.119	280.201	308.196	336.076	391.233	409.240	418.198	432.128	529.176	571.318^{+2}	588.312	610.837^{+2}	619.841^{+2}	642.258	685.366^{+2}	717.353	726.299	743.313	830.434	931.479	1141.616	1238.688
Frac. Inten.(% of TIC)	0.00	0.03	3.82	1.03	0.99	1.08	1.75	0.97	1.38	2.23	2.29	1.53	1.18	2.48	2.33	52.86	0.84	3.53	2.44	0.88	1.31	3.66	3.62	5.65	2.11
Rel. Inten.(% of BP)	0.01	0.06	7.23	1.95	1.88	2.04	3.31	1.83	2.61	4.22	4.33	2.90	2.23	4.69	4.41	100.00	1.59	6.68	4.62	1.67	2.47	6.92	6.84	10.69	3.99
Score	0.20	0.22	-0.07	1.50	0.50	0.75	0.50	0.50	0.75	1.50	0.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50	0.25	0.50	1.50	1.50	1.50	1.50
Ion-type	PR	LI		y_1	PPL-28	PPL	b_2	PPLT-H_2O	PPLT	y_3	b_3	b_4	y_{10}^{+2}	y_5	y_{11}-H_2O^{+2}	y_{11}^{+2}	b_5	y_{12}^{+2}	y_6	b_6-H_2O	b_6	y_7	y_8	y_{10}	y_{11}
Delta ppm	22.5	4.3		1.4	-7.3	-6.4	4.8	-5.1	-14.5	-15.5	-2.4	-8.3	2.8	2.7	2.3	1.3	-7.9	6.1	0.0	-1.8	1.8	-3.7	-5.6	-5.1	-5.2

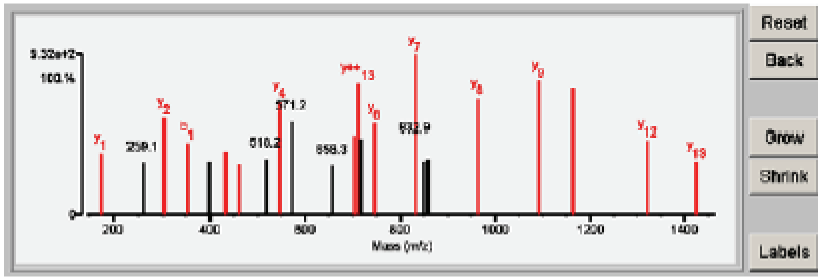
S3

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.88	69.7	11	10/25	(G) K|T/G T/A/E/M/S/S I/L/E/E/R (I)	1774.7809	0.0085	4.8	59760.8/9.16	HUMAN	P25705	44289	ATP synthase subunit alpha, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	84.083	175.122	259.063	304.163	362.111	389.116	433.199	460.198	518.185	546.296	571.204	658.277	703.338^{+2}
Frac. Inten.(% of TIC)	2.68	3.04	2.60	4.71	3.53	2.62	3.11	2.50	2.78	5.51	4.55	2.48	3.86
Rel. Inten.(% of BP)	34.12	38.71	33.12	60.11	45.02	33.38	39.66	31.88	35.48	70.30	57.97	31.61	49.21
Score	-0.34	1.50	-0.33	1.50	0.50	-0.33	1.50	0.75	-0.35	1.50	-0.58	-0.32	0.50
Ion-type		y_1		y_2	b_1		y_3	TGTAE		y_4			$y_{13}-H_2O^{+2}$
Delta ppm		15.7		6.1	-13.0		-11.2	-14.3		12.4			4.1

Fragment-Ion (m/z)	712.360	718.261	746.402	832.878	833.436	849.443^{+2}	869.159	964.473	1088.620	1164.548	1322.620	1423.666
Frac. Inten.(% of TIC)	6.38	3.75	4.47	3.43	7.84	2.68	2.79	5.64	6.55	6.23	3.63	2.65
Rel. Inten.(% of BP)	81.35	47.79	57.01	43.77	100.00	34.11	35.62	71.94	83.46	79.47	46.31	33.81
Score	1.50	-0.48	1.50	-0.44	1.50	-0.34	-0.36	1.50	1.50	1.50	1.50	1.50
Ion-type	y^{++}_{13}		y_6		y_7			y_8	y_9	y_{10}	y_{12}	y_{13}
Delta ppm	13.5		-2.9		0.1			-3.4	0.8	-7.3	-4.3	-12.4



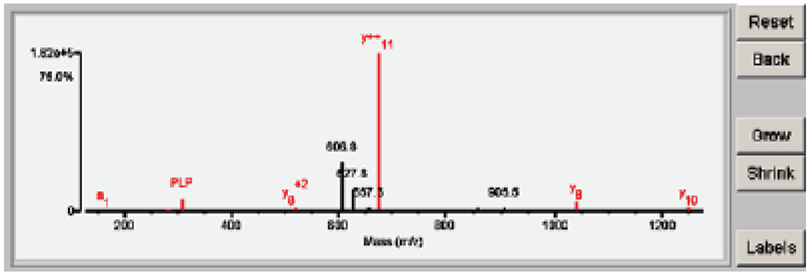
S4

Detailed Results

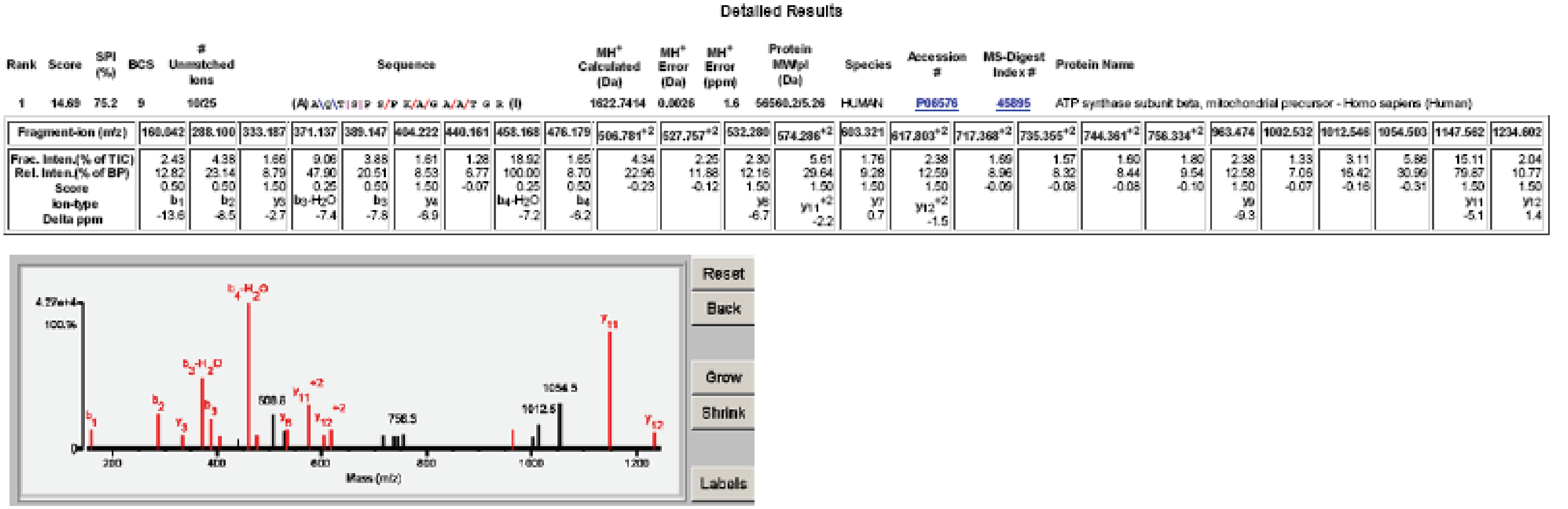
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.89	70.7	4	12/26	(P) V/P|P L/P E Y G G K V/R (Y)	1534.7545	0.0028	1.8	28908.8/9.37	HUMAN	P24539	39497	ATP synthase subunit b, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	72.081	86.096	160.076	175.118	233.060	276.114	280.198	285.126	308.194	474.214	520.761^{+2}	606.836
Frac. Inten.(% of TIC)	0.00	0.01	0.03	0.38	0.34	0.42	0.55	0.50	0.56	3.83	0.42	0.96	14.09
Rel. Inten.(% of BP)	0.00	0.02	0.05	0.62	0.57	0.70	0.91	0.83	0.94	6.35	0.69	1.59	23.41
Score	0.20	0.50	0.22	0.50	1.50	-0.01	-0.01	0.50	0.50	0.75	-0.01	1.50	-0.23
Ion-type	PR	V	LI	a_1	y_1			PLP-28	b_2	PLP		y_8^{+2}	
Delta ppm	-1.8	8.7	-15.4	-23.5	-17.4			-17.7	-9.2	-13.8		-3.7	

Fragment-Ion (m/z)	607.842^{+2}	625.813^{+2}	627.816^{+2}	657.347^{+2}	674.343	676.832	866.479	906.479	947.425	1040.486	1116.619	1260.627
Frac. Inten.(% of TIC)	3.15	0.42	6.50	0.90	60.20	0.65	0.78	1.07	0.41	2.69	0.34	0.82
Rel. Inten.(% of BP)	5.23	0.69	10.80	1.50	100.00	1.09	1.29	1.77	0.67	4.46	0.57	1.36
Score	-0.05	1.50	-0.11	-0.01	1.50	-0.01	-0.01	-0.02	-0.01	1.50	-0.01	1.50
Ion-type		y_{10}^{+2}			y^{++}_{11}					y_8		y_{10}
Delta ppm		-12.9			-6.3					-11.4		-6.6



S5

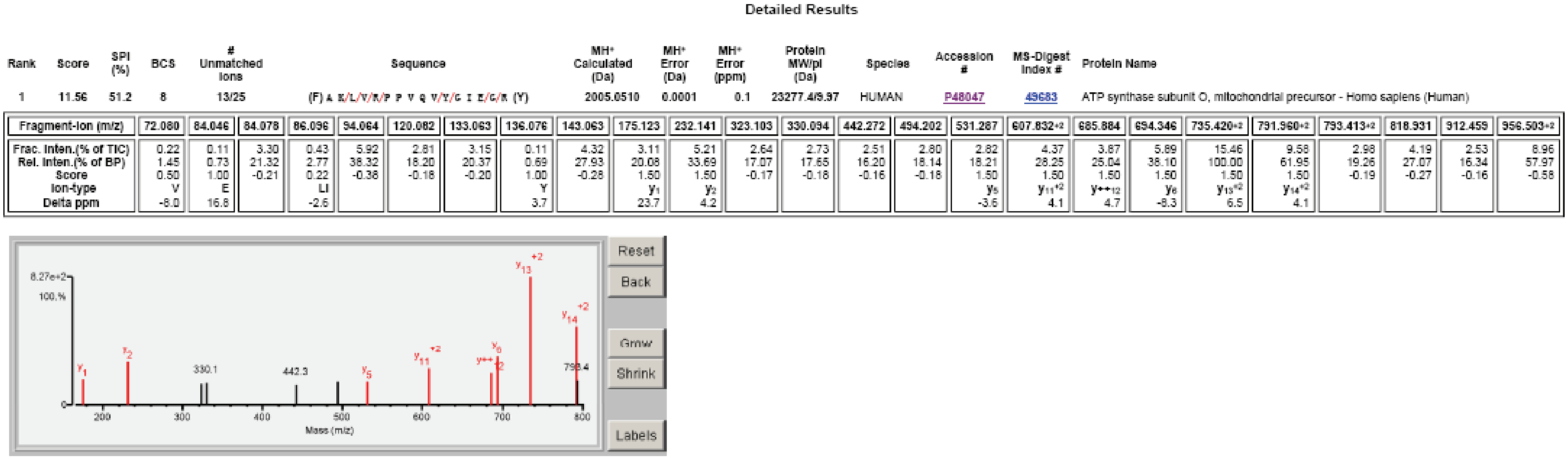


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.69	75.2	9	10/25	(A) A\Q\T|S|P S/P K/A/G A/A/T G R (I)	1622.7414	0.0026	1.6	56560.2/5.26	HUMAN	P06576	45895	ATP synthase subunit beta, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	160.042	288.100	333.187	371.137	389.147	404.222	440.161	458.168	476.179	506.781^{+2}	527.757^{+2}	532.288	574.286^{+2}	603.321	617.803^{+2}	717.368^{+2}	735.355^{+2}	744.361^{+2}	756.334^{+2}	963.474	1002.532	1012.546	1054.503	1147.562	1234.602
Frac. Inten.(% of TIC)	2.43	4.38	1.66	9.06	3.88	1.61	1.28	18.92	1.65	4.34	2.25	2.30	5.61	1.76	2.38	1.69	1.57	1.60	1.80	2.38	1.33	3.11	5.86	15.11	2.04
Rel. Inten.(% of BP)	12.82	23.14	8.79	47.90	20.51	8.53	6.77	100.00	8.70	22.96	11.88	12.16	29.64	9.28	12.59	8.96	8.32	8.44	9.54	12.58	7.06	16.42	30.99	79.87	10.77
Score	0.50	0.50	1.50	0.25	0.50	1.50	-0.07	0.25	0.50	-0.23	-0.12	1.50	1.50	1.50	1.50	-0.09	-0.08	-0.08	-0.10	1.50	-0.07	-0.16	-0.31	1.50	1.50
Ion-type	b_1	b_2	y_3	b_3-H_2O	b_3	y_4		b_4-H_2O	b_4			y_6	y_{11}^{+2}	y_7	y_{12}^{+2}					y_9				y_{11}	y_{12}
Delta ppm	-13.6	-6.5	-2.7	-7.4	-7.8	-6.9		-7.2	-6.2			-6.7	-2.2	0.7	-1.5					-9.3				-5.1	1.4

S6

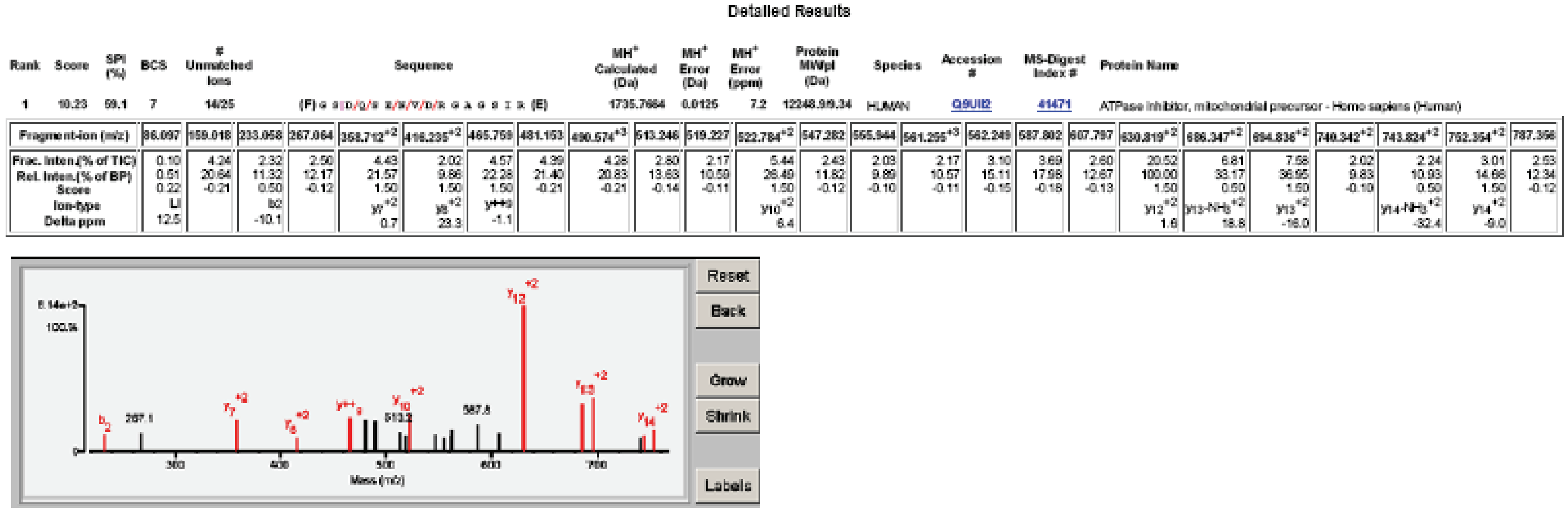


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.56	51.2	8	13/25	(F) A K/L/V/R/P P V Q V/Y/G I E/G/R (Y)	2005.0510	0.0001	0.1	23277.4/9.97	HUMAN	P48047	49683	ATP synthase subunit O, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	84.046	84.078	86.096	94.064	120.082	133.063	136.076	143.063	175.123	232.141	323.103	330.094	442.272	494.202	531.287	607.832^{+2}	685.884	694.346	735.420^{+2}	791.960^{+2}	793.413^{+2}	818.931	912.459	956.503^{+2}
Frac. Inten.(% of TIC)	0.22	0.11	3.30	0.43	5.92	2.81	3.15	0.11	4.32	3.11	5.21	2.64	2.73	2.51	2.80	2.82	4.37	3.87	5.89	15.46	9.58	2.98	4.19	2.53	8.96
Rel. Inten.(% of BP)	1.45	0.73	21.32	2.77	38.32	18.20	20.37	0.69	27.93	20.08	33.69	17.07	17.65	16.20	18.14	18.21	28.25	25.04	38.10	100.00	61.95	19.26	27.07	16.34	57.97
Score	0.50	1.00	-0.21	0.22	-0.36	-0.18	-0.20	1.00	-0.28	1.50	1.50	-0.17	-0.18	-0.16	-0.18	1.50	1.50	1.50	1.50	1.50	1.50	-0.19	-0.27	-0.16	-0.58
Ion-type	V	E		LI				Y		y_1	y_2					y_5	y_{11}^{+2}	y^{++}_{12}	y_6	y_{13}^{+2}	y_{14}^{+2}				
Delta ppm	-6.0	16.8		-2.6				3.7		23.7	4.2					-3.6	4.1	4.7	-8.3	6.5	4.1				

S7



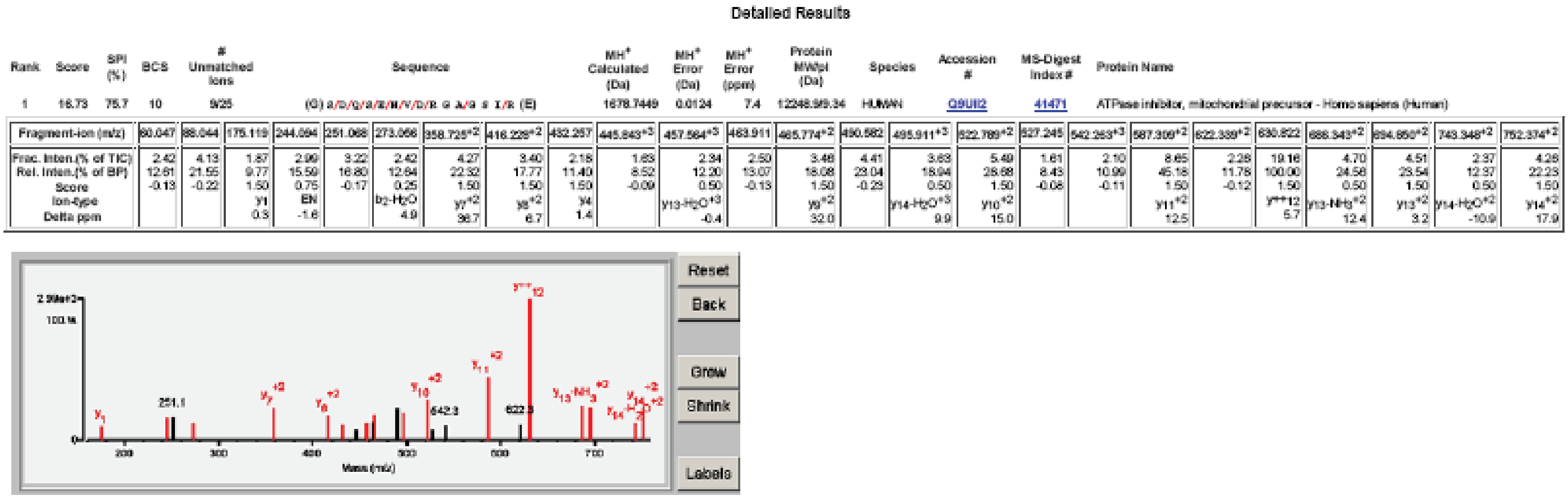
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.23	59.1	7	14/25	(F) G S D/Q/S E/N/V/D/R G A G S I R (E)	1735.7684	0.0125	7.2	12248.9/9.34	HUMAN	Q9UII2	41471	ATPase inhibitor, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	86.097	159.018	233.058	267.064	358.712^{+2}	416.235^{+2}	465.759	481.153	490.574^{+3}	513.246	519.227	522.784^{+2}
Frac. Inten.(% of TIC)	0.10	4.24	2.32	2.50	4.43	2.02	4.57	4.39	4.28	2.80	2.17	5.44
Rel. Inten.(% of BP)	0.51	20.64	11.32	12.17	21.57	9.86	22.28	21.40	20.83	13.63	10.59	26.49
Score	0.22	-0.21	0.50	-0.12	1.50	1.50	1.50	-0.21	-0.21	-0.14	-0.11	1.50
Ion-type	LI		b_2		y_7^{+2}	y_8^{+2}	y^{++}_9					y_{10}^{+2}
Delta ppm	12.5		-10.1		0.7	23.3	-1.1					6.4

Fragment-ion (m/z)	547.282	555.944	561.295^{+3}	562.249	587.802	607.797	630.819^{+2}	686.347^{+2}	694.836^{+2}	740.342^{+2}	743.824^{+2}	752.354^{+2}	787.356
Frac. Inten.(% of TIC)	2.43	2.03	2.17	3.10	3.69	2.60	20.52	6.81	7.58	2.02	2.24	3.01	2.53
Rel. Inten.(% of BP)	11.82	9.89	10.57	15.11	17.98	12.67	100.00	33.17	36.95	9.83	10.93	14.66	12.34
Score	-0.12	-0.10	-0.11	-0.15	-0.18	-0.13	1.50	0.50	1.50	-0.10	0.50	1.50	-0.12
Ion-type							y_{12}^{+2}	y_{13}-NH$_3^{+2}$	y_{13}^{+2}		y_{14}-NH$_3^{+2}$	y_{14}^{+2}	
Delta ppm							1.6	18.8	-16.0		-32.4	-9.0	

S8



Detailed Results

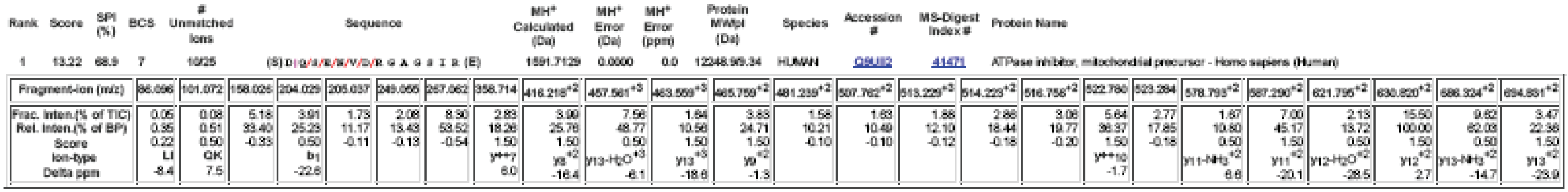
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.73	75.7	10	9/25	(G) S/D/Q/S/E/N/V/D/R G A/G S I/R (E)	1678.7449	0.0124	7.4	12248.9/9.34	HUMAN	Q9UII2	41471	ATPase inhibitor, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	80.047	88.044	175.119	244.094	251.068	273.056	358.725^{+2}	416.228^{+2}	432.257	445.843^{+3}	457.564^{+3}	463.911
Frac. Inten.(% of TIC)	2.42	4.13	1.87	2.99	3.22	2.42	4.27	3.40	2.18	1.63	2.34	2.50
Rel. Inten.(% of BP)	12.61	21.55	9.77	15.59	16.80	12.64	22.32	17.77	11.40	8.52	12.20	13.07
Score	-0.13	-0.22	1.50	0.75	-0.17	0.25	1.50	1.50	1.50	-0.09	0.50	-0.13
Ion-type			y_1	EN		b_2-H$_2$O	y_7^{+2}	y_8^{+2}	y_4		y_{13}-H$_2$O^{+3}	
Delta ppm			0.3	-1.6		4.9	36.7	6.7	1.4		-0.4	

Fragment-ion (m/z)	465.774^{+2}	490.582	495.911^{+3}	522.789^{+2}	527.245	542.263^{+3}	587.309^{+2}	622.339^{+2}	630.822	688.343^{+2}	694.850^{+2}	743.348^{+2}	752.374^{+2}
Frac. Inten.(% of TIC)	3.46	4.41	3.63	5.49	1.61	2.10	8.65	2.26	19.16	4.70	4.51	2.37	4.26
Rel. Inten.(% of BP)	18.08	23.04	18.94	28.68	8.43	10.99	45.18	11.78	100.00	24.58	23.54	12.37	22.23
Score	1.50	-0.23	0.50	1.50	-0.08	-0.11	1.50	-0.12	1.50	0.50	1.50	0.50	1.50
Ion-type	y_9^{+2}		y_{14}-H$_2$O^{+3}	y_{10}^{+2}			y_{11}^{+2}		$y^{++}12$	y_{13}-NH$_3^{+2}$	y_{13}^{+2}	y_{14}-H$_2$O^{+2}	y_{14}^{+2}
Delta ppm	32.0		9.9	15.0			12.5		5.7	12.4	3.2	-10.9	17.9

S9

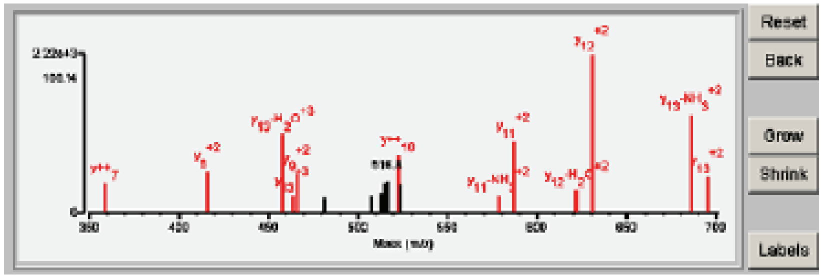
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.22	68.9	7	10/25	(S) D|Q/S/E/N/V/D/R G A G S I R (E)	1591.7129	0.0000	0.0	12248.9/9.34	HUMAN	Q9UII2	41471	ATPase inhibitor, mitochondrial precursor - Homo sapiens (Human)

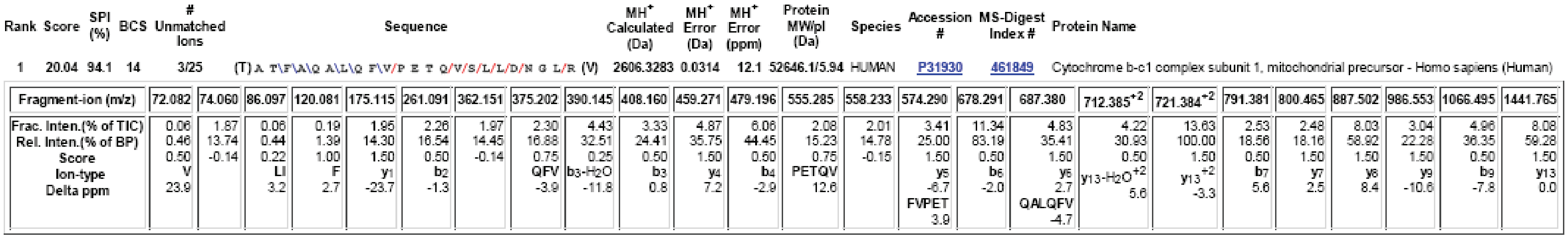
Fragment-ion (m/z)	86.096	101.072	158.026	204.029	205.037	249.065	257.062	358.714	416.218^{+2}	457.561^{+3}	463.559^{+3}	465.759^{+2}	481.239^{+2}
Frac. Inten.(% of TIC)	0.05	0.08	5.18	3.91	1.73	2.08	8.30	2.83	3.99	7.56	1.64	3.83	1.58
Rel. Inten.(% of BP)	0.35	0.51	33.40	25.23	11.17	13.43	53.52	18.26	25.78	48.77	10.58	24.71	10.21
Score	0.22	0.50	-0.33	0.50	-0.11	-0.13	-0.54	1.50	1.50	0.50	1.50	1.50	-0.10
Ion-type	LI	QK		b_1				y^{++}_7	y_8^{+2}	$y_{13}\text{-}H_2O^{+3}$	y_{13}^{+3}	y_9^{+2}	
Delta ppm	-8.4	7.5		-22.6				6.0	-16.4	-6.1	-18.6	-1.3	

Fragment-ion (m/z)	507.762^{+2}	513.229^{+2}	514.223^{+2}	516.756^{+2}	522.780	523.284	578.793^{+2}	587.290^{+2}	621.795^{+2}	630.820^{+2}	686.324^{+2}	694.831^{+2}
Frac. Inten.(% of TIC)	1.63	1.88	2.86	3.08	5.64	2.77	1.67	7.00	2.13	15.50	9.62	3.47
Rel. Inten.(% of BP)	10.49	12.10	18.44	19.77	36.37	17.85	10.80	45.17	13.72	100.00	62.03	22.38
Score	-0.10	-0.12	-0.18	-0.20	1.50	-0.18	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type					y^{++}_{10}		$y_{11}\text{-}NH_3^{+2}$	y_{11}^{+2}	$y_{12}\text{-}H_2O^{+2}$	y_{12}^{+2}	$y_{13}\text{-}NH_3^{+2}$	y_{13}^{+2}
Delta ppm					-1.7		6.6	-20.1	-28.5	2.7	-14.7	-23.9



S10

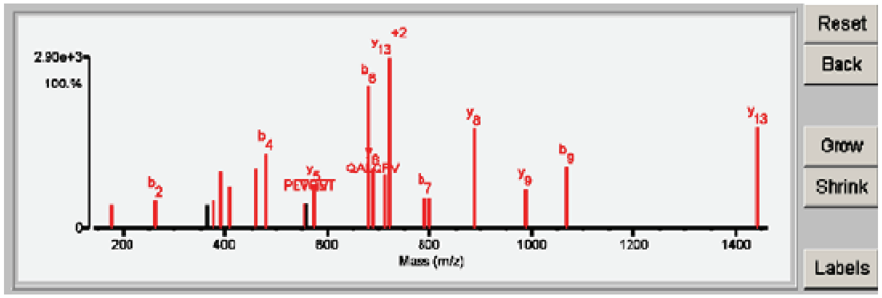
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.04	94.1	14	3/25	(T) A T\F\A\Q A\L\Q F\V/P E T Q/V/S/L/L/D/N G L/R (V)	2606.3283	0.0314	12.1	52646.1/5.94	HUMAN	P31930	461849	Cytochrome b-c1 complex subunit 1, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	74.060	86.097	120.081	175.115	261.091	362.151	375.202	390.145	408.160	459.271	479.196	555.285
Frac. Inten.(% of TIC)	0.06	1.87	0.06	0.19	1.95	2.26	1.97	2.30	4.43	3.33	4.87	6.06	2.08
Rel. Inten.(% of BP)	0.46	13.74	0.44	1.39	14.30	16.54	14.45	16.88	32.51	24.41	35.75	44.45	15.23
Score	0.50	-0.14	0.22	1.00	1.50	0.50	-0.14	0.75	0.25	0.50	1.50	0.50	0.75
Ion-type	V		LI	F	y_1	b_2		QFV	$b_3\text{-}H_2O$	b_3	y_4	b_4	PETQV
Delta ppm	23.9		3.2	2.7	-23.7	-1.3		-3.9	-11.8	0.8	7.2	-2.9	12.6

Fragment-ion (m/z)	558.233	574.290	678.291	687.380	712.385^{+2}	721.384^{+2}	791.381	800.465	887.502	986.553	1066.495	1441.765
Frac. Inten.(% of TIC)	2.01	3.41	11.34	4.83	4.22	13.63	2.53	2.48	8.03	3.04	4.96	8.08
Rel. Inten.(% of BP)	14.78	25.00	83.19	35.41	30.93	100.00	18.56	18.16	58.92	22.28	36.35	59.28
Score	-0.15	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50	0.50	1.50
Ion-type		y_5	b_6	y_6	$y_{13}\text{-}H_2O^{+2}$	y_{13}^{+2}	b_7	y_7	y_8	y_9	b_9	y_{13}
Delta ppm		-6.7	-2.0	2.7	5.6	-3.3	5.6	2.5	8.4	-10.6	-7.8	0.0
		FVPET		QALQFV								
		3.9		-4.7								



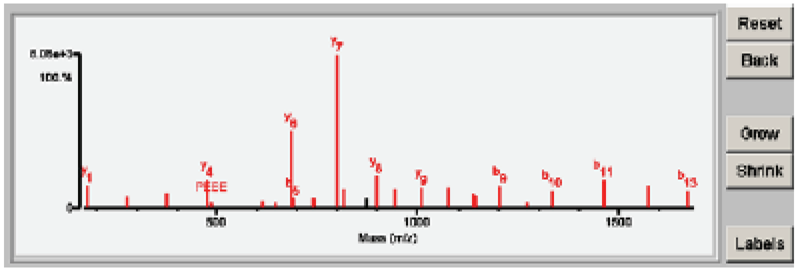
S11

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.84	98.4	16	1/25	(G) D/P E E E\E\E\E\E|E|E|L|V|D/P L/T/T/V/R (E)	2475.0803	0.0034	1.4	10738.8/4.39	HUMAN	P07919	481887	Cytochrome b-c1 complex subunit 6, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	175.118	274.184	375.234	476.273	486.182	614.217	646.212	686.416	688.215	743.271	801.441	817.246	872.288
Frac. Inten.(% of TIC)	3.75	1.84	2.43	4.60	1.01	1.22	0.95	12.64	1.63	1.53	25.16	3.14	1.56
Rel. Inten.(% of BP)	14.92	7.31	9.65	18.27	4.03	4.86	3.79	50.25	6.47	6.09	100.00	12.47	6.18
Score	1.50	1.50	1.50	1.50	0.75	0.75	0.75	1.50	0.50	0.75	1.50	0.50	-0.06
Ion-type	y_1	y_2	y_3	y_4	PEEE	PEEEE	EEEEE	y_6	b_5	PEEEEE	y_7	b_6	
Delta ppm	-4.3	-11.5	-2.3	-19.6	5.3	-24.4	-15.1	-5.5	1.7	-4.3	-7.5	-13.5	

Fragment-ion (m/z)	900.510	946.289	1013.601	1075.336	1138.517^{+2}	1142.643	1204.378	1271.680	1333.424	1462.461	1575.542	1674.608
Frac. Inten.(% of TIC)	5.38	3.20	3.28	3.27	2.25	2.12	3.56	1.02	2.93	4.66	3.86	3.01
Rel. Inten.(% of BP)	21.37	12.70	13.04	12.99	8.95	8.45	14.17	4.06	11.64	18.53	15.34	11.94
Score	1.50	0.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50	0.50	0.50	0.50
Ion-type	y_8	b_7	y_9	b_8	y_{19}^{+2}	y_{10}	b_9	y_{11}	b_{10}	b_{11}	b_{12}	b_{13}
Delta ppm	-6.0	-11.2	2.1	-6.7	-3.8	1.5	-5.5	-3.0	-2.7	-5.7	-7.3	-8.8



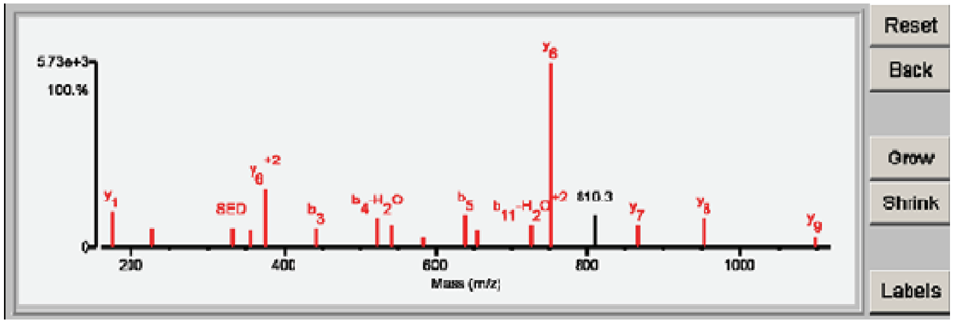
S12

Detailed Results

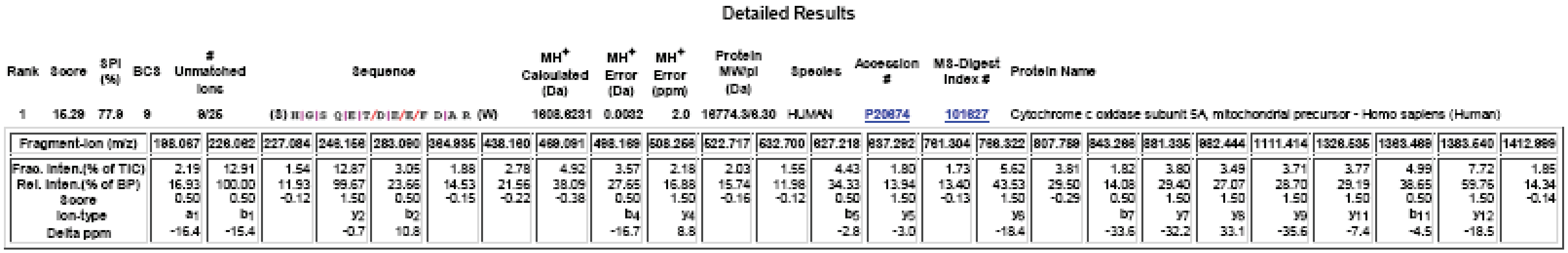
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.24	87.6	12	4/25	(A) H\E\S\V\V\K S E D/F/S/L/P/A/Y M D/R (R)	2333.0035	0.0115	4.9	19576.8/9.52	HUMAN	P13073	101541	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.082	84.045	86.097	120.079	141.102	175.119	226.062	332.111	355.104	376.679^{+2}	442.138	523.197
Frac. Inten.(% of TIC)	0.00	0.11	0.06	0.28	0.31	2.17	5.58	3.00	3.01	2.77	9.34	3.02	4.58
Rel. Inten.(% of BP)	0.01	0.37	0.20	0.98	1.09	7.55	19.40	10.43	10.47	9.62	32.47	10.49	15.92
Score	0.20	0.50	1.00	0.22	1.00	-0.08	1.50	0.50	0.75	0.50	1.50	0.50	0.25
Ion-type	PR	V	E	LI	F		y1	b1	SED	b2	$y6^{+2}$	b3	b4-H2O
Delta ppm	-8.9	19.8	2.5	0.9	-12.3		0.8	-16.2	4.4	-12.6	14.5	-5.6	-2.0

Fragment-ion (m/z)	541.205	584.252	640.276	655.288	725.782^{+2}	752.336	810.318	865.410	952.451	1099.545	1141.429	1357.508
Frac. Inten.(% of TIC)	3.54	1.93	5.14	2.72	3.44	28.76	5.02	3.51	4.66	1.83	2.70	2.54
Rel. Inten.(% of BP)	12.31	6.72	17.87	9.46	11.97	100.00	17.44	12.21	16.19	6.38	9.38	8.82
Score	0.50	1.50	0.50	1.50	0.25	1.50	-0.17	1.50	1.50	1.50	-0.09	-0.09
Ion-type	b4	y4	b5	y5	$b11-H2O^{+2}$	y6		y7	y8	y9		
Delta ppm	-6.7	4.1	-1.9	2.4	-15.1	-4.8		-16.0	-4.8	18.7		



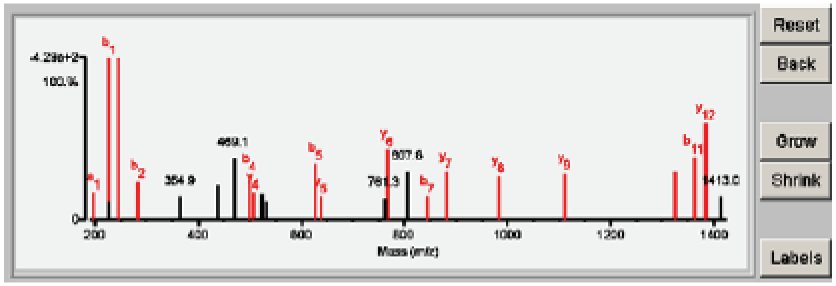
S13



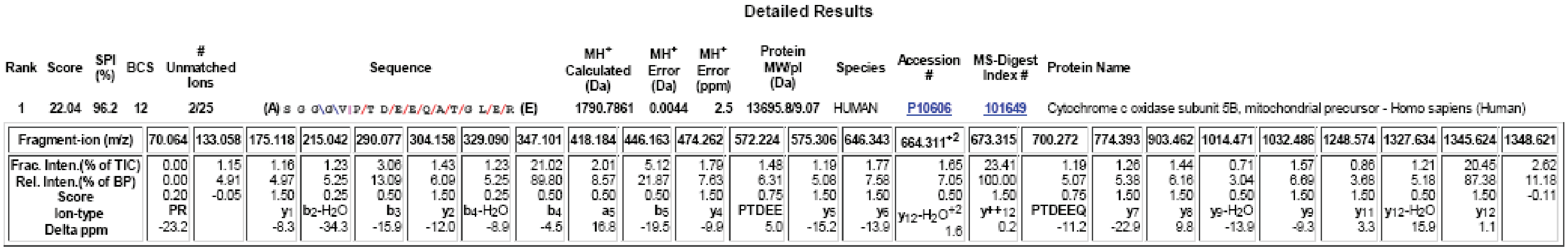
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.29	77.8	9	8/26	(S) H|G|S Q|E|T/D|E/E/F D|A R (W)	1608.6231	0.0032	2.0	16774.3/6.30	HUMAN	P20674	101627	Cytochrome c oxidase subunit 5A, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	188.087	226.082	227.084	246.158	283.090	364.935	438.160	469.091	498.169	508.268	522.717	632.700	627.218	637.292	761.304	768.322	807.789	843.268	881.336	882.444	1111.414	1326.535	1363.489	1383.640	1412.989
Frac. Inten.(% of TIC)	2.19	12.91	1.54	12.87	3.05	1.88	2.78	4.92	3.57	2.18	2.03	1.55	4.43	1.80	1.73	5.62	3.81	1.82	3.80	3.49	3.71	3.77	4.99	7.72	1.85
Rel. Inten.(% of BP)	16.93	100.00	11.93	99.67	23.66	14.53	21.56	38.09	27.65	16.88	15.74	11.98	34.33	13.94	13.40	43.53	29.50	14.08	29.40	27.07	28.70	29.19	38.65	59.76	14.34
Score	0.50	0.50	-0.12	1.50	0.50	-0.15	-0.22	-0.38	0.50	1.50	-0.16	-0.12	0.50	1.50	-0.13	1.50	-0.29	0.50	1.50	1.50	1.50	1.50	0.50	1.50	-0.14
Ion-type	a_1	b_1		y_2	b_2				b_4	y_4			b_5	y_5		y_6		b_7	y_7	y_8	y_9	y_{11}	b_{11}	y_{12}	
Delta ppm	-16.4	-15.4		-0.7	10.8				-16.7	8.8			-2.8	-3.0		-18.4		-33.6	-32.2	33.1	-35.6	-7.4	-4.5	-18.5	



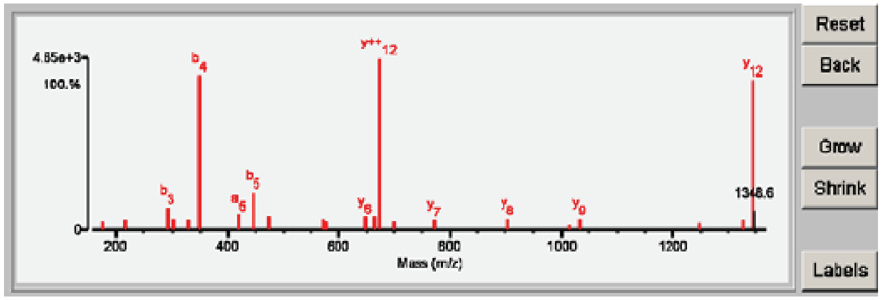
S14



Detailed Results

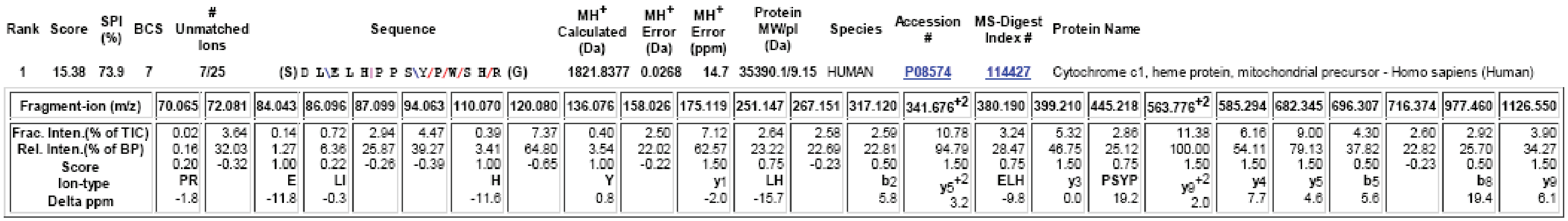
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.04	96.2	12	2/25	(A) S G G\G\V|P/T D/E/E/Q/A/T/G L/E/R (E)	1790.7861	0.0044	2.5	13695.8/9.07	HUMAN	P10606	101649	Cytochrome c oxidase subunit 5B, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	133.058	175.118	215.042	290.077	304.158	329.090	347.101	418.184	446.163	474.262	572.224	575.306	646.343	664.311^{+2}	673.315	700.272	774.393	903.462	1014.471	1032.486	1248.574	1327.634	1345.624	1348.621
Frac. Inten.(% of TIC)	0.00	1.15	1.16	1.23	3.06	1.43	1.23	21.02	2.01	5.12	1.79	1.48	1.19	1.77	1.65	23.41	1.19	1.26	1.44	0.71	1.57	0.86	1.21	20.45	2.62
Rel. Inten.(% of BP)	0.00	4.91	4.97	5.25	13.09	6.09	5.25	89.80	8.57	21.87	7.63	6.31	5.08	7.58	7.05	100.00	5.07	5.38	6.16	3.04	6.69	3.68	5.18	87.38	11.18
Score	0.20	-0.05	1.50	0.25	0.50	1.50	0.25	0.50	0.50	0.50	1.50	0.75	1.50	1.50	0.50	1.50	0.75	1.50	1.50	0.50	1.50	1.50	0.50	1.50	-0.11
Ion-type	PR		y_1	b_2-H$_2$O	b_3	y_2	b_4-H$_2$O	b_4	a_5	b_5	y_4	PTDEE	y_5	y_6	y_{12}-H$_2$O^{+2}	y^{++}_{12}	PTDEEQ	y_7	y_8	y_9-H$_2$O	y_9	y_{11}	y_{12}-H$_2$O	y_{12}	
Delta ppm	-23.2		-8.3	-34.3	-15.9	-12.0	-8.9	-4.5	16.8	-19.5	-9.9	5.0	-15.2	-13.9	1.6	0.2	-11.2	-22.9	9.8	-13.9	-9.3	3.3	15.9	1.1	



S15

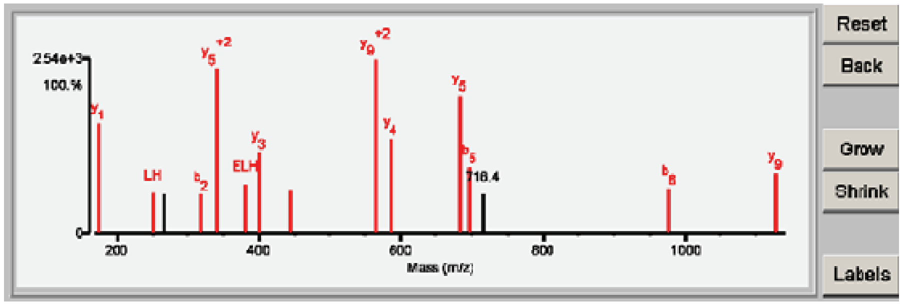
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.38	73.9	7	7/25	(S) D L\E L H|P P S\Y/P/W/S H/R (G)	1821.8377	0.0268	14.7	35390.1/9.15	HUMAN	P08574	114427	Cytochrome c1, heme protein, mitochondrial precursor - Homo sapiens (Human)

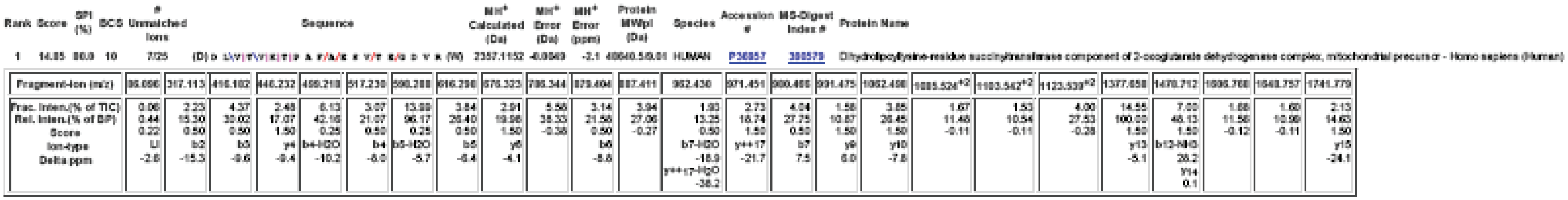
Fragment-ion (m/z)	70.065	72.081	84.043	86.096	87.099	94.063	110.070	120.080	136.076	158.026	175.119	251.147
Frac. Inten.(% of TIC)	0.02	3.64	0.14	0.72	2.94	4.47	0.39	7.37	0.40	2.50	7.12	2.64
Rel. Inten.(% of BP)	0.16	32.03	1.27	6.36	25.87	39.27	3.41	64.80	3.54	22.02	62.57	23.22
Score	0.20	-0.32	1.00	0.22	-0.26	-0.39	1.00	-0.65	1.00	-0.22	1.50	0.75
Ion-type	PR		E	LI			H		Y		y1	LH
Delta ppm	-1.8		-11.8	-0.3			-11.6		0.8		-2.0	-15.7

Fragment-ion (m/z)	267.151	317.120	341.676^{+2}	380.190	399.210	445.218	563.776^{+2}	585.294	682.345	696.307	716.374	977.460	1126.550
Frac. Inten.(% of TIC)	2.58	2.59	10.78	3.24	5.32	2.86	11.38	6.16	9.00	4.30	2.60	2.92	3.90
Rel. Inten.(% of BP)	22.69	22.81	94.79	28.47	46.75	25.12	100.00	54.11	79.13	37.82	22.82	25.70	34.27
Score	-0.23	0.50	1.50	0.75	1.50	0.75	1.50	1.50	1.50	0.50	-0.23	0.50	1.50
Ion-type		b2	y5^{+2}	ELH	y3	PSYP	y9^{+2}	y4	y5	b5		b8	y9
Delta ppm		5.8	3.2	-9.8	0.0	19.2	2.0	7.7	4.6	5.6		19.4	6.1



S16

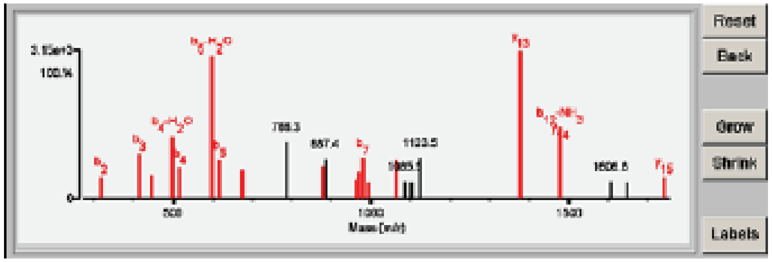
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.85	80.0	10	7/25	(D) D L\V|T\V|K|T|P A F/A/E E V/T E/G D V K (W)	2357.1152	-0.0049	-2.1	48840.5/6.01	HUMAN	P36957	380579	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	317.113	416.182	446.232	499.218	517.230	598.288	616.298	676.323	706.344	879.404	887.411
Frac. Inten.(% of TIC)	0.06	2.23	4.37	2.48	6.13	3.07	13.99	3.84	2.91	5.58	3.14	3.94
Rel. Inten.(% of BP)	0.44	15.30	30.02	17.07	42.16	21.07	96.17	26.40	19.98	38.33	21.58	27.06
Score	0.22	0.50	0.50	1.50	0.25	0.50	0.25	0.50	1.50	-0.38	0.50	-0.27
Ion-type	LI	b2	b3	y4	b4-H2O	b4	b5-H2O	b5	y6		b6	
Delta ppm	-2.6	-15.3	-9.6	-9.4	-10.2	-8.0	-5.7	-6.4	-4.1		-8.8	

Fragment-ion (m/z)	962.430	971.451	980.466	991.475	1062.498	1085.524^{+2}	1103.542^{+2}	1123.539^{+2}	1377.658	1470.712	1606.768	1640.757	1741.779
Frac. Inten.(% of TIC)	1.93	2.73	4.04	1.58	3.85	1.67	1.53	4.00	14.55	7.00	1.68	1.60	2.13
Rel. Inten.(% of BP)	13.25	18.74	27.75	10.87	26.45	11.48	10.54	27.53	100.00	48.13	11.58	10.99	14.63
Score	0.50	1.50	0.50	1.50	1.50	-0.11	-0.11	-0.28	1.50	1.50	-0.12	-0.11	1.50
Ion-type	b7-H2O y++17-H2O	y++17	b7	y9	y10				y13	b12-NH3 y14			y15
Delta ppm	-18.9 -38.2	-21.7	7.5	6.0	-7.8				-5.1	28.2 0.1			-24.1

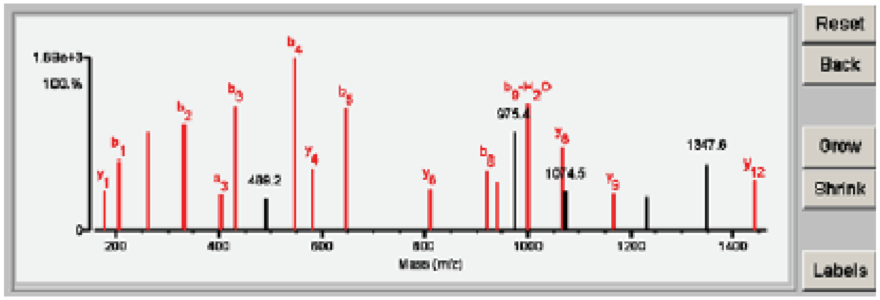


S17

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.41	78.3	12	7/25	(D) D\E\V\D\V|D G T|V/E/E/D L/G K/S/R (E)	2085.8740	-0.0200	-9.6	92469.3/4.76	HUMAN	P14625	185471	Endoplasmin precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	88.095	128.068	176.118	204.030	262.148	333.073	404.183	432.137	488.221	547.168	582.273	648.236	810.386	919.324	939.412	975.406	1000.386	1068.480	1071.324	1074.486	1187.687	1232.524	1347.567	1440.614
Frac. Inten.(% of TIC)	0.12	0.10	2.59	2.49	4.23	5.98	6.42	2.25	7.60	2.04	10.53	3.82	7.43	2.58	3.73	3.00	5.97	7.72	4.96	2.38	2.49	2.26	2.13	4.06	3.08
Rel. Inten.(% of BP)	1.16	0.98	24.63	23.62	40.20	56.85	61.00	21.36	72.21	19.42	100.00	36.33	70.57	24.55	35.46	28.49	56.75	73.30	47.11	22.63	23.70	21.48	20.27	38.59	29.25
Score	0.50	0.22	-0.25	1.50	0.50	1.50	0.50	0.50	0.50	-0.19	0.50	1.50	0.50	1.50	0.50	1.50	-0.57	0.25	1.50	-0.23	-0.24	1.50	-0.20	-0.39	1.50
Ion-type	V	LI		y_1	b_1	y_2	b_2	a_3	b_3		b_4	y_4	b_5	y_6	b_8	y_7		b_9-H_2O	y_8			y_9			y_{12}
Delta ppm	1.7	-16.6		-2.0	-18.6	-17.5	-8.7	33.4	-16.7		-22.2	-14.2	-6.3	-9.5	-13.4	-24.7		-9.2	-16.4			17.8			-19.9

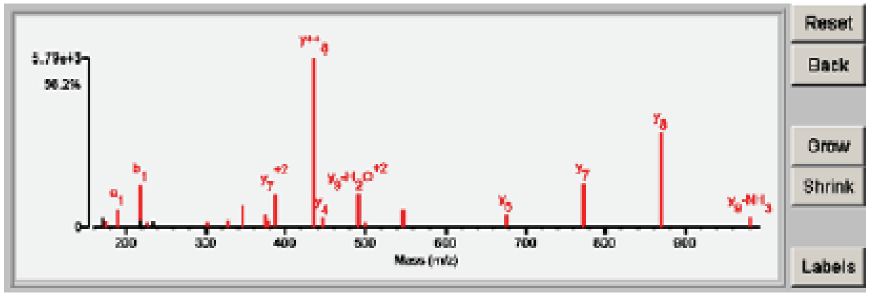


S18

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.82	96.7	9	3/25	(E) E|Q|P/P/E/T/A/A/Q/R (C)	1214.6470	0.0039	3.2	54388.0/6.48	HUMAN	Q96HE7	187919	ERO1-like protein alpha precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	84.043	101.072	172.041	176.118	190.062	218.060	219.060	227.100	236.074	303.176	328.146	348.105	374.217	377.700^{+2}	388.702^{+2}	436.229	446.248	490.265^{+2}	499.268^{+2}	546.303	675.349	772.391	869.446	980.488
Frac. Inten.(% of TIC)	0.00	0.06	0.17	1.41	0.95	2.50	5.91	1.04	0.63	0.87	0.65	1.16	3.09	1.75	1.10	4.51	42.25	1.32	4.67	0.72	2.45	1.78	6.22	13.32	1.45
Rel. Inten.(% of BP)	0.00	0.15	0.39	3.34	2.25	5.91	13.98	2.47	1.49	2.07	1.55	2.76	7.31	4.15	2.61	10.66	100.00	3.13	11.06	1.71	5.81	4.21	14.72	31.54	3.42
Score	0.20	1.00	0.50	-0.03	1.50	0.50	0.50	-0.02	0.75	-0.02	1.50	0.75	0.50	1.50	0.50	1.50	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	0.50
Ion-type	PR	E	QK		y_1	a_1	b_1		PE		y_2	PET	b_2	y_3	y_7-H_2O^{+2}	y_7^{+2}	y^{++}_8	y_4	y_9-H_2O^{+2}	y_9^{+2}	y_5	y_6	y_7	y_8	y_9-NH_3
Delta ppm	-0.4	-21.3	11.5		0.3	-11.8	1.6		-17.7		-5.7	-16.5	-9.3	7.6	12.6	2.2	4.8	-7.8	6.5	5.2	5.6	10.6	-5.4	-2.8	-10.9



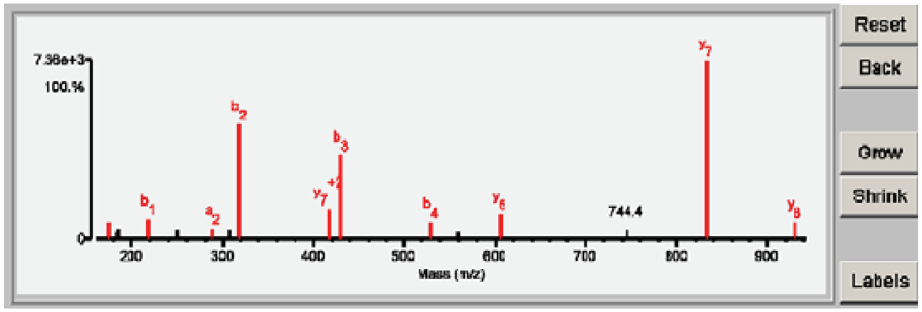
S19

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.34	83.4	6	10/25	(R) E\V\L|V|P E/G P L Y/R (V)	1359.6977	-0.0086	-6.3	65034.6/8.23	HUMAN	Q969P0	268031	Immunoglobulin superfamily member 8 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.047	86.096	94.066	101.071	110.071	136.076	157.130	175.121	183.121	185.084
Frac. Inten.(% of TIC)	0.01	0.23	0.08	0.28	1.64	1.28	3.41	0.11	1.30	2.86	1.18	1.80
Rel. Inten.(% of BP)	0.02	0.82	0.27	1.00	5.79	4.50	12.02	0.39	4.59	10.09	4.14	6.35
Score	0.20	0.50	1.00	0.22	-0.06	-0.05	-0.12	1.00	-0.05	1.50	-0.04	-0.06
Ion-type	PR	V	E	LI				Y		y1		
Delta ppm	8.2	18.4	31.1	-6.1				2.3		12.8		

Fragment-ion (m/z)	218.047	251.066	289.117	308.220	317.116	416.229^{+2}	430.198	529.267	558.252	605.335	744.354	831.433	930.496
Frac. Inten.(% of TIC)	3.18	1.51	1.86	1.63	18.42	4.72	13.51	2.82	1.34	4.10	1.55	28.39	2.78
Rel. Inten.(% of BP)	11.19	5.33	6.56	5.74	64.89	16.62	47.58	9.95	4.71	14.43	5.45	100.00	9.78
Score	0.50	-0.05	0.50	-0.06	0.50	1.50	0.50	0.50	-0.05	1.50	-0.05	1.50	1.50
Ion-type	b1		a2		b2	$y7^{+2}$	b3	b4		y6		y7	y8
Delta ppm	-8.5		-18.9		-4.6	16.8	-8.2	-5.9		-8.9		-4.1	-8.8



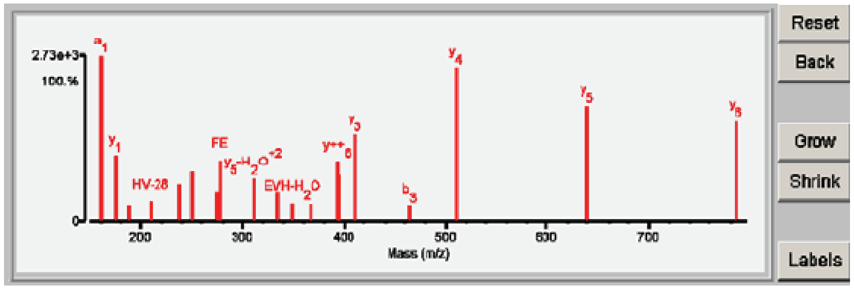
S20

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.64	95.8	6	2/25	(K) V|F|E|V/H/V/R (P)	973.4924	0.0033	3.4	30654.5/7.10	HUMAN	P13598	262037	Intercellular adhesion molecule 2 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.082	86.097	110.071	120.081	121.083	160.078	175.119	188.074	209.136	237.134	249.125
Frac. Inten.(% of TIC)	0.00	0.42	2.00	0.24	0.80	2.21	13.69	5.50	1.38	1.74	3.14	4.13
Rel. Inten.(% of BP)	0.01	3.05	14.60	1.72	5.87	16.14	100.00	40.14	10.09	12.74	22.96	30.17
Score	0.20	0.50	-0.15	1.00	1.00	-0.16	0.50	1.50	0.50	0.50	0.75	0.50
Ion-type	PR	V		H	F		a1	y1	b1	HV-28	HV	FE-28
Delta ppm	-14.6	10.0		-0.7	-2.3		-12.2	-2.6	-7.8	-23.8	-7.2	1.7

Fragment-ion (m/z)	274.186	277.116	311.171^{+2}	335.141	348.173	366.178	393.718	394.215	411.243	464.195	510.309	639.355	786.422
Frac. Inten.(% of TIC)	2.51	5.09	3.58	2.47	1.60	1.49	4.93	3.90	7.14	1.38	12.70	9.54	8.42
Rel. Inten.(% of BP)	18.31	37.19	26.17	18.04	11.70	10.90	35.98	28.52	52.16	10.07	92.75	69.70	61.48
Score	1.50	0.75	0.50	0.50	0.50	0.75	1.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	y2	FE	$y5\text{-}H_2O^{+2}$	b2	EVH-H_2O	EVH	y++6	y3-NH_3	y3	b3	y4	y5	y6
Delta ppm	-4.6	-11.5	-18.3	-7.7	16.0	-1.9	3.3	-11.0	-8.9	19.6	-11.3	-3.1	-4.8



S21

Detailed Results

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<tr><td>1</td><td>18.86</td><td>90.9</td><td>11</td><td>5/25</td><td>(S) T Q A\A|T|Q/V|V|L/N/V|P E/T/R (V)</td><td>1714.8792</td><td>0.0017</td><td>1.0</td><td>54366.5/6.38</td><td>HUMAN</td><td>O75439</td><td>341571</td><td>Mitochondrial-processing peptidase subunit beta, mitochondrial precursor - Homo sapiens (Human)</td></tr>
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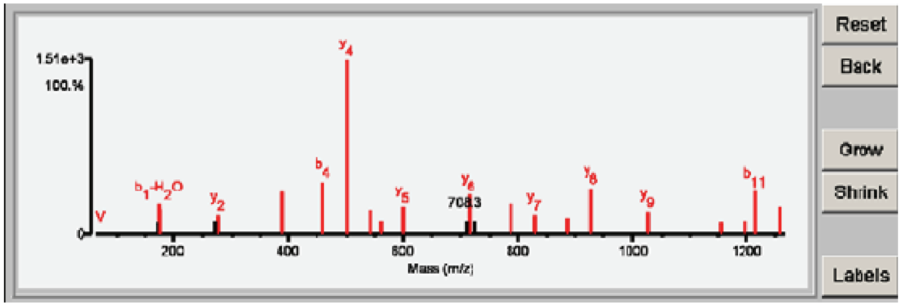
Fragment-ion (m/z)	72.081	169.132	172.039	175.119	272.117	272.171	276.164	389.144	460.183	502.262	543.229	561.243	601.332
Frac. Inten.(% of TIC)	0.07	1.61	4.08	3.55	1.75	1.89	2.71	5.69	6.92	23.06	3.18	1.82	3.62
Rel. Inten.(% of BP)	0.28	7.00	17.68	15.38	7.61	8.18	11.77	24.65	30.00	100.00	13.80	7.88	15.71
Score	0.50	-0.07	0.25	1.50	-0.08	-0.08	1.50	0.50	0.50	1.50	0.25	0.50	1.50
Ion-type	V		b1-H2O	y1			y2	b3	b4	y4	b5-H2O	b5	y5
Delta ppm	-1.0		-27.2	3.1			-11.0	-16.3	-8.1	-0.4	8.2	14.4	2.8

Fragment-ion (m/z)	708.311	715.369	725.307	788.360	828.454	887.414	927.523	1026.587	1154.666	1196.569	1213.618	1255.713
Frac. Inten.(% of TIC)	1.94	5.17	1.86	4.13	2.59	2.31	6.17	3.01	1.59	1.88	5.73	3.67
Rel. Inten.(% of BP)	8.42	22.42	8.05	17.91	11.24	10.02	26.76	13.07	6.88	8.16	24.83	15.90
Score	-0.08	1.50	-0.08	0.50	1.50	0.50	1.50	1.50	1.50	0.25	0.50	1.50
Ion-type		y6		b7	y7	b8	y8	y9	y10	b11-NH3	b11	y11
Delta ppm		-6.8		-1.8	-3.6	-17.7	-3.0	-7.4	11.0	-24.8	-6.5	10.0



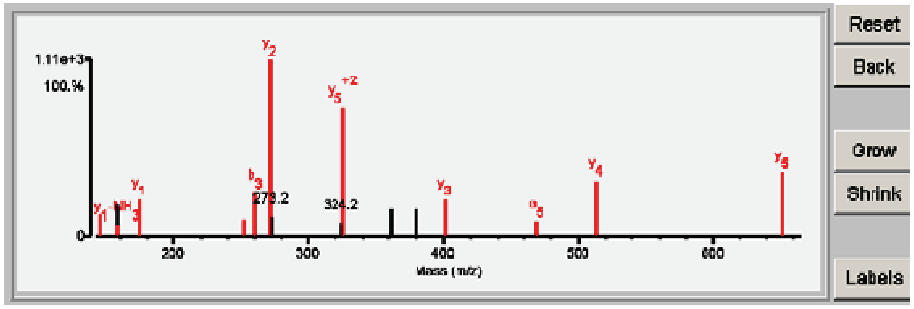
S22

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.57	74.3	7	10/25	(A) G\G G\V/H/I/E/P/R (Y)	1009.4884	0.0027	2.7	12058.5/5.47	HUMAN	O95178	368021	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.079	93.044	95.064	110.070	111.072	112.089	115.085	140.079	146.027	158.029	158.094
Frac. Inten.(% of TIC)	0.01	0.09	1.78	1.88	0.55	3.00	0.06	2.30	2.05	2.76	3.87	1.60
Rel. Inten.(% of BP)	0.03	0.43	8.43	8.89	2.61	14.14	0.27	10.87	9.68	13.05	18.27	7.54
Score	0.20	0.50	-0.08	-0.09	1.00	-0.14	0.33	-0.11	-0.10	0.50	-0.18	0.50
Ion-type	PR	V			H		R			b1		y1-NH3
Delta ppm	-3.2	-28.8			-11.6		17.6			-10.4		12.0

Fragment-ion (m/z)	175.117	251.149	260.073	272.171	273.179	324.179	326.183^{+2}	362.183	379.241	401.205	468.208	514.293	651.350
Frac. Inten.(% of TIC)	4.41	2.03	5.27	21.18	2.43	1.69	15.51	3.31	3.39	4.39	1.95	6.85	7.64
Rel. Inten.(% of BP)	20.84	9.57	24.88	100.00	11.45	7.99	73.24	15.61	15.99	20.71	9.20	32.36	36.07
Score	1.50	0.75	0.50	1.50	-0.11	-0.08	1.50	-0.16	-0.16	1.50	0.50	1.50	1.50
Ion-type	y1	HI	b3	y2			$y5^{+2}$			y3	a5	y4	y5
Delta ppm	-14.0	-10.2	6.3	-1.5			3.7			-22.7	8.8	-9.5	-11.5

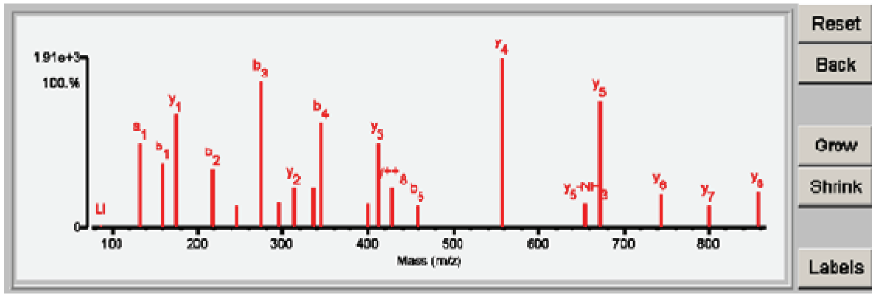


S23

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.92	100.0	8	0/25	(G) A|G|G|A|L|F/V/H/R (D)	1015.5142	0.0021	2.1	27391.7/8.21	HUMAN	P19404	368451	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.066	0.00	0.02	0.20	PR	8.2
72.080	0.08	0.59	0.50	V	-5.2
86.096	0.22	1.70	0.22	LI	-6.1
110.069	0.10	0.73	1.00	H	-18.8
120.083	0.07	0.53	1.00	F	16.0
132.048	6.63	50.37	0.50	a1	-8.8
160.043	5.02	38.15	0.50	b1	-3.6
175.117	8.69	66.07	1.50	y1	-11.7
217.065	4.55	34.60	0.50	b2	-1.1
246.093	1.75	13.29	0.50	a3	5.3
274.086	11.30	85.90	0.50	b3	-4.4
295.153	1.92	14.61	0.50	y2-NH3	5.7
312.176	3.08	23.40	1.50	y2	-6.6
336.200^{+2}	3.06	23.29	1.50	$y5^{+2}$	-9.9
345.120	8.20	62.32	0.50	b4	-10.5
400.225^{+2}	1.85	14.05	1.50	$y7^{+2}$	-17.5
411.245	6.62	50.32	1.50	y3	-2.6
428.745	3.08	23.40	1.50	y++8	4.8
458.196	1.72	13.04	0.50	b5	-25.1
558.310	13.16	100.00	1.50	y4	-8.9
654.370	1.83	13.88	0.50	y5-NH3	-2.8
671.397	9.90	75.21	1.50	y5	-2.8
742.441	2.62	19.92	1.50	y6	6.6
799.455	1.79	13.64	1.50	y7	-2.8
856.460	2.76	20.94	1.50	y8	-21.8



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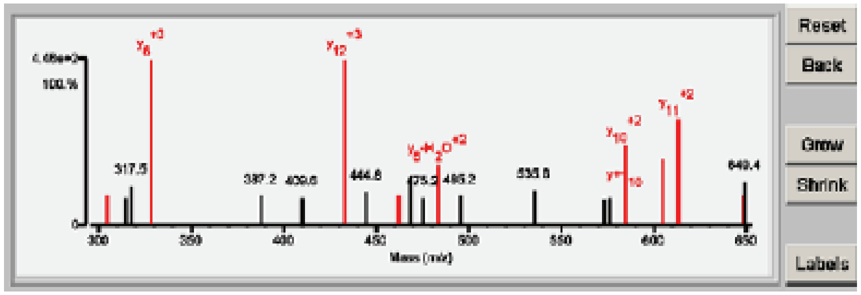
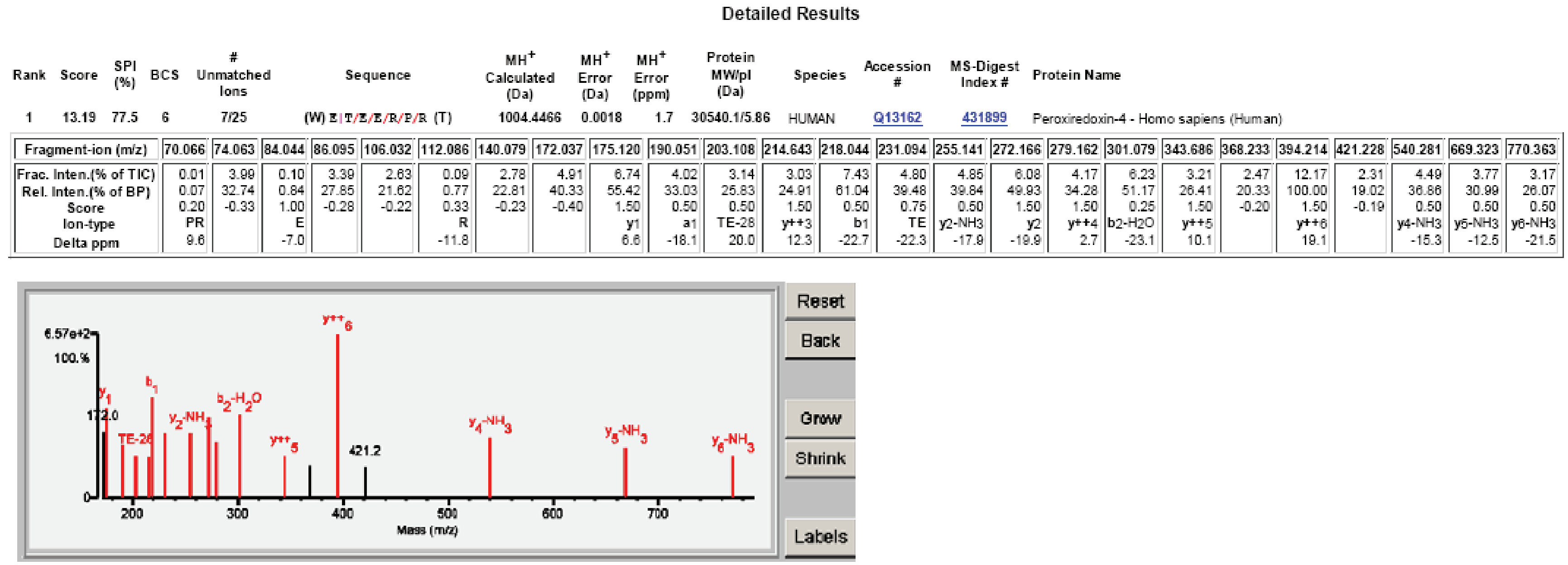
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.43	62.4	4	14/26	(E) S/A/G|A D/T R P T V R P R (N)	1471.7434	0.0061	4.2	30241.7/6.98	HUMAN	O75489	388277	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.066	0.00	0.02	0.20	PR	9.6
251.074	2.45	18.03	-0.18		
285.807	3.10	22.83	-0.23		
304.100	2.41	17.74	0.50	b_3	8.0
314.163	2.29	16.87	-0.17		
317.647	3.23	23.82	-0.24		
328.208^{+3}	13.55	99.82	1.50	$y8^{+3}$	19.9
387.183	2.37	17.45	-0.17		
409.686^{+3}	2.22	16.38	-0.16		
432.914^{+3}	13.57	100.00	1.50	$y12^{+3}$	12.2
444.849	2.70	19.91	-0.20		
461.932^{+3}	2.37	17.49	1.50	$y13^{+3}$	1.8
468.030	3.76	27.70	-0.28		
476.232	2.22	16.35	-0.16		
482.797^{+2}	4.93	36.33	0.50	$y8\text{-}H_2O^{+2}$	6.7
486.177	2.40	17.67	-0.18		
535.776	2.89	21.27	-0.21		
573.281	2.16	15.88	-0.16		
576.290^{+2}	2.30	16.98	-0.17		
584.814	2.83	20.84	1.50	y++10	-29.2
584.841^{+2}	6.42	47.34	1.50	$y10^{+2}$	16.9
604.828^{+2}	5.38	39.61	0.50	$y11\text{-}NH_3^{+2}$	1.2
613.340^{+2}	8.61	63.45	1.50	$y11^{+2}$	-2.8
648.873	2.33	17.20	1.50	y++12	19.9
649.366	3.52	25.96	-0.26		



S25



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.19	77.5	6	7/25	(W) E|T/E/E/R/P/R (T)	1004.4466	0.0018	1.7	30540.1/5.86	HUMAN	Q13162	431899	Peroxiredoxin-4 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	74.063	84.044	86.095	106.032	112.086	140.079	172.037	175.120	190.051	203.108	214.643
Frac. Inten.(% of TIC)	0.01	3.99	0.10	3.39	2.63	0.09	2.78	4.91	6.74	4.02	3.14	3.03
Rel. Inten.(% of BP)	0.07	32.74	0.84	27.85	21.62	0.77	22.81	40.33	55.42	33.03	25.83	24.91
Score	0.20	-0.33	1.00	-0.28	-0.22	0.33	-0.23	-0.40	1.50	0.50	0.50	1.50
Ion-type	PR		E			R			y1	a1	TE-28	y++3
Delta ppm	9.6		-7.0			-11.8			6.6	-18.1	20.0	12.3

Fragment-ion (m/z)	218.044	231.094	255.141	272.166	279.162	301.079	343.686	368.233	394.214	421.228	540.281	669.323	770.363
Frac. Inten.(% of TIC)	7.43	4.80	4.85	6.08	4.17	6.23	3.21	2.47	12.17	2.31	4.49	3.77	3.17
Rel. Inten.(% of BP)	61.04	39.48	39.84	49.93	34.28	51.17	26.41	20.33	100.00	19.02	36.86	30.99	26.07
Score	0.50	0.75	0.50	1.50	1.50	0.25	1.50	-0.20	1.50	-0.19	0.50	0.50	0.50
Ion-type	b1	TE	y2-NH3	y2	y++4	b2-H2O	y++5		y++6		y4-NH3	y5-NH3	y6-NH3
Delta ppm	-22.7	-22.3	-17.9	-19.9	2.7	-23.1	10.1		19.1		-15.3	-12.5	-21.5

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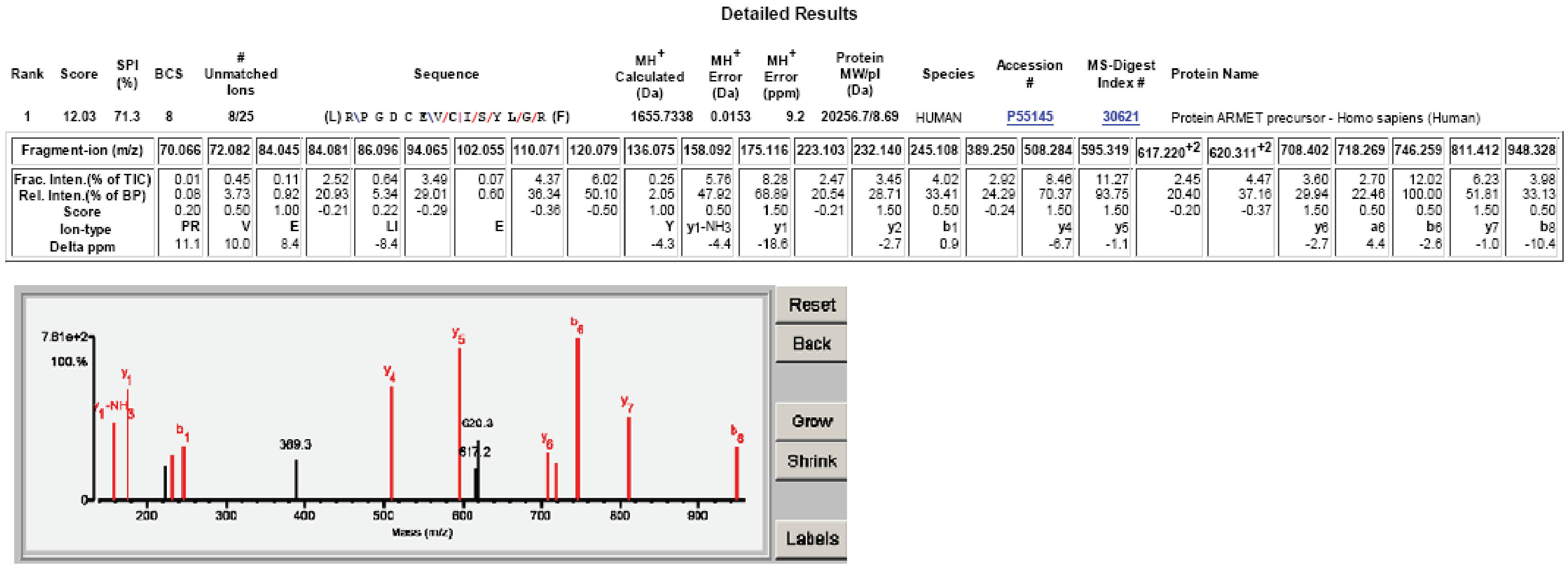

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.03	71.3	8	8/25	(L) R\P G D C E\V/C|I/S/Y L/G/R (F)	1655.7338	0.0153	9.2	20256.7/8.69	HUMAN	P55145	30621	Protein ARMET precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.045	84.081	86.096	94.065	102.055	110.071	120.079	136.075	158.092	175.116
Frac. Inten.(% of TIC)	0.01	0.45	0.11	2.52	0.64	3.49	0.07	4.37	6.02	0.25	5.76	8.28
Rel. Inten.(% of BP)	0.08	3.73	0.92	20.93	5.34	29.01	0.60	36.34	50.10	2.05	47.92	68.89
Score	0.20	0.50	1.00	-0.21	0.22	-0.29		-0.36	-0.50	1.00	0.50	1.50
Ion-type	PR	V	E		LI		E			Y	y1-NH3	y1
Delta ppm	11.1	10.0	8.4		-8.4					-4.3	-4.4	-18.6

Fragment-ion (m/z)	223.103	232.140	245.108	389.250	508.284	595.319	617.220^{+2}	620.311^{+2}	708.402	718.269	746.259	811.412	948.328
Frac. Inten.(% of TIC)	2.47	3.45	4.02	2.92	8.46	11.27	2.45	4.47	3.60	2.70	12.02	6.23	3.98
Rel. Inten.(% of BP)	20.54	28.71	33.41	24.29	70.37	93.75	20.40	37.16	29.94	22.46	100.00	51.81	33.13
Score	-0.21	1.50	0.50	-0.24	1.50	1.50	-0.20	-0.37	1.50	0.50	0.50	1.50	0.50
Ion-type		y2	b1		y4	y5			y6	a6	b6	y7	b8
Delta ppm		-2.7	0.9		-6.7	-1.1			-2.7	4.4	-2.6	-1.0	-10.4

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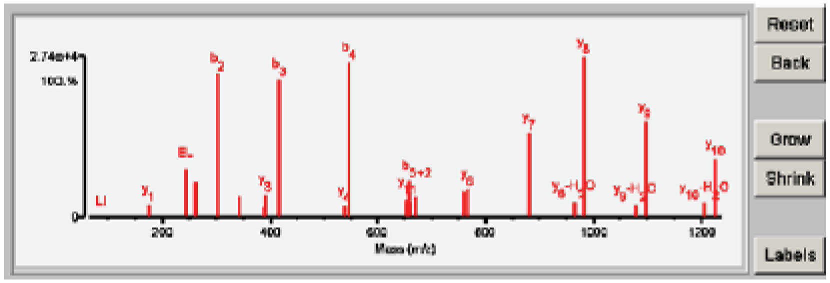
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.72	100.0	11	0/26	(S) D V|L|E|L|T|D/D/N/F/E/S/R (I)	1640.7108	0.0033	2.0	58782.7/5.98	HUMAN	P30101	406819	Protein disulfide-isomerase A3 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.096	175.118	243.133	262.150	303.100	342.200	388.190	391.183	416.184	538.269
Frac. Inten.(% of TIC)	0.10	0.10	1.06	4.09	3.00	12.06	1.80	0.87	1.93	11.62	1.03
Rel. Inten.(% of BP)	0.71	0.75	7.81	30.22	22.16	89.21	13.30	6.46	14.31	85.91	7.63
Score	0.50	0.22	1.50	0.75	1.50	0.50	0.75	0.50	1.50	0.50	1.50
Ion-type	V	LI	y_1	EL	y_2	b_2	VLE	a_3	y_3	b_3	y_4
Delta ppm	11.4	-2.6	-3.2	-9.2	-3.4	-5.7	-9.8	-2.7	-2.5	-4.5	-5.7

Fragment-ion (m/z)	545.226	652.302	658.310	680.813^{+2}	688.814^{+2}	759.357	767.330	882.364	866.388	883.403	1078.483	1096.489	1207.521	1225.531
Frac. Inten.(% of TIC)	12.97	1.47	3.01	1.37	1.68	2.30	2.35	7.11	1.27	13.52	1.14	8.00	1.21	4.95
Rel. Inten.(% of BP)	95.91	10.84	22.26	10.15	12.39	16.99	17.37	52.56	9.42	100.00	8.40	59.16	8.92	36.58
Score	0.50	1.50	0.50	0.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	b_4	y_5	b_5	y_{11}-H_2O^{+2}	y_{11}^{+2}	b_6	y_6	y_7	y_8-H_2O	y_8	y_9-H_2O	y_9	y_{10}-H_2O	y_{10}
Delta ppm	-5.6	-4.0	-4.0	9.9	2.5	-4.1	-2.6	-5.3	-7.6	-3.6	2.3	-1.7	-1.5	-1.9



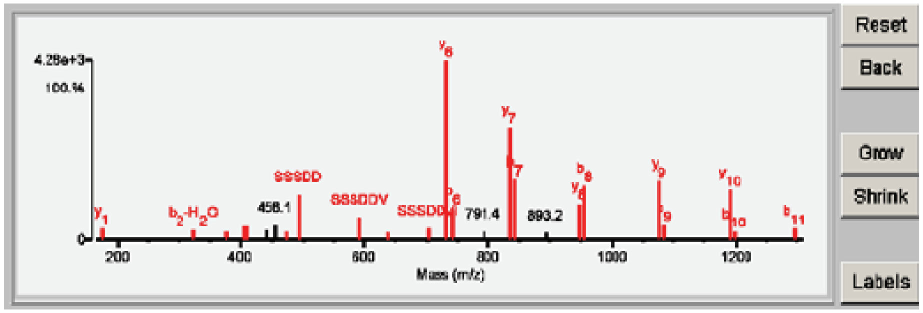
S28

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.02	94.8	8	4/25	(L) Y S S S D D\V|I|E|L|T|P/S N F N/R (E)	2031.8964	0.0311	15.3	48121.6/4.95	HUMAN	Q15084	406851	Protein disulfide-isomerase A6 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	175.120	321.085	377.138	405.135	408.122	440.187	456.140	474.144	492.151	591.234	637.301
Frac. Inten.(% of TIC)	1.41	1.20	1.01	1.63	1.61	1.26	1.89	1.04	5.59	2.74	0.93
Rel. Inten.(% of BP)	6.33	5.39	4.56	7.36	7.27	5.67	8.52	4.69	25.16	12.34	4.20
Score	1.50	0.25	0.75	0.75	0.25	-0.06	-0.09	0.50	0.75	0.75	1.50
Ion-type	y_1	b_2-H_2O	SSSD SSDD-28	SSDD	b_3-H_2O			SSSDD-H_2O	SSSDD	SSSDDV	y_5
Delta ppm	8.8	-20.1	16.4 16.4	22.2	-3.9			-9.0	-14.5	11.9	-6.7

Fragment-ion (m/z)	704.320	734.359	743.232	791.373	835.412	842.293	893.188	948.501	955.380	1077.543	1084.433	1190.640	1197.463	1298.555
Frac. Inten.(% of TIC)	1.36	22.20	3.93	1.10	13.97	7.50	0.90	4.44	6.66	7.31	1.78	6.17	1.03	1.33
Rel. Inten.(% of BP)	6.14	100.00	17.72	4.95	62.92	33.76	4.07	19.98	30.00	32.94	8.03	27.80	4.63	6.00
Score	0.75	1.50	0.50	-0.05	1.50	0.50	-0.04	1.50	0.50	1.50	0.50	1.50	0.50	0.50
Ion-type	SSSDDVI	y_6	b_6		y_7	b_7		y_8	b_8	y_9	b_9	y_{10}	b_{10}	b_{11}
Delta ppm	12.9	0.9	16.1		7.2	5.4		12.2	8.2	10.2	16.4	19.4	-30.2	6.2

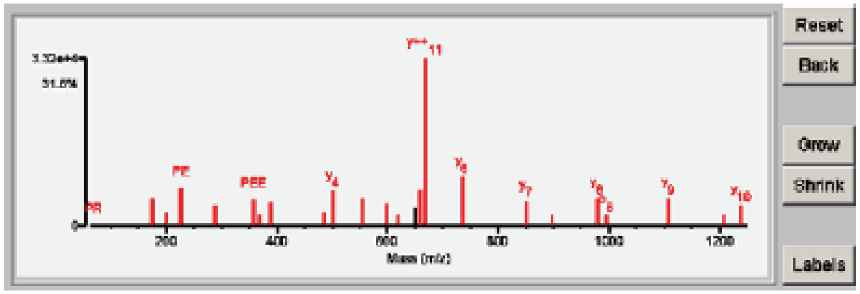


S29

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	28.66	98.1	11	1/26	(D) A/P/E/E/E/D/H|V|L/V|L/R (K)	1494.7267	0.0112	7.5	57116.6/4.76	HUMAN	P07237	406797	Protein disulfide-isomerase precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	175.117	199.106	227.101	288.203	356.143	368.747^{+2}	387.271	485.181	500.356	555.306^{+2}	599.422	600.212	619.828^{+2}	650.338^{+2}	659.347^{+2}	668.350	736.488	851.508	896.309	980.547	995.376	1109.590	1207.527	1238.634
Frac. Inten.(% of TIC)	0.00	2.57	1.35	3.62	1.94	2.50	1.05	2.21	1.23	3.33	2.67	2.01	2.09	1.07	1.85	3.42	49.82	4.62	2.33	1.03	2.64	1.06	2.61	1.00	1.98
Rel. Inten.(% of BP)	0.01	5.17	2.70	7.26	3.89	5.01	2.11	4.43	2.46	6.68	5.36	4.04	4.19	2.16	3.72	6.86	100.00	9.27	4.68	2.06	5.30	2.13	5.24	2.02	3.98
Score	0.20	1.50	0.50	0.75	1.50	0.75	1.50	1.50	0.75	1.50	1.50	1.50	0.75	1.50	-0.04	0.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	PR	y1	PE-28	PE	y2	PEE	y6^{+2}	y3	PEEE	y4	y9^{+2}	y5	PEEED	y10^{+2}		y11-H_2O^{+2}	y++11	y6	y7	b7	y8	b8	y9	b10	y10
Delta ppm	3.9	-11.7	-14.1	-9.8	1.3	-8.8	5.0	-1.1	-15.9	-0.2	7.5	-3.5	-6.4	11.0		5.8	2.3	4.9	-3.9	-1.5	-5.8	-2.5	0.3	-3.4	-2.5

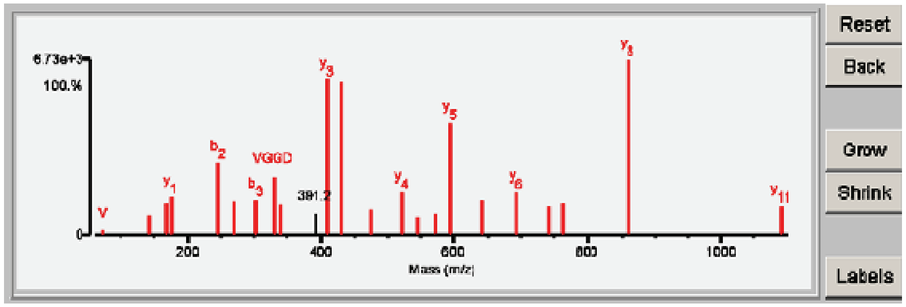


S30

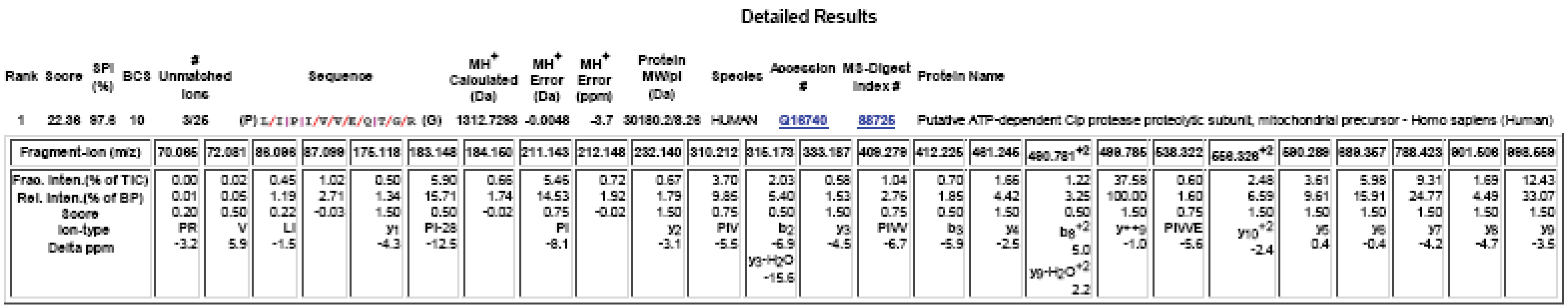
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.30	98.3	9	1/25	(D) G V|G\G D|P|A|V|A/L/P H/R (R)	1333.6681	0.0004	0.3	57549.2/6.30	HUMAN	P49257	309375	Protein ERGIC-53 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	86.097	141.103	169.096	175.119	245.095	268.166	302.118	329.144	339.203	391.216	409.231	430.759^{+2}	474.165	522.314	545.293	571.208	593.347	642.256	692.415	741.327	763.459	860.512	1089.574
Frac. Inten.(% of TIC)	0.00	0.40	0.05	1.69	2.66	3.12	5.89	2.79	2.87	4.80	2.55	1.72	12.64	12.42	2.09	3.54	1.59	1.81	9.13	2.83	3.54	2.45	2.69	14.34	2.40
Rel. Inten.(% of BP)	0.02	2.78	0.35	11.78	18.53	21.74	41.11	19.47	20.02	33.47	17.76	11.98	88.19	86.60	14.59	24.67	11.06	12.63	63.67	19.75	24.69	17.09	18.75	100.00	16.75
Score	0.20	0.50	0.22	0.50	0.75	1.50	0.50	0.75	0.50	0.75	0.75	-0.12	1.50	1.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50
Ion-type	PR	V	LI	PA-28	PA	y1	b2	PAV	b3	VGGD	PAVA		y3	y8^{+2}	b5	y4	y++11	b6	y5	b7	y6	b8	y7	y8	y11
Delta ppm	5.3	8.7	0.9	-3.1	-11.5	-0.9	-4.2	-4.3	-0.7	-8.1	-2.3		-0.1	0.7	-3.8	-1.5	-1.1	-20.3	-7.4	-0.4	-7.2	2.8	1.9	2.2	-5.2



S31

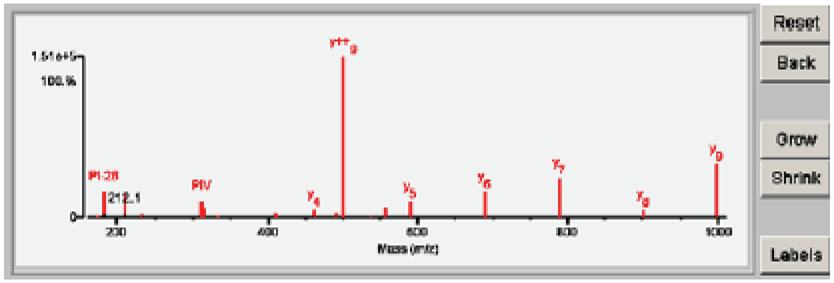


Detailed Results

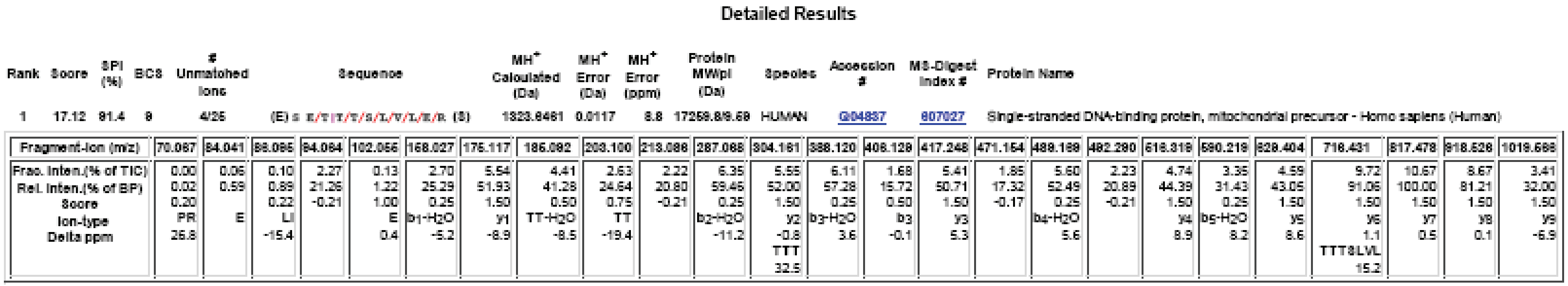
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.38	97.6	10	3/26	(P) L/I|P|I/V/V/E/Q|T/G/R (G)	1312.7293	-0.0048	-3.7	30180.2/8.26	HUMAN	Q16740	88726	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	72.081	86.096	87.099	175.118	183.148	184.160	211.143	212.148	232.140	310.212	315.173	333.187
Frac. Inten.(% of TIC)	0.00	0.02	0.45	1.02	0.50	5.90	0.66	5.46	0.72	0.67	3.70	2.03	0.58
Rel. Inten.(% of BP)	0.01	0.05	1.19	2.71	1.34	15.71	1.74	14.53	1.92	1.79	9.85	5.40	1.53
Score	0.20	0.50	0.22	-0.03	1.50	0.50	-0.02	0.75	-0.02	1.50	0.75	0.50	1.50
Ion-type	PR	V	LI		y_1	PI-28		PI		y_2	PIV	b_2 y_3-H_2O	y_3
Delta ppm	-3.2	5.9	-1.5		-4.3	-12.5		-8.1		-3.1	-5.5	-6.9 -15.6	-4.5

Fragment-Ion (m/z)	409.279	412.225	461.246	490.781^{+2}	499.785	538.322	556.328^{+2}	590.289	689.357	788.423	901.506	998.558
Frac. Inten.(% of TIC)	1.04	0.70	1.66	1.22	37.58	0.60	2.48	3.61	5.98	9.31	1.69	12.43
Rel. Inten.(% of BP)	2.76	1.85	4.42	3.25	100.00	1.60	6.59	9.61	15.91	24.77	4.49	33.07
Score	0.75	0.50	1.50	0.50	1.50	0.75	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	PIVV	b_3	y_4	b_8^{+2} y_9-H_2O^{+2}	y^{++}_9	PIVVE	y_{10}^{+2}	y_5	y_6	y_7	y_8	y_9
Delta ppm	-6.7	-5.9	-2.5	5.0 2.2	-1.0	-5.6	-2.4	0.4	-0.4	-4.2	-4.7	-3.5



S32

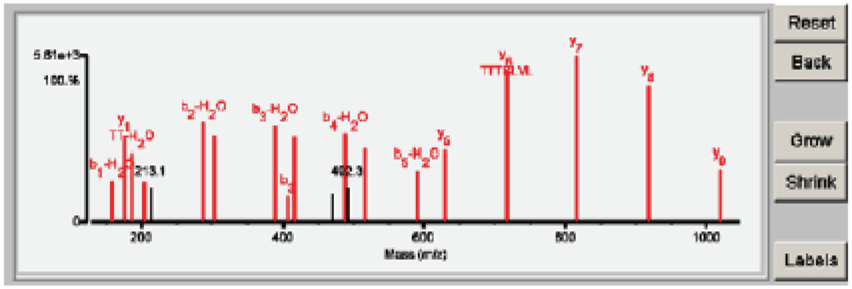


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.12	91.4	9	4/25	(E) s E/T|T/T/S/L/V/L/E/R (S)	1323.6461	0.0117	8.8	17259.8/9.68	HUMAN	Q04837	807027	Single-stranded DNA-binding protein, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.067	84.041	86.095	94.064	102.056	168.027	175.117	185.092	203.100	213.086	287.068	304.161	388.120
Frac. Inten.(% of TIC)	0.00	0.06	0.10	2.27	0.13	2.70	5.54	4.41	2.63	2.22	6.35	5.55	6.11
Rel. Inten.(% of BP)	0.02	0.59	0.89	21.26	1.22	25.29	51.93	41.28	24.64	20.80	59.46	52.00	57.28
Score	0.20		0.22	-0.21	1.00	0.25	1.50	0.50	0.75	-0.21	0.25	1.50	0.25
Ion-type	PR	E	LI		E	b_1-H_2O	y_1	TT-H_2O	TT		b_2-H_2O	y_2 TTT	b_3-H_2O
Delta ppm	26.8		-15.4		0.4	-5.2	-8.9	-8.5	-19.4		-11.2	-0.8 32.5	3.6

Fragment-Ion (m/z)	406.128	417.248	471.154	489.169	492.290	516.319	590.219	629.404	716.431	817.478	918.526	1019.566
Frac. Inten.(% of TIC)	1.68	5.41	1.85	5.60	2.23	4.74	3.35	4.59	9.72	10.67	8.67	3.41
Rel. Inten.(% of BP)	15.72	50.71	17.32	52.49	20.89	44.39	31.43	43.05	91.06	100.00	81.21	32.00
Score	0.50	1.50	-0.17	0.25	-0.21	1.50	0.25	1.50	1.50	1.50	1.50	1.50
Ion-type	b_3	y_3		b_4-H_2O		y_4	b_5-H_2O	y_5	y_6 TTTSLVL	y_7	y_8	y_9
Delta ppm	-0.1	5.3		5.6		8.9	8.2	8.6	1.1 15.2	0.5	0.1	-6.9



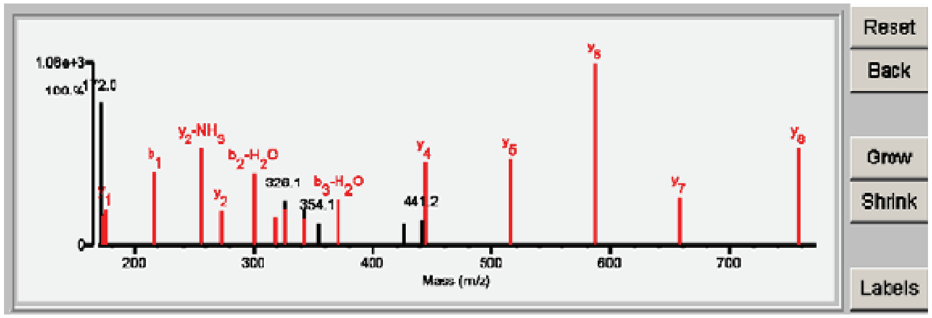
S33

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.11	69.8	8	9/25	(A) Q|T|A/A/A/T/A/P/R (I)	974.4724	0.0019	2.0	31629.9/9.03	HUMAN	P21912	135967	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	74.063	84.045	86.096	172.040	173.093	175.115	217.065	255.148	272.173	300.101	318.111	326.113
Frac. Inten.(% of TIC)	0.00	1.54	6.25	1.43	10.05	2.31	2.57	5.22	6.95	2.44	5.15	2.00	3.16
Rel. Inten.(% of BP)	0.02	11.91	48.44	11.09	77.85	17.87	19.91	40.42	53.81	18.92	39.87	15.53	24.51
Score	0.20	-0.12	-0.48	-0.11	-0.78	0.75	1.50	0.50	0.50	1.50	0.25	0.50	-0.25
Ion-type	PR					TA	y1	b1	y2-NH3	y2	b2-H2O	b2	
Delta ppm	5.3					-3.8	-20.3	-2.0	11.1	4.0	-4.2	-5.1	

Fragment-ion (m/z)	326.182	343.148	343.210	354.110	371.136	425.232	441.210	444.252	515.296	586.327	657.362	758.411
Frac. Inten.(% of TIC)	2.66	2.65	2.06	1.64	3.22	1.58	1.85	5.96	6.13	12.91	3.36	6.90
Rel. Inten.(% of BP)	20.59	20.50	15.98	12.68	24.91	12.23	14.35	46.15	47.48	100.00	26.00	53.47
Score	0.50	-0.21	1.50	-0.13	0.25	-0.12	-0.14	1.50	1.50	1.50	1.50	1.50
Ion-type	y3-NH3		y3		b3-H2O			y4	y5	y6	y7	y8
Delta ppm	-1.2		2.8		-8.5			-10.4	4.6	-6.9	-8.4	-5.7



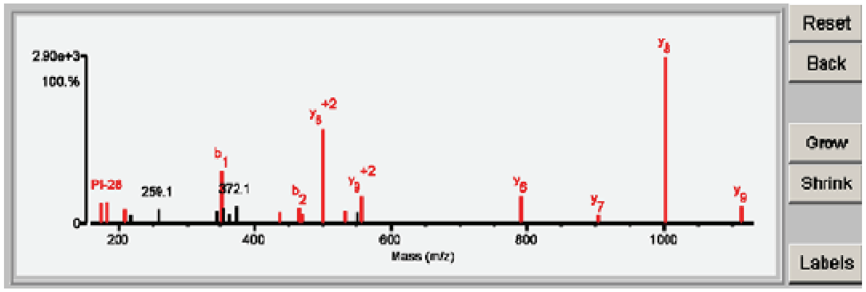
S34

Detailed Results

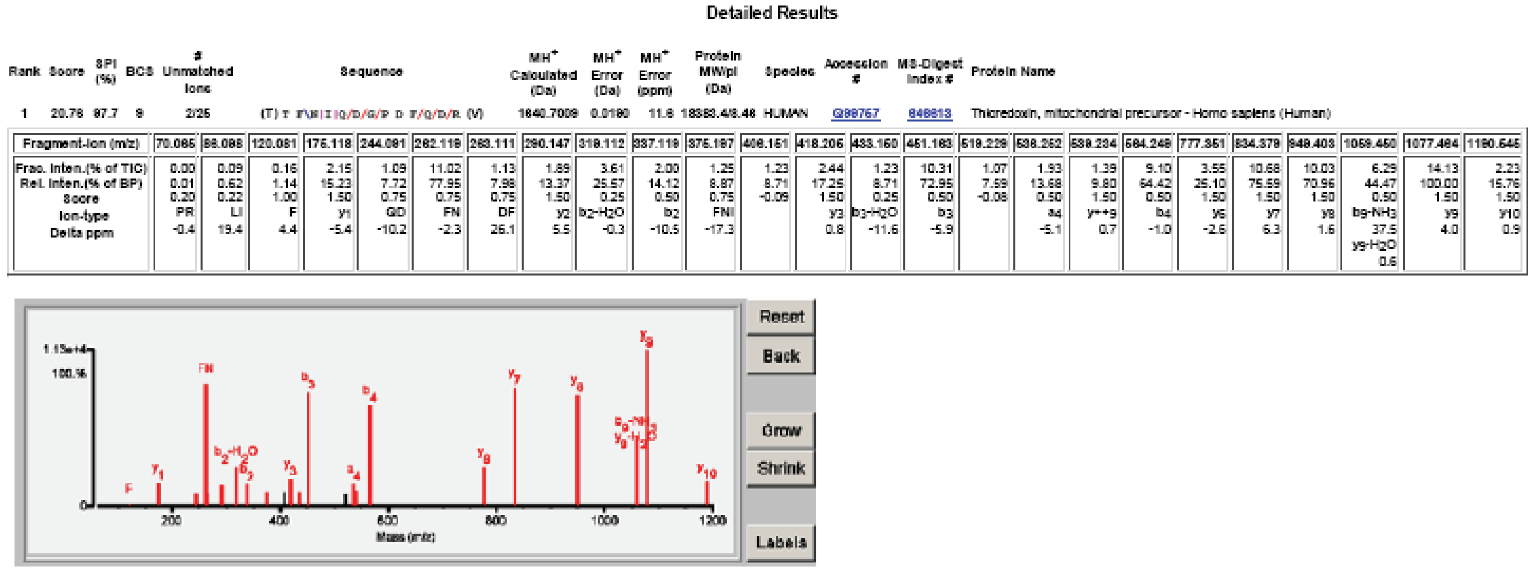
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.11	79.0	6	9/25	(F) K|I|P/I/E E/L E D/R (V)	1464.6861	0.0034	2.3	18929.7/5.30	HUMAN	P04234	73447	T-cell surface glycoprotein CD3 delta chain precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.063	84.081	86.096	94.065	175.116	183.148	211.144	219.091	259.060	344.149	352.116	354.111	362.181
Frac. Inten.(% of TIC)	0.00	1.95	0.50	4.09	3.30	3.32	2.32	1.53	2.36	2.13	8.19	2.59	1.65
Rel. Inten.(% of BP)	0.01	7.56	1.94	15.88	12.79	12.87	9.02	5.93	9.17	8.25	31.79	10.05	6.39
Score	0.20	-0.08	0.22	-0.16	1.50	0.50	0.75	-0.06	-0.09	-0.08	0.50	-0.10	-0.06
Ion-type	PR		LI		y1	PI-28	PI				b1		
Delta ppm	-24.6		-3.8		-15.1	-14.1	-3.3				1.2		

Fragment-ion (m/z)	372.125	437.203	465.197	469.226	500.752^{+2}	532.270	551.509	557.291^{+2}	790.342	903.464	1000.488	1113.577
Frac. Inten.(% of TIC)	2.83	1.98	2.43	1.71	14.57	2.10	1.93	4.30	4.28	1.50	25.77	2.68
Rel. Inten.(% of BP)	10.97	7.68	9.42	6.65	56.55	8.14	7.47	16.70	16.61	5.83	100.00	10.42
Score	-0.11	0.50	0.50	0.75	1.50	1.50	-0.07	1.50	1.50	1.50	1.50	1.50
Ion-type		a2	b2	PIEE	y_8^{+2}	y4		y_9^{+2}	y6	y7	y8	y9
Delta ppm		-5.6	-7.0	-10.4	1.8	-4.6		-4.0	-20.5	25.0	-6.3	-1.7



S35

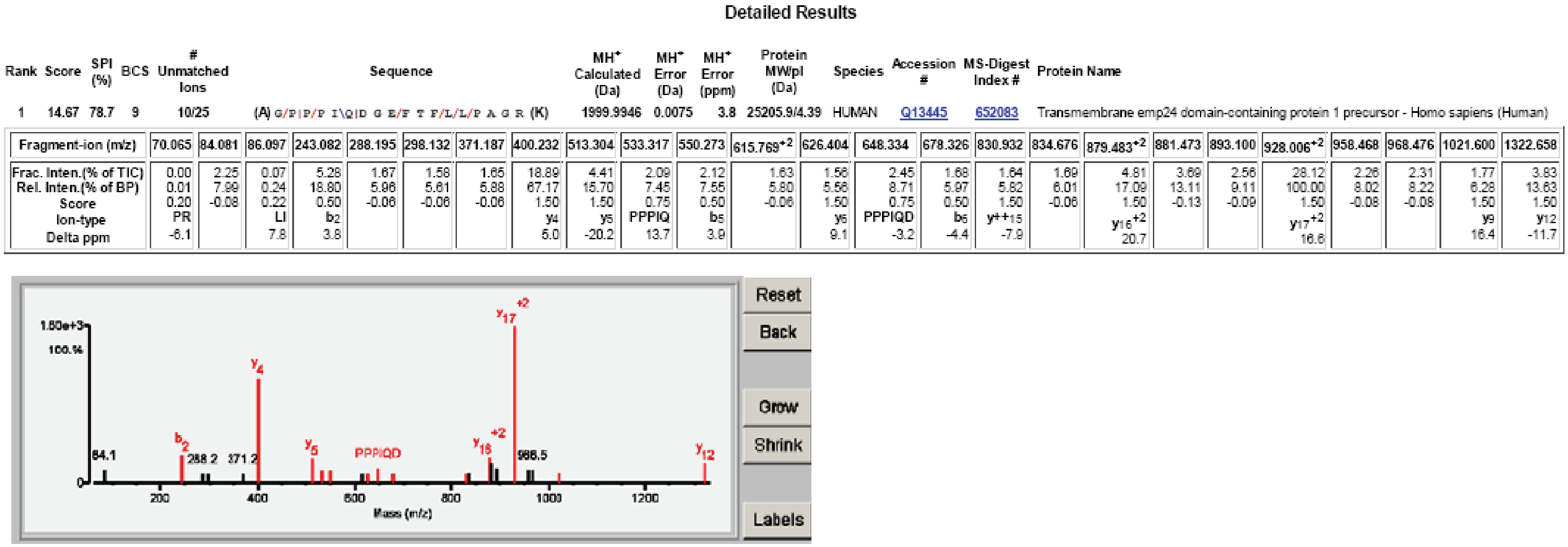


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.76	87.7	9	2/25	(T) T F\N|I|Q/D/G/P D F/Q/D/R (V)	1640.7009	0.0190	11.6	18383.4/8.48	HUMAN	Q99757	848813	Thioredoxin, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	86.098	120.081	175.118	244.091	262.119	263.111	290.147	318.112	337.119	375.197	406.161	418.206	433.160	451.163	519.229	538.252	539.234	584.249	777.351	834.379	949.403	1059.450	1077.464	1190.545
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -0.4	0.09 0.62 0.22 LI 19.4	0.16 1.14 1.00 F 4.4	2.15 15.23 1.50 y_1 -5.4	1.09 7.72 0.75 GD -10.2	11.02 77.95 0.75 FN -2.3	1.13 7.98 0.75 DF 26.1	1.89 13.37 1.50 y_2 5.5	3.61 25.57 0.25 b_2-H_2O -0.3	2.00 14.12 0.50 b_2 -10.5	1.25 8.87 0.75 FNI -17.3	1.23 8.71 -0.09	2.44 17.25 1.50 y_3 0.8	1.23 8.71 0.25 b_3-H_2O -11.6	10.31 72.95 0.50 b_3 -5.9	1.07 7.59 -0.08	1.93 13.68 0.50 a_4 -5.1	1.39 9.80 1.50 $y{+}{+}_9$ 0.7	9.10 64.42 0.50 b_4 -1.0	3.55 25.10 1.50 y_6 -2.6	10.68 75.59 1.50 y_7 6.3	10.03 70.96 1.50 y_8 1.6	6.29 44.47 0.50 b_9-NH_3 37.5 y_9-H_2O 0.6	14.13 100.00 1.50 y_9 4.0	2.23 15.76 1.50 y_{10} 0.9

S36



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.67	78.7	9	10/25	(A) G/P|P/P I\Q|D G E/F T F/L/L/P A G R (K)	1999.9946	0.0075	3.8	25205.9/4.39	HUMAN	Q13445	652083	Transmembrane emp24 domain-containing protein 1 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	84.081	86.097	243.082	288.195	298.132	371.187	400.232	513.304	533.317	550.273	615.769^{+2}	626.404	648.334	678.326	830.932	834.676	879.483^{+2}	881.473	893.100	928.006^{+2}	958.468	968.476	1021.600	1322.658
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR -6.1	2.25 7.99 -0.08	0.07 0.24 0.22 LI 7.8	5.28 18.80 0.50 b_2 3.8	1.67 5.96 -0.06	1.58 5.61 -0.06	1.65 5.88 -0.06	18.89 67.17 1.50 y_4 5.0	4.41 15.70 1.50 y_5 -20.2	2.09 7.45 0.75 PPPIQ 13.7	2.12 7.55 0.50 b_5 3.9	1.63 5.80 -0.06	1.56 5.56 1.50 y_6 9.1	2.45 8.71 0.75 PPPIQD -3.2	1.68 5.97 0.50 b_6 -4.4	1.64 5.82 1.50 $y{+}{+}_{15}$ -7.9	1.69 6.01 -0.06	4.81 17.09 1.50 $y_{16}{}^{+2}$ 20.7	3.69 13.11 -0.13	2.56 9.11 -0.09	28.12 100.00 1.50 $y_{17}{}^{+2}$ 16.6	2.26 8.02 -0.08	2.31 8.22 -0.08	1.77 6.28 1.50 y_9 16.4	3.83 13.63 1.50 y_{12} -11.7

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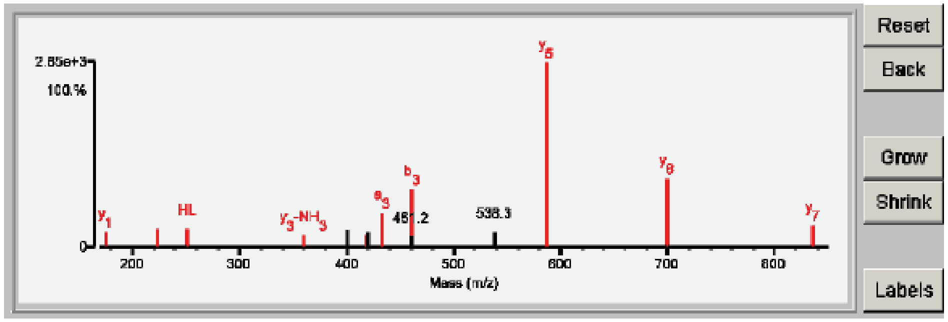
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.84	74.6	4	11/25	(I) S F/H|L/P I N S/R (K)	1158.5724	-0.0001	-0.1	24976.1/6.98	HUMAN	P49755	652147	Transmembrane emp24 domain-containing protein 10 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.047	86.096	87.044	89.061	94.065	110.071	111.076	120.079	157.122	175.117	223.156	251.147	359.163	400.222	418.741	419.176	432.165	460.162	461.153	538.295	586.329	699.416	836.472
Frac. Inten.(% of TIC)	0.00	2.53	1.77	0.18	2.27	3.20	1.97	0.85	2.11	0.20	1.95	2.61	2.97	3.05	2.06	2.70	1.85	2.49	5.72	9.53	1.81	2.62	30.63	11.47	3.46
Rel. Inten.(% of BP)	0.01	8.25	5.77	0.60	7.42	10.46	6.42	2.76	6.88	0.66	6.36	8.52	9.68	9.97	6.74	8.83	6.02	8.11	18.67	31.11	5.89	8.55	100.00	37.46	11.31
Score	0.20	-0.08	-0.06	0.22	-0.07	-0.10	-0.06	1.00	-0.07	1.00	-0.06	1.50	0.50	0.75	0.50	-0.09	1.50	-0.08	0.50	0.50	-0.06	-0.09	1.50	1.50	1.50
Ion-type	PR			LI				H		F		y1	HL-28	HL	y3-NH3		y++7		a3	b3			y5	y6	y7
Delta ppm	12.5			-2.6				-1.6		-16.5		-12.3	-1.5	-15.7	-13.2		2.4		-14.1	-8.3			-3.6	2.1	-1.4

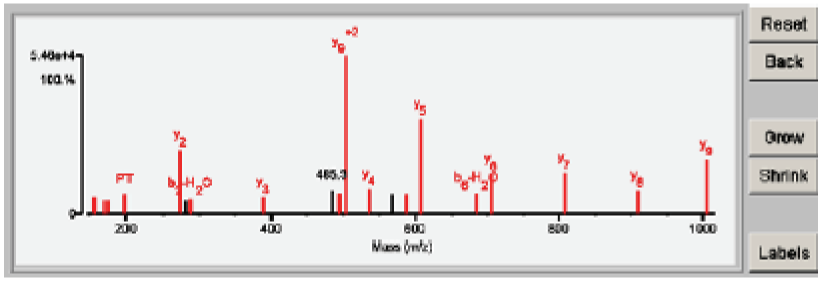


S38

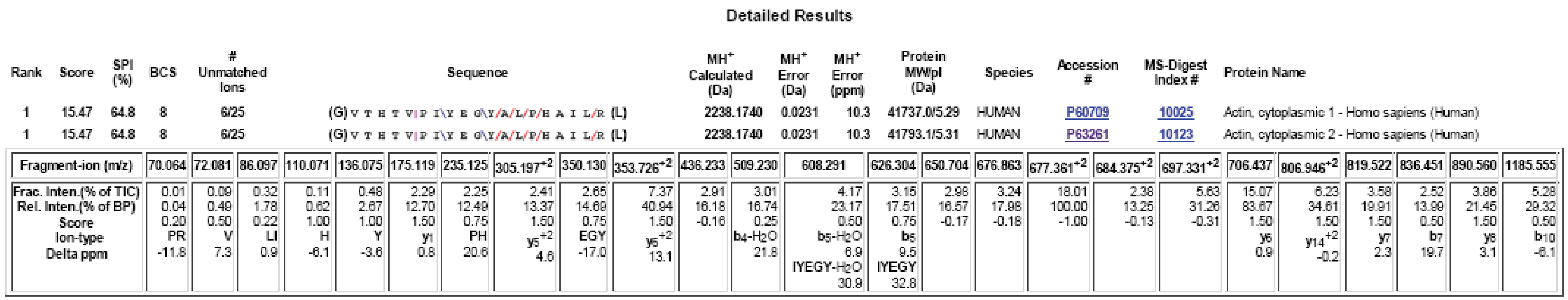
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.63	88.0	9	5/25	(V) S E/P/T/T/V/A/F/D/V/R (P)	1309.6093	0.0030	2.3	18795.3/6.20	HUMAN	Q969H8	107821	UPF0556 protein C19orf10 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	102.056	120.080	130.049	136.076	158.027	171.112	175.118	199.104	274.188	282.144	287.070	389.215	485.262^{+2}	494.266^{+2}	503.273^{+2}	536.280	568.206	586.217	607.319	685.286	706.387	807.436	908.487	1005.534
Frac. Inten.(% of TIC)	0.01	0.14	0.10	1.80	2.58	2.32	1.85	1.89	2.65	8.42	1.95	1.99	2.24	3.09	2.83	20.96	3.27	2.61	2.67	12.67	2.82	5.24	5.47	3.14	7.32
Rel. Inten.(% of BP)	0.02	0.67	0.47	8.60	12.30	11.08	8.83	9.00	12.63	40.20	9.30	9.48	10.68	14.73	13.49	100.00	15.60	12.45	12.76	60.44	13.47	25.02	26.09	14.98	34.91
Score	0.20	1.00	1.00	-0.09	-0.12	0.25	0.75	1.50	0.75	1.50	-0.09	0.25	1.50	-0.15	0.50	1.50	1.50	-0.12	0.25	1.50	0.25	1.50	1.50	1.50	1.50
Ion-type	PR	E	F			b_1-H_2O	VA PT-28	y_1	PT	y_2		b_2-H_2O	y_3		y_9-H_2O^{+2}	y_9^{+2}	y_4		b_5-H_2O	y_5	b_6-H_2O	y_6	y_7	y_8	y_9
Delta ppm	3.9	-0.5	-3.1			-7.1	-11.7 -11.7	-6.0	-22.7	1.2		-3.9	1.3		-3.3	1.7	-4.1		-3.8	-1.2	-1.5	-1.9	-1.0	3.6	-2.3



C1

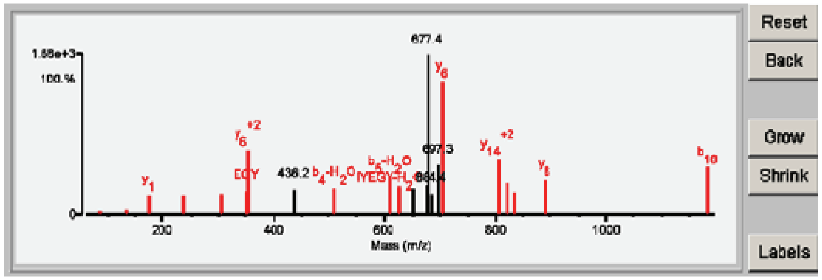


Detailed Results

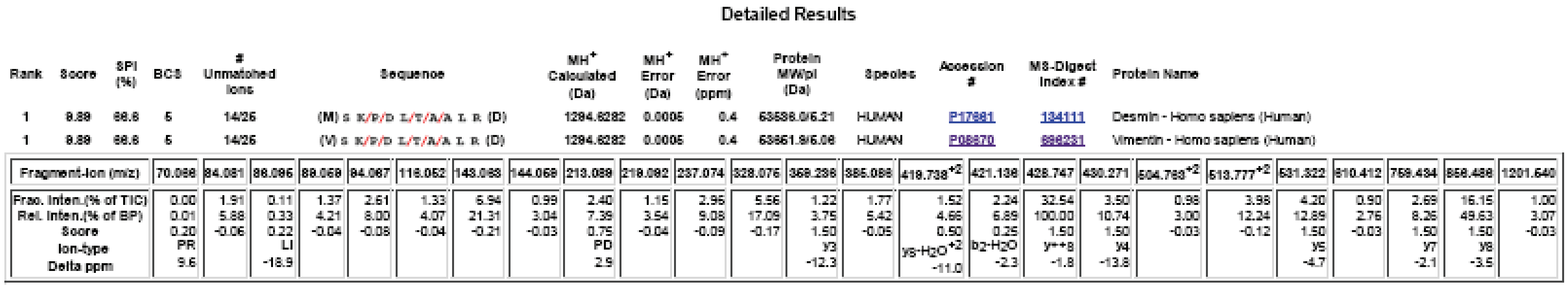
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.47	64.8	8	6/25	(G) V T H T V|P I\Y E G\Y/A/L/P/H A I L/R (L)	2238.1740	0.0231	10.3	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	15.47	64.8	8	6/25	(G) V T H T V|P I\Y E G\Y/A/L/P/H A I L/R (L)	2238.1740	0.0231	10.3	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.081	86.097	110.071	136.075	175.119	235.125	305.197^{+2}	350.130	353.726^{+2}	436.233	509.230	608.291
Frac. Inten.(% of TIC)	0.01	0.09	0.32	0.11	0.48	2.29	2.25	2.41	2.65	7.37	2.91	3.01	4.17
Rel. Inten.(% of BP)	0.04	0.49	1.78	0.62	2.67	12.70	12.49	13.37	14.69	40.94	16.18	16.74	23.17
Score	0.20	0.50	0.22	1.00	1.00	1.50	0.75	1.50	0.75	1.50	-0.16	0.25	0.50
Ion-type	PR	V	LI	H	Y	y_1	PH	y_5^{+2}	EGY	y_6^{+2}		b_4-H_2O	b_5-H_2O IYEGY-H_2O
Delta ppm	-11.8	7.3	0.9	-6.1	-3.6	0.8	20.6	4.6	-17.0	13.1		21.8	6.9 30.9

Fragment-ion (m/z)	626.304	650.704	676.863	677.361^{+2}	684.375^{+2}	697.331^{+2}	706.437	806.946^{+2}	819.522	836.451	890.560	1185.555
Frac. Inten.(% of TIC)	3.15	2.98	3.24	18.01	2.38	5.63	15.07	6.23	3.58	2.52	3.86	5.28
Rel. Inten.(% of BP)	17.51	16.57	17.98	100.00	13.25	31.26	83.67	34.61	19.91	13.99	21.45	29.32
Score	0.75	-0.17	-0.18	-1.00	-0.13	-0.31	1.50	1.50	1.50	0.50	1.50	0.50
Ion-type	b_5 IYEGY						y_6	y_{14}^{+2}	y_7	b_7	y_8	b_{10}
Delta ppm	9.5 32.8						0.9	-0.2	2.3	19.7	3.1	-6.1



C2

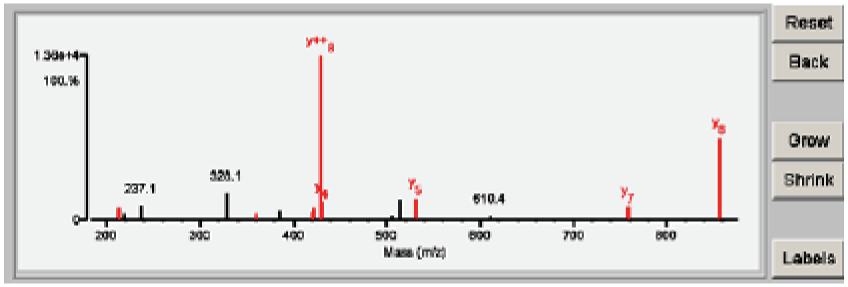


Detailed Results

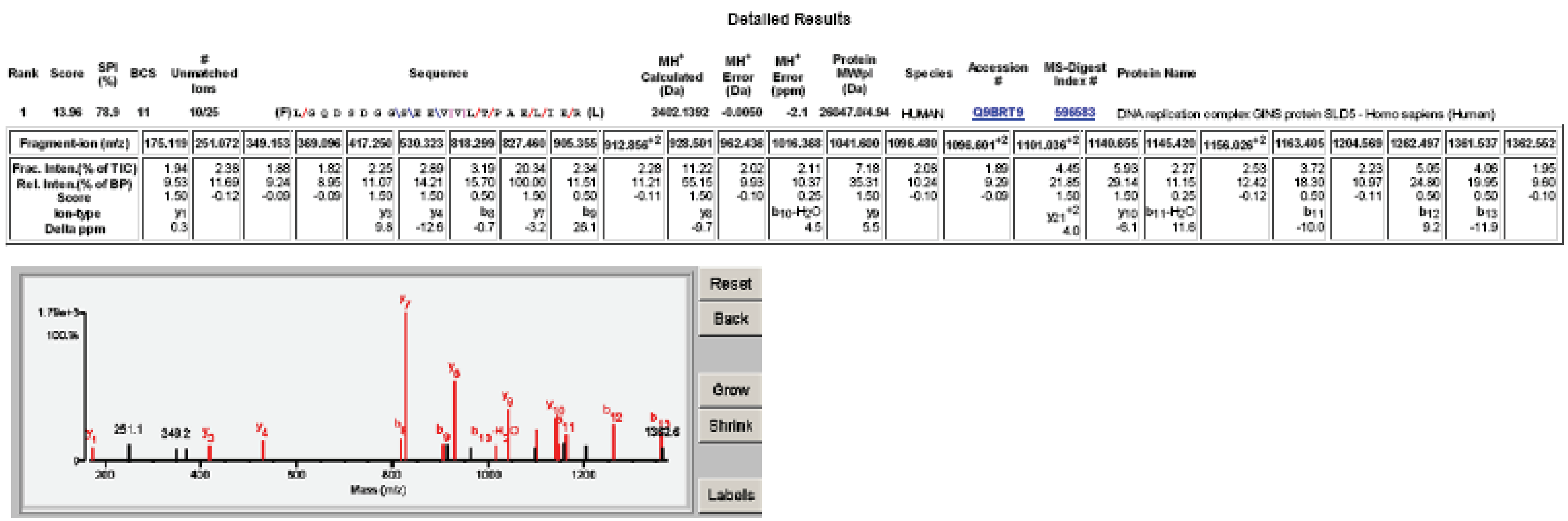
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.89	68.6	5	14/26	(M) S K/P/D L/T/A/A L R (D)	1294.6282	0.0005	0.4	53536.0/5.21	HUMAN	P17661	134111	Desmin - Homo sapiens (Human)
1	8.89	68.6	5	14/26	(V) S K/P/D L/T/A/A L R (D)	1294.6282	0.0005	0.4	53651.9/5.06	HUMAN	P08670	698231	Vimentin - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	84.081	86.096	88.039	84.067	116.052	143.083	144.069	213.088	219.082	237.074	328.076	359.236
Frac. Inten.(% of TIC)	0.00	1.91	0.11	1.37	2.61	1.33	6.94	0.99	2.40	1.15	2.96	5.56	1.22
Rel. Inten.(% of BP)	0.01	5.88	0.33	4.21	8.00	4.07	21.31	3.04	7.39	3.54	9.08	17.09	3.75
Score	0.20	-0.06	0.22	-0.04	-0.08	-0.04	-0.21	-0.03	0.75	-0.04	-0.09	-0.17	1.50
Ion-type	PR		LI						PD				y_3
Delta ppm	9.6		-18.9						2.9				-12.3

Fragment-ion (m/z)	385.086	419.738^{+2}	421.138	428.747	430.271	504.763^{+2}	513.777^{+2}	531.322	610.412	759.434	856.488	1201.640
Frac. Inten.(% of TIC)	1.77	1.52	2.24	32.54	3.50	0.98	3.98	4.20	0.90	2.69	16.15	1.00
Rel. Inten.(% of BP)	5.42	4.66	6.89	100.00	10.74	3.00	12.24	12.89	2.76	8.26	49.63	3.07
Score	-0.05	0.50	0.25	1.50	1.50	-0.03	-0.12	1.50	-0.03	1.50	1.50	-0.03
Ion-type		y_8-H_2O^{+2}	b_2-H_2O	y++8	y_4			y_5		y_7	y_8	
Delta ppm		-11.0	-2.3	-1.8	-13.8			-4.7		-2.1	-3.5	



C3



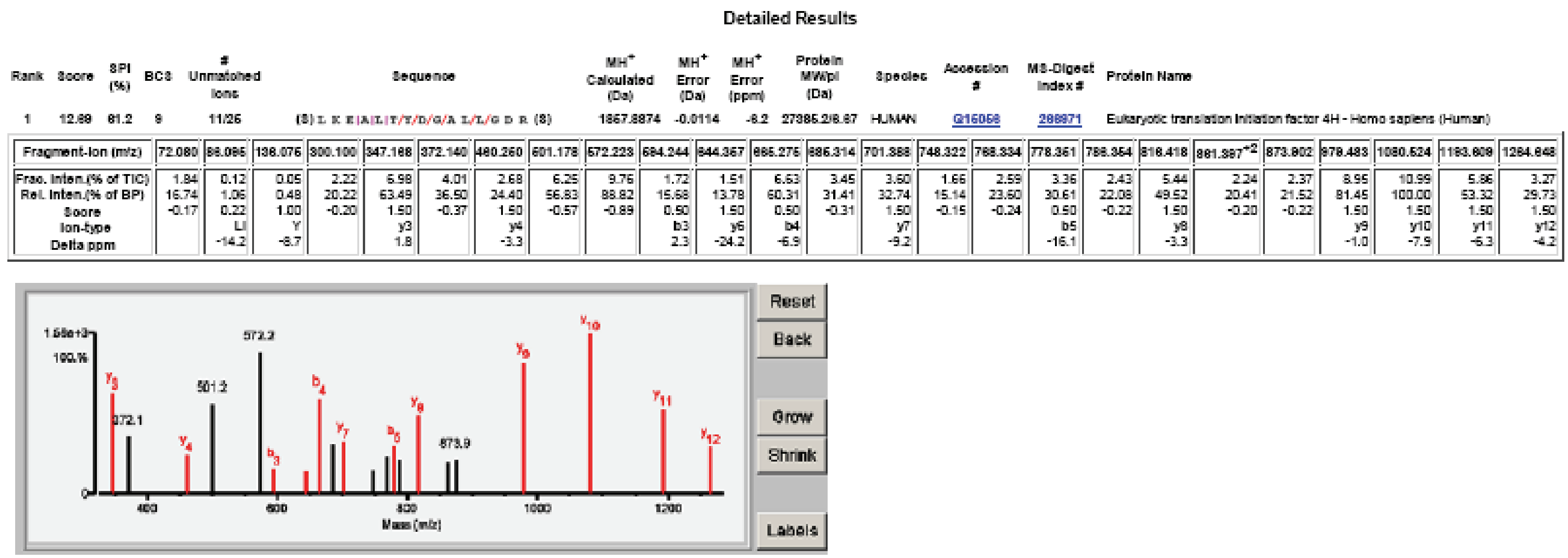
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.96	78.9	11	10/25	(F)L/G Q D S D G G\S\E E\V|V|L/T/P A E/L/I E/R (L)	2402.1392	-0.0050	-2.1	26047.0/4.94	HUMAN	Q9BRT9	596583	DNA replication complex GINS protein SLD5 - Homo sapiens (Human)

Fragment-Ion (m/z)	175.119	251.072	349.153	369.096	417.250	530.323	818.299	827.460	905.355	912.856^{+2}	928.501	962.436	1016.368
Frac. Inten.(% of TIC)	1.94	2.38	1.88	1.82	2.25	2.89	3.19	20.34	2.34	2.28	11.22	2.02	2.11
Rel. Inten.(% of BP)	9.53	11.69	9.24	8.95	11.07	14.21	15.70	100.00	11.51	11.21	55.15	9.93	10.37
Score	1.50	-0.12	-0.09	-0.09	1.50	1.50	0.50	1.50	0.50	-0.11	1.50	-0.10	0.25
Ion-type	y_1				y_3	y_4	b_8	y_7	b_9		y_8		b_{10}-H_2O
Delta ppm	0.3				9.8	-12.6	-0.7	-3.2	28.1		-9.7		4.5

Fragment-Ion (m/z)	1041.600	1096.480	1096.601^{+2}	1101.036^{+2}	1140.655	1145.420	1156.026^{+2}	1163.405	1204.569	1262.497	1361.537	1362.552
Frac. Inten.(% of TIC)	7.18	2.08	1.89	4.45	5.93	2.27	2.53	3.72	2.23	5.06	4.06	1.95
Rel. Inten.(% of BP)	35.31	10.24	9.29	21.85	29.14	11.15	12.42	18.30	10.97	24.80	19.95	9.60
Score	1.50	-0.10	-0.09	1.50	1.50	0.25	-0.12	0.50	-0.11	0.50	0.50	-0.10
Ion-type	y_9			y_{21}^{+2}	y_{10}	b_{11}-H_2O		b_{11}		b_{12}	b_{13}	
Delta ppm	5.5			4.0	-6.1	11.6		-10.0		9.2	-11.9	

C4



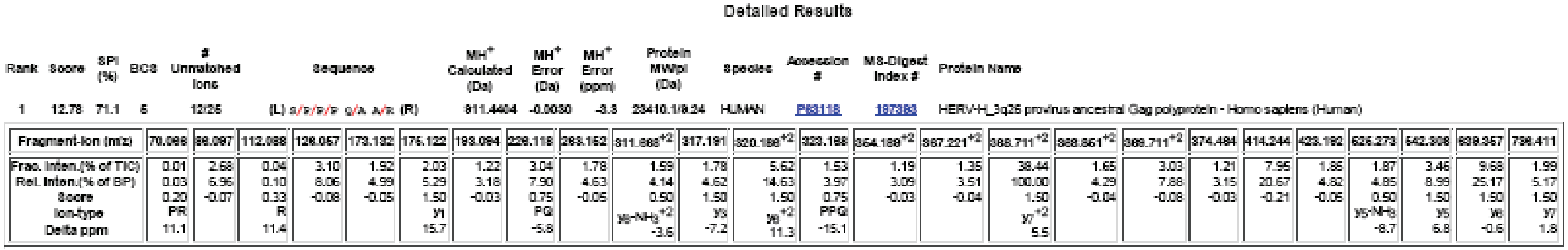
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.69	81.2	9	11/26	(S)L K E|A|L|T/Y/D/G/A L/L/G D R (S)	1867.8874	-0.0114	-6.2	27385.2/6.67	HUMAN	Q15056	288971	Eukaryotic translation initiation factor 4H - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	86.096	136.076	300.100	347.168	372.140	460.260	501.178	572.223	584.244	644.367	685.275	686.314
Frac. Inten.(% of TIC)	1.84	0.12	0.05	2.22	6.98	4.01	2.68	6.25	9.76	1.72	1.51	6.63	3.45
Rel. Inten.(% of BP)	16.74	1.06	0.48	20.22	63.49	36.50	24.40	56.83	88.82	15.68	13.78	60.31	31.41
Score	-0.17	0.22	1.00	-0.20	1.50	-0.37	1.50	-0.57	-0.89	0.50	1.50	0.50	-0.31
Ion-type		LI	Y		y3		y4			b3	y6	b4	
Delta ppm		-14.2	-8.7		1.8		-3.3			2.3	-24.2	-6.9	

Fragment-Ion (m/z)	701.388	748.322	768.334	778.361	786.354	816.418	861.397^{+2}	873.902	979.483	1080.524	1193.608	1264.646
Frac. Inten.(% of TIC)	3.60	1.66	2.59	3.36	2.43	5.44	2.24	2.37	8.95	10.99	5.86	3.27
Rel. Inten.(% of BP)	32.74	15.14	23.60	30.61	22.08	49.52	20.41	21.52	81.45	100.00	53.32	29.73
Score	1.50	-0.15	-0.24	0.50	-0.22	1.50	-0.20	-0.22	1.50	1.50	1.50	1.50
Ion-type	y7			b5		y8			y9	y10	y11	y12
Delta ppm	-9.2			-16.1		-3.3			-1.0	-7.9	-6.3	-4.2

C5

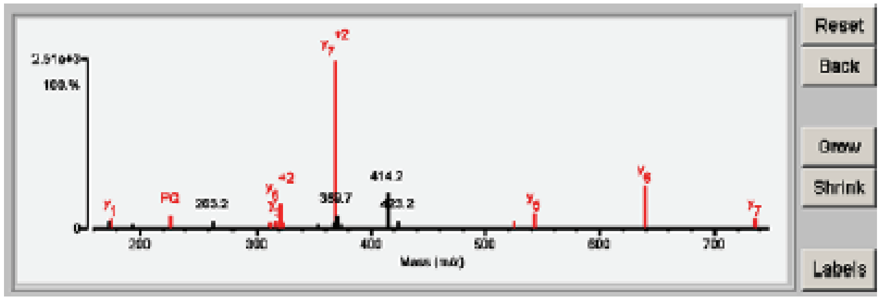


Detailed Results

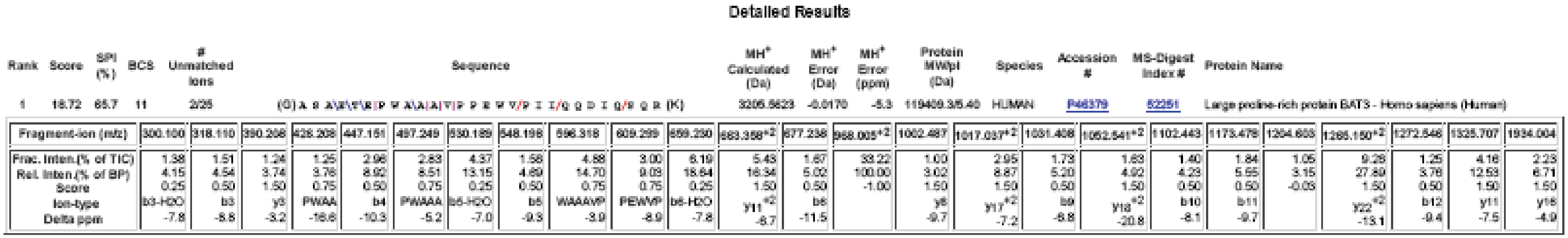
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.78	71.1	5	12/25	(L) S/P/P/P Q/A A/R (R)	811.4404	-0.0030	-3.3	23410.1/8.24	HUMAN	P63118	187383	HERV-H_3q26 provirus ancestral Gag polyprotein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	86.097	112.088	126.057	173.132	175.122	193.094	228.118	283.152	311.668^{+2}	317.191	320.186^{+2}	323.168
Frac. Inten.(% of TIC)	0.01	2.68	0.04	3.10	1.92	2.03	1.22	3.04	1.78	1.59	1.78	5.62	1.53
Rel. Inten.(% of BP)	0.03	6.96	0.10	8.06	4.99	5.29	3.18	7.90	4.63	4.14	4.62	14.63	3.97
Score	0.20	-0.07	0.33	-0.08	-0.05	1.50	-0.03	0.75	-0.05	0.50	1.50	1.50	0.75
Ion-type	PR		R			y_1		PQ		y_6-NH_3^{+2}	y_3	y_6^{+2}	PPQ
Delta ppm	11.1		11.4			15.7		-5.8		-3.6	-7.2	11.3	-15.1

Fragment-ion (m/z)	364.186^{+2}	367.221^{+2}	368.711^{+2}	368.861^{+2}	369.711^{+2}	374.484	414.244	423.192	526.273	542.308	639.357	736.411
Frac. Inten.(% of TIC)	1.19	1.35	38.44	1.65	3.03	1.21	7.95	1.85	1.87	3.46	9.68	1.99
Rel. Inten.(% of BP)	3.09	3.51	100.00	4.29	7.88	3.15	20.67	4.82	4.85	8.99	25.17	5.17
Score	-0.03	-0.04	1.50	-0.04	-0.08	-0.03	-0.21	-0.05	0.50	1.50	1.50	1.50
Ion-type			y_7^{+2}						y_5-NH_3	y_5	y_6	y_7
Delta ppm			5.5						-8.7	6.8	-0.6	1.8



C6

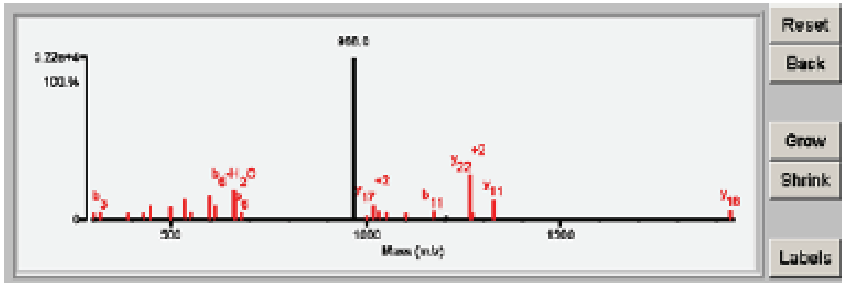


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.72	65.7	11	2/25	(G) A S A\E\T\R|P W A\A|A|V|P P E W V/P I I/Q Q D I Q/S Q R (K)	3205.5623	-0.0170	-5.3	119409.3/5.40	HUMAN	P46379	52251	Large proline-rich protein BAT3 - Homo sapiens (Human)

Fragment-ion (m/z)	300.100	318.110	390.206	426.208	447.151	497.249	530.189	548.196	596.318	609.299	659.230	683.358^{+2}	677.238
Frac. Inten.(% of TIC)	1.38	1.51	1.24	1.25	2.96	2.83	4.37	1.56	4.88	3.00	6.19	5.43	1.67
Rel. Inten.(% of BP)	4.15	4.54	3.74	3.76	8.92	8.51	13.15	4.69	14.70	9.03	18.64	16.34	5.02
Score	0.25	0.50	1.50	0.75	0.50	0.75	0.25	0.50	0.75	0.75	0.25	1.50	0.50
Ion-type	b_3-H_2O	b_3	y_3	PWAA	b_4	PWAAA	b_5-H_2O	b_5	WAAAVP	PEWVP	b_6-H_2O	y_{11}^{+2}	b_6
Delta ppm	-7.8	-8.8	-3.2	-16.6	-10.3	-5.2	-7.0	-9.3	-3.9	-8.9	-7.8	-8.7	-11.5

Fragment-ion (m/z)	968.005^{+2}	1002.487	1017.037^{+2}	1031.408	1052.541^{+2}	1102.443	1173.478	1204.603	1265.150^{+2}	1272.546	1325.707	1934.004
Frac. Inten.(% of TIC)	33.22	1.00	2.95	1.73	1.63	1.40	1.84	1.05	9.28	1.25	4.16	2.23
Rel. Inten.(% of BP)	100.00	3.02	8.87	5.20	4.92	4.23	5.55	3.15	27.89	3.76	12.53	6.71
Score	-1.00	1.50	1.50	0.50	1.50	0.50	0.50	-0.03	1.50	0.50	1.50	1.50
Ion-type		y_8	y_{17}^{+2}	b_9	y_{18}^{+2}	b_{10}	b_{11}		y_{22}^{+2}	b_{12}	y_{11}	y_{16}
Delta ppm		-9.7	-7.2	-8.8	-20.8	-8.1	-9.7		-13.1	-9.4	-7.5	-4.9



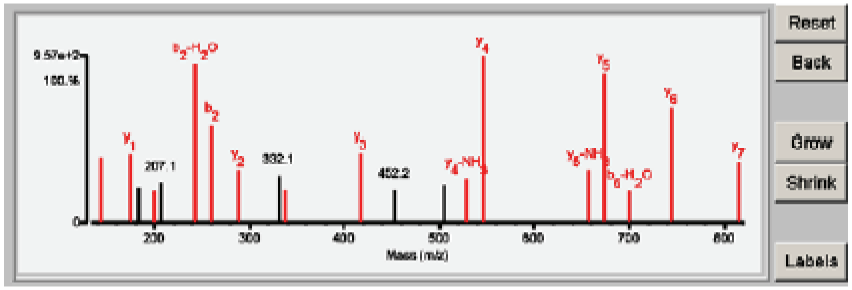
C7

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.28	79.4	7	8/26	(T) T/A|A/Q/Q/E/L/R (T)	1004.4830	-0.0000	-0.0	228840.2/5.44	HUMAN	P35580	359021	Myosin-10 - Homo sapiens (Human)
1	14.28	79.4	7	8/26	(S) T/A|A/Q/Q/E/L/R (S)	1004.4830	-0.0000	-0.0	228533.4/5.60	HUMAN	P35579	359139	Myosin-9 - Homo sapiens (Human)

Fragment-ion (m/z)	70.084	72.082	74.081	110.069	116.086	143.084	175.120	183.078	200.103	207.078	243.080	261.092	288.201
Frac. Inten.(% of TIC)	0.00	3.38	2.31	2.25	2.11	4.27	4.39	2.34	2.03	2.59	10.17	6.27	3.40
Rel. Inten.(% of BP)	0.02	31.57	21.54	20.96	19.68	39.90	41.06	21.85	19.01	24.20	95.07	58.60	31.76
Score	0.20	-0.32	-0.22	-0.21	0.50	0.75	1.50	-0.22	0.75	-0.24	0.25	0.50	1.50
Ion-type	PR				AA-28	AA	y_1		AQ		$b_2\text{-}H_2O$	b_2	y_2
Delta ppm	-16.1				-24.2	10.5	4.8		-7.3		-2.8	1.7	-7.7

Fragment-ion (m/z)	332.128^{+2}	337.196^{+2}	417.262	452.157	506.248	628.270	645.302	656.348	673.362	698.266	744.381	816.426
Frac. Inten.(% of TIC)	3.10	2.19	4.54	2.17	2.47	2.91	10.70	3.46	9.53	2.07	7.37	3.99
Rel. Inten.(% of BP)	28.99	20.43	42.45	20.23	23.11	27.16	100.00	32.32	89.02	19.36	68.82	37.24
Score	-0.29	1.50	1.50	-0.20	-0.23	0.50	1.50	0.50	1.50	0.25	1.50	1.50
Ion-type		y_5^{+2}	y_3			$y_4\text{-}NH_3$	y_4	$y_5\text{-}NH_3$	y_5	$b_6\text{-}H_2O$	y_6	y_7
Delta ppm		29.6	14.6			-14.3	-3.5	18.7	-0.4	-33.2	-11.7	-13.8



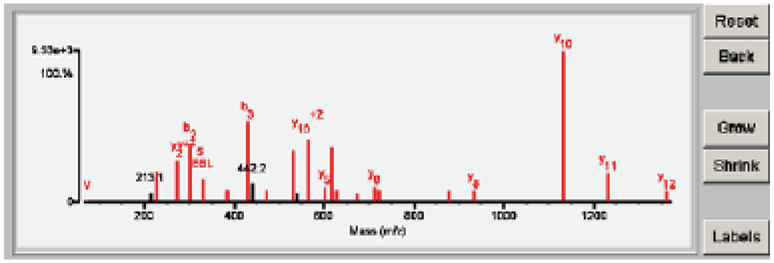
C8

Detailed Results

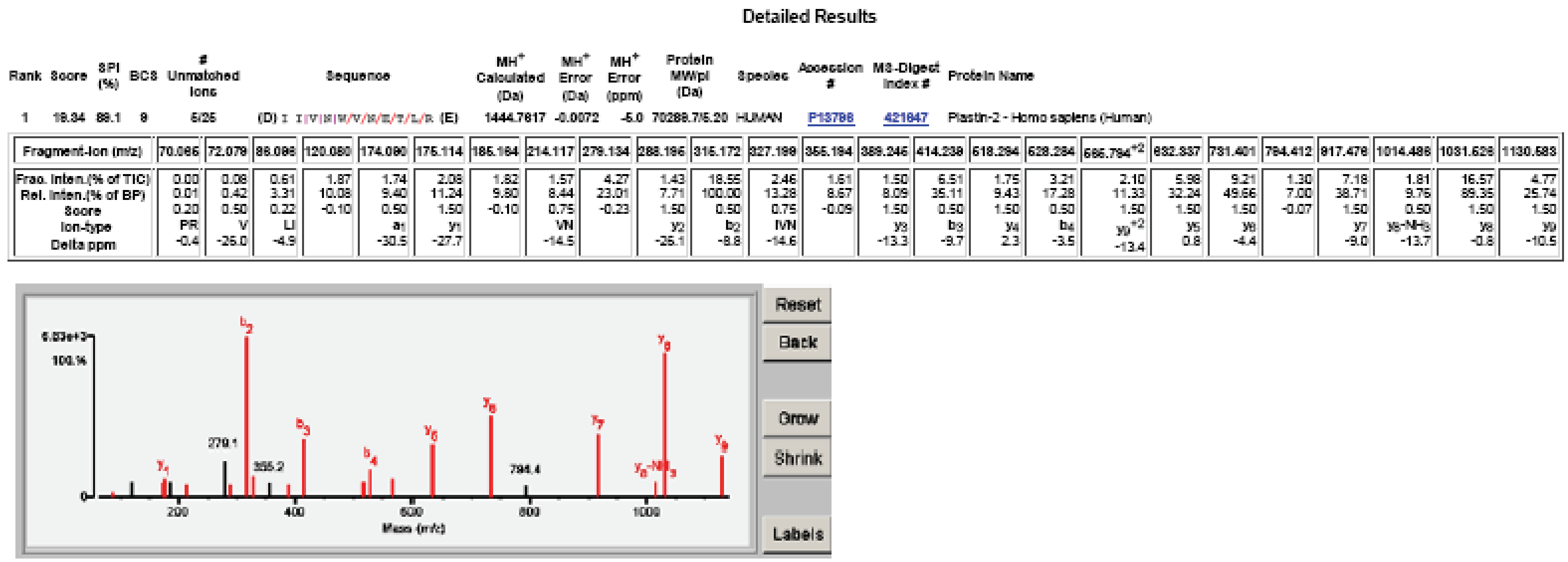
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.97	94.8	11	3/25	(G) L V|E|T|P\T/G/Y/I/E/S/L/P R (V)	1662.8407	0.0014	0.8	45374.4/4.36	HUMAN	P55209	375961	Nucleosome assembly protein 1-like 1 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.097	213.084	229.117	272.171	301.158	330.164	385.253	430.199	442.170	472.287	531.247	541.232
Frac. Inten.(% of TIC)	0.26	0.05	1.33	4.13	5.66	7.85	3.13	1.67	10.58	2.58	1.64	6.93	1.25
Rel. Inten.(% of BP)	1.27	0.24	6.61	20.45	28.04	38.90	15.52	8.27	52.45	12.78	8.11	34.33	6.19
Score	0.50	0.22	-0.07	0.75	1.50	1.50	0.75	1.50	0.50	-0.13	1.50	0.50	-0.06
Ion-type	V	LI		VE	y_2	b_2 y^{++}_5	ESL	y_3	b_3		y_4	b_4	
Delta ppm	7.3	2.0		-12.1	-3.4	-3.1 -35.3	-8.4	-7.2	-5.6		-0.9	-3.8	

Fragment-ion (m/z)	566.804^{+2}	601.328	617.326^{+2}	628.277	672.838^{+2}	714.416	722.879^{+2}	877.469	934.501	1132.597	1233.642	1362.688
Frac. Inten.(% of TIC)	8.57	1.96	7.52	1.72	1.16	2.05	1.68	1.39	1.43	20.18	3.90	1.41
Rel. Inten.(% of BP)	42.45	9.70	37.30	8.53	5.77	10.14	8.32	6.88	7.10	100.00	19.31	6.97
Score	1.50	1.50	1.50	0.50	0.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	y_{10}^{+2}	y_5	y_{11}^{+2}	b_6	$y_{12}\text{-}H_2O^{+2}$	y_6	$y_{13}\text{-}NH_3^{+2}$	y_7	y_8	y_{10}	y_{11}	y_{12}
Delta ppm	0.2	-4.3	-2.3	-39.4	-8.1	2.4	13.3	-9.7	1.8	-2.8	-4.4	-2.8



C9

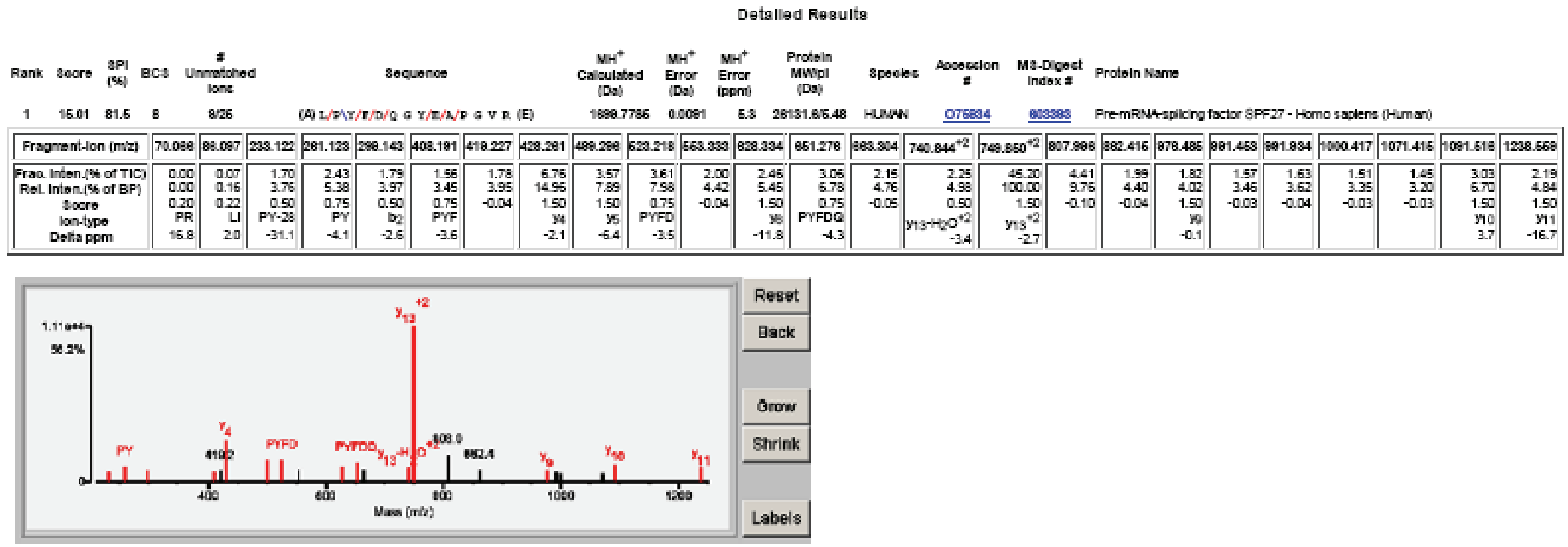


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.34	89.1	9	6/25	(D) I I|V|N|W/V/N/E/T/L/R (E)	1444.7817	-0.0072	-5.0	70288.7/5.20	HUMAN	P13796	421847	Plastin-2 - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.066	0.00	0.01	0.20	PR	-0.4
72.079	0.08	0.42	0.50	V	-26.0
86.096	0.61	3.31	0.22	LI	-4.9
120.080	1.87	10.08	-0.10		
174.090	1.74	9.40	0.50	a_1	-30.5
175.114	2.08	11.24	1.50	y_1	-27.7
185.164	1.82	9.80	-0.10		
214.117	1.57	8.44	0.75	VN	-14.5
279.134	4.27	23.01	-0.23		
288.196	1.43	7.71	1.50	y_2	-25.1
315.172	18.55	100.00	0.50	b_2	-8.8
327.199	2.46	13.28	0.75	IVN	-14.6
355.194	1.61	8.67	-0.09		
389.246	1.50	8.09	1.50	y_3	-13.3
414.238	6.51	35.11	0.50	b_3	-9.7
518.294	1.75	9.43	1.50	y_4	2.3
528.284	3.21	17.28	0.50	b_4	-3.5
565.794^{+2}	2.10	11.33	1.50	y_9^{+2}	-13.4
632.337	5.98	32.24	1.50	y_5	0.8
731.401	9.21	49.66	1.50	y_6	-4.4
794.412	1.30	7.00	-0.07		
917.476	7.18	38.71	1.50	y_7	-9.0
1014.486	1.81	9.76	0.50	y_8-NH_3	-13.7
1031.526	16.57	89.35	1.50	y_8	-0.8
1130.583	4.77	25.74	1.50	y_9	-10.5

C10



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.01	81.5	8	8/26	(A) L/P\Y/F/D/Q G Y/E/A/P G V R (E)	1698.7786	0.0091	5.3	26131.6/6.48	HUMAN	O75934	803393	Pre-mRNA-splicing factor SPF27 - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.066	0.00	0.00	0.20	PR	16.8
86.097	0.07	0.16	0.22	LI	2.0
233.122	1.70	3.76	0.50	PY-28	-31.1
261.123	2.43	5.38	0.75	PY	-4.1
298.143	1.79	3.97	0.50	b_2	-2.6
408.191	1.56	3.45	0.75	PYF	-3.6
418.227	1.78	3.95	-0.04		
428.261	6.76	14.96	1.50	y_4	-2.1
499.296	3.57	7.89	1.50	y_5	-6.4
523.218	3.61	7.98	0.75	PYFD	-3.5
563.333	2.00	4.42	-0.04		
628.334	2.46	5.45	1.50	y_6	-11.8
651.276	3.06	6.78	0.75	PYFDQ	-4.3
663.304	2.15	4.76	-0.05		
740.844^{+2}	2.25	4.98	0.50	y_{13}-H_2O^{+2}	-3.4
749.850^{+2}	45.20	100.00	1.50	y_{13}^{+2}	-2.7
807.986	4.41	9.76	-0.10		
862.416	1.99	4.40	-0.04		
976.485	1.82	4.02	1.50	y_9	-0.1
981.453	1.57	3.46	-0.03		
991.934	1.63	3.62	-0.04		
1000.417	1.51	3.35	-0.03		
1071.416	1.45	3.20	-0.03		
1091.516	3.03	6.70	1.50	y_{10}	3.7
1238.568	2.19	4.84	1.50	y_{11}	-16.7

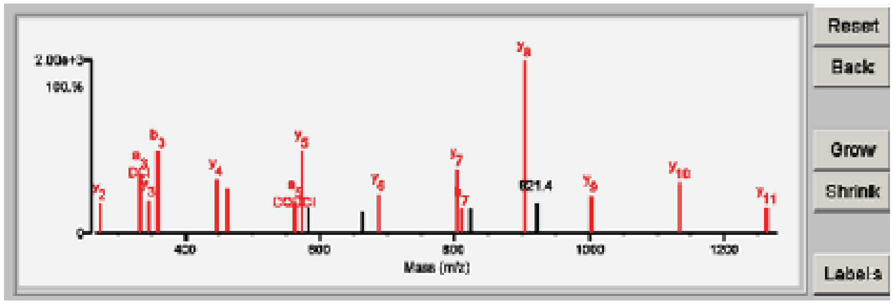
C11

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.41	78.9	13	8/25	(N) G D V\C\Q D C\I/Q/M/V/T/D/I/Q/T/A/V R (T)	2182.9800	0.0173	7.9	58113.1/5.07	HUMAN	P07602	583787	Proactivator polypeptide precursor [Contains: Saposin-A - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.097	104.066	188.087	206.097	262.121	274.186	332.129	346.227	360.120	448.269	463.130	563.188
Frac. Inten.(% of TIC)	0.91	0.25	2.74	2.98	3.64	2.10	2.86	5.67	3.03	7.68	5.02	4.19	2.93
Rel. Inten.(% of BP)	5.63	1.54	17.01	18.50	22.66	13.03	17.76	35.22	18.84	47.72	31.22	26.07	18.18
Score	0.50	0.22	-0.17	-0.18	-0.23	-0.13	1.50	0.75	1.50	0.50	1.50	0.50	0.75
Ion-type	V	LI					y2	a3	y3	b3	y4	b4	a5
Delta ppm	8.7	5.5					-3.9	1.6 DCI 1.6	6.4	-11.1	-6.9	-5.1	-15.5 CQDCI -15.5

Fragment-Ion (m/z)	674.322	683.230	682.291	687.404	802.441	809.227	822.308	903.484	921.378	1002.568	1133.588	1261.652
Frac. Inten.(% of TIC)	7.68	2.45	2.18	3.70	5.95	2.25	2.25	16.09	2.80	3.54	4.75	2.38
Rel. Inten.(% of BP)	47.72	15.20	13.54	22.97	36.97	14.01	13.95	100.00	17.39	22.00	29.51	14.79
Score	1.50	-0.15	-0.14	1.50	1.50	0.50	-0.14	1.50	-0.17	1.50	1.50	1.50
Ion-type	y5			y6	y7	b7		y8		y9	y10	y11
Delta ppm	-16.1			-16.3	-0.8	-0.1		5.3		1.1	-9.4	-4.0



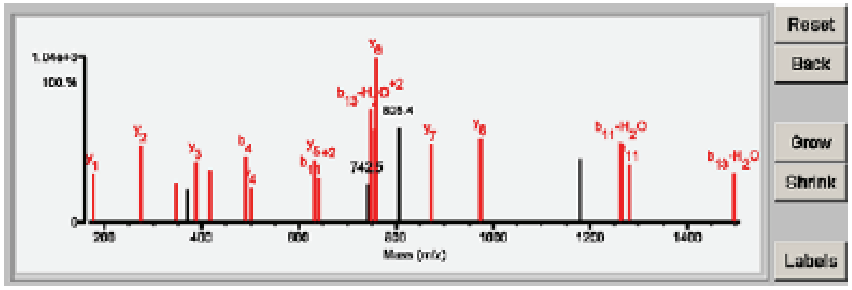
C12

Detailed Results

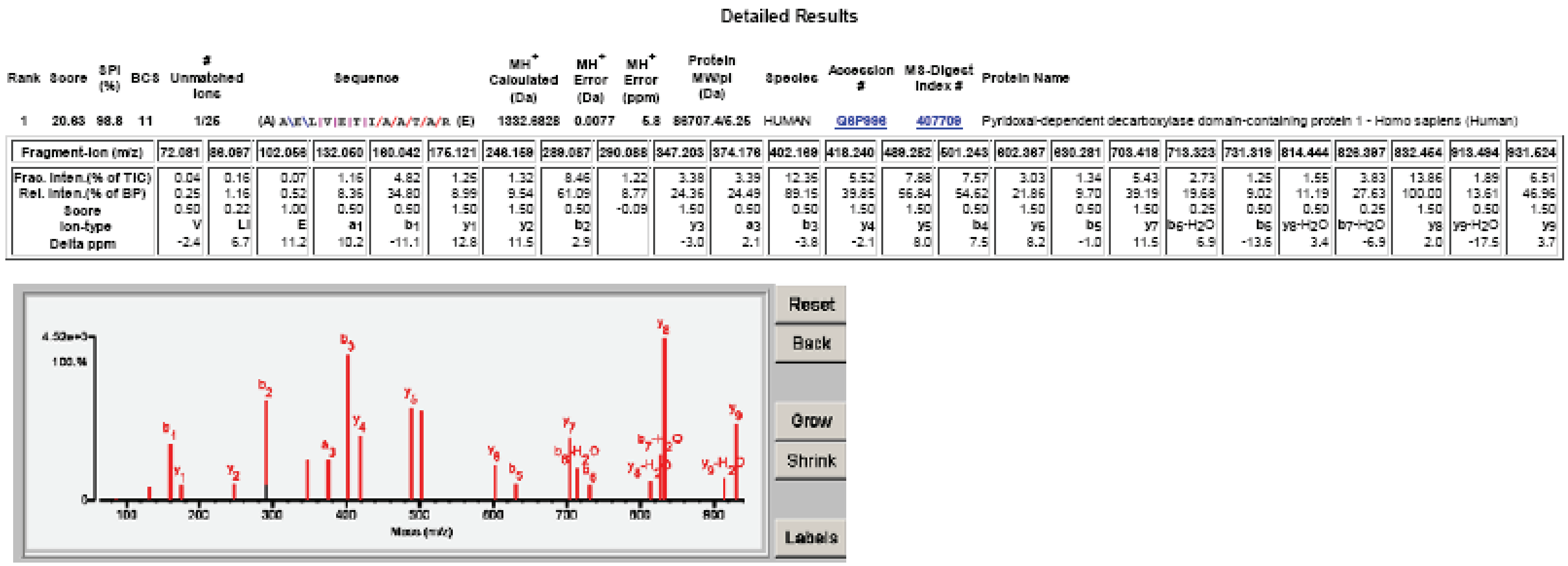
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.19	79.1	12	5/26	(N) E E\A\A\L L E E E A T\M/T|I/E/R/L/L/T/R (Y)	2387.1469	0.0080	3.3	59271.8/4.27	HUMAN	O15355	429683	Protein phosphatase 1G - Homo sapiens (Human)

Fragment-Ion (m/z)	86.099	102.068	104.053	175.118	276.167	347.081	371.883^{+2}	389.253	418.126	489.165	502.341	631.373	632.777^{+2}
Frac. Inten.(% of TIC)	0.28	0.08	6.45	3.05	4.76	2.46	2.09	3.74	3.33	4.12	2.17	3.88	3.23
Rel. Inten.(% of BP)	2.73	0.75	62.79	29.64	46.35	23.96	20.37	36.42	32.40	40.06	21.10	37.73	31.44
Score	0.22	1.00	-0.63	1.50	1.50	0.50	-0.20	1.50	0.50	0.50	1.50	1.50	0.25
Ion-type	LI	E		y_1	y_2	b_2		y_3	b_3	b_4	y_4	y_5	b_{11}-H_2O^{+2}
Delta ppm	25.3	26.9		-8.3	-33.4	-30.1		5.2	-8.3	-22.4	13.2	-7.4	-4.7

Fragment-Ion (m/z)	641.784^{+2}	742.616^{+3}	748.828^{+2}	767.826^{+2}	780.419	806.353	873.601	874.543	1181.482	1264.656	1282.582	1496.623
Frac. Inten.(% of TIC)	2.79	2.43	7.09	5.83	10.28	5.93	4.92	5.26	4.00	4.98	3.67	3.16
Rel. Inten.(% of BP)	27.17	23.64	69.02	56.74	100.00	57.66	47.82	51.21	38.96	48.45	35.66	30.79
Score	0.50	-0.24	0.25	0.50	1.50	-0.58	1.50	1.50	-0.39	0.25	0.50	0.25
Ion-type	b_{11}^{+2}		b_{13}-H_2O^{+2}	b_{13}^{+2}	y_6		y_7	y_8		b_{11}-H_2O	b_{11}	b_{13}-H_2O
Delta ppm	-1.1		4.8	-4.0	-1.4		-3.0	-6.4		2.0	-1.2	-12.0



C13

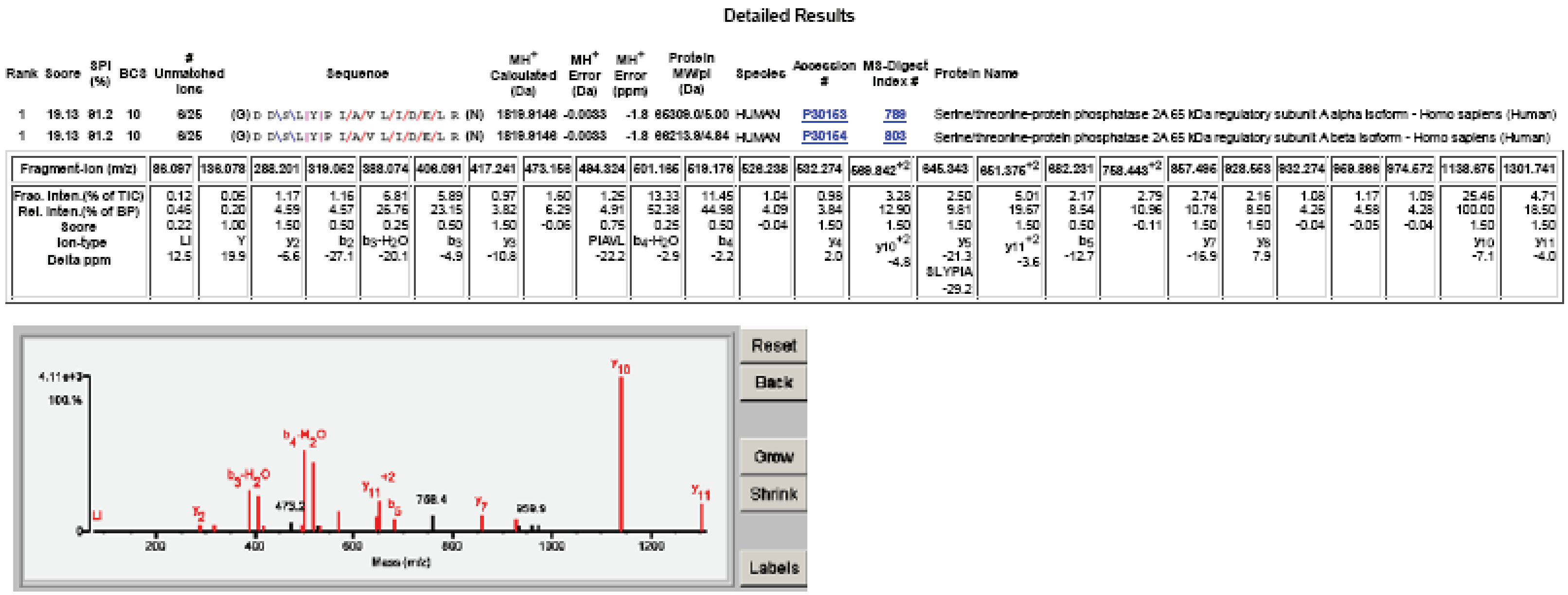


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.63	98.8	11	1/26	(A) A\E\L|V|E|T|I/A/A/T/A/R (E)	1332.6828	0.0077	5.8	86707.4/6.25	HUMAN	Q6P996	407708	Pyridoxal-dependent decarboxylase domain-containing protein 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.097	102.056	132.060	160.042	176.121	248.159	289.087	290.088	347.203	374.178	402.169	418.240	489.282	501.243	602.367	630.281	703.418	713.323	731.319	814.444	826.397	832.464	913.494	931.524
Frac. Inten.(% of TIC)	0.04	0.16	0.07	1.16	4.82	1.25	1.32	8.46	1.22	3.38	3.39	12.35	5.52	7.88	7.57	3.03	1.34	5.43	2.73	1.25	1.55	3.83	13.86	1.89	6.51
Rel. Inten.(% of BP)	0.25	1.16	0.52	8.36	34.80	8.99	9.54	61.09	8.77	24.36	24.49	89.15	39.85	56.84	54.62	21.86	9.70	39.19	19.68	9.02	11.19	27.63	100.00	13.61	46.96
Score	0.50	0.22	1.00	0.50	0.50	1.50	1.50	0.50	-0.09	1.50	0.50	0.50	1.50	1.50	0.50	1.50	0.50	1.50	0.25	0.50	0.50	0.25	1.50	0.50	1.50
Ion-type	V	LI	E	a_1	b_1	y_1	y_2	b_2		y_3	a_3	b_3	y_4	y_5	b_4	y_6	b_5	y_7	b_6-H_2O	b_6	y_8-H_2O	b_7-H_2O	y_8	y_9-H_2O	y_9
Delta ppm	-2.4	6.7	11.2	10.2	-11.1	12.8	11.5	2.9		-3.0	2.1	-3.8	-2.1	8.0	7.5	8.2	-1.0	11.5	6.9	-13.6	3.4	-6.9	2.0	-17.5	3.7

C14

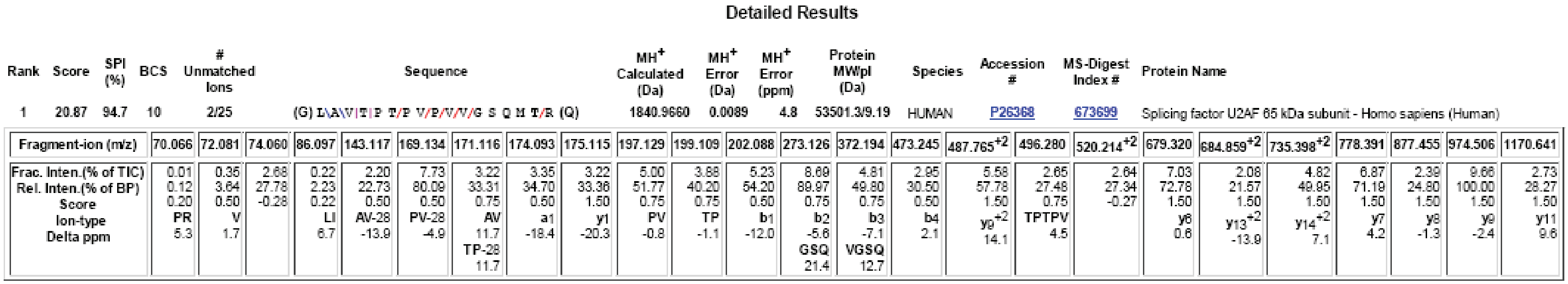


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.13	91.2	10	6/25	(G) D D\S\L|Y|P I/A/V L/I/D/E/L R (N)	1819.9148	-0.0033	-1.8	65309.0/5.00	HUMAN	P30153	789	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform - Homo sapiens (Human)
1	19.13	91.2	10	6/25	(G) D D\S\L|Y|P I/A/V L/I/D/E/L R (N)	1819.9148	-0.0033	-1.8	66213.8/4.84	HUMAN	P30154	803	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	136.076	288.201	319.062	388.074	406.081	417.241	473.156	484.324	501.166	519.176	526.238	532.274	589.842^{+2}	645.343	651.376^{+2}	682.231	758.443^{+2}	857.496	928.563	932.274	969.886	974.672	1138.676	1301.741
Frac. Inten.(% of TIC)	0.12	0.05	1.17	1.16	6.81	5.89	0.97	1.60	1.25	13.33	11.45	1.04	0.98	3.28	2.50	5.01	2.17	2.79	2.74	2.16	1.08	1.17	1.09	25.46	4.71
Rel. Inten.(% of BP)	0.46	0.20	4.59	4.57	26.76	23.15	3.82	6.29	4.91	52.38	44.98	4.09	3.84	12.90	9.81	19.67	8.54	10.96	10.78	8.50	4.26	4.58	4.28	100.00	18.50
Score	0.22	1.00	1.50	0.50	0.25	0.50	1.50	-0.06	0.75	0.25	0.50	-0.04	1.50	1.50	1.50	1.50	0.50	-0.11	1.50	1.50	-0.04	-0.05	-0.04	1.50	1.50
Ion-type	LI	Y	y_2	b_2	b_3-H_2O	b_3	y_3		PIAVL	b_4-H_2O	b_4		y_4	$y10^{+2}$	y_5		$y11^{+2}$	b_5		y_7	y_8			y_{10}	y_{11}
Delta ppm	12.5	19.9	-6.6	-27.1	-20.1	-4.9	-10.8		-22.2	-2.9	-2.2		2.0	-4.8	-21.3 SLYPIA -29.2	-3.6	-12.7		-16.9	7.9				-7.1	-4.0

C15

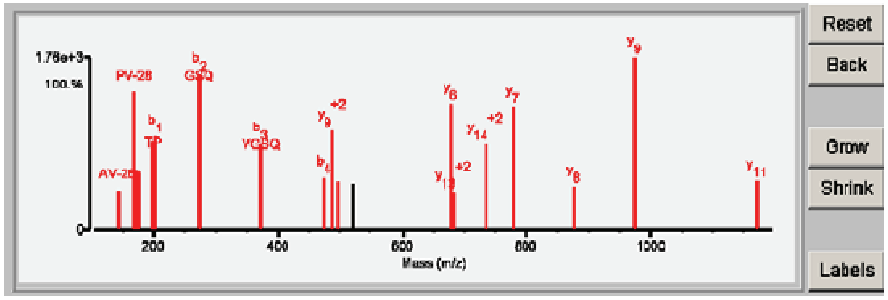


Detailed Results

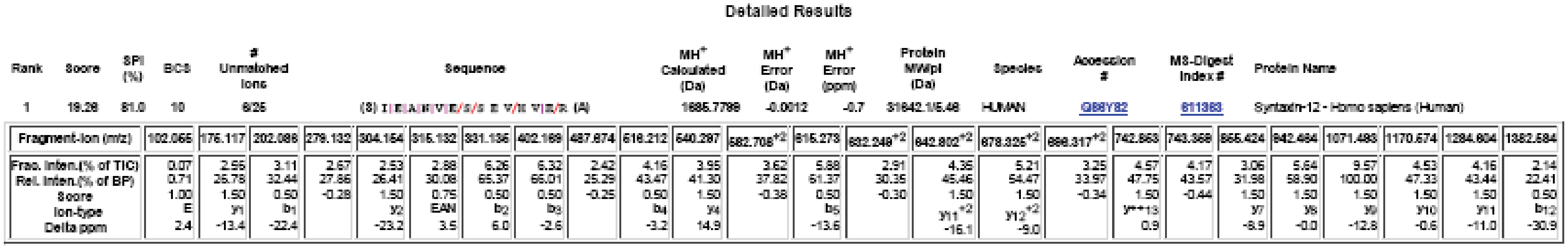
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.87	94.7	10	2/25	(G) L\A\V|T|P T/P V/P/V/V/G S Q M T/R (Q)	1840.9660	0.0089	4.8	53501.3/9.19	HUMAN	P26368	673699	Splicing factor U2AF 65 kDa subunit - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	74.060	86.097	143.117	169.134	171.116	174.093	175.115	197.129	199.109	202.088	273.126
Frac. Inten.(% of TIC)	0.01	0.35	2.68	0.22	2.20	7.73	3.22	3.35	3.22	5.00	3.88	5.23	8.69
Rel. Inten.(% of BP)	0.12	3.64	27.78	2.23	22.73	80.09	33.31	34.70	33.36	51.77	40.20	54.20	89.97
Score	0.20	0.50	-0.28	0.22	0.50	0.50	0.75	0.50	1.50	0.75	0.75	0.50	0.75
Ion-type	PR	V		LI	AV-28	PV-28	AV TP-28	a1	y1	PV	TP	b1	b2 GSQ
Delta ppm	5.3	1.7		6.7	-13.9	-4.9	11.7 11.7	-18.4	-20.3	-0.8	-1.1	-12.0	-5.6 21.4

Fragment-ion (m/z)	372.194	473.245	487.765^{+2}	496.280	520.214^{+2}	679.320	684.859^{+2}	735.398^{+2}	778.391	877.455	974.506	1170.641
Frac. Inten.(% of TIC)	4.81	2.95	5.58	2.65	2.64	7.03	2.08	4.82	6.87	2.39	9.66	2.73
Rel. Inten.(% of BP)	49.80	30.50	57.78	27.48	27.34	72.78	21.57	49.95	71.19	24.80	100.00	28.27
Score	0.75	0.50	1.50	0.75	-0.27	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	b3 VGSQ	b4	y9^{+2}	TPTPV		y6	y13^{+2}	y14^{+2}	y7	y8	y9	y11
Delta ppm	-7.1 12.7	2.1	14.1	4.5		0.6	-13.9	7.1	4.2	-1.3	-2.4	9.6



C16

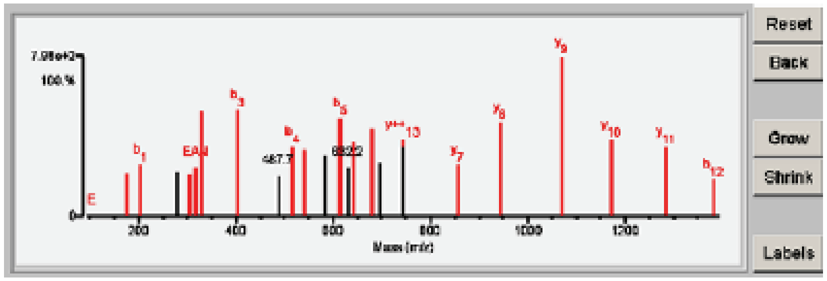


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.28	81.0	10	6/25	(S) I|E|A|N|V|E/S/S E V/H V|E/R (A)	1685.7799	-0.0012	-0.7	31642.1/5.48	HUMAN	Q86Y82	811383	Syntaxin-12 - Homo sapiens (Human)

Fragment-ion (m/z)	102.066	176.117	202.088	279.132	304.164	315.132	331.136	402.169	487.674	516.212	540.287	582.708^{+2}	615.273
Frac. Inten.(% of TIC)	0.07	2.56	3.11	2.67	2.53	2.88	6.26	6.32	2.42	4.16	3.95	3.62	5.88
Rel. Inten.(% of BP)	0.71	26.78	32.44	27.86	26.41	30.08	65.37	66.01	25.29	43.47	41.30	37.82	61.37
Score	1.00	1.50	0.50	-0.28	1.50	0.75	0.50	0.50	-0.25	0.50	1.50	-0.38	0.50
Ion-type	E	y1	b1		y2	EAN	b2	b3		b4	y4		b5
Delta ppm	2.4	-13.4	-22.4		-23.2	3.5	6.0	-2.6		-3.2	14.9		-13.6

Fragment-ion (m/z)	632.248^{+2}	642.802^{+2}	678.325^{+2}	698.317^{+2}	742.863	743.368	865.424	942.464	1071.483	1170.674	1284.604	1382.584
Frac. Inten.(% of TIC)	2.91	4.36	5.21	3.25	4.57	4.17	3.06	5.64	9.57	4.53	4.16	2.14
Rel. Inten.(% of BP)	30.35	45.46	54.47	33.97	47.75	43.57	31.98	58.90	100.00	47.33	43.44	22.41
Score	-0.30	1.50	1.50	-0.34	1.50	-0.44	1.50	1.50	1.50	1.50	1.50	0.50
Ion-type		y11^{+2}	y12^{+2}		y++13		y7	y8	y9	y10	y11	b12
Delta ppm		-16.1	-9.0		0.9		-8.9	-0.0	-12.8	-0.6	-11.0	-30.9



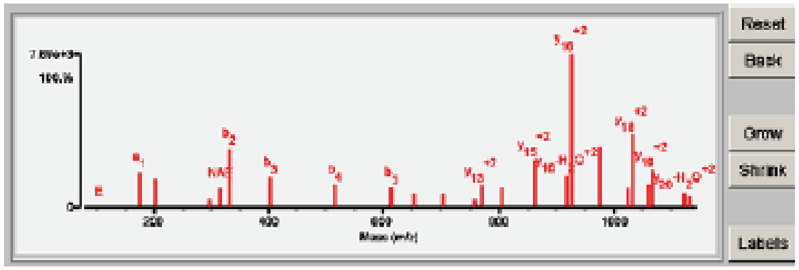
C17

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.97	100.0	10	0/25	(S) I|E|A|H|V|E/E/A/E/V/H V Q Q A E Q Q L S E (A)	2465.1038	0.0173	7.0	28816.7/5.41	HUMAN	O15400	611483	Syntaxin-7 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	102.054	174.093	202.089	297.119	315.133	331.138	402.170	516.212	615.283	654.855^{+2}	704.378^{+2}	755.376^{+3}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.06 0.31 0.22 LI -0.3	0.07 0.35 1.00 E -6.4	4.67 23.71 0.50 a_1 -15.6	3.63 18.47 0.50 b_1 -7.0	1.03 5.25 0.50 NAE-H_2O -4.5	2.52 12.82 0.75 NAE 6.6	7.72 39.22 0.50 b_2 -0.7	3.97 20.19 0.50 b_3 -0.3	2.97 15.10 0.50 b_4 -2.0	2.68 13.62 0.50 b_5 1.5	1.69 8.59 1.50 y_{11}^{+2} 19.4	1.78 9.03 1.50 y_{12}^{+2} 2.7	1.09 5.55 1.50 y_{20}^{+3} 4.9

Fragment-Ion (m/z)	768.888^{+2}	834.418^{+2}	861.446^{+2}	916.964^{+2}	925.965^{+2}	975.493^{+2}	1024.009^{+2}	1032.522^{+2}	1059.518^{+2}	1068.037^{+2}	1123.600^{+2}	1132.544^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.71 13.79 1.50 y_{13}^{+2} -11.8	2.58 13.11 1.50 y_{14}^{+2} 2.8	6.22 31.60 1.50 y_{15}^{+2} 9.1	4.07 20.67 0.50 y_{16}-H_2O^{+2} 0.8	19.68 100.00 1.50 y_{16}^{+2} 6.2	7.86 39.96 1.50 y_{17}^{+2} 0.2	2.43 12.33 0.50 y_{18}-NH_3^{+2} 7.8	9.39 47.70 1.50 y_{18}^{+2} 7.6	3.01 15.32 0.50 y_{19}-NH_3^{+2} -1.4	4.80 24.41 1.50 y_{19}^{+2} 3.3	1.87 9.51 0.50 y_{20}-H_2O^{+2} -38.2	1.49 7.57 1.50 y_{20}^{+2} -8.9



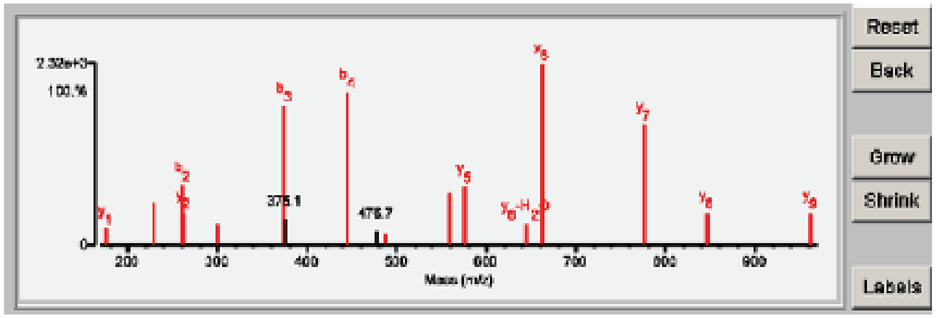
C18

Detailed Results

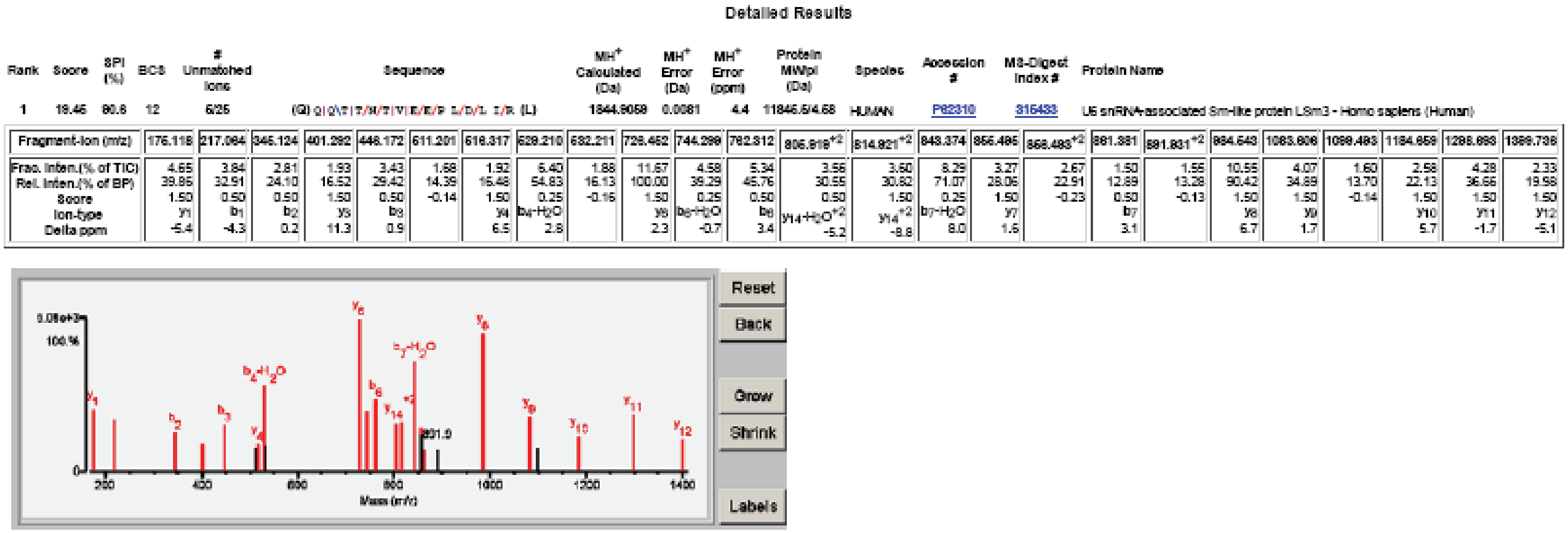
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.32	85.6	8	9/25	(A) G I|D|A|I|S/S/I I/S/R (Q)	1219.6361	-0.0018	-1.5	28906.8/4.91	HUMAN	Q9UNK0	611497	Syntaxin-8 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	88.087	94.066	102.053	120.082	136.076	166.086	176.114	229.117	259.109	262.148	299.171	300.158
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	3.05 19.12 -0.19	0.45 2.82 0.22 LI 3.2	1.46 9.15 -0.09	1.21 7.59 -0.08	1.85 11.62 -0.12	1.18 7.39 -0.07	1.30 8.13 -0.08	1.42 8.94 1.50 y_1 -26.6	3.68 23.12 0.75 LD -10.8	5.26 33.02 0.50 b_2 -13.5	2.76 17.34 1.50 y_2 -9.8	1.00 6.28 -0.06	1.87 11.75 0.75 DAL -1.3

Fragment-Ion (m/z)	374.138	375.150	446.176	479.703^{+2}	488.322	568.259	576.348	644.380	662.382	776.463	848.612	961.633
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	12.13 76.17 0.50 b_3 -3.3	2.27 14.23 -0.14	13.41 84.19 0.50 b_4 -2.6	1.10 6.90 -0.07	1.08 6.80 1.50 y_4 5.5	4.57 28.70 0.50 b_5 -3.1	5.13 32.21 1.50 y_5 -8.2	1.79 11.22 0.50 y_6-H_2O 12.3	15.93 100.00 1.50 y_6 -1.2	10.54 66.18 1.50 y_7 -4.8	2.82 17.69 1.50 y_8 8.7	2.76 17.34 1.50 y_9 1.4



C19



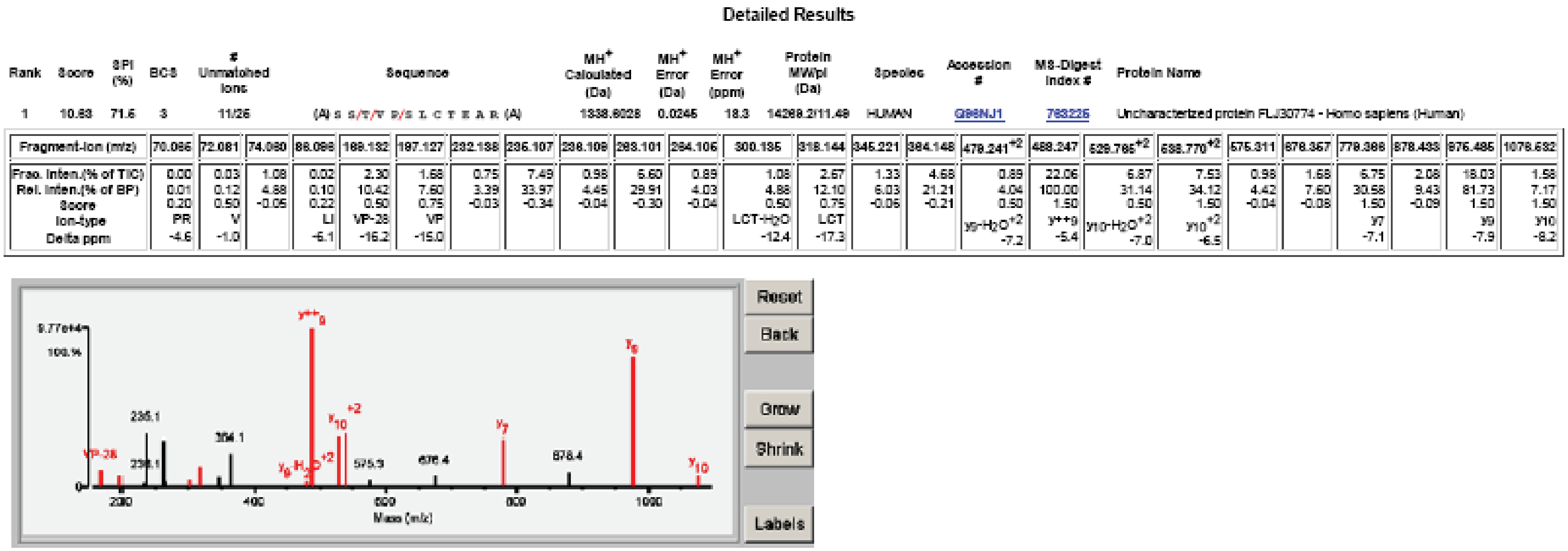
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.46	80.6	12	6/25	(Q) Q|Q\T|T/H/T|V|E/E/P L/D/L I/R (L)	1844.9059	0.0081	4.4	11846.6/4.68	HUMAN	P62310	316433	U6 snRNA-associated Sm-like protein LSm3 - Homo sapiens (Human)

Fragment-Ion (m/z)	176.118	217.084	345.124	401.292	446.172	611.201	616.317	629.210	632.211	726.452	744.299	782.312	806.919^{+2}
Frac. Inten.(% of TIC)	4.65	3.84	2.81	1.93	3.43	1.68	1.92	6.40	1.88	11.67	4.58	5.34	3.56
Rel. Inten.(% of BP)	39.86	32.91	24.10	16.52	29.42	14.39	16.48	54.83	16.13	100.00	39.29	45.76	30.55
Score	1.50	0.50	0.50	1.50	0.50	-0.14	1.50	0.25	-0.16	1.50	0.25	0.50	0.50
Ion-type	y_1	b_1	b_2	y_3	b_3		y_4	b_4-H$_2$O		y_6	b_6-H$_2$O	b_6	y_{14}-H$_2$O^{+2}
Delta ppm	-5.4	-4.3	0.2	11.3	0.9		6.5	2.8		2.3	-0.7	3.4	-5.2

Fragment-Ion (m/z)	814.921^{+2}	843.374	856.495	868.483^{+2}	881.381	891.831^{+2}	984.643	1083.606	1099.483	1184.659	1298.693	1399.736
Frac. Inten.(% of TIC)	3.60	8.29	3.27	2.67	1.50	1.55	10.55	4.07	1.60	2.58	4.28	2.33
Rel. Inten.(% of BP)	30.82	71.07	28.06	22.91	12.89	13.28	90.42	34.89	13.70	22.13	36.66	19.98
Score	1.50	0.25	1.50	-0.23	0.50	-0.13	1.50	1.50	-0.14	1.50	1.50	1.50
Ion-type	y_{14}^{+2}	b_7-H$_2$O	y_7		b_7		y_8	y_9		y_{10}	y_{11}	y_{12}
Delta ppm	-8.8	8.0	1.6		3.1		6.7	1.7		5.7	-1.7	-5.1

C20



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.63	71.6	3	11/26	(A) S S/T/V P/S L C T E A R (A)	1338.6028	0.0245	18.3	14269.2/11.49	HUMAN	Q96NJ1	783226	Uncharacterized protein FLJ30774 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.081	74.060	86.096	169.132	197.127	232.138	236.107	238.109	263.101	264.106	300.135	318.144
Frac. Inten.(% of TIC)	0.00	0.03	1.08	0.02	2.30	1.68	0.75	7.49	0.98	6.60	0.89	1.08	2.67
Rel. Inten.(% of BP)	0.01	0.12	4.88	0.10	10.42	7.60	3.39	33.97	4.45	29.91	4.03	4.88	12.10
Score	0.20	0.50	-0.05	0.22	0.50	0.75	-0.03	-0.34	-0.04	-0.30	-0.04	0.50	0.75
Ion-type	PR	V		LI	VP-28	VP						LCT-H$_2$O	LCT
Delta ppm	-4.6	-1.0		-6.1	-16.2	-15.0						-12.4	-17.3

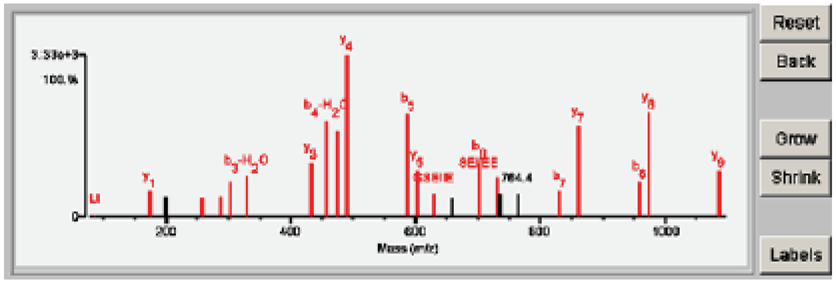
Fragment-Ion (m/z)	345.221	364.148	479.241^{+2}	488.247	529.785^{+2}	538.770^{+2}	575.311	676.367	778.388	878.433	976.485	1078.632
Frac. Inten.(% of TIC)	1.33	4.68	0.89	22.06	6.87	7.53	0.98	1.68	6.75	2.08	18.03	1.58
Rel. Inten.(% of BP)	6.03	21.21	4.04	100.00	31.14	34.12	4.42	7.60	30.58	9.43	81.73	7.17
Score	-0.06	-0.21	0.50	1.50	0.50	1.50	-0.04	-0.08	1.50	-0.09	1.50	1.50
Ion-type			y_9-H$_2$O^{+2}	y++9	y_{10}-H$_2$O^{+2}	y_{10}^{+2}			y_7		y_9	y_{10}
Delta ppm			-7.2	-5.4	-7.0	-6.5			-7.1		-7.9	-8.2

C21

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.70	93.1	10	4/25	(Q) I G\S E|I|I|E|E|L/G/E/Q/R (D)	1580.7674	-0.0009	-0.6	26688.6/8.02	HUMAN	Q9UEU0	701461	Vesicle transport through interaction with t-SNAREs homolog 1B - Homo sapiens (Human)

Fragment-Ion (m/z)	86.098	174.093	176.117	199.070	269.111	288.146	303.178	328.132	432.220	467.173	476.182	489.238	588.269	602.324	629.318	667.288	701.364	731.380	734.363^{+2}	764.392^{+2}	830.389	860.404	969.441	973.489	1086.676
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.14 1.03 0.22 LI 18.3	1.61 12.09 0.50 a_1 -17.9	2.06 15.48 1.50 y_1 -8.9	1.60 11.99 -0.12	1.54 11.56 0.50 b_2 -3.8	1.68 12.60 0.50 y_2-NH_3 -18.5	2.88 21.64 1.50 y_2 -5.7	3.31 24.90 0.25 b_3-H_2O -5.6	4.46 33.50 1.50 y_3 0.6	7.92 59.49 0.25 b_4-H_2O -6.2	7.16 53.81 0.50 b_4 -10.1	13.31 100.00 1.50 y_4 -7.3	8.44 63.38 0.50 b_5 -2.3	3.83 28.79 1.50 y_5 -2.9	1.93 14.48 0.75 GSEIIE 5.3	1.56 11.75 -0.12	4.53 34.00 0.75 b_6 -1.6 SEIIEE 24.9	3.28 24.62 1.50 y_6 -12.0	1.87 14.03 -0.14	1.89 14.21 -0.14	2.14 16.06 0.50 b_7 -10.6	7.49 56.30 1.50 y_7 -7.5	2.94 22.07 0.50 b_8 1.2	8.60 64.60 1.50 y_8 -6.3	3.83 28.79 1.50 y_9 -2.5

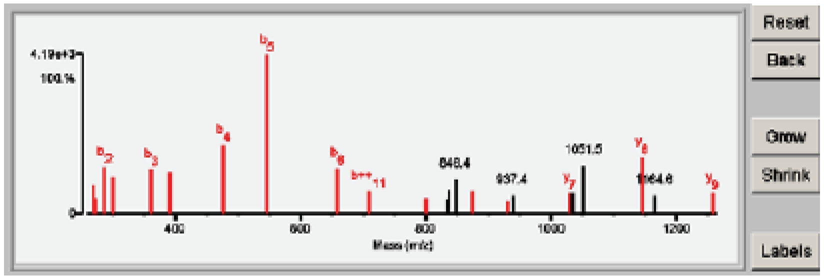


C22

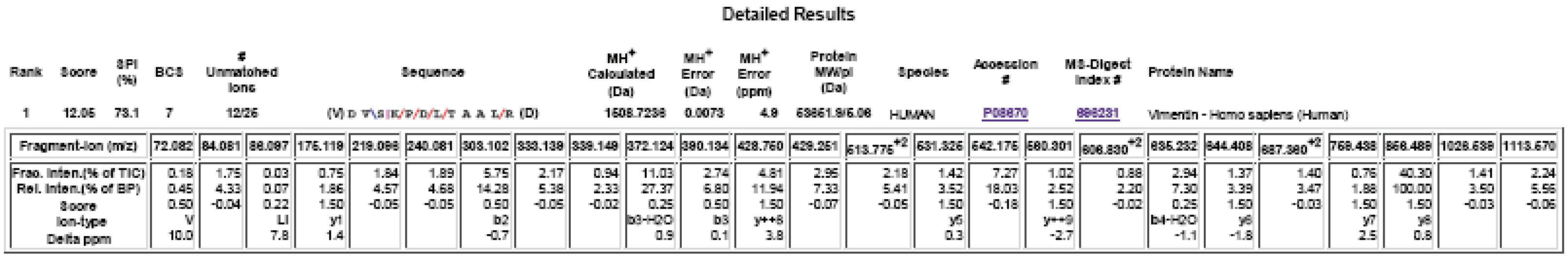
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.00	77.3	10	8/26	(F) S L\A\D\A|I|N/T|E/F K|N/T R (T)	1602.8200	0.0149	8.3	53651.9/5.06	HUMAN	P08670	698231	Vimentin - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	271.111	276.168	289.121	300.167	380.160	390.209	475.187	546.224	659.312	707.329	800.390	834.838	838.378	846.386^{+2}	874.386	929.419	937.411	1030.490	1034.468	1051.481	1144.624	1164.562	1257.600	1360.680
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.17 0.92 0.22 LI 6.7	3.34 17.99 0.25 b_2-H_2O -3.6	1.84 9.90 1.50 y_2 4.2	5.45 29.34 0.50 b_2 -7.4	4.38 23.57 0.75 DAI 0.7	5.16 27.81 0.50 b_3 0.1	4.92 26.48 1.50 y_3 -1.7	8.07 43.47 0.50 b_4 0.4	18.57 100.00 0.50 b_5 0.7	5.39 29.02 0.50 b_6 5.3	2.54 13.70 0.50 b^{++}_{11} 23.1	1.80 9.71 1.50 y_5 3.5	1.66 8.96 -0.09	2.76 14.89 -0.15	4.02 21.67 -0.22	2.63 14.19 0.50 b_8 -3.2	1.58 8.49 1.50 y_6 -11.5	2.17 11.66 -0.12	2.52 13.57 1.50 y_7 12.1	2.44 13.14 -0.13	5.69 30.64 -0.31	6.52 35.09 1.50 y_8 3.4	2.14 11.54 -0.12	2.44 13.14 1.50 y_9 -3.3	1.79 9.65 -0.10



C23

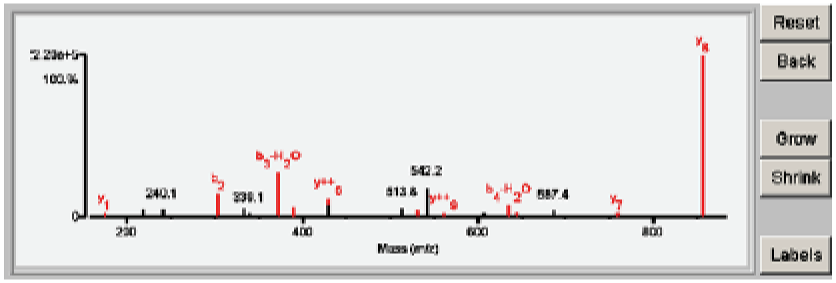


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.05	73.1	7	12/26	(V) D V\S|K/P/D/L/T A A L/R (D)	1608.7236	0.0073	4.9	53661.9/5.06	HUMAN	P08670	896231	Vimentin - Homo sapiens (Human)

Fragment-Ion (m/z)	72.082	84.081	86.097	175.119	219.098	240.081	303.102	333.139	339.148	372.124	390.134	428.760	429.261
Frac. Inten.(% of TIC)	0.18	1.75	0.03	0.75	1.84	1.89	5.75	2.17	0.94	11.03	2.74	4.81	2.95
Rel. Inten.(% of BP)	0.45	4.33	0.07	1.86	4.57	4.68	14.28	5.38	2.33	27.37	6.80	11.94	7.33
Score	0.50	-0.04	0.22	1.50	-0.05	-0.05	0.50	-0.05	-0.02	0.25	0.50	1.50	-0.07
Ion-type	V		LI	y1			b2			b3-H2O	b3	y++6	
Delta ppm	10.0		7.8	1.4			-0.7			0.9	0.1	3.8	

Fragment-Ion (m/z)	613.775^{+2}	631.326	642.176	580.301	606.830^{+2}	635.232	644.408	687.380^{+2}	769.438	868.489	1028.639	1113.670
Frac. Inten.(% of TIC)	2.18	1.42	7.27	1.02	0.88	2.94	1.37	1.40	0.76	40.30	1.41	2.24
Rel. Inten.(% of BP)	5.41	3.52	18.03	2.52	2.20	7.30	3.39	3.47	1.88	100.00	3.50	5.56
Score	-0.05	1.50	-0.18	1.50	-0.02	0.25	1.50	-0.03	1.50	1.50	-0.03	-0.06
Ion-type		y5		y++9		b4-H2O	y6		y7	y8		
Delta ppm		0.3		-2.7		-1.1	-1.8		2.5	0.8		



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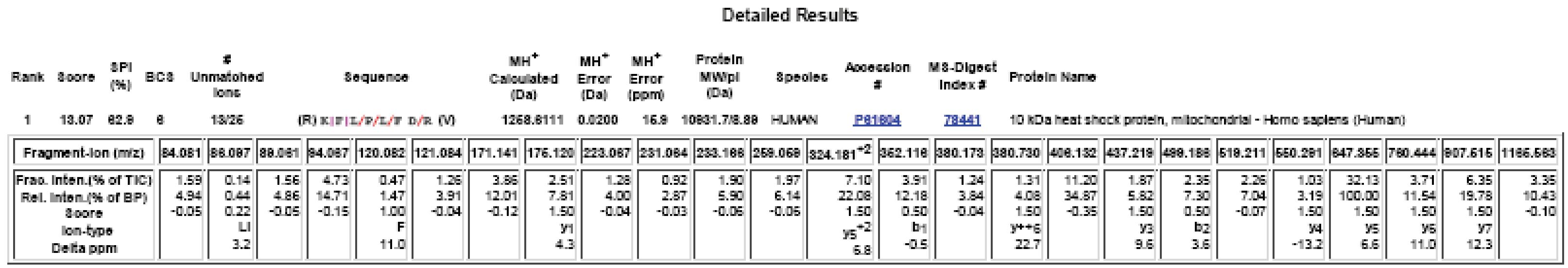
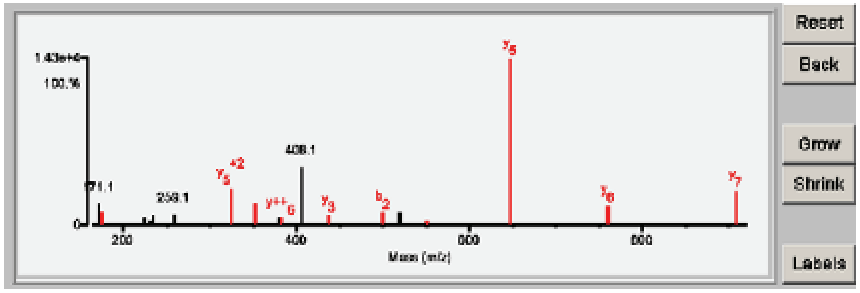


Detailed Results

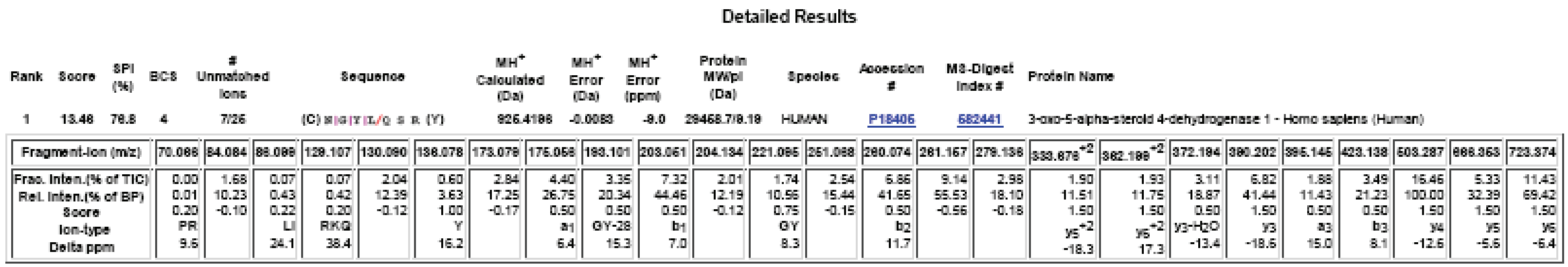
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.07	62.9	6	13/26	(R) K|F|L/P/L/F D/R (V)	1268.6111	0.0200	16.9	10931.7/8.89	HUMAN	P61604	78441	10 kDa heat shock protein, mitochondrial - Homo sapiens (Human)

Fragment-Ion (m/z)	84.081	86.097	88.061	94.067	120.082	121.084	171.141	175.120	223.087	231.084	233.166	259.069
Frac. Inten.(% of TIC)	1.59	0.14	1.56	4.73	0.47	1.26	3.86	2.51	1.28	0.92	1.90	1.97
Rel. Inten.(% of BP)	4.94	0.44	4.86	14.71	1.47	3.91	12.01	7.81	4.00	2.87	5.90	6.14
Score	-0.05	0.22	-0.05	-0.15	1.00	-0.04	-0.12	1.50	-0.04	-0.03	-0.06	-0.06
Ion-type		LI			F			y1				
Delta ppm		3.2			11.0			4.3				

Fragment-Ion (m/z)	324.181^{+2}	362.116	380.173	380.730	406.132	437.219	499.188	519.211	550.291	647.355	760.444	907.515	1166.583
Frac. Inten.(% of TIC)	7.10	3.91	1.24	1.31	11.20	1.87	2.35	2.26	1.03	32.13	3.71	6.35	3.35
Rel. Inten.(% of BP)	22.08	12.18	3.84	4.08	34.87	5.82	7.30	7.04	3.19	100.00	11.54	19.78	10.43
Score	1.50	0.50	-0.04	1.50	-0.35	1.50	0.50	-0.07	1.50	1.50	1.50	1.50	-0.10
Ion-type	y5^{+2}	b1		y++6		y3	b2		y4	y5	y6	y7	
Delta ppm	6.8	-0.5		22.7		9.6	3.6		-13.2	6.6	11.0	12.3	



I2

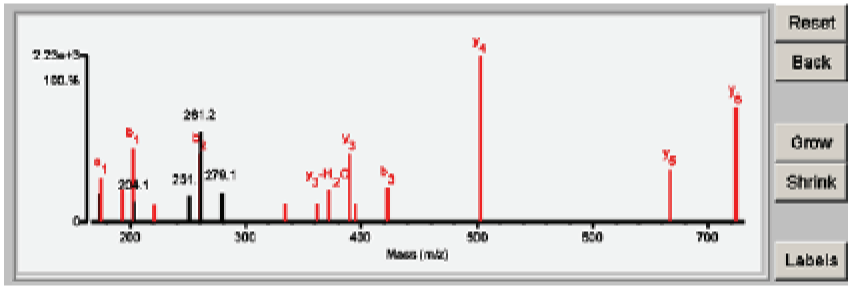


Detailed Results

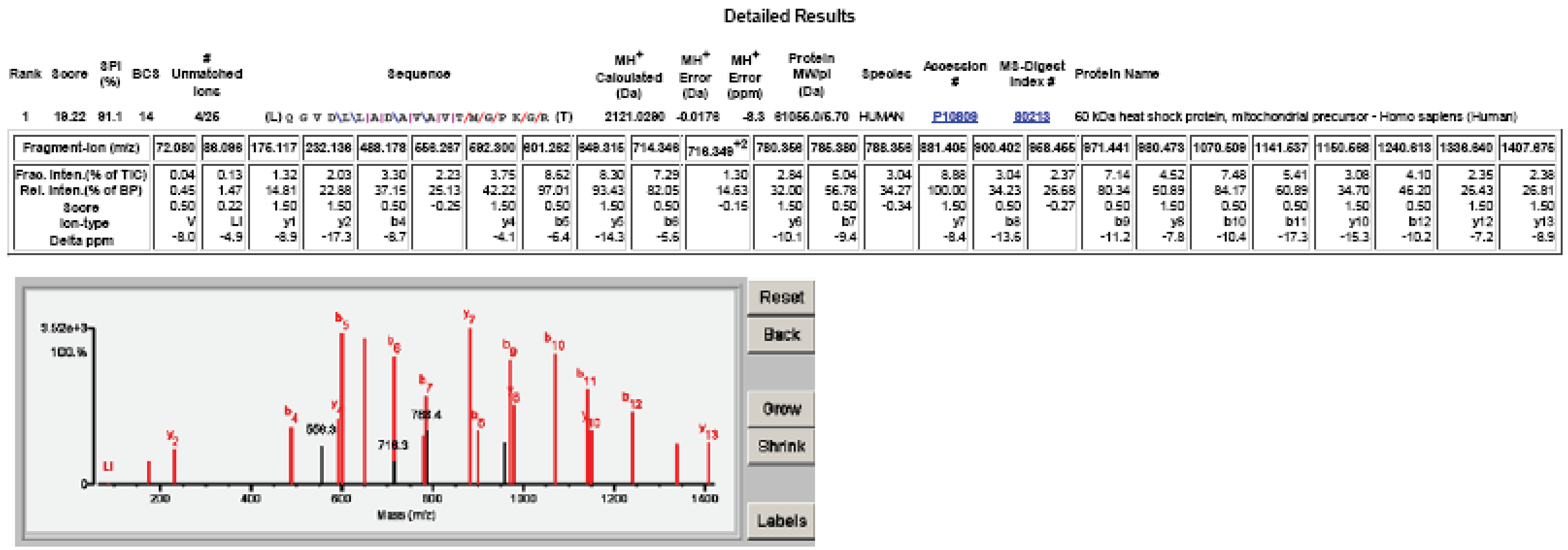
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.48	76.8	4	7/26	(C) N|G|Y|L/Q S R (Y)	926.4186	-0.0083	-9.0	29468.7/9.19	HUMAN	P18405	682441	3-oxo-5-alpha-steroid 4-dehydrogenase 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	84.084	86.099	129.107	130.090	136.078	173.079	175.056	193.101	203.061	204.134	221.095	251.068
Frac. Inten.(% of TIC)	0.00	1.68	0.07	0.07	2.04	0.60	2.84	4.40	3.35	7.32	2.01	1.74	2.54
Rel. Inten.(% of BP)	0.01	10.23	0.43	0.42	12.39	3.63	17.25	26.75	20.34	44.46	12.19	10.56	15.44
Score	0.20	-0.10	0.22	0.20	-0.12	1.00	-0.17	0.50	0.50	0.50	-0.12	0.75	-0.15
Ion-type	PR		LI	RKQ		Y		a1	GY-28	b1		GY	
Delta ppm	9.6		24.1	38.4		16.2		6.4	15.3	7.0		8.3	

Fragment-Ion (m/z)	260.074	261.167	279.136	333.676^{+2}	362.199^{+2}	372.194	390.202	395.145	423.138	503.287	666.363	723.374
Frac. Inten.(% of TIC)	6.86	9.14	2.98	1.90	1.93	3.11	6.82	1.88	3.49	16.46	5.33	11.43
Rel. Inten.(% of BP)	41.65	55.53	18.10	11.51	11.75	18.87	41.44	11.43	21.23	100.00	32.39	69.42
Score	0.50	-0.56	-0.18	1.50	1.50	0.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	b2			y5^{+2}	y6^{+2}	y3-H2O	y3	a3	b3	y4	y5	y6
Delta ppm	11.7			-18.3	17.3	-13.4	-18.6	15.0	8.1	-12.6	-5.6	-6.4



I3



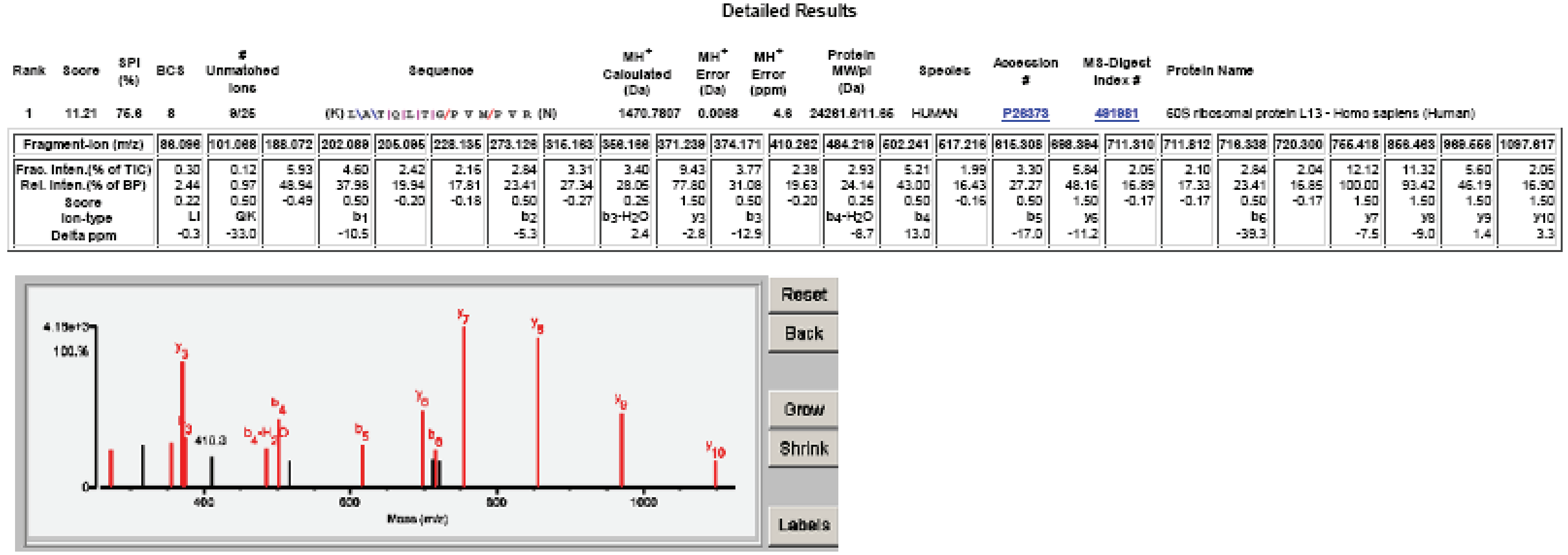
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.22	91.1	14	4/26	(L) Q G V D\L\L|A|D\A|V\A|V|T/M/G/P K/G/R (T)	2121.0290	-0.0178	-8.3	61056.0/6.70	HUMAN	P10809	80213	60 kDa heat shock protein, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	86.096	176.117	232.138	488.178	656.267	692.300	601.262	649.316	714.346	718.349+2	780.358	785.380
Frac. Inten.(% of TIC)	0.04	0.13	1.32	2.03	3.30	2.23	3.75	8.62	8.30	7.29	1.30	2.84	5.04
Rel. Inten.(% of BP)	0.45	1.47	14.81	22.88	37.15	25.13	42.22	97.01	93.43	82.05	14.63	32.00	56.78
Score	0.50	0.22	1.50	1.50	0.50	-0.25	1.50	0.50	1.50	0.50	-0.15	1.50	0.50
Ion-type	V	LI	y1	y2	b4		y4	b5	y5	b6		y6	b7
Delta ppm	-8.0	-4.9	-6.9	-17.3	-8.7		-4.1	-6.4	-14.3	-5.6		-10.1	-9.4

Fragment-Ion (m/z)	788.356	881.405	900.402	968.465	971.441	980.473	1070.509	1141.537	1150.688	1240.613	1336.640	1407.676
Frac. Inten.(% of TIC)	3.04	8.88	3.04	2.37	7.14	4.52	7.48	5.41	3.08	4.10	2.35	2.38
Rel. Inten.(% of BP)	34.27	100.00	34.23	26.68	80.34	50.89	84.17	60.89	34.70	46.20	25.43	26.81
Score	-0.34	1.50	0.50	-0.27	0.50	1.50	0.50	0.50	1.50	0.50	1.50	1.50
Ion-type		y7	b8		b9	y8	b10	b11	y10	b12	y12	y13
Delta ppm		-8.4	-13.6		-11.2	-7.8	-10.4	-17.3	-15.3	-10.2	-7.2	-8.9

I4



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.21	76.8	8	8/25	(K) I\A\T|Q|L|T|G/P V M/P V R (N)	1470.7807	0.0068	4.6	24261.6/11.66	HUMAN	P26373	491881	60S ribosomal protein L13 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	101.068	188.072	202.089	205.095	228.135	273.126	316.183	358.166	371.239	374.171	410.282	484.219
Frac. Inten.(% of TIC)	0.30	0.12	5.93	4.60	2.42	2.16	2.84	3.31	3.40	9.43	3.77	2.38	2.93
Rel. Inten.(% of BP)	2.44	0.97	48.94	37.98	19.94	17.81	23.41	27.34	28.05	77.80	31.08	19.63	24.14
Score	0.22	0.50	-0.49	0.50	-0.20	-0.18	0.50	-0.27	0.25	1.50	0.50	-0.20	0.25
Ion-type	LI	Q/K		b_1			b_2		b_3-H_2O	y_3	b_3		b_4-H_2O
Delta ppm	-0.3	-33.0		-10.5			-5.3		2.4	-2.8	-12.9		-8.7

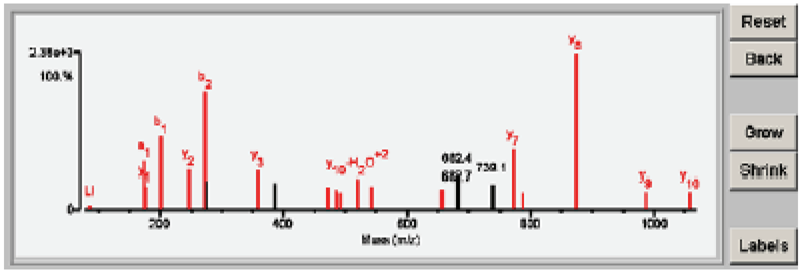
Fragment-Ion (m/z)	502.241	617.218	615.308	698.384	711.310	711.812	716.338	720.300	766.418	866.483	969.566	1097.817
Frac. Inten.(% of TIC)	5.21	1.99	3.30	5.84	2.05	2.10	2.84	2.04	12.12	11.32	5.60	2.05
Rel. Inten.(% of BP)	43.00	16.43	27.27	48.16	16.89	17.33	23.41	16.85	100.00	93.42	46.19	16.90
Score	0.50	-0.16	0.50	1.50	-0.17	-0.17	0.50	-0.17	1.50	1.50	1.50	1.50
Ion-type	b_4		b_5	y_6			b_6		y_7	y_8	y_9	y_{10}
Delta ppm	13.0		-17.0	-11.2			-39.3		-7.5	-9.0	1.4	3.3

I5

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.22	82.9	10	6/25	(R) I|A|L/T|D/H/A|L/I/A/R (S)	1268.6824	0.0053	4.2	29226.8/10.66	HUMAN	P18124	524483	60S ribosomal protein L7 - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
86.096	0.33	1.94	0.22	LI	-6.1
174.096	5.15	30.04	0.50	a_1	0.5
175.118	2.54	14.82	1.50	y_1	-3.7
202.092	7.81	45.54	0.50	b_1	6.3
248.158	4.38	25.55	1.50	y_2	9.1
273.127	12.77	74.42	0.50	b_2	-2.3
274.128	3.19	18.59	-0.19		
359.238	4.18	24.39	1.50	y_3	-7.0
388.210^{+2}	2.87	16.73	-0.17		
472.319	2.47	14.37	1.50	y_4	-11.4
484.792^{+2}	2.06	12.00	0.50	$y_9\text{-}H_2O^{+2}$	25.2
487.258	1.82	10.58	0.50	b_4	-8.2
493.779^{+2}	1.79	10.46	1.50	y_9^{+2}	-12.4
520.284^{+2}	3.34	19.49	0.50	$y_{10}\text{-}H_2O^{+2}$	-8.6
543.350	2.55	14.88	1.50	y_5	-21.2
657.403	2.14	12.45	1.50	y_6	-1.3
682.384	3.69	21.54	-0.22		
682.738	1.88	10.98	-0.11		
738.087	2.74	15.99	-0.16		
738.427	2.74	15.97	-0.16		
772.425	6.46	37.65	1.50	y_7	-7.5
787.382	1.91	11.11	0.50	b_7	-5.2
873.476	17.16	100.00	1.50	y_8	-3.4
956.570	1.98	11.55	1.50	y_9	6.8
1057.680	2.03	11.84	1.50	y_{10}	-19.4

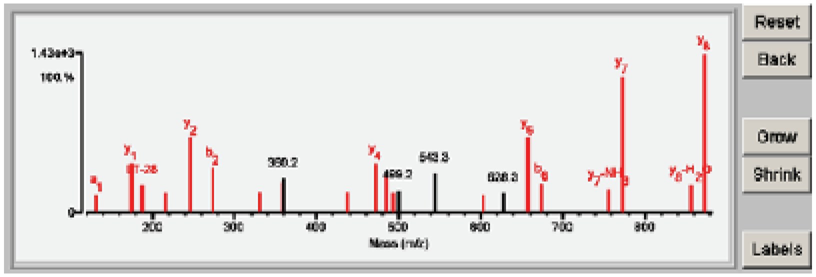


I6

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.31	88.1	9	5/25	(I) A/L|T/D/H\A|L/I/A/R (S)	1145.6983	-0.0066	-5.8	29226.8/10.66	HUMAN	P18124	524483	60S ribosomal protein L7 - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
86.096	1.01	6.60	0.22	LI	-8.4
87.101	2.72	17.87	-0.16		
132.048	1.80	11.79	0.50	a_1	-6.5
176.118	4.81	31.60	1.50	y_1	-3.2
187.146	2.64	17.33	0.50	LT-28	-0.5
216.138	1.91	12.51	0.75	LT	-11.7
248.158	7.26	47.62	1.50	y_2	0.5
273.127	4.41	28.92	0.50	b_2	-3.8
331.127	2.04	13.39	0.75	TDN	2.0
359.244	2.99	19.65	1.50	y_3	11.9
380.238^{+2}	3.36	22.07	-0.22		
437.250^{+2}	2.07	13.60	1.50	y_8^{+2}	16.1
472.323	4.79	31.45	1.50	y_4	-3.2
484.773^{+2}	3.48	22.85	0.50	$y_9\text{-}H_2O^{+2}$	-14.5
493.784^{+2}	1.95	12.77	1.50	y_9^{+2}	-2.8
499.233	2.16	14.16	-0.14		
543.349^{+2}	3.86	25.32	-0.25		
603.241	1.82	11.95	0.50	b_5	-7.8
628.285	1.84	12.06	-0.12		
657.406	7.25	47.62	1.50	y_6	1.9
674.277	2.78	18.27	0.50	b_6	-7.9
756.385	2.22	14.55	0.50	$y_7\text{-}NH_3$	-25.3
772.431	12.97	85.13	1.50	y_7	-0.7
856.468	2.63	17.29	0.50	$y_8\text{-}H_2O$	-13.9
873.471	15.24	100.00	1.50	y_8	-9.6



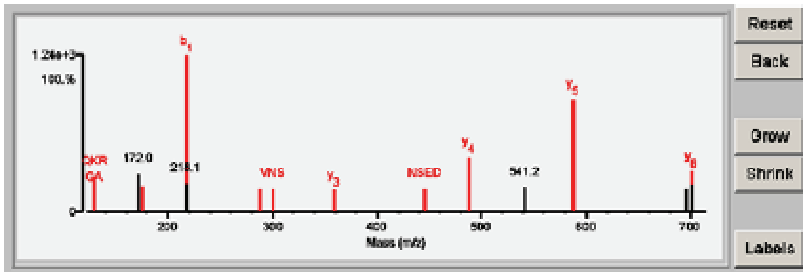
I7

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.27	80.2	7	13/25	(T) Q\V N S E D K G A L A K/L/V/E/A/I/R (T)	2299.1032	0.0011	0.6	29995.8/10.61	HUMAN	P62424	523981	60S ribosomal protein L7a - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.096	88.068	94.084	117.087	120.078	129.065	172.040	176.123	217.084	218.068	288.203	301.147
Frac. Inten.(% of TIC)	0.11	0.35	2.94	3.12	2.81	2.27	4.08	4.33	2.98	18.04	3.24	2.62	2.77
Rel. Inten.(% of BP)	0.61	1.93	16.29	17.29	15.55	12.58	22.61	24.00	16.52	100.00	17.96	14.54	15.38
Score	0.50	0.22	-0.16	-0.17	-0.16	-0.13	0.75	-0.24	1.50	0.50	-0.18	1.50	0.75
Ion-type	V	LI					GKR GA		y_1	b_1		y_2	VNS
Delta ppm	18.4	-0.3					-9.7 -18.2		21.4	-6.6		0.3	-14.8

Fragment-ion (m/z)	359.241	446.162	488.278	541.188^{+2}	587.351	686.274	700.439	701.408^{+3}	822.461^{+2}	823.394	870.486	941.629
Frac. Inten.(% of TIC)	2.51	2.65	6.35	2.92	13.09	2.66	4.70	3.16	2.29	2.81	2.86	4.36
Rel. Inten.(% of BP)	13.93	14.69	35.22	16.20	72.57	14.74	26.08	17.52	12.70	15.56	15.85	24.16
Score	1.50	0.75	1.50	-0.16	1.50	-0.15	1.50	-0.18	-0.13	-0.16	-0.16	-0.24
Ion-type	y_3	NSED	y_4		y_5		y_6					
Delta ppm	3.5	-1.0	-10.3		0.1		6.1					



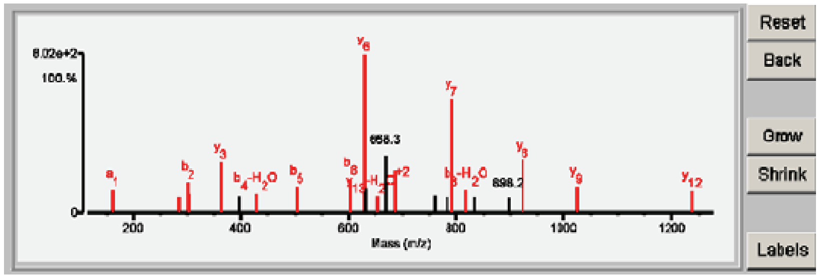
I8

Detailed Results

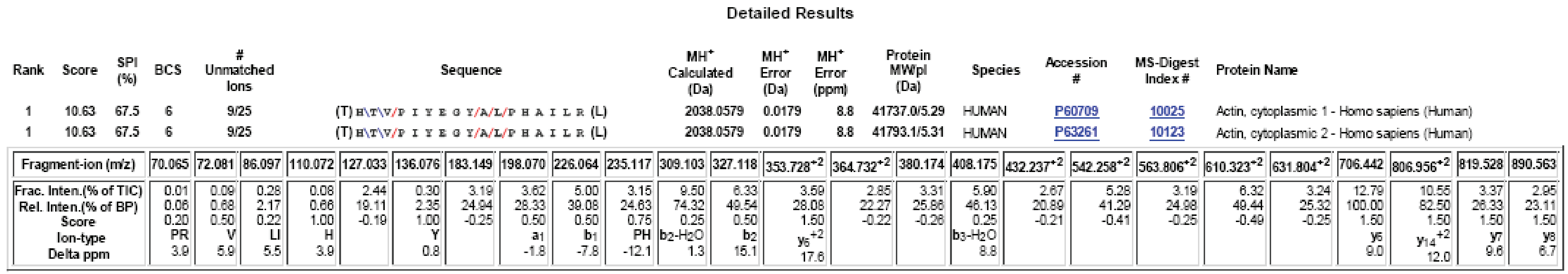
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.57	78.8	8	8/25	(N) V L\S/G G\T|T/H/Y/P G I/A D R (M)	1625.7662	0.0285	17.6	42009.2/5.24	HUMAN	P62736	9969	Actin, aortic smooth muscle - Homo sapiens (Human)
1	12.57	78.8	8	8/25	(T) V L\S/G G\T|T/M/Y/P G I/A D R (M)	1625.7662	0.0285	17.6	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	12.57	78.8	8	8/25	(N) V L\S/G G\T|T/H/Y/P G I/A D R (M)	1625.7662	0.0285	17.6	42019.2/5.23	HUMAN	P68032	10091	Actin, alpha cardiac muscle 1 - Homo sapiens (Human)
1	12.57	78.8	8	8/25	(T) V L\S/G G\T|T/M/Y/P G I/A D R (M)	1625.7662	0.0285	17.6	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)
1	12.57	78.8	8	8/25	(N) V L\S/G G\T|T/H/Y/P G I/A D R (M)	1625.7662	0.0285	17.6	41877.1/5.31	HUMAN	P63267	10161	Actin, gamma-enteric smooth muscle - Homo sapiens (Human)

Fragment-ion (m/z)	70.061	86.097	160.077	285.126	301.160	303.132	361.181	398.200^{+2}	427.217	502.240	603.279	628.346	632.312^{+2}
Frac. Inten.(% of TIC)	2.17	0.24	2.79	1.75	3.53	2.28	5.93	1.93	2.26	3.01	4.02	18.45	2.98
Rel. Inten.(% of BP)	11.75	1.32	15.13	9.51	19.13	12.35	32.16	10.44	12.24	16.34	21.80	100.00	16.14
Score	-0.12	0.22	0.50	0.50	0.50	0.75	1.50	-0.10	0.25	0.50	0.50	1.50	-0.16
Ion-type		LI	a_1	SGGT-H_2O	b_2	SGGT	y_3		b_4-H_2O	b_5	b_6	y_6	
Delta ppm		9.0	-19.1	20.2	1.5	4.3	-5.3		36.1	11.6	-4.3	7.5	

Fragment-ion (m/z)	654.313^{+2}	668.309	686.334	759.983	783.373	791.415	817.368	831.411	898.151	922.474	1023.529	1238.601
Frac. Inten.(% of TIC)	2.01	6.67	4.93	2.21	1.76	13.10	2.70	1.74	1.74	6.10	3.09	2.61
Rel. Inten.(% of BP)	10.90	36.18	26.74	11.97	9.53	71.04	14.65	9.44	9.41	33.09	16.73	14.12
Score	0.50	-0.36	0.25	-0.12	-0.10	1.50	0.25	-0.09	-0.09	1.50	1.50	1.50
Ion-type	y_{13}-H_2O^{+2}		b_7-H_2O			y_7	b_8-H_2O			y_8	y_9	y_{12}
Delta ppm	10.4		22.5			12.9	10.9			30.9	35.6	14.3



I9

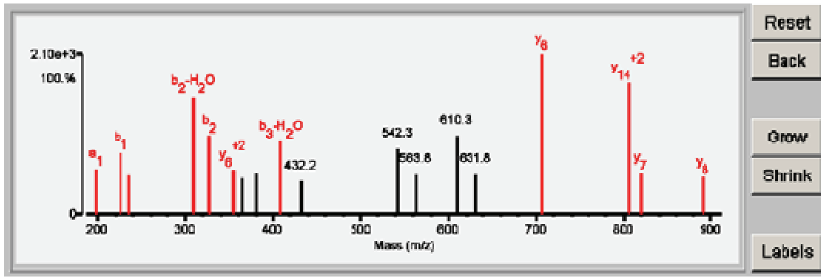


Detailed Results

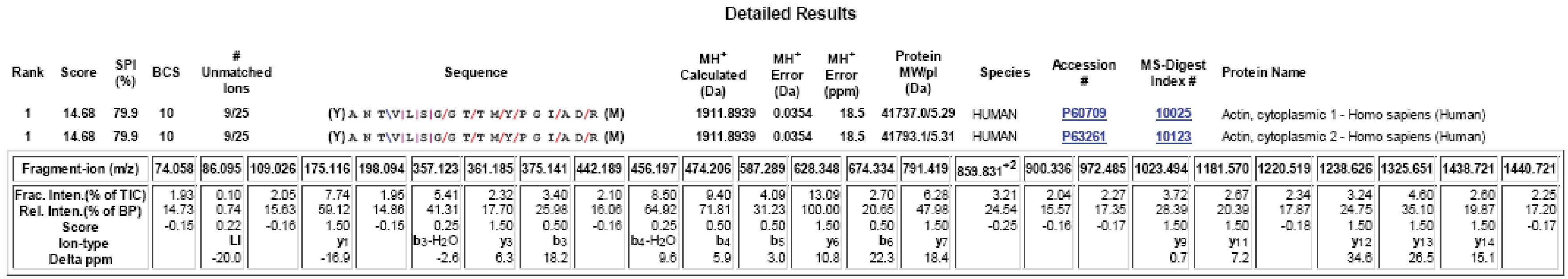
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.63	67.5	6	9/25	(T) H\T\V/P I Y E G Y/A/L/P H A I L R (L)	2038.0579	0.0179	8.8	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	10.63	67.5	6	9/25	(T) H\T\V/P I Y E G Y/A/L/P H A I L R (L)	2038.0579	0.0179	8.8	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.097	110.072	127.033	136.076	183.149	198.070	226.064	235.117	309.103	327.118	353.728^{+2}
Frac. Inten.(% of TIC)	0.01	0.09	0.28	0.08	2.44	0.30	3.19	3.62	5.00	3.15	9.50	6.33	3.59
Rel. Inten.(% of BP)	0.06	0.68	2.17	0.66	19.11	2.35	24.94	28.33	39.08	24.63	74.32	49.54	28.08
Score	0.20	0.50	0.22	1.00	-0.19	1.00	-0.25	0.50	0.50	0.75	0.25	0.50	1.50
Ion-type	PR	V	LI	H		Y		a_1	b_1	PH	b_2-H_2O	b_2	y_6^{+2}
Delta ppm	3.9	5.9	5.5	3.9		0.8		-1.8	-7.8	-12.1	1.3	15.1	17.6

Fragment-ion (m/z)	364.732^{+2}	380.174	408.175	432.237^{+2}	542.258^{+2}	563.806^{+2}	610.323^{+2}	631.804^{+2}	706.442	806.956^{+2}	819.528	890.563
Frac. Inten.(% of TIC)	2.85	3.31	5.90	2.67	5.28	3.19	6.32	3.24	12.79	10.55	3.37	2.95
Rel. Inten.(% of BP)	22.27	25.86	46.13	20.89	41.29	24.98	49.44	25.32	100.00	82.50	26.33	23.11
Score	-0.22	-0.26	0.25	-0.21	-0.41	-0.25	-0.49	-0.25	1.50	1.50	1.50	1.50
Ion-type			b_3-H_2O						y_6	y_{14}^{+2}	y_7	y_8
Delta ppm			8.8						9.0	12.0	9.6	6.7



I10

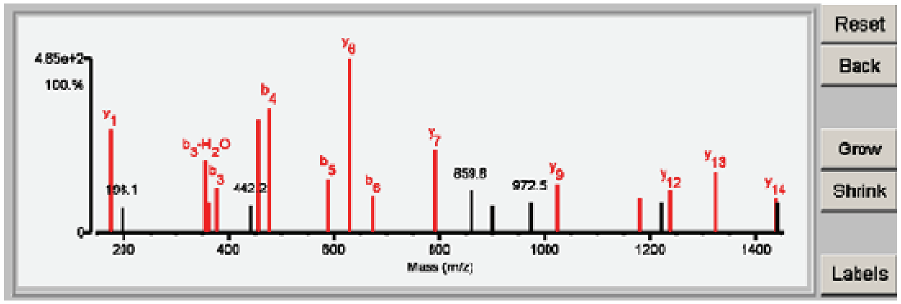


Detailed Results

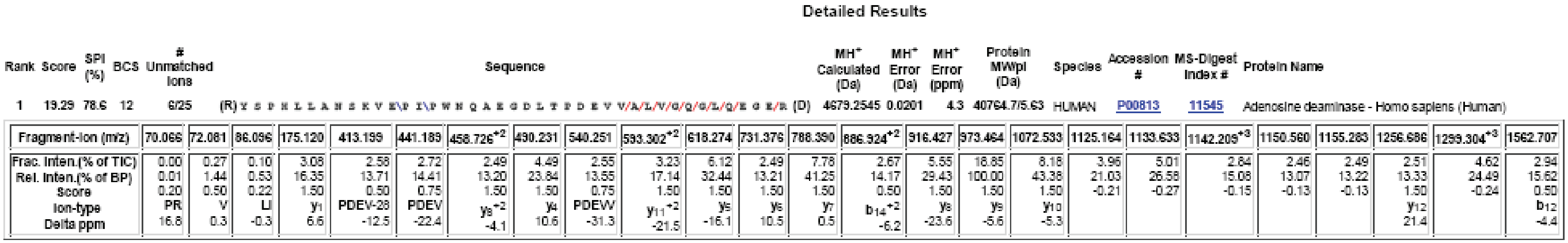
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.68	79.9	10	9/25	(Y) A N T\V|L|S|G/G T/T M/Y/P G I/A D/R (M)	1911.8939	0.0354	18.5	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	14.68	79.9	10	9/25	(Y) A N T\V|L|S|G/G T/T M/Y/P G I/A D/R (M)	1911.8939	0.0354	18.5	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)

Fragment-ion (m/z)	74.058	86.095	109.026	175.116	198.094	357.123	361.185	375.141	442.189	456.197	474.206	587.289	628.348
Frac. Inten.(% of TIC)	1.93	0.10	2.05	7.74	1.95	5.41	2.32	3.40	2.10	8.50	9.40	4.09	13.09
Rel. Inten.(% of BP)	14.73	0.74	15.63	59.12	14.86	41.31	17.70	25.98	16.06	64.92	71.81	31.23	100.00
Score	-0.15	0.22	-0.16	1.50	-0.15	0.25	1.50	0.50	-0.16	0.25	0.50	0.50	1.50
Ion-type		LI		y_1		b_3-H_2O	y_3	b_3		b_4-H_2O	b_4	b_5	y_6
Delta ppm		-20.0		-16.9		-2.6	6.3	18.2		9.6	5.9	3.0	10.8

Fragment-ion (m/z)	674.334	791.419	859.831^{+2}	900.336	972.485	1023.494	1181.570	1220.519	1238.626	1325.651	1438.721	1440.721
Frac. Inten.(% of TIC)	2.70	6.28	3.21	2.04	2.27	3.72	2.67	2.34	3.24	4.60	2.60	2.25
Rel. Inten.(% of BP)	20.65	47.98	24.54	15.57	17.35	28.39	20.39	17.87	24.75	35.10	19.87	17.20
Score	0.50	1.50	-0.25	-0.16	-0.17	1.50	1.50	-0.18	1.50	1.50	1.50	-0.17
Ion-type	b_6	y_7				y_9	y_{11}		y_{12}	y_{13}	y_{14}	
Delta ppm	22.3	18.4				0.7	7.2		34.6	26.5	15.1	



I11

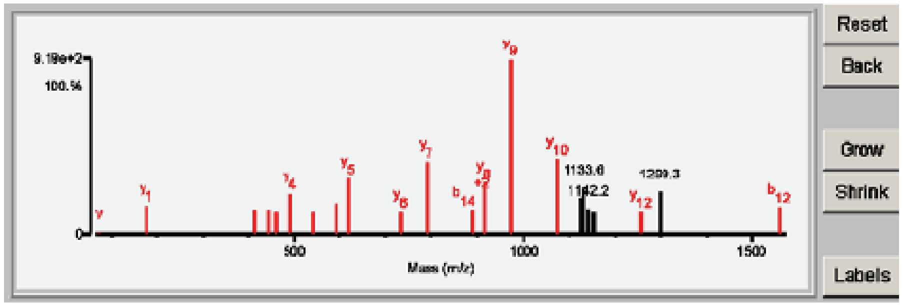


Detailed Results

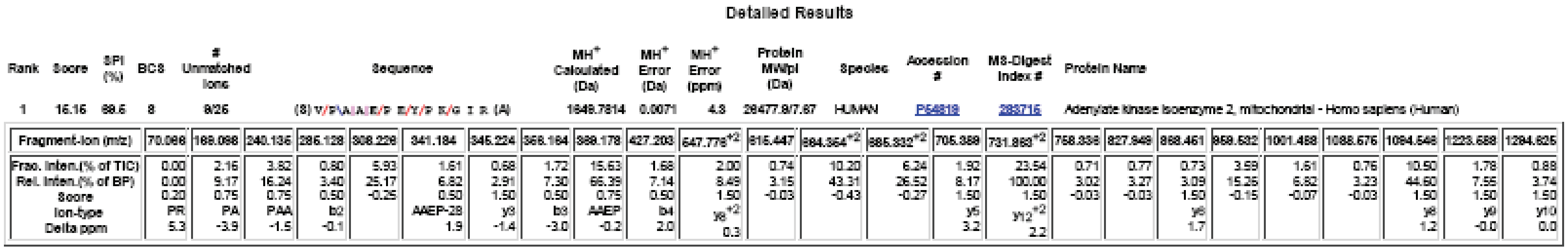
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.29	78.6	12	6/25	(R) Y S P H L L A N S K V E\P I\P W N Q A E G D L T P D E V V/A/L/V/G/Q/G/L/Q/E G E/R (D)	4679.2545	0.0201	4.3	40764.7/5.63	HUMAN	P00813	11545	Adenosine deaminase - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.081	86.096	175.120	413.199	441.189	458.726^{+2}	490.231	540.251	593.302^{+2}	618.274	731.376	788.390
Frac. Inten.(% of TIC)	0.00	0.27	0.10	3.08	2.58	2.72	2.49	4.49	2.55	3.23	6.12	2.49	7.78
Rel. Inten.(% of BP)	0.01	1.44	0.53	16.35	13.71	14.41	13.20	23.84	13.55	17.14	32.44	13.21	41.25
Score	0.20	0.50	0.22	1.50	0.50	0.75	1.50	1.50	0.75	1.50	1.50	1.50	1.50
Ion-type	PR	V	LI	y_1	PDEV-28	PDEV	$y_8{}^{+2}$	y_4	PDEVV	$y_{11}{}^{+2}$	y_5	y_6	y_7
Delta ppm	16.8	0.3	-0.3	6.6	-12.5	-22.4	-4.1	10.6	-31.3	-21.5	-16.1	10.5	0.5

Fragment-Ion (m/z)	886.924^{+2}	916.427	973.464	1072.533	1125.164	1133.633	1142.209^{+3}	1150.560	1155.283	1256.686	1299.304^{+3}	1562.707
Frac. Inten.(% of TIC)	2.67	5.55	18.85	8.18	3.96	5.01	2.84	2.46	2.49	2.51	4.62	2.94
Rel. Inten.(% of BP)	14.17	29.43	100.00	43.38	21.03	26.58	15.08	13.07	13.22	13.33	24.49	15.62
Score	0.50	1.50	1.50	1.50	-0.21	-0.27	-0.15	-0.13	-0.13	1.50	-0.24	0.50
Ion-type	$b_{14}{}^{+2}$	y_8	y_9	y_{10}						y_{12}		b_{12}
Delta ppm	-6.2	-23.6	-5.6	-5.3						21.4		-4.4



I12

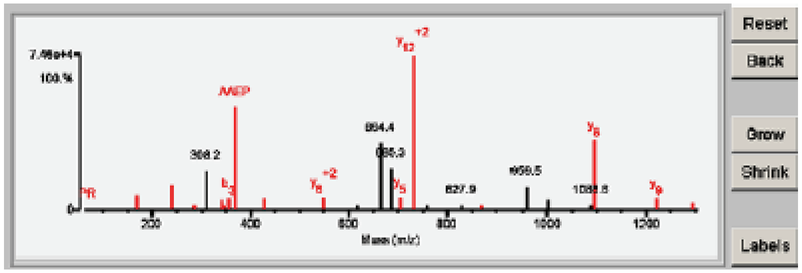


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.16	88.6	8	8/26	(S) V/P\A|A|E/P E/Y/P K/G I R (A)	1648.7814	0.0071	4.3	26477.8/7.67	HUMAN	P54819	283716	Adenylate kinase isoenzyme 2, mitochondrial - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	169.098	240.136	285.128	308.226	341.184	345.224	356.164	369.178	427.203	647.776^{+2}	615.447	664.364^{+2}
Frac. Inten.(% of TIC)	0.00	2.16	3.82	0.80	5.93	1.61	0.68	1.72	15.63	1.68	2.00	0.74	10.20
Rel. Inten.(% of BP)	0.00	9.17	16.24	3.40	25.17	6.82	2.91	7.30	66.39	7.14	8.49	3.15	43.31
Score	0.20	0.75	0.75	0.50	-0.25	0.50	1.50	0.50	0.75	0.50	1.50	-0.03	-0.43
Ion-type	PR	PA	PAA	b2		AAEP-28	y3	b3	AAEP	b4	$y_8{}^{+2}$		
Delta ppm	5.3	-3.9	-1.5	-0.1		1.9	-1.4	-3.0	-0.2	2.0	0.3		

Fragment-Ion (m/z)	685.332^{+2}	705.388	731.868^{+2}	758.336	827.949	868.461	959.532	1001.488	1088.676	1094.546	1223.688	1294.626
Frac. Inten.(% of TIC)	6.24	1.92	23.54	0.71	0.77	0.73	3.59	1.61	0.76	10.50	1.78	0.88
Rel. Inten.(% of BP)	26.52	8.17	100.00	3.02	3.27	3.09	15.26	6.82	3.23	44.60	7.55	3.74
Score	-0.27	1.50	1.50	-0.03	-0.03	1.50	-0.15	-0.07	-0.03	1.50	1.50	1.50
Ion-type		y5	$y_{12}{}^{+2}$			y6				y8	y9	y10
Delta ppm		3.2	2.2			1.7				1.2	-0.0	0.0

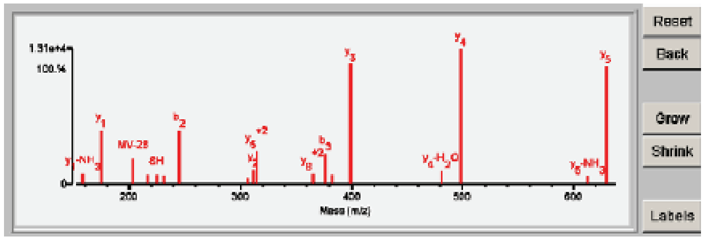


I13

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.10	84.8	6	4/24	(W) G/V|M|V/S/H/R (S)	873.4070	0.0030	3.4	47169.2/7.01	HUMAN	P06733	164186	Alpha-enolase - Homo sapiens (Human)
1	17.10	84.8	6	4/24	(W) G/V|M|V/S/H/R (S)	873.4070	0.0030	3.4	46987.1/7.58	HUMAN	P13929	164208	Beta-enolase - Homo sapiens (Human)
1	17.10	84.8	6	4/24	(W) G/V|M|V/S/H/R (S)	873.4070	0.0030	3.4	47268.8/4.91	HUMAN	P09104	164228	Gamma-enolase - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	73.084	86.096	104.053	110.070	143.119	158.097	175.119	203.120	217.100	225.097	231.115	245.096	306.166^{+2}	312.178	315.165^{+2}	364.697^{+2}	378.136	382.182	399.210	480.265	498.280	612.297	629.318
Frac. Inten.(% of TIC)	0.79	1.30	1.09	12.04	0.03	0.80	1.39	6.69	3.28	1.19	1.27	1.08	6.71	0.85	1.87	4.07	1.38	3.85	1.25	14.96	1.66	16.86	0.97	14.63
Rel. Inten.(% of BP)	4.70	7.71	6.46	71.43	0.20	4.77	8.25	39.65	19.43	7.08	7.53	6.40	39.81	5.02	11.07	24.14	8.16	22.83	7.39	88.71	9.83	100.00	5.77	86.79
Score	0.50	-0.08	-0.06	-0.71	1.00	-0.05	0.50	1.50	0.50	0.50	0.75	0.75	0.50	0.50	1.50	1.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type	V				H		y_1-NH_3	y_1	MV-28	a_2	SH	MV	b_2	y_5-H_2O^{+2}	y_2	y_5^{+2}	y_6^{+2}	b_3	y_3-NH_3	y_3	y_4-H_2O	y_4	y_5-NH_3	y_5
Delta ppm	5.9				-9.8		29.1	-3.7	-12.6	-7.5	-11.6	-9.4	-7.5	-4.7	3.3	7.2	-0.1	-4.8	-4.8	1.0	-6.5	2.6	8.4	-1.9

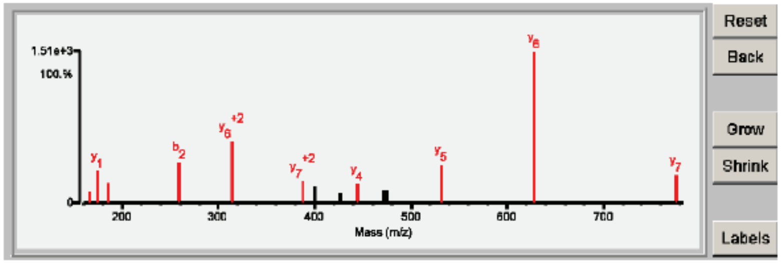


I14

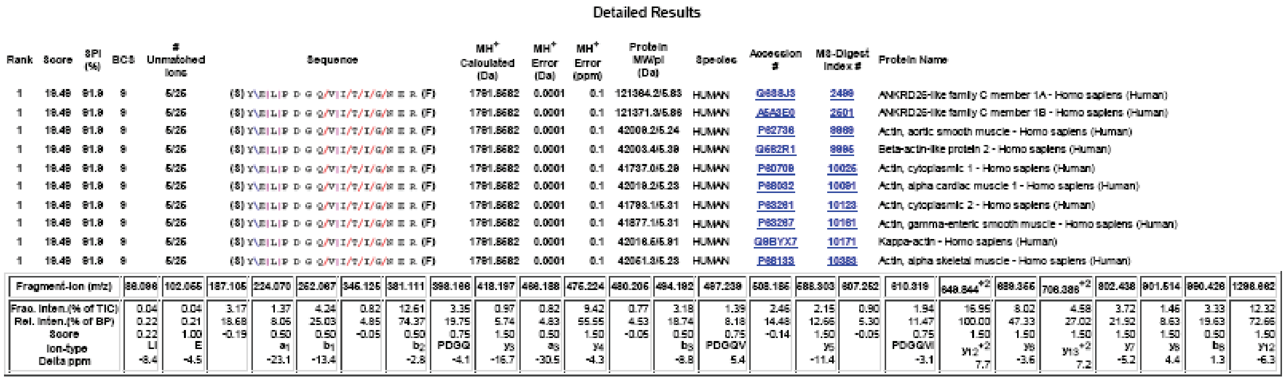
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	121364.2/5.83	HUMAN	Q6S8J3	2499	ANKRD26-like family C member 1A - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	121371.3/5.86	HUMAN	A5A3E0	2501	ANKRD26-like family C member 1B - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	42009.2/5.24	HUMAN	P62736	9969	Actin, aortic smooth muscle - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	42019.2/5.23	HUMAN	P68032	10091	Actin, alpha cardiac muscle 1 - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	41877.1/5.31	HUMAN	P63267	10161	Actin, gamma-enteric smooth muscle - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(Q) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	42016.5/5.91	HUMAN	Q9BYX7	10171	Kappa-actin - Homo sapiens (Human)
1	13.74	78.8	5	9/24	(R) A V|F/P/S/I V G/R (P)	1033.5499	-0.0026	-2.5	42051.3/5.23	HUMAN	P68133	10383	Actin, alpha skeletal muscle - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	71.082	72.081	84.080	86.097	94.067	112.084	120.080	156.078	167.087	175.118	185.096	259.114	314.692^{+2}	388.226^{+2}	400.227	427.248	444.295	471.743	474.898	531.326	628.374	775.451	793.837
Frac. Inten.(% of TIC)	0.01	2.84	0.65	2.00	0.37	2.25	0.07	0.49	2.74	1.99	5.82	3.72	7.37	11.28	3.92	2.84	1.88	3.35	2.16	2.19	7.04	27.59	5.16	2.26
Rel. Inten.(% of BP)	0.03	10.29	2.35	7.24	1.35	8.15	0.26	1.79	9.94	7.20	21.11	13.49	26.73	40.88	14.22	10.29	6.83	12.13	7.82	7.94	25.53	100.00	18.72	8.20
Score	0.20	-0.10	0.50	-0.07	0.22	-0.08	0.33	1.00	-0.10	0.50	1.50	0.75	0.50	1.50	1.50	-0.10	-0.07	1.50	-0.08	-0.08	1.50	1.50	1.50	-0.08
Ion-type	PR		V		LI		R	F		PS-H_2O	y_1	PS	b_2	y_6^{+2}	y_7^{+2}			y_4			y_5	y_6	y_7	
Delta ppm	9.6		-1.0		10.2		-28.8	-7.3		23.3	-4.9	14.2	8.5	-1.2	-2.5			4.5			2.6	-6.3	5.7	



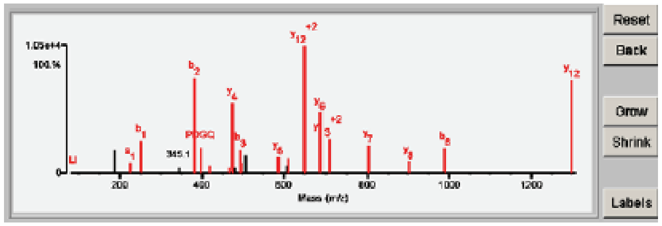
I15



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	121384.2/5.83	HUMAN	Q6S8J3	2489	ANKRD26-like family C member 1A - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	121371.3/5.88	HUMAN	A5A3E0	2501	ANKRD26-like family C member 1B - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	42009.2/5.24	HUMAN	P62736	9969	Actin, aortic smooth muscle - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	42003.4/5.39	HUMAN	Q562R1	9985	Beta-actin-like protein 2 - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	41737.0/5.29	HUMAN	P60709	10026	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	42019.2/5.23	HUMAN	P68032	10081	Actin, alpha cardiac muscle 1 - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	41877.1/5.31	HUMAN	P63267	10161	Actin, gamma-enteric smooth muscle - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	42018.6/5.91	HUMAN	Q9BYX7	10171	Kappa-actin - Homo sapiens (Human)
1	19.49	91.8	9	5/26	(S) Y\E|L|P D G Q/V|I/T/I/G/N E R (F)	1791.8682	0.0001	0.1	42051.3/5.23	HUMAN	P68133	10383	Actin, alpha skeletal muscle - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	102.065	187.105	224.070	262.087	346.125	381.111	398.166	418.197	466.188	476.224	480.206	494.182	497.239	508.186	588.303	607.252	610.319	648.844^{+2}	689.366	706.386^{+2}	802.438	901.514	960.428	1298.662
Frac. Inten.(% of TIC)	0.04	0.04	3.17	1.37	4.24	0.82	12.61	3.35	0.97	0.82	9.42	0.77	3.18	1.39	2.46	2.15	0.90	1.94	16.95	8.02	4.58	3.72	1.46	3.33	12.32
Rel. Inten.(% of BP)	0.22	0.21	18.68	8.06	25.03	4.85	74.37	19.75	5.74	4.83	55.55	4.53	18.74	8.18	14.48	12.66	5.30	11.47	100.00	47.33	27.02	21.92	8.63	19.63	72.66
Score	0.22	1.00	-0.19	0.50	0.50	-0.05	0.50	0.75	1.50	0.50	1.50	-0.05	0.50	0.75	-0.14	1.50	-0.05	0.75	1.50	1.50	1.50	1.50	1.50	0.50	1.50
Ion-type	LI	E		a_1	b_1		b_2	PDGQ	y_3	a_5	y_4		b_5	PDGQV		y_5		PDGQVI	y_{12}^{+2}	y_6	y_{13}^{+2}	y_7	y_8	b_9	y_{12}
Delta ppm	-8.4	-4.5		-23.1	-13.4		-2.8	-4.1	-16.7	-30.5	-4.3		-8.8	5.4		-11.4		-3.1	7.7	-3.6	7.2	-5.2	4.4	1.3	-6.3



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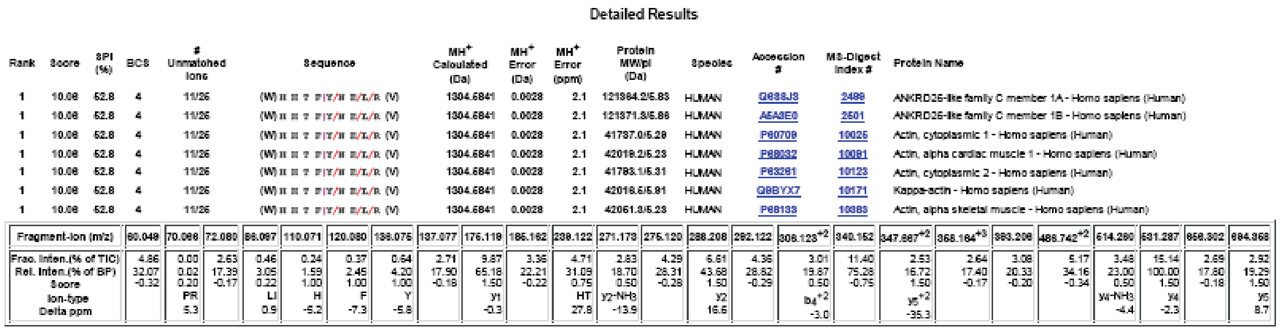
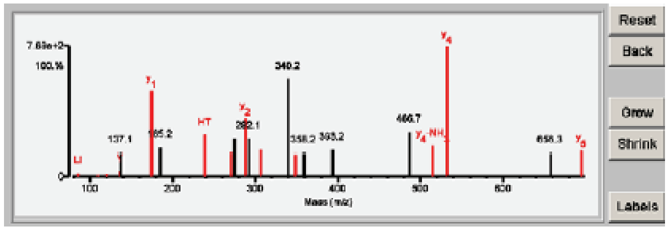


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	121384.2/5.83	HUMAN	Q6S8J3	2489	ANKRD26-like family C member 1A - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	121371.3/5.88	HUMAN	A5A3E0	2501	ANKRD26-like family C member 1B - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	41737.0/5.29	HUMAN	P60709	10026	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	42019.2/5.23	HUMAN	P68032	10081	Actin, alpha cardiac muscle 1 - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	42018.6/5.91	HUMAN	Q9BYX7	10171	Kappa-actin - Homo sapiens (Human)
1	10.08	52.8	4	11/26	(W) H H T F|Y/N E/L/R (V)	1304.6841	0.0028	2.1	42051.3/5.23	HUMAN	P68133	10383	Actin, alpha skeletal muscle - Homo sapiens (Human)

Fragment-Ion (m/z)	60.049	70.066	72.080	86.097	110.071	120.080	136.075	137.077	176.119	185.162	238.122	271.173	275.120	288.208	292.122	308.123^{+2}	340.152	347.687^{+2}	368.164^{+3}	393.206	486.742^{+2}	614.280	631.287	658.302	694.368
Frac. Inten.(% of TIC)	4.86	0.00	2.63	0.46	0.24	0.37	0.64	2.71	9.87	3.36	4.71	2.83	4.29	6.61	4.36	3.01	11.40	2.53	2.64	3.08	5.17	3.48	15.14	2.69	2.92
Rel. Inten.(% of BP)	32.07	0.02	17.39	3.05	1.59	2.45	4.20	17.90	65.18	22.21	31.09	18.70	28.31	43.68	28.82	19.87	75.28	16.72	17.40	20.33	34.16	23.00	100.00	17.80	19.29
Score	-0.32	0.20	-0.17	0.22	1.00	1.00	1.00	-0.18	1.50	-0.22	0.75	0.50	-0.28	1.50	-0.29	0.50	-0.75	1.50	-0.17	-0.20	-0.34	0.50	1.50	-0.18	1.50
Ion-type		PR		LI	H	F	Y		y_1		HT	y_2-NH$_3$		y_2		b_4^{+2}		y_5^{+2}				y_4-NH$_3$	y_4		y_5
Delta ppm		5.3		0.9	-5.2	-7.3	-5.8		-0.3		27.8	-13.9		16.6		-3.0		-35.3				-4.4	-2.3		8.7



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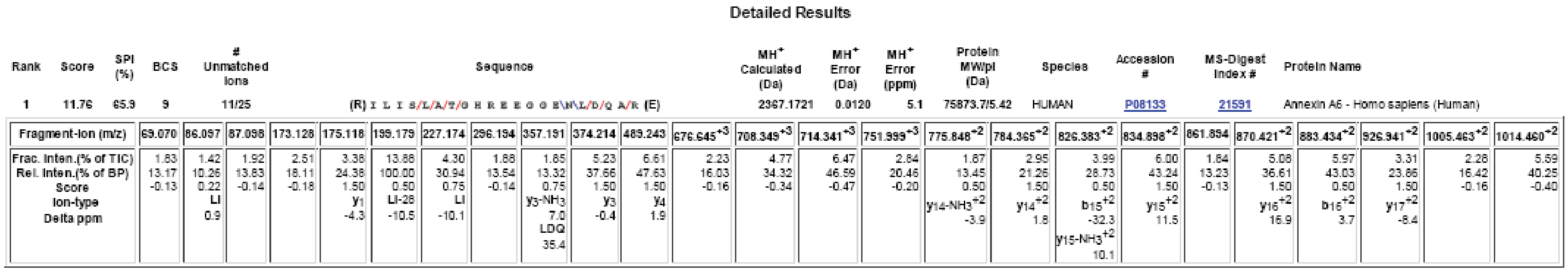
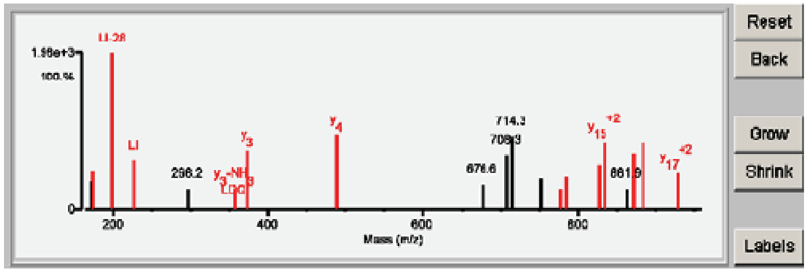


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.76	65.9	9	11/25	(R) I L I S/L/A/T/G H R E E G G E\N\L/D/Q A/R (E)	2367.1721	0.0120	5.1	75873.7/5.42	HUMAN	P08133	21591	Annexin A6 - Homo sapiens (Human)

Fragment-ion (m/z)	69.070	86.097	87.098	173.128	175.118	199.179	227.174	296.194	357.191	374.214	489.243	676.645^{+3}	708.349^{+3}	714.341^{+3}	751.999^{+3}	775.848^{+2}	784.365^{+2}	826.383^{+2}	834.898^{+2}	861.894	870.421^{+2}	883.434^{+2}	926.941^{+2}	1005.463^{+2}	1014.460^{+2}
Frac. Inten.(% of TIC)	1.63	1.42	1.92	2.51	3.36	13.86	4.30	1.88	1.65	5.23	6.61	2.23	4.77	6.47	2.84	1.67	2.95	3.99	6.00	1.64	5.08	5.97	3.31	2.26	5.59
Rel. Inten.(% of BP)	13.17	10.26	13.63	18.11	24.38	100.00	30.94	13.54	13.32	37.66	47.63	16.03	34.32	46.59	20.46	13.45	21.26	28.73	43.24	13.23	36.61	43.03	23.86	16.42	40.25
Score	-0.13	0.22	-0.14	-0.18	1.50	0.50	0.75	-0.14	0.75	1.50	1.50	-0.16	-0.34	-0.47	-0.20	0.50	1.50	0.50	1.50	-0.13	1.50	0.50	1.50	-0.16	-0.40
Ion-type		LI			y_1	LI-28	LI		y_3-NH_3 LDQ	y_3	y_4					y_{14}-NH_3^{+2}	y_{14}^{+2}	b_{15}^{+2} y_{15}-NH_3^{+2}	y_{15}^{+2}		y_{16}^{+2}	b_{16}^{+2}	y_{17}^{+2}		
Delta ppm		0.9			-4.3	-10.5	-10.1		7.0 35.4	-0.4	1.9					-3.9	1.8	-32.3 10.1	11.5		16.9	3.7	-8.4		



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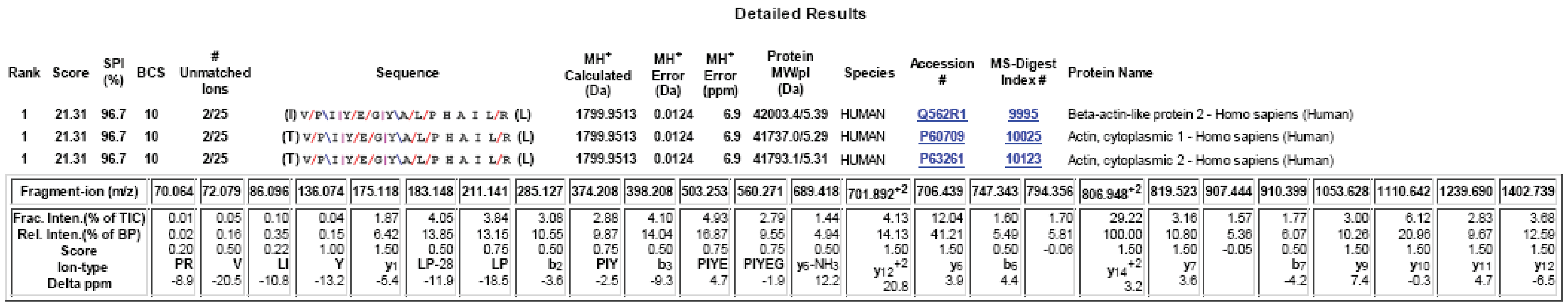
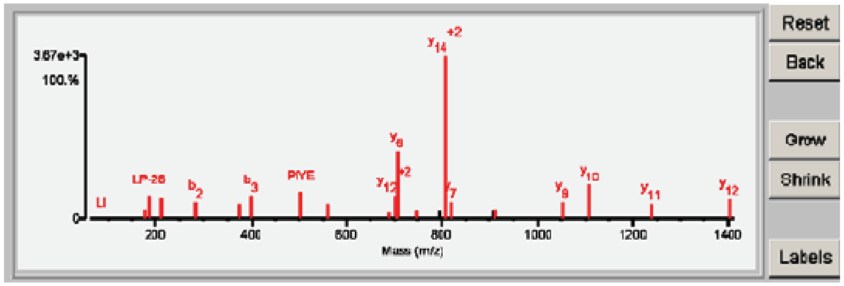


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.31	96.7	10	2/25	(I) V/P\I|Y/E/G|Y\A/L/P H A I L/R (L)	1799.9513	0.0124	6.9	42003.4/5.39	HUMAN	Q562R1	9995	Beta-actin-like protein 2 - Homo sapiens (Human)
1	21.31	96.7	10	2/25	(T) V/P\I|Y/E/G|Y\A/L/P H A I L/R (L)	1799.9513	0.0124	6.9	41737.0/5.29	HUMAN	P60709	10025	Actin, cytoplasmic 1 - Homo sapiens (Human)
1	21.31	96.7	10	2/25	(T) V/P\I|Y/E/G|Y\A/L/P H A I L/R (L)	1799.9513	0.0124	6.9	41793.1/5.31	HUMAN	P63261	10123	Actin, cytoplasmic 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.079	86.096	136.074	175.118	183.148	211.141	285.127	374.208	398.208	503.253	560.271	689.418	701.892^{+2}	706.439	747.343	794.356	806.948^{+2}	819.523	907.444	910.399	1053.628	1110.642	1239.690	1402.739
Frac. Inten.(% of TIC)	0.01	0.05	0.10	0.04	1.87	4.05	3.84	3.08	2.88	4.10	4.93	2.79	1.44	4.13	12.04	1.60	1.70	29.22	3.16	1.57	1.77	3.00	6.12	2.83	3.68
Rel. Inten.(% of BP)	0.02	0.16	0.35	0.15	6.42	13.85	13.15	10.55	9.87	14.04	16.87	9.55	4.94	14.13	41.21	5.49	5.81	100.00	10.80	5.36	6.07	10.26	20.96	9.67	12.59
Score	0.20	0.50	0.22	1.00	1.50	0.50	0.75	0.50	0.75	0.50	0.75	0.75	0.50	1.50	1.50	0.50	-0.06	1.50	1.50	-0.05	0.50	1.50	1.50	1.50	1.50
Ion-type	PR	V	LI	Y	y_1	LP-28	LP	b_2	PIY	b_3	PIYE	PIYEG	y_6-NH_3	y_{12}^{+2}	y_6	b_6		y_{14}^{+2}	y_7		b_7	y_9	y_{10}	y_{11}	y_{12}
Delta ppm	-8.9	-20.5	-10.8	-13.2	-5.4	-11.9	-18.5	-3.6	-2.5	-9.3	4.7	-1.9	12.2	20.8	3.9	4.4		3.2	3.6		-4.2	7.4	-0.3	4.7	-6.5

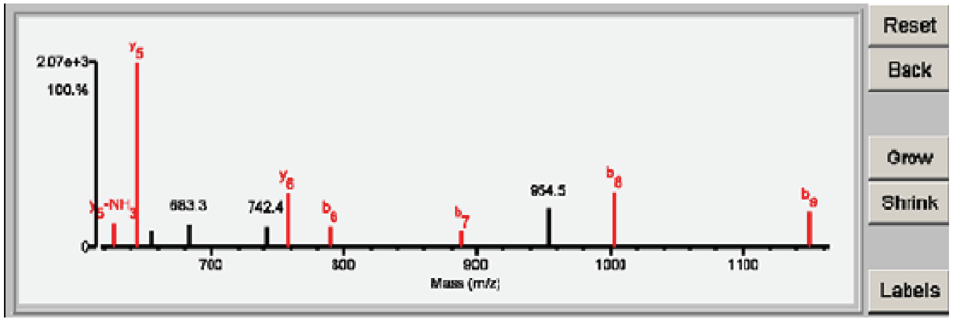


I19

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.27	61.7	7	10/25	(R) D V F H T T\V\N\F|I/N/Q N L/R (T)	1905.9276	0.0144	7.5	21994.8/5.27	HUMAN	P55957	54843	BH3-interacting domain death agonist - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.080	86.096	87.056	110.071	120.080	175.123	187.106	442.216^{+2}	478.265	530.304	590.313^{+2}	600.273	609.302^{+2}	627.324	644.345	655.320	683.317	742.445	757.437	789.329	888.381	954.520	1002.439	1149.501
Frac. Inten.(% of TIC)	0.01	0.27	0.75	0.13	0.09	0.41	2.69	3.23	2.83	3.49	2.49	8.84	2.45	3.57	3.39	25.76	2.30	3.13	3.02	7.69	2.99	2.21	5.49	7.73	5.06
Rel. Inten.(% of BP)	0.03	1.06	2.92	0.51	0.36	1.57	10.45	12.53	10.98	13.53	9.68	34.34	9.50	13.87	13.17	100.00	8.94	12.16	11.71	29.84	11.60	8.58	21.30	30.00	19.63
Score	0.20	0.50	0.22	0.33	1.00	1.00	1.50	-0.13	-0.11	-0.14	1.50	-0.34	-0.09	-0.14	0.50	1.50	-0.09	-0.12	-0.12	1.50	0.50	0.50	-0.21	0.50	0.50
Ion-type	PR	V	LI	NR	H	F	y1				y4				y5-NH3	y5				y6	b6	b7		b8	b9
Delta ppm	15.3	-5.2	-2.6	11.6	-0.7	-4.8	20.3				-1.0				5.1	-3.8				7.6	5.4	-14.0		3.1	-3.3

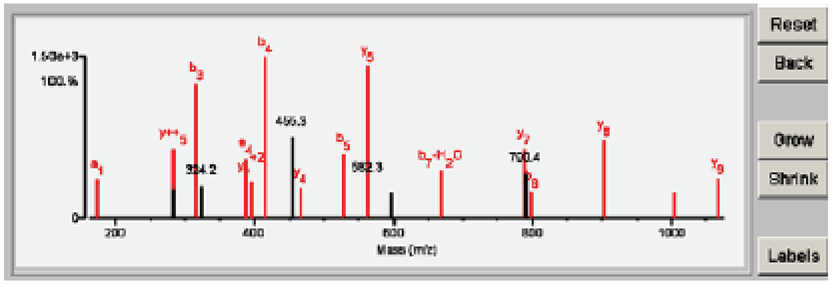


I20

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.21	78.5	9	7/26	(I) L G G\V|T\S A I\S E A A A Q/Y/N/P E/P/P P P R (T)	2422.2071	0.0039	1.6	28316.9/6.06	HUMAN	P04632	104127	Calpain small subunit 1 - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.085	118.086	136.077	174.090	282.171	282.670	316.134	324.218	387.203	396.205^{+2}	416.199	465.320	486.279	528.279	582.263	583.325	597.318^{+2}	668.340	789.424	790.430^{+2}	799.433	903.482	1004.501	1068.617
Frac. Inten.(% of TIC)	0.08	0.14	2.98	0.07	2.96	5.26	2.13	10.11	2.40	4.56	2.73	12.17	6.05	2.36	4.85	2.62	11.47	1.92	3.56	5.27	3.40	2.01	5.83	1.95	3.11
Rel. Inten.(% of BP)	0.67	1.18	24.51	0.56	24.33	43.25	17.49	83.08	19.71	37.46	22.44	100.00	49.70	19.40	39.90	21.55	94.24	15.77	29.29	43.35	27.94	16.51	47.95	16.04	25.59
Score	0.50	0.22	-0.25	1.00	0.50	1.50	-0.17	0.50	-0.20	0.50	1.50	0.50	-0.50	1.50	0.50	-0.22	1.50	-0.16	0.25	1.50	-0.28	0.50	1.50	1.50	1.50
Ion-type	V	LI		Y	a1	y++5		b3		a4	y7^{+2}	b4		y4	b6		y5		b7-H2O	y7		b8	y8	y++19	y9
Delta ppm	14.2	-17.7		13.3	-35.1	6.9		1.4		-11.2	-27.4	-8.3		3.6	-13.7		-8.4		-6.4	-2.0		-8.5	-6.4	-9.4	-14.1



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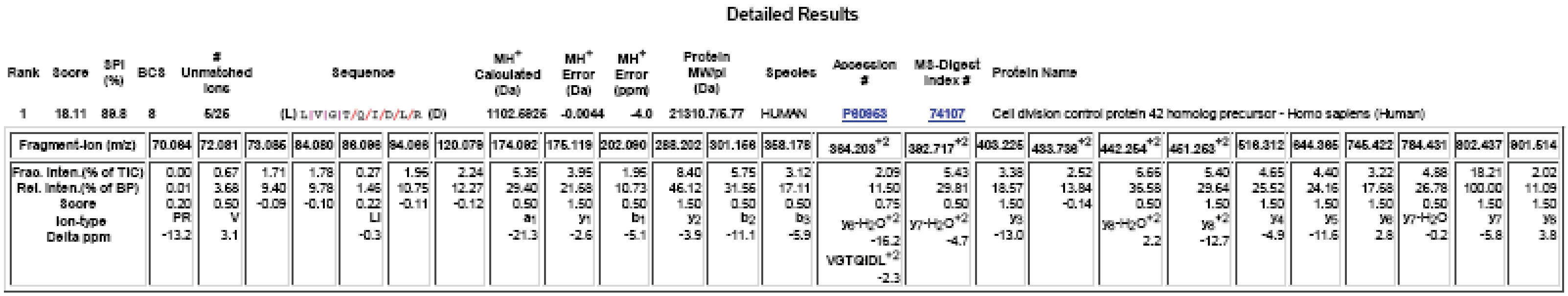
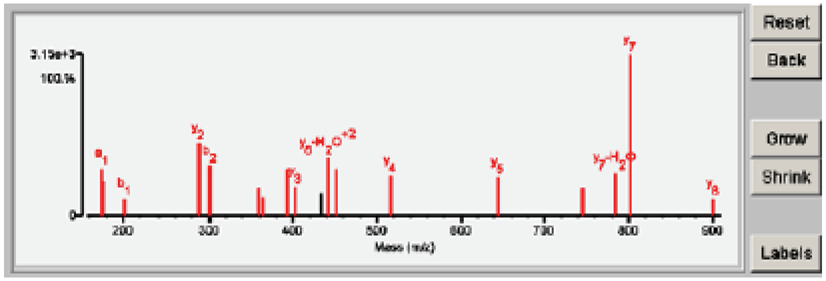


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.11	88.8	8	5/26	(L) L|V|G|T/Q/I/D/L/R (D)	1102.6826	-0.0044	-4.0	21310.7/6.77	HUMAN	P60953	74107	Cell division control protein 42 homolog precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.084	72.081	73.086	84.080	86.096	94.066	120.079	174.082	175.119	202.090	288.202	301.168	358.178
Frac. Inten.(% of TIC)	0.00	0.67	1.71	1.78	0.27	1.95	2.24	5.35	3.95	1.95	8.40	5.75	3.12
Rel. Inten.(% of BP)	0.01	3.68	9.40	9.78	1.46	10.75	12.27	29.40	21.68	10.73	46.12	31.56	17.11
Score	0.20	0.50	-0.09	-0.10	0.22	-0.11	-0.12	0.50	1.50	0.50	1.50	0.50	0.50
Ion-type	PR	V			LI			a_1	y_1	b_1	y_2	b_2	b_3
Delta ppm	-13.2	3.1			-0.3			-21.3	-2.6	-5.1	-3.9	-11.1	-5.9

Fragment-Ion (m/z)	364.203^{+2}	382.717^{+2}	403.225	433.738^{+2}	442.254^{+2}	461.263^{+2}	516.312	644.365	745.422	784.431	802.437	901.514
Frac. Inten.(% of TIC)	2.09	5.43	3.38	2.52	6.66	5.40	4.65	4.40	3.22	4.88	18.21	2.02
Rel. Inten.(% of BP)	11.50	29.81	18.57	13.84	36.58	29.64	25.52	24.16	17.68	26.78	100.00	11.09
Score	0.75	0.50	1.50	-0.14	0.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	y_6-H_2O^{+2}	y_7-H_2O^{+2}	y_3		y_8-H_2O^{+2}	y_8^{+2}	y_4	y_5	y_6	y_7-H_2O	y_7	y_8
Delta ppm	-16.2 VGTQIDL^{+2} -2.3	-4.7	-13.0		2.2	-12.7	-4.9	-11.6	2.8	-0.2	-5.8	3.8



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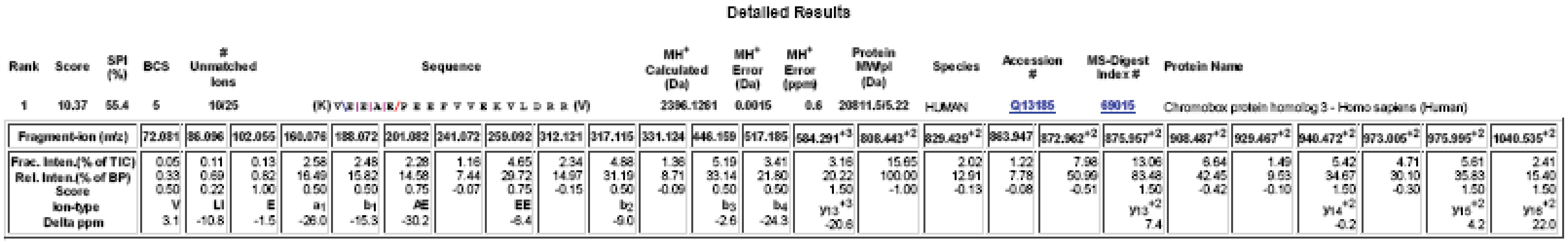
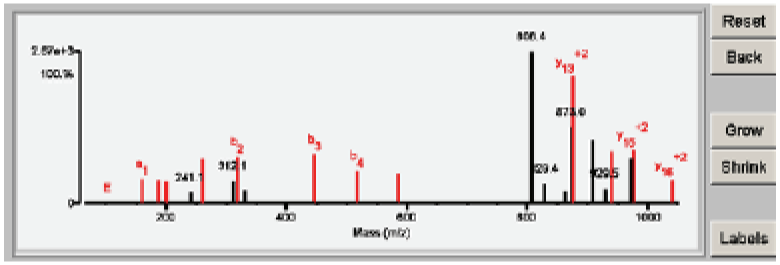


Detailed Results

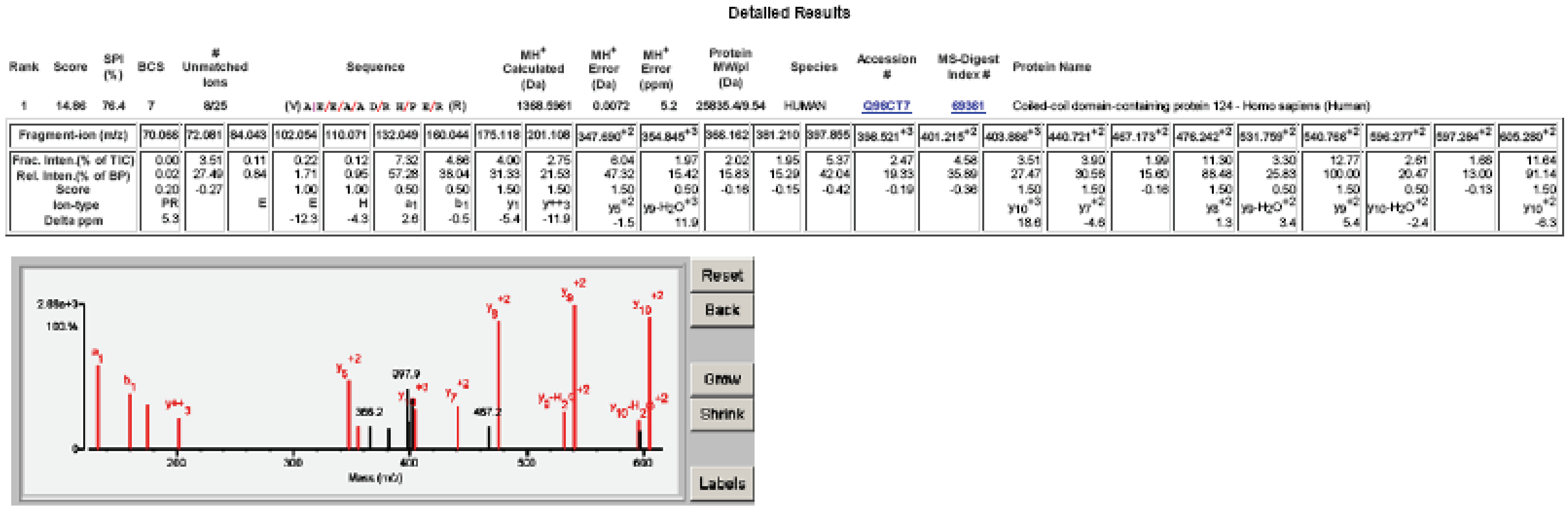
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.37	55.4	5	10/25	(K) V\E|E|A|K/P E E F V V E K V L D R R (V)	2396.1261	0.0015	0.6	20811.5/5.22	HUMAN	Q13185	69015	Chromobox protein homolog 3 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.096	102.055	160.076	188.072	201.082	241.072	259.092	312.121	317.115	331.124	446.159	517.185
Frac. Inten.(% of TIC)	0.05	0.11	0.13	2.58	2.48	2.28	1.16	4.65	2.34	4.88	1.36	5.19	3.41
Rel. Inten.(% of BP)	0.33	0.69	0.82	16.49	15.82	14.58	7.44	29.72	14.97	31.19	8.71	33.14	21.80
Score	0.50	0.22	1.00	0.50	0.50	0.75	-0.07	0.75	-0.15	0.50	-0.09	0.50	0.50
Ion-type	V	LI	E	a_1	b_1	AE		EE		b_2		b_3	b_4
Delta ppm	3.1	-10.8	-1.5	-26.0	-15.3	-30.2		-6.4		-9.0		-2.6	-24.3

Fragment-Ion (m/z)	584.291^{+3}	808.443^{+2}	829.429^{+2}	863.947	872.962^{+2}	875.957^{+2}	908.487^{+2}	929.467^{+2}	940.472^{+2}	973.005^{+2}	975.995^{+2}	1040.535^{+2}
Frac. Inten.(% of TIC)	3.16	15.65	2.02	1.22	7.98	13.06	6.64	1.49	5.42	4.71	5.61	2.41
Rel. Inten.(% of BP)	20.22	100.00	12.91	7.78	50.99	83.48	42.45	9.53	34.67	30.10	35.83	15.40
Score	1.50	-1.00	-0.13	-0.08	-0.51	1.50	-0.42	-0.10	1.50	-0.30	1.50	1.50
Ion-type	y_{13}^{+3}					y_{13}^{+2}			y_{14}^{+2}		y_{15}^{+2}	y_{16}^{+2}
Delta ppm	-20.6					7.4			-0.2		4.2	22.0



I23



Detailed Results

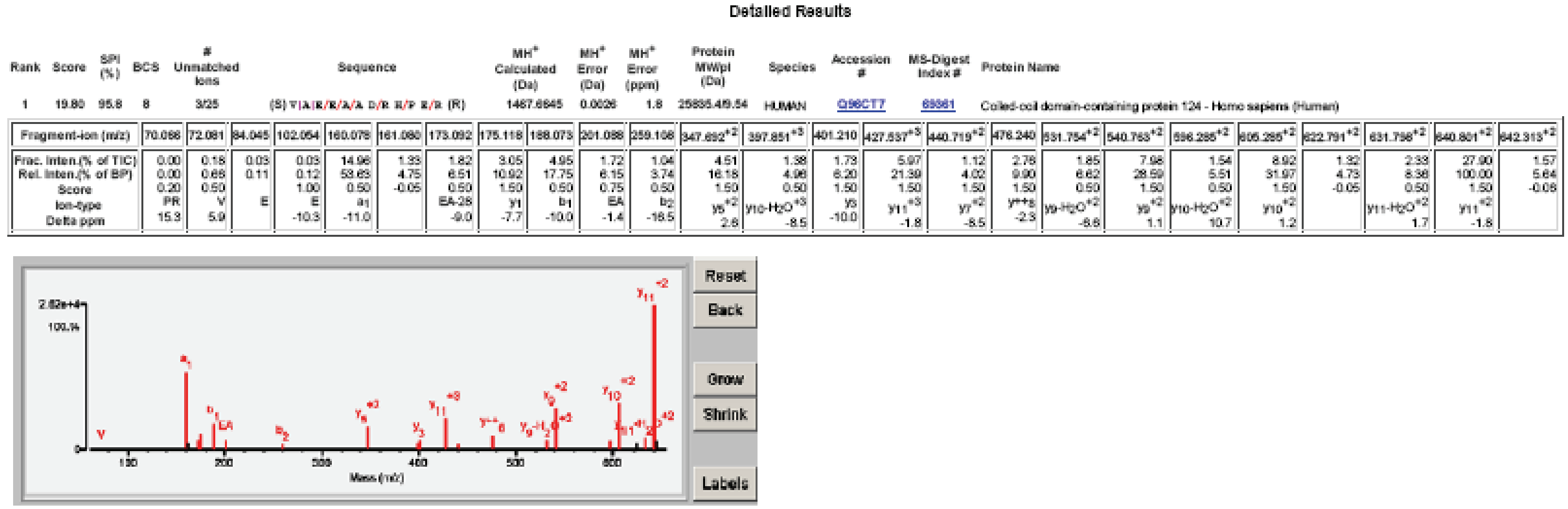
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.86	76.4	7	8/25	(V) A|E/E/A/A D/R H/P E/R (R)	1368.5961	0.0072	5.2	25835.4/9.54	HUMAN	Q96CT7	69361	Coiled-coil domain-containing protein 124 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.043	102.054	110.071	132.049	160.044	175.118	201.108
Frac. Inten.(% of TIC)	0.00	3.51	0.11	0.22	0.12	7.32	4.86	4.00	2.75
Rel. Inten.(% of BP)	0.02	27.49	0.84	1.71	0.95	57.28	38.04	31.33	21.53
Score	0.20	-0.27		1.00	1.00	0.50	0.50	1.50	1.50
Ion-type	PR		E	E	H	a_1	b_1	y_1	y^{++}_3
Delta ppm	5.3			-12.3	-4.3	2.6	-0.5	-5.4	-11.9

Fragment-ion (m/z)	347.690^{+2}	354.845^{+3}	366.162	381.210	397.855	398.521^{+3}	401.215^{+2}	403.886^{+3}
Frac. Inten.(% of TIC)	6.04	1.97	2.02	1.95	5.37	2.47	4.58	3.51
Rel. Inten.(% of BP)	47.32	15.42	15.83	15.29	42.04	19.33	35.89	27.47
Score	1.50	0.50	-0.16	-0.15	-0.42	-0.19	-0.36	1.50
Ion-type	y_5^{+2}	$y_9\text{-}H_2O^{+3}$						y_{10}^{+3}
Delta ppm	-1.5	11.9						18.6

Fragment-ion (m/z)	440.721^{+2}	457.173^{+2}	476.242^{+2}	531.759^{+2}	540.766^{+2}	596.277^{+2}	597.284^{+2}	605.280^{+2}
Frac. Inten.(% of TIC)	3.90	1.99	11.30	3.30	12.77	2.61	1.66	11.64
Rel. Inten.(% of BP)	30.56	15.60	88.48	25.83	100.00	20.47	13.00	91.14
Score	1.50	-0.16	1.50	0.50	1.50	0.50	-0.13	1.50
Ion-type	y_7^{+2}		y_8^{+2}	$y_9\text{-}H_2O^{+2}$	y_9^{+2}	$y_{10}\text{-}H_2O^{+2}$		y_{10}^{+2}
Delta ppm	-4.6		1.3	3.4	5.4	-2.4		-6.3

I24



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.80	95.8	8	3/25	(S) V|A|E/E/A/A D/R H/P E/R (R)	1467.6645	0.0026	1.8	25835.4/9.54	HUMAN	Q96CT7	69361	Coiled-coil domain-containing protein 124 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.045	102.054	160.076	161.080	173.092	175.118	188.073
Frac. Inten.(% of TIC)	0.00	0.18	0.03	0.03	14.96	1.33	1.82	3.05	4.95
Rel. Inten.(% of BP)	0.00	0.66	0.11	0.12	53.63	4.75	6.51	10.92	17.75
Score	0.20	0.50		1.00	0.50	-0.05	0.50	1.50	0.50
Ion-type	PR	V	E	E	a_1		EA-28	y_1	b_1
Delta ppm	15.3	5.9		-10.3	-11.0		-9.0	-7.7	-10.0

Fragment-ion (m/z)	201.088	259.108	347.692^{+2}	397.851^{+3}	401.210	427.537^{+3}	440.719^{+2}	476.240
Frac. Inten.(% of TIC)	1.72	1.04	4.51	1.38	1.73	5.97	1.12	2.76
Rel. Inten.(% of BP)	6.15	3.74	16.16	4.96	6.20	21.39	4.02	9.90
Score	0.75	0.50	1.50	0.50	1.50	1.50	1.50	1.50
Ion-type	EA	b_2	y_5^{+2}	$y_{10}\text{-}H_2O^{+3}$	y_3	y_{11}^{+3}	y_7^{+2}	y^{++}_8
Delta ppm	-1.4	-16.5	2.6	-8.5	-10.0	-1.8	-8.5	-2.3

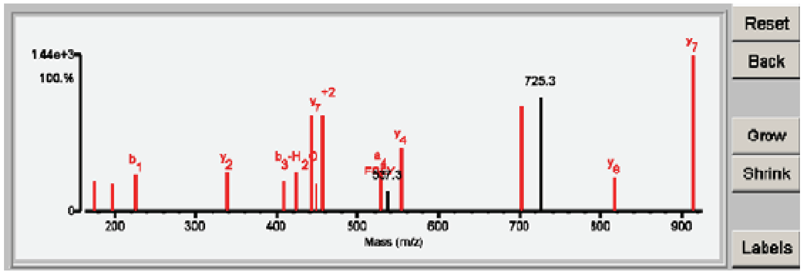
Fragment-ion (m/z)	531.754^{+2}	540.763^{+2}	596.285^{+2}	605.285^{+2}	622.791^{+2}	631.798^{+2}	640.801^{+2}	642.313^{+2}
Frac. Inten.(% of TIC)	1.85	7.98	1.54	8.92	1.32	2.33	27.90	1.57
Rel. Inten.(% of BP)	6.62	28.59	5.51	31.97	4.73	8.36	100.00	5.64
Score	0.50	1.50	0.50	1.50	-0.05	0.50	1.50	-0.06
Ion-type	$y_9\text{-}H_2O^{+2}$	y_9^{+2}	$y_{10}\text{-}H_2O^{+2}$	y_{10}^{+2}		$y_{11}\text{-}H_2O^{+2}$	y_{11}^{+2}	
Delta ppm	-6.6	1.1	10.7	1.2		1.7	-1.8	

I25

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.17	75.2	9	6/25	(S) H\T D\I K\V/P/D/F/S E/Y/R (R)	1829.7986	0.0124	6.8	30815.5/9.04	HUMAN	P0C7P4	678539	Cytochrome b-c1 complex subunit Rieske-like protein 1 - Homo sapiens (Human)
1	15.17	75.2	9	6/25	(S) H\T D\I K\V/P/D/F/S E/Y/R (R)	1829.7986	0.0124	6.8	29668.1/8.55	HUMAN	P47985	678563	Cytochrome b-c1 complex subunit Rieske, mitochondrial precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	84.080	86.099	94.066	110.073	116.049	120.085	143.064	175.115	198.070	226.067	338.180	409.671^{+2}	424.115	442.137	448.190^{+2}	457.212^{+2}	527.233	537.252	554.247	701.331	725.271	816.357	913.403
Frac. Inten.(% of TIC)	0.01	0.33	2.04	0.09	5.74	0.06	1.85	0.07	2.94	2.73	2.49	3.33	3.55	2.78	3.58	8.69	2.50	8.71	3.67	1.94	5.82	9.49	10.32	3.10	14.19
Rel. Inten.(% of BP)	0.04	2.33	14.41	0.60	40.49	0.40	13.01	0.51	20.69	19.25	17.54	23.44	24.99	19.59	25.24	61.24	17.59	61.36	25.90	13.68	41.00	66.92	72.75	21.83	100.00
Score	0.20	0.50	-0.14	0.22	-0.40	1.00	-0.13	1.00	-0.21	1.50	0.50	0.50	1.50	0.50	0.25	0.50	0.50	1.50	0.75	-0.14	1.50	1.50	-0.73	1.50	1.50
Ion-type	PR	V		LI		H		F		y1	a1	b1	y2	b_5^{+2}	b_3-H$_2$O	b3	y_7-H$_2$O^{+2}	y_7^{+2}	a4 FSEY		y4	y5		y6	y7
Delta ppm	-0.4	5.9		33.4		19.3		36.8		-23.1	-3.3	6.8	-7.9	0.5	-35.0	-6.3	-23.4	11.9	6.6 34.3		-17.3	7.4		5.8	-2.4

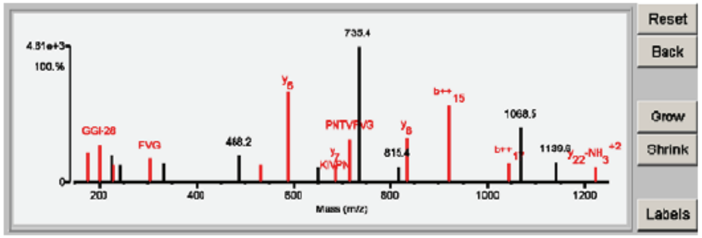


I26

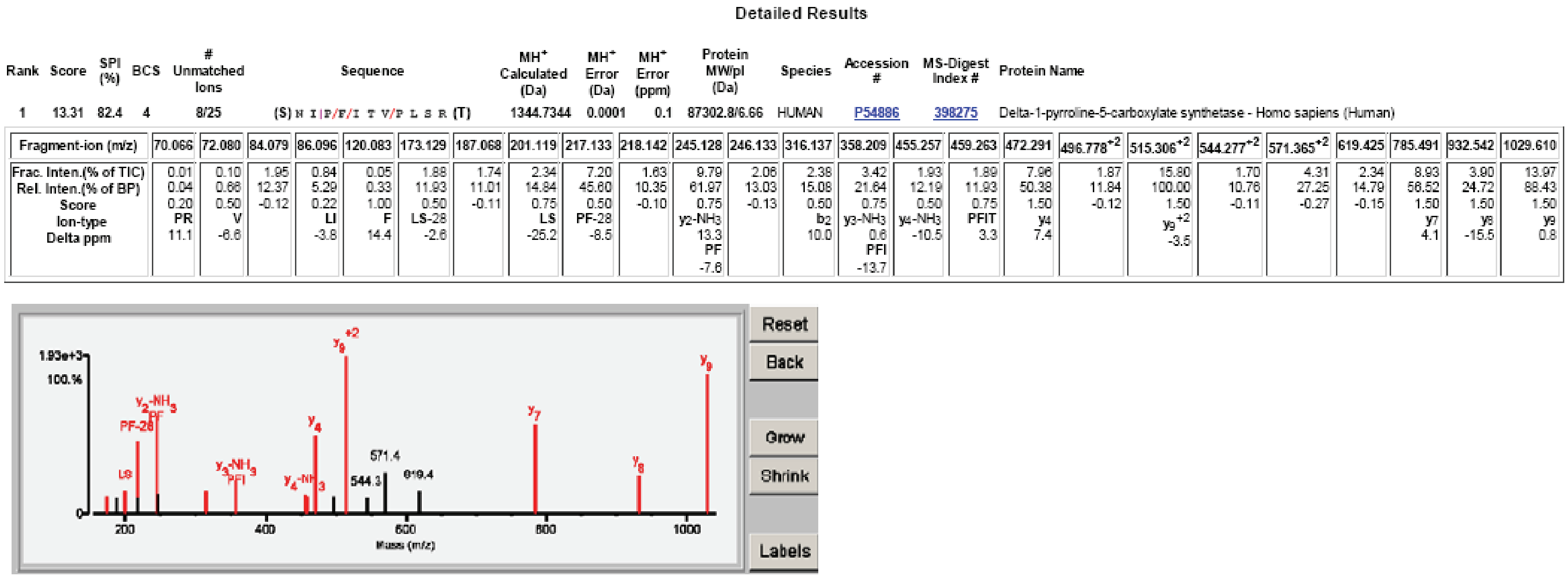
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	82764.9/9.36	HUMAN	Q9NQZ3	126217	Deleted in azoospermia protein 1 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	82764.9/9.36	HUMAN	Q9NQZ3	126217	Deleted in azoospermia protein 1 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	82764.9/9.36	HUMAN	Q9NQZ3	126217	Deleted in azoospermia protein 1 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	63132.0/8.84	HUMAN	Q13117	126219	Deleted in azoospermia protein 2 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	54988.9/8.90	HUMAN	Q9NR90	126221	Deleted in azoospermia protein 3 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	64785.3/9.23	HUMAN	Q86SG3	126223	Deleted in azoospermia protein 4 - Homo sapiens (Human)
1	12.02	56.8	5	9/25	(S) Q G W V L P E G K I V P N T V|F/V|G/G I D A/R (M)	2675.3473	0.0140	5.2	64785.3/9.23	HUMAN	Q86SG3	126223	Deleted in azoospermia protein 4 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.096	102.053	120.079	175.118	200.139	226.121	228.133	243.135	304.161	330.133	488.249	531.289	588.310	651.797^{+2}	687.352	715.375	735.377	815.384	834.446	921.475	1044.543	1068.544	1139.580	1221.620^{+2}
Frac. Inten.(% of TIC)	0.07	0.24	0.07	0.10	3.90	4.88	3.50	2.29	2.29	3.05	2.42	3.48	2.30	11.64	2.05	2.31	5.68	17.62	2.09	5.73	10.04	2.49	7.08	2.66	2.00
Rel. Inten.(% of BP)	0.41	1.34	0.38	0.58	22.11	27.71	19.89	12.99	13.00	17.29	13.75	19.75	13.07	66.09	11.65	13.14	32.23	100.00	11.86	32.54	56.99	14.15	40.20	15.08	11.36
Score	0.50	0.22	1.00	1.00	1.50	0.50	-0.20	0.75	-0.13	0.75	-0.14	-0.20	1.50	1.50	-0.12	1.50	0.75	-1.00	-0.12	1.50	0.50	0.50	-0.40	-0.15	0.50
Ion-type	V	LI	E	F	y_1	GGI-28		GGI		FVG			y_5	y_6		y_7 KIVPN	PNTVFVG			y_8	b^{++}_{15}	b^{++}_{17}			y_{22}-NH$_3^{+2}$
Delta ppm	4.5	-7.3	-17.2	-14.8	-4.9	-6.2		-9.5		-17.6			0.7	-0.7		-38.0 -19.6	-4.8			-1.4	18.3	16.1			-12.7



I27



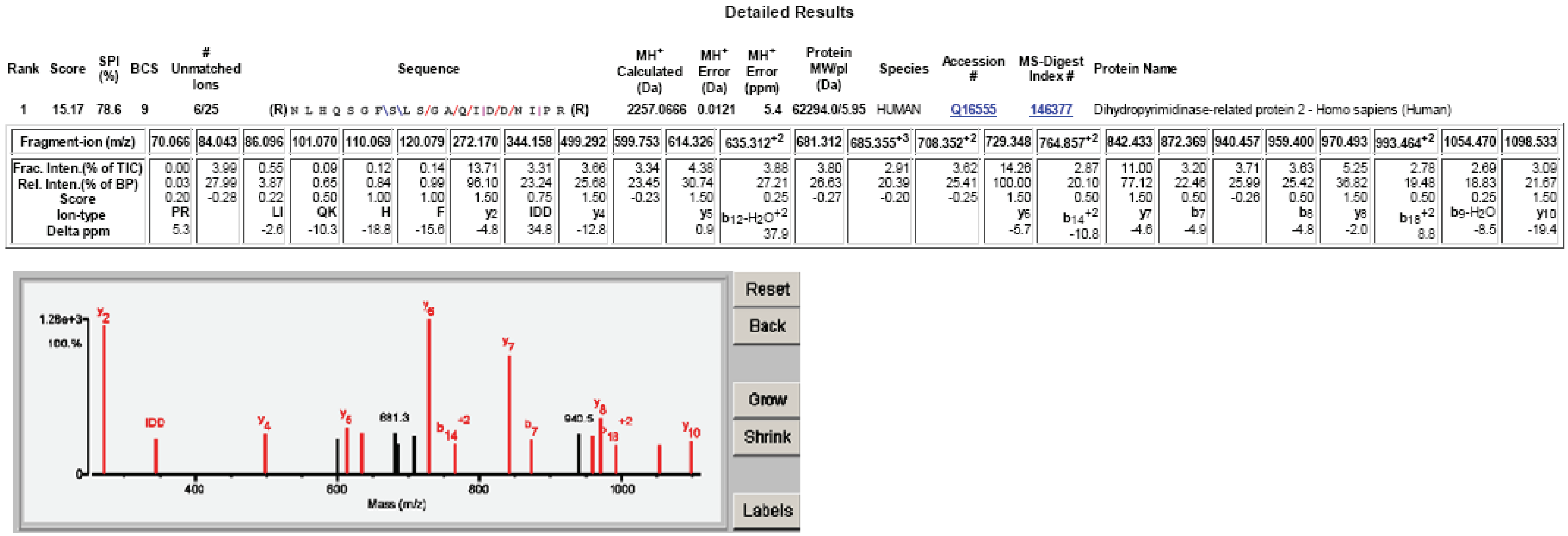
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.31	82.4	4	8/25	(S) N I|P/F/I T V/P L S R (T)	1344.7344	0.0001	0.1	87302.8/6.66	HUMAN	P54886	398275	Delta-1-pyrroline-5-carboxylate synthetase - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.080	84.079	86.096	120.083	173.129	187.068	201.119	217.133	218.142	245.128	246.133
Frac. Inten.(% of TIC)	0.01	0.10	1.95	0.84	0.05	1.88	1.74	2.34	7.20	1.63	9.79	2.06
Rel. Inten.(% of BP)	0.04	0.66	12.37	5.29	0.33	11.93	11.01	14.84	45.60	10.35	61.97	13.03
Score	0.20	0.50	-0.12	0.22	1.00	0.50	-0.11	0.75	0.50	-0.10	0.75	-0.13
Ion-type	PR	V		LI	F	LS-28		LS	PF-28		y_2-NH$_3$ 13.3 PF	
Delta ppm	11.1	-6.6		-3.8	14.4	-2.6		-25.2	-8.5		-7.6	

Fragment-ion (m/z)	316.137	358.209	455.257	459.263	472.291	496.778^{+2}	515.306^{+2}	544.277^{+2}	571.365^{+2}	619.425	785.491	932.542	1029.610
Frac. Inten.(% of TIC)	2.38	3.42	1.93	1.89	7.96	1.87	15.80	1.70	4.31	2.34	8.93	3.90	13.97
Rel. Inten.(% of BP)	15.08	21.64	12.19	11.93	50.38	11.84	100.00	10.76	27.25	14.79	56.52	24.72	88.43
Score	0.50	0.75	0.50	0.75	1.50	-0.12	1.50	-0.11	-0.27	-0.15	1.50	1.50	1.50
Ion-type	b_2	y_3-NH$_3$ 0.6 PFI	y_4-NH$_3$	PFIT	y_4		y_9^{+2}				y_7	y_8	y_9
Delta ppm	10.0	-13.7	-10.5	3.3	7.4		-3.5				4.1	-15.5	0.8

I28



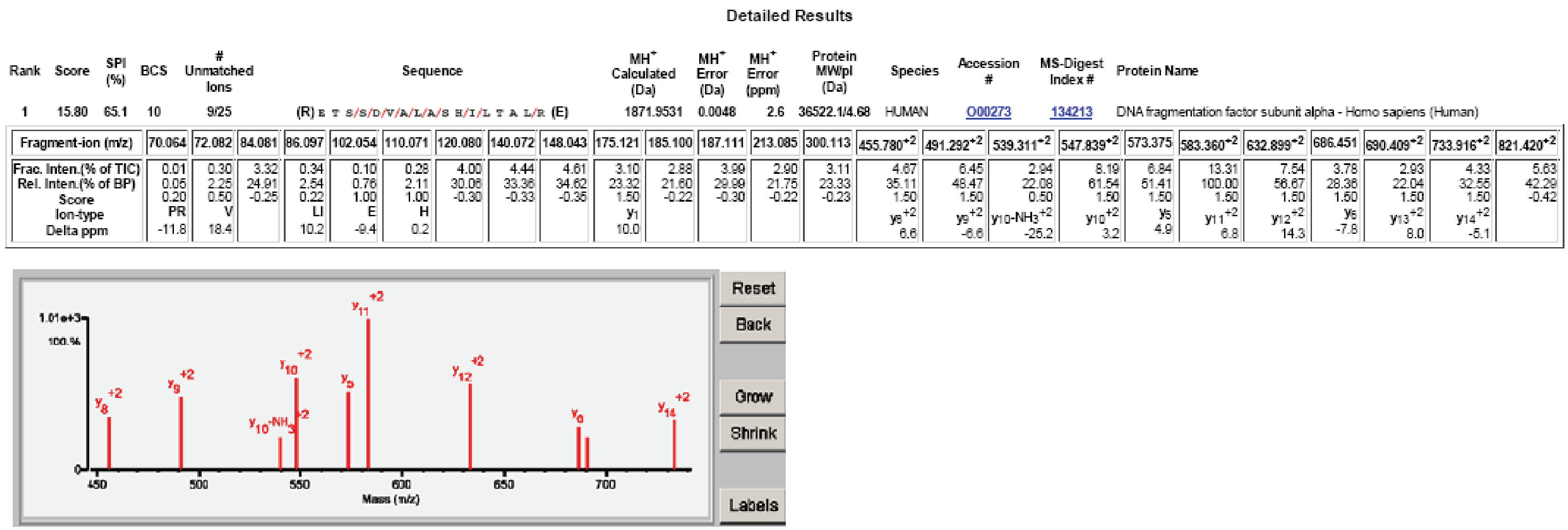
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.17	78.6	9	6/25	(R) N L H Q S G F\S\L S/G A/Q/I|D/D/N I|P R (R)	2257.0666	0.0121	5.4	62294.0/5.95	HUMAN	Q16555	146377	Dihydropyrimidinase-related protein 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	84.043	86.096	101.070	110.069	120.079	272.170	344.158	499.292	599.753	614.326	635.312^{+2}
Frac. Inten.(% of TIC)	0.00	3.99	0.55	0.09	0.12	0.14	13.71	3.31	3.66	3.34	4.38	3.88
Rel. Inten.(% of BP)	0.03	27.99	3.87	0.65	0.84	0.99	96.10	23.24	25.68	23.45	30.74	27.21
Score	0.20	-0.28	0.22	0.50	1.00	1.00	1.50	0.75	1.50	-0.23	1.50	0.25
Ion-type	PR		LI	QK	H	F	y_2	IDD	y_4		y_5	b_{12}-H$_2$O^{+2}
Delta ppm	5.3		-2.6	-10.3	-18.8	-15.6	-4.8	34.8	-12.8		0.9	37.9

Fragment-ion (m/z)	681.312	685.355^{+3}	708.352^{+2}	729.348	764.857^{+2}	842.433	872.369	940.457	959.400	970.493	993.464^{+2}	1054.470	1098.533
Frac. Inten.(% of TIC)	3.80	2.91	3.62	14.26	2.87	11.00	3.20	3.71	3.63	5.25	2.78	2.69	3.09
Rel. Inten.(% of BP)	26.63	20.39	25.41	100.00	20.10	77.12	22.46	25.99	25.42	36.82	19.48	18.83	21.67
Score	-0.27	-0.20	-0.25	1.50	0.50	1.50	0.50	-0.26	0.50	1.50	0.50	0.25	1.50
Ion-type				y_6	b_{14}^{+2}	y_7	b_7		b_8	y_8	b_{18}^{+2}	b_9-H$_2$O	y_{10}
Delta ppm				-5.7	-10.8	-4.6	-4.9		-4.8	-2.0	8.8	-8.5	-19.4

I29



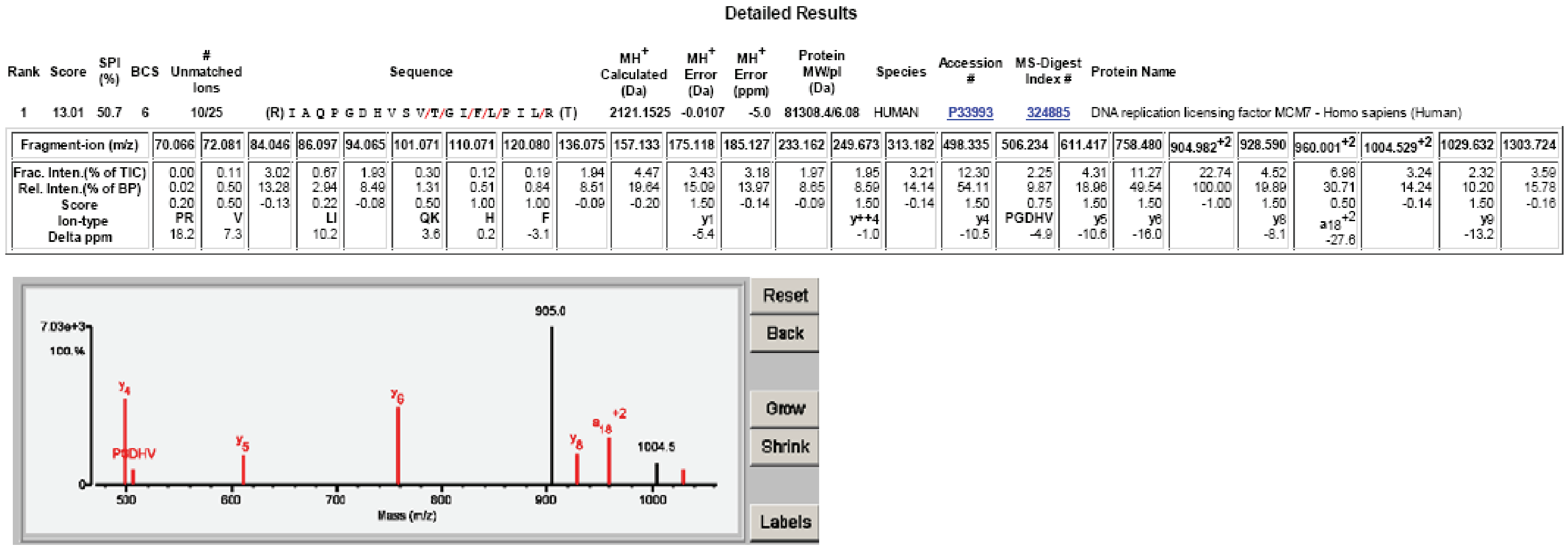
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.80	65.1	10	9/25	(R) E T S/S/D/V/A/L/A/S H/I/L T A L/R (E)	1871.9531	0.0048	2.6	36522.1/4.68	HUMAN	O00273	134213	DNA fragmentation factor subunit alpha - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.082	84.081	86.097	102.054	110.071	120.080	140.072	148.043	175.121	185.100	187.111	213.085
Frac. Inten.(% of TIC)	0.01	0.30	3.32	0.34	0.10	0.28	4.00	4.44	4.61	3.10	2.88	3.99	2.90
Rel. Inten.(% of BP)	0.05	2.25	24.91	2.54	0.76	2.11	30.06	33.36	34.62	23.32	21.60	29.99	21.75
Score	0.20	0.50	-0.25	0.22	1.00	1.00	-0.30	-0.33	-0.35	1.50	-0.22	-0.30	-0.22
Ion-type	PR	V		LI	E	H				y_1			
Delta ppm	-11.8	18.4		10.2	-9.4	0.2				10.0			

Fragment-ion (m/z)	300.113	455.780^{+2}	491.292^{+2}	539.311^{+2}	547.839^{+2}	573.375	583.360^{+2}	632.899^{+2}	686.451	690.409^{+2}	733.916^{+2}	821.420^{+2}
Frac. Inten.(% of TIC)	3.11	4.67	6.45	2.94	8.19	6.84	13.31	7.54	3.78	2.93	4.33	5.63
Rel. Inten.(% of BP)	23.33	35.11	48.47	22.08	61.54	51.41	100.00	56.67	28.36	22.04	32.55	42.29
Score	-0.23	1.50	1.50	0.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	-0.42
Ion-type		y_8^{+2}	y_9^{+2}	$y_{10}\text{-}NH_3^{+2}$	y_{10}^{+2}	y_5	y_{11}^{+2}	y_{12}^{+2}	y_6	y_{13}^{+2}	y_{14}^{+2}	
Delta ppm		6.6	-6.6	-25.2	3.2	4.9	6.8	14.3	-7.8	8.0	-5.1	

I30



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.01	50.7	6	10/25	(R) I A Q P G D H V S V/T/G I/F/L/P I L/R (T)	2121.1525	-0.0107	-5.0	81308.4/6.08	HUMAN	P33993	324885	DNA replication licensing factor MCM7 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.046	86.097	94.065	101.071	110.071	120.080	136.075	157.133	175.118	185.127	233.162
Frac. Inten.(% of TIC)	0.00	0.11	3.02	0.67	1.93	0.30	0.12	0.19	1.94	4.47	3.43	3.18	1.97
Rel. Inten.(% of BP)	0.02	0.50	13.28	2.94	8.49	1.31	0.51	0.84	8.51	19.64	15.09	13.97	8.65
Score	0.20	0.50	-0.13	0.22	-0.08	0.50	1.00	1.00	-0.09	-0.20	1.50	-0.14	-0.09
Ion-type	PR	V		LI		QK	H	F			y_1		
Delta ppm	18.2	7.3		10.2		3.6	0.2	-3.1			-5.4		

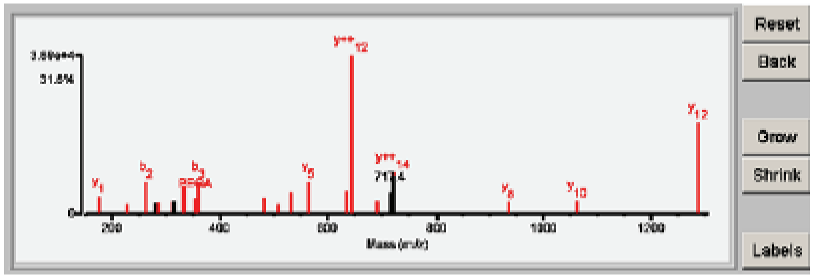
Fragment-ion (m/z)	249.673	313.182	498.335	506.234	611.417	758.480	904.982^{+2}	928.590	960.001^{+2}	1004.529^{+2}	1029.632	1303.724
Frac. Inten.(% of TIC)	1.95	3.21	12.30	2.25	4.31	11.27	22.74	4.52	6.98	3.24	2.32	3.59
Rel. Inten.(% of BP)	8.59	14.14	54.11	9.87	18.96	49.54	100.00	19.89	30.71	14.24	10.20	15.78
Score	1.50	-0.14	1.50	0.75	1.50	1.50	-1.00	1.50	0.50	-0.14	1.50	-0.16
Ion-type	y++4		y_4	PGDHV	y_5	y_6		y_8	a_{18}^{+2}		y_9	
Delta ppm	-1.0		-10.5	-4.9	-10.6	-16.0		-8.1	-27.6		-13.2	

I31

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.33	81.8	10	4/25	(K) D/G|V|P E/G A/Q L/Q/G/P V/E/R (N)	1647.7908	0.0048	2.9	40090.1/9.77	HUMAN	P16989	127231	DNA-binding protein A - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
72.082	0.12	0.25	0.50	V	10.0
176.118	1.65	3.36	1.50	y_1	-3.2
227.102	0.81	1.64	0.75	PE	-6.3
261.063	3.13	6.37	0.50	b_2	-6.0
279.132	0.93	1.90	-0.02		
284.125	1.01	2.05	0.75	PEG	0.0
312.177	1.14	2.31	1.50	y_2	-4.0
314.117	1.29	2.61	-0.03		
332.127	2.70	5.49	0.50	a_3	-4.1
356.161	1.35	2.75	0.75	PEGA	-3.1
360.123	3.08	6.26	0.50	b_3	-0.2
483.221	1.54	3.13	0.75	PEGAQ	0.2
508.301	0.82	1.67	1.50	y_4	3.3
531.784^{+2}	2.03	4.13	1.50	y_{10}^{+2}	0.6
586.318	3.09	6.28	1.50	y_5	-3.5
635.832^{+2}	2.20	4.47	0.50	$y_{12}\text{-}H_2O^{+2}$	-6.7
644.842	49.24	100.00	1.50	$y^{++}12$	1.0
693.378	1.33	2.70	1.50	y_6	-1.9
694.381^{+2}	0.98	2.00	1.50	y_{13}^{+2}	7.8
717.369^{+2}	2.10	4.26	-0.04		
722.884	4.11	8.34	1.50	$y^{++}14$	-3.7
723.387	3.85	7.81	-0.08		
934.616	1.19	2.42	1.50	y_8	-6.1
1062.577	1.24	2.52	1.50	y_{10}	-2.8
1288.671	9.05	18.38	1.50	y_{12}	-3.3

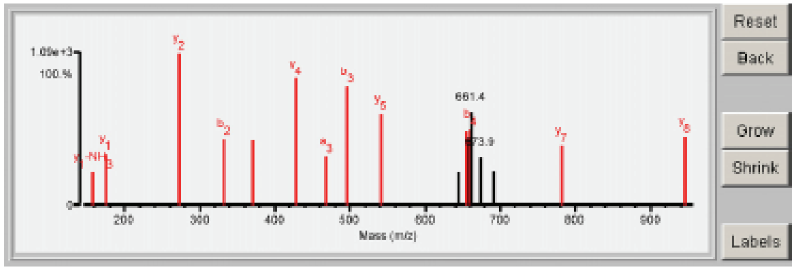


I32

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.78	72.1	9	8/25	(K) E D\Y|Y|Q/I/L/G/V/P/R (N)	1440.6828	0.0166	11.6	52538.1/9.38	HUMAN	Q96EY1	141863	DnaJ homolog subfamily A member 3, mitochondrial precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.066	0.01	0.05	0.20	PR	13.9
72.081	0.12	1.11	0.50	V	-1.0
84.081	3.41	32.32	-0.32		
86.097	0.33	3.15	0.22	LI	0.9
94.066	2.72	25.79	-0.26		
120.081	2.89	27.38	-0.27		
136.074	0.54	5.12	1.00	Y	-14.6
158.095	2.33	22.10	0.50	$y_1\text{-}NH_3$	13.3
176.118	3.53	33.46	1.50	y_1	-6.6
272.170	10.56	100.00	1.50	y_2	-5.6
333.074	4.53	42.88	0.50	b_2	-5.4
371.236	4.47	42.37	1.50	y_3	-15.2
428.268	8.72	82.54	1.50	y_4	-8.4
468.144	3.39	32.12	0.50	a_3	-0.2
496.139	8.16	77.25	0.50	b_3	-14.0
541.342	6.26	59.32	1.50	y_5	-6.2
644.320	2.27	21.50	-0.22		
654.422	5.06	47.92	1.50	y_6	-11.8
658.344	4.62	43.75	-0.44		
659.196	5.21	49.33	0.50	b_4	-11.0
661.374+2	6.36	60.23	-0.60		
673.869+2	3.30	31.21	-0.31		
681.352	2.37	22.42	-0.22		
782.488	4.11	38.89	1.50	y_7	-0.9
945.559	4.72	44.67	1.50	y_8	8.2

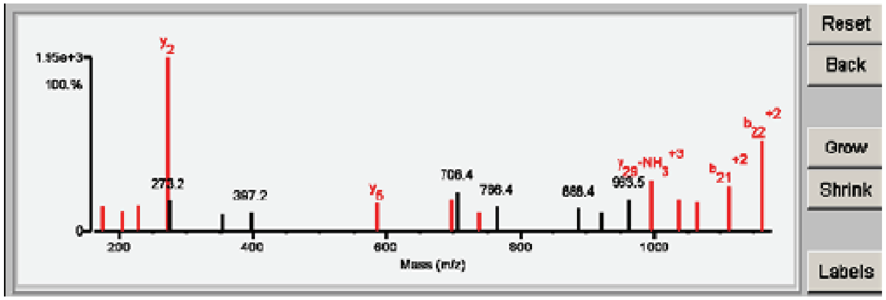


I33

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.29	70.5	7	10/25	(R) I G P E P T T D S F I A V M H G P T E G\V\V|P G N A/L/V V D/P/R (R)	3360.6603	-0.0061	-1.8	60627.2/6.35	HUMAN	Q9H4M9	160101	EH domain-containing protein 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.064	72.080	86.098	136.077	143.113	175.115	203.105	227.106	272.171	273.173	353.724	397.205	585.335	698.417	706.435	737.399	766.421	888.413	920.473	963.467^{+3}	996.818^{+3}	1037.574	1063.496^{+2}	1113.032^{+2}	1162.555^{+2}
Frac. Inten.(% of TIC)	0.00	0.26	0.33	2.51	2.03	2.97	2.47	3.19	21.31	3.80	2.12	2.30	3.28	3.95	4.83	2.28	3.04	2.87	2.19	3.85	6.24	3.89	3.51	5.59	11.18
Rel. Inten.(% of BP)	0.02	1.22	1.53	11.77	9.51	13.96	11.60	14.98	100.00	17.83	9.95	10.79	15.41	18.53	22.65	10.72	14.26	13.47	10.27	18.08	29.28	18.25	16.47	26.25	52.48
Score	0.20	0.50	0.22	-0.12	-0.10	1.50	0.75	0.75	1.50	-0.18	-0.10	-0.11	1.50	1.50	-0.23	0.75	-0.14	-0.13	-0.10	-0.18	0.50	1.50	0.50	0.50	0.50
Ion-type	PR	V	LI			y_1	TT	EP	y_2				y_5	y_6		PTEGVVPG					y_{29}-NH_3^{+3}	y_{10}	b_{20}^{+2}	b_{21}^{+2}	b_{22}^{+2}
Delta ppm	-10.4	-8.0	13.6			-20.9	5.3	9.1	-0.8				-1.3	-4.1		20.6					-13.0	0.2	12.8	13.5	3.7

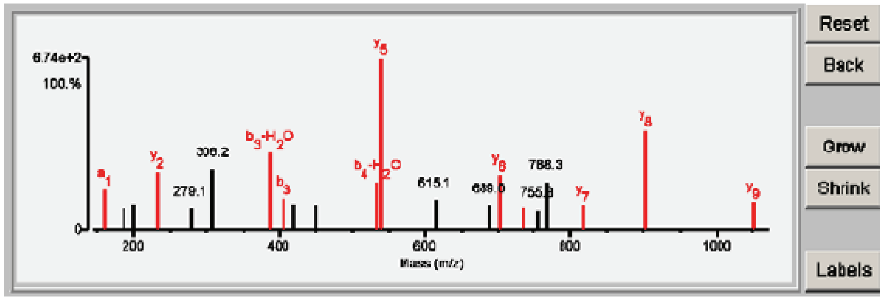


I34

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.70	68.7	6	10/25	(C) V E S|F/S/D/Y/P P L/G R (F)	1454.6620	0.0075	5.1	50141.1/9.10	HUMAN	P68104	153989	Elongation factor 1-alpha 1 - Homo sapiens (Human)
1	11.70	68.7	6	10/25	(C) V E S|F/S/D/Y/P P L/G R (F)	1454.6620	0.0075	5.1	50185.3/9.15	HUMAN	Q5VTE0	154035	Elongation factor 1-alpha-like 3 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.079	102.052	120.080	160.074	186.086	199.069	232.143	279.131	308.223	386.140	404.147	419.209	450.213	533.200	539.329	615.093	688.984	702.401	735.258	755.327	768.278	817.404	904.454	1051.506
Frac. Inten.(% of TIC)	0.00	0.11	0.10	0.09	4.24	2.16	2.63	6.10	2.19	6.38	8.06	3.29	2.69	2.53	4.96	17.92	3.11	2.58	5.76	2.35	2.10	4.93	2.55	10.30	2.88
Rel. Inten.(% of BP)	0.01	0.59	0.53	0.49	23.66	12.03	14.70	34.04	12.21	35.60	45.00	18.37	15.01	14.09	27.67	100.00	17.33	14.40	32.17	13.13	11.73	27.53	14.21	57.50	16.07
Score	0.20	0.50	1.00	1.00	0.50	-0.12	-0.15	1.50	-0.12	-0.36	0.25	0.50	-0.15	-0.14	0.25	1.50	-0.17	-0.14	1.50	0.25	-0.12	-0.28	1.50	1.50	1.50
Ion-type	PR	V	E	F	a_1			y_2			b_3-H_2O	b_3			b_4-H_2O	y_5			y_6	b_6-H_2O			y_7	y_8	y_9
Delta ppm	-16.1	-19.1	-29.9	-6.5	-39.1			9.8			1.2	-5.4			-14.7	-1.5			10.8	-11.0			-19.4	1.4	-13.9

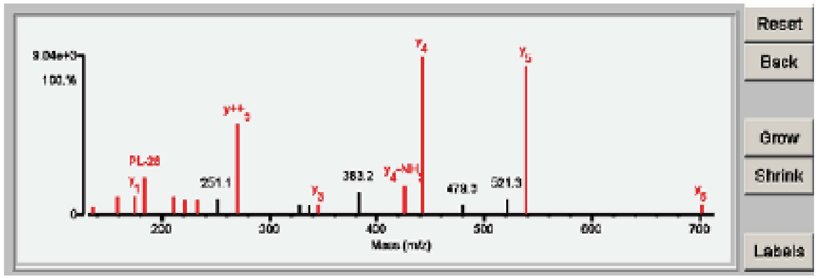


I35

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.89	82.2	6	10/25	(S) D/T/P/P/L/G/R (F)	805.4188	0.0048	5.3	60141.1/9.10	HUMAN	P68104	163988	Elongation factor 1-alpha 1 - Homo sapiens (Human)
1	14.89	82.2	6	10/25	(S) D/T/P/P/L/G/R (F)	805.4188	0.0048	5.3	60186.3/9.16	HUMAN	Q5VTE0	164036	Elongation factor 1-alpha-like 3 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	86.095	98.094	100.048	118.050	126.056	136.074	168.092	176.118	183.148	211.141	221.642	232.138	251.070	270.168	328.204^{+2}	338.232	346.232	383.231	426.253	442.278	479.291	521.316	539.329	702.389
Frac. Inten.(% of TIC)	0.02	0.04	1.86	1.20	1.41	1.41	1.14	2.47	2.61	5.45	2.38	1.96	2.02	2.32	12.93	1.42	1.19	1.49	3.28	4.21	22.78	1.48	2.25	21.30	1.37
Rel. Inten.(% of BP)	0.10	0.17	8.16	5.25	6.21	6.21	5.01	10.82	11.44	23.93	10.44	8.60	8.89	10.18	56.76	6.23	5.24	6.55	14.41	18.49	100.00	6.49	9.89	93.49	6.01
Score	0.20	0.22	-0.08	-0.05	-0.06	-0.06	1.00	0.50	1.50	0.50	0.75	1.50	1.50	-0.10	1.50	-0.06	-0.05	1.50	-0.14	0.50	1.50	-0.06	-0.10	1.50	1.50
Ion-type	PR	LI					Y	y_1-NH$_3$	y_1	PL-28	PL	y++4	y_2		y++5			y_3		y_4-NH$_3$	y_4			y_5	y_6
Delta ppm	3.9	-13.1					-14.6	-3.8	-4.9	-14.1	-20.8	-1.6	-20.3		-2.0			22.9		5.0	1.7			-2.2	-6.2

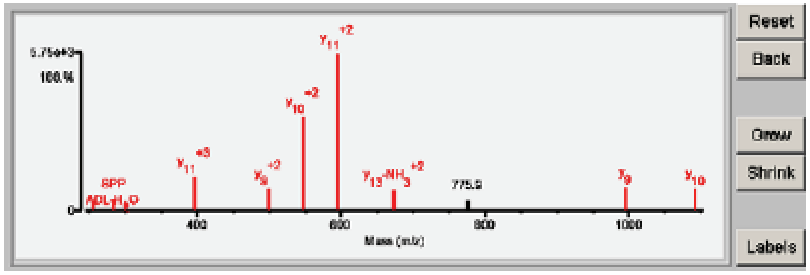


I36

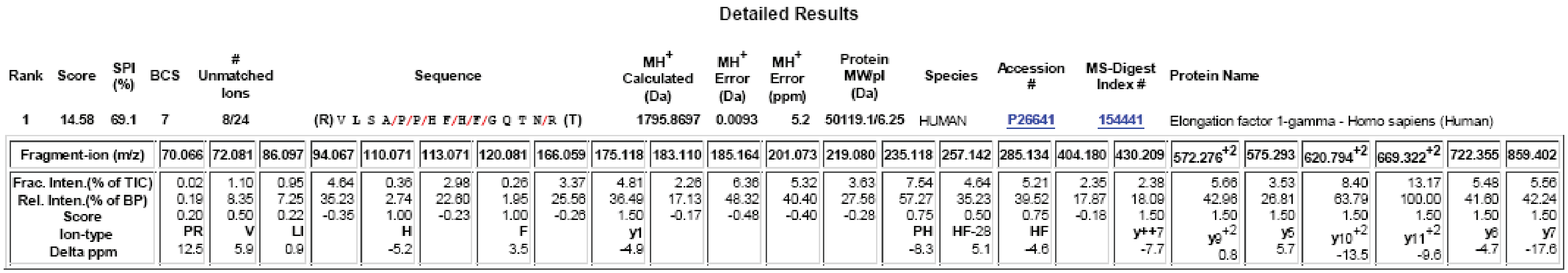
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.81	75.8	5	10/25	(F) E A V S S/P/P/P A D L/C H A L/R (W)	1750.8251	0.0030	1.7	24763.8/4.50	HUMAN	P24534	164311	Elongation factor 1-beta - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	72.081	84.043	86.096	94.066	126.064	136.076	143.080	173.085	175.120	183.074	199.106	201.088	227.077	254.142	282.147	300.161	387.207^{+3}	498.260^{+2}	548.782^{+2}	696.311^{+2}	673.813^{+2}	775.861^{+2}	896.503	1092.561
Frac. Inten.(% of TIC)	0.00	0.34	0.07	0.24	1.97	2.59	1.85	1.57	1.89	1.71	3.84	1.60	5.05	2.12	1.78	2.00	1.64	6.23	4.11	17.05	28.35	3.81	1.87	4.35	3.93
Rel. Inten.(% of BP)	0.02	1.21	0.26	0.84	6.97	9.15	6.51	5.55	6.68	6.04	13.54	5.66	17.80	7.46	6.29	7.05	5.79	21.97	14.51	60.14	100.00	13.45	6.60	15.33	13.87
Score	0.20	0.50	1.00	0.22	-0.07	-0.09	-0.07	-0.06	-0.07	1.50	-0.14	-0.05	-0.18	-0.07	0.50	0.75	1.50	1.50	1.50	1.50	1.50	0.50	-0.07	1.50	1.50
Ion-type	PR	V	E	LI						y_1					SPP-28	SPP	y++5	y_{11}^{+3}	y_9^{+2}	y_{10}^{+2}	y_{11}^{+2}	y_{13}-NH$_3^{+2}$		y_9	y_{10}
Delta ppm	-0.4	8.7	-16.5	-9.6						3.7					-35.9	3.1 ADL-H$_2$O 3.1	10.2 ADL 14.3	-6.6	-17.5	-4.3	-0.8	-25.4		-6.0	-10.4



I37



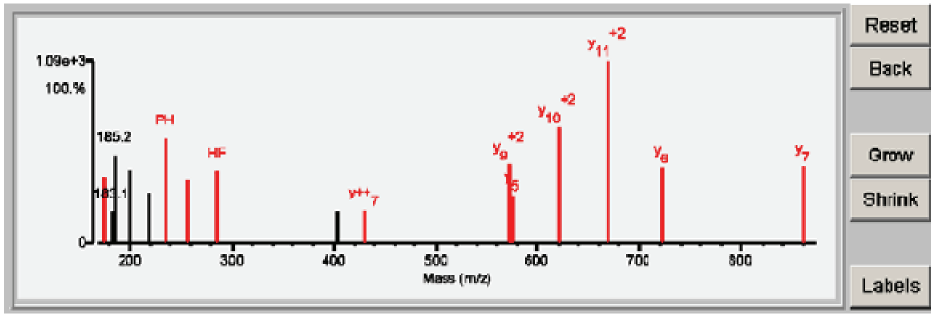
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.58	69.1	7	8/24	(R) V L S A/P/P/H F/H/F/G Q T N/R (T)	1795.8697	0.0093	5.2	50119.1/6.25	HUMAN	P26641	154441	Elongation factor 1-gamma - Homo sapiens (Human)

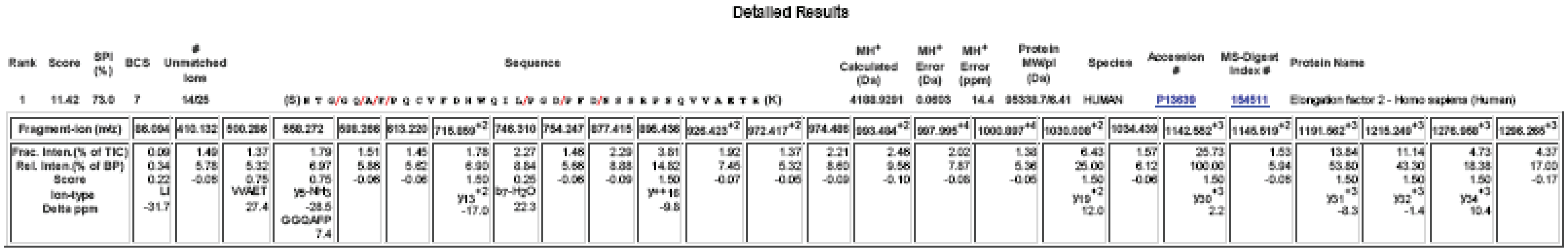
Fragment-ion (m/z)	70.066	72.081	86.097	94.067	110.071	113.071	120.081	166.059
Frac. Inten.(% of TIC)	0.02	1.10	0.95	4.64	0.36	2.98	0.26	3.37
Rel. Inten.(% of BP)	0.19	8.35	7.25	35.23	2.74	22.60	1.95	25.56
Score	0.20	0.50	0.22	-0.35	1.00	-0.23	1.00	-0.26
Ion-type	PR	V	LI		H		F	
Delta ppm	12.5	5.9	0.9		-5.2		3.5	

Fragment-ion (m/z)	175.118	183.110	185.164	201.073	219.080	235.118	257.142	285.134
Frac. Inten.(% of TIC)	4.81	2.26	6.36	5.32	3.63	7.54	4.64	5.21
Rel. Inten.(% of BP)	36.49	17.13	48.32	40.40	27.56	57.27	35.23	39.52
Score	1.50	-0.17	-0.48	-0.40	-0.28	0.75	0.50	0.75
Ion-type	y1					PH	HF-28	HF
Delta ppm	-4.9					-8.3	5.1	-4.6

Fragment-ion (m/z)	404.180	430.209	572.276^{+2}	575.293	620.794^{+2}	669.322^{+2}	722.355	859.402
Frac. Inten.(% of TIC)	2.35	2.38	5.66	3.53	8.40	13.17	5.48	5.56
Rel. Inten.(% of BP)	17.87	18.09	42.96	26.81	63.79	100.00	41.60	42.24
Score	-0.18	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type		y++7	$y9^{+2}$	y5	$y10^{+2}$	$y11^{+2}$	y6	y7
Delta ppm		-7.7	0.8	5.7	-13.5	-9.6	-4.7	-17.6



I38



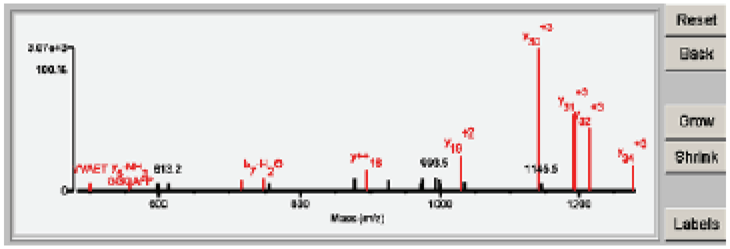
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.42	73.0	7	14/25	(S) N T G/G Q/A/F/P Q C V F D H W Q I L/P G D/P F D/N S S R P S Q V V A E T R (K)	4108.9281	0.0603	14.4	95338.7/6.41	HUMAN	P13639	154511	Elongation factor 2 - Homo sapiens (Human)

Fragment-ion (m/z)	86.094	410.132	500.286	558.272	598.286	613.220	715.859^{+2}	746.310	754.247
Frac. Inten.(% of TIC)	0.09	1.49	1.37	1.79	1.51	1.45	1.78	2.27	1.46
Rel. Inten.(% of BP)	0.34	5.78	5.32	6.97	5.88	5.62	6.90	8.84	5.66
Score	0.22	-0.05	0.75	0.75	-0.06	-0.06	1.50	0.25	-0.06
Ion-type	LI		VVAET	$y5\text{-}NH_3$ GGQAFP			$y13^{+2}$	$b7\text{-}H_2O$	
Delta ppm	-31.7		27.4	-28.5 7.4			-17.0	22.3	

Fragment-ion (m/z)	877.415	896.436	926.423^{+2}	972.417^{+2}	974.486	993.484^{+2}	997.995^{+4}	1000.997^{+4}
Frac. Inten.(% of TIC)	2.29	3.81	1.92	1.37	2.21	2.46	2.02	1.38
Rel. Inten.(% of BP)	8.88	14.82	7.46	5.32	8.60	9.56	7.87	5.36
Score	-0.09	1.50	-0.07	-0.06	-0.09	-0.10	-0.08	-0.05
Ion-type		y++16						
Delta ppm		-9.8						

Fragment-ion (m/z)	1030.008^{+2}	1034.439	1142.582^{+3}	1146.619^{+2}	1191.662^{+3}	1215.249^{+3}	1276.868^{+3}	1296.265^{+3}
Frac. Inten.(% of TIC)	6.43	1.57	25.73	1.53	13.84	11.14	4.73	4.37
Rel. Inten.(% of BP)	25.00	6.12	100.00	5.94	53.80	43.30	18.38	17.00
Score	1.50	-0.06	1.50	-0.05	1.50	1.50	1.50	-0.17
Ion-type	$y19^{+2}$		$y30^{+3}$		$y31^{+3}$	$y32^{+3}$	$y34^{+3}$	
Delta ppm	12.0		2.2		-8.3	-1.4	10.4	



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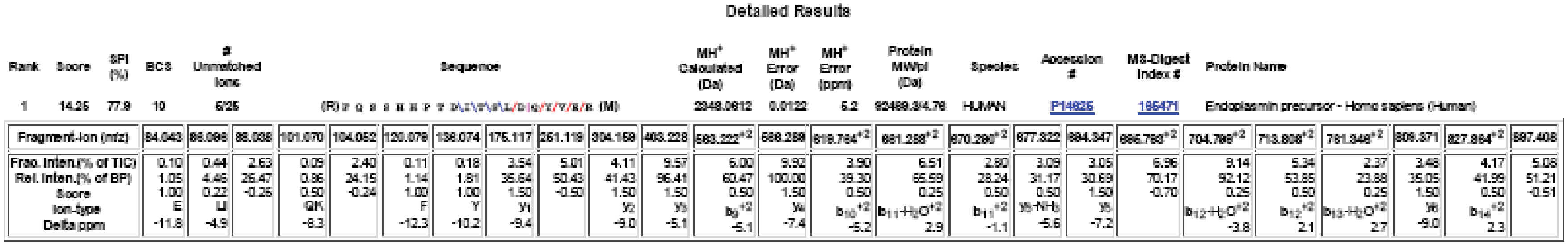
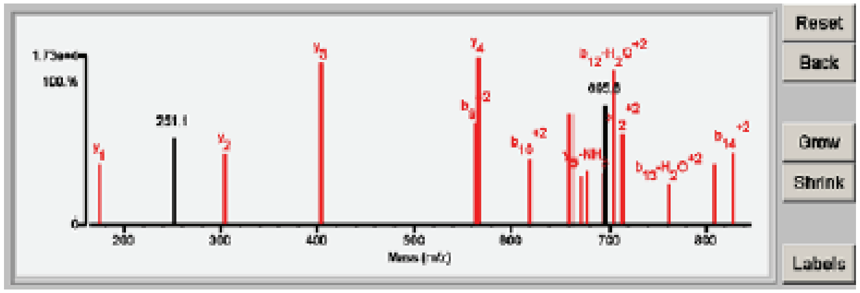


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.25	77.9	10	6/25	(R) F Q S S H H P T D\I\T\S\L/D|Q/Y/V/E/R (M)	2348.0812	0.0122	6.2	92469.3/4.76	HUMAN	P14625	185471	Endoplasmin precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	84.043	86.096	88.038	101.070	104.052	120.079	136.074	175.117	261.119	304.159	403.228	583.222^{+2}	688.289
Frac. Inten.(% of TIC)	0.10	0.44	2.63	0.09	2.40	0.11	0.18	3.54	5.01	4.11	9.57	6.00	9.92
Rel. Inten.(% of BP)	1.05	4.46	26.47	0.86	24.15	1.14	1.81	35.64	50.43	41.43	96.41	60.47	100.00
Score	1.00	0.22	-0.26	0.50	-0.24	1.00	1.00	1.50	-0.50	1.50	1.50	0.50	1.50
Ion-type	E	LI		QK		F	Y	y_1		y_2	y_3	b_9^{+2}	y_4
Delta ppm	-11.8	-4.9		-8.3		-12.3	-10.2	-9.4		-9.0	-5.1	-5.1	-7.4

Fragment-Ion (m/z)	618.764^{+2}	661.288^{+2}	670.290^{+2}	677.322	694.347	696.763^{+2}	704.789^{+2}	713.808^{+2}	761.348^{+2}	809.371	827.884^{+2}	897.408
Frac. Inten.(% of TIC)	3.90	6.51	2.80	3.09	3.05	6.96	9.14	5.34	2.37	3.48	4.17	5.08
Rel. Inten.(% of BP)	39.30	65.59	28.24	31.17	30.69	70.17	92.12	53.85	23.88	35.05	41.99	51.21
Score	0.50	0.25	0.50	0.50	1.50	-0.70	0.25	0.50	0.25	1.50	0.50	-0.51
Ion-type	b_{10}^{+2}	b_{11}-H_2O^{+2}	b_{11}^{+2}	y_5-NH_3	y_5		b_{12}-H_2O^{+2}	b_{12}^{+2}	b_{13}-H_2O^{+2}	y_6	b_{14}^{+2}	
Delta ppm	-5.2	2.9	-1.1	-5.6	-7.2		-3.8	2.1	2.7	-9.0	2.3	



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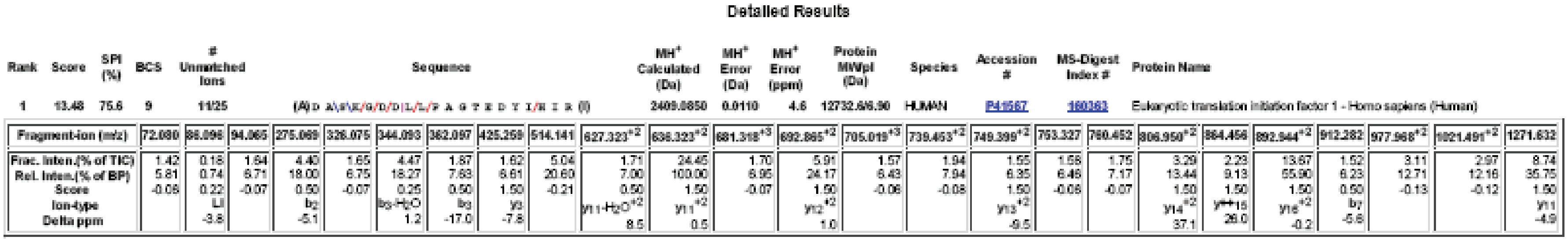
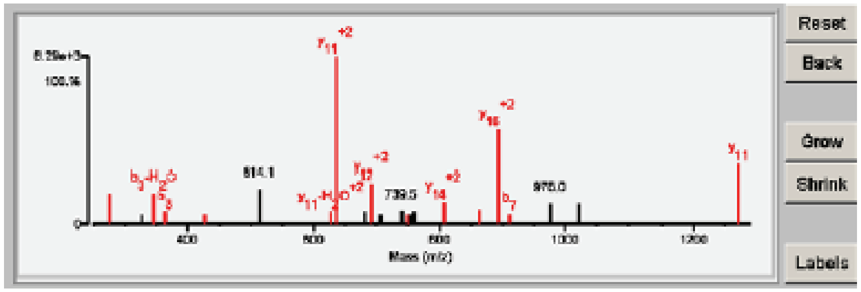


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.48	75.6	9	11/25	(A) D A\S\K/G/D/D|L/L/P A G T E D Y I/H I R (I)	2409.0850	0.0110	4.6	12732.6/6.90	HUMAN	P41567	160363	Eukaryotic translation initiation factor 1 - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	86.096	94.065	275.089	326.075	344.093	362.097	425.259	514.141	627.323^{+2}	636.323^{+2}	681.318^{+3}	692.865^{+2}
Frac. Inten.(% of TIC)	1.42	0.18	1.64	4.40	1.65	4.47	1.87	1.62	5.04	1.71	24.45	1.70	5.91
Rel. Inten.(% of BP)	5.81	0.74	6.71	18.00	6.75	18.27	7.63	6.61	20.60	7.00	100.00	6.95	24.17
Score	-0.08	0.22	-0.07	0.50	-0.07	0.25	0.50	1.50	-0.21	0.50	1.50	-0.07	1.50
Ion-type		LI		b_2		b_3-H_2O	b_3	y_3		y_{11}-H_2O^{+2}	y_{11}^{+2}		y_{12}^{+2}
Delta ppm		-3.8		-5.1		1.2	-17.0	-7.8		8.5	0.5		1.0

Fragment-Ion (m/z)	705.019^{+3}	739.453^{+2}	749.399^{+2}	753.327	760.452	806.950^{+2}	864.456	892.944^{+2}	912.282	977.968^{+2}	1021.491^{+2}	1271.632
Frac. Inten.(% of TIC)	1.57	1.94	1.55	1.58	1.75	3.29	2.23	13.67	1.52	3.11	2.97	8.74
Rel. Inten.(% of BP)	6.43	7.94	6.35	6.46	7.17	13.44	9.13	55.90	6.23	12.71	12.16	35.75
Score	-0.06	-0.08	1.50	-0.08	-0.07	1.50	1.50	1.50	0.50	-0.13	-0.12	1.50
Ion-type			y_{13}^{+2}			y_{14}^{+2}	y^{++}_{15}	y_{16}^{+2}	b_7			y_{11}
Delta ppm			-9.5			37.1	26.0	-0.2	-5.6			-4.9



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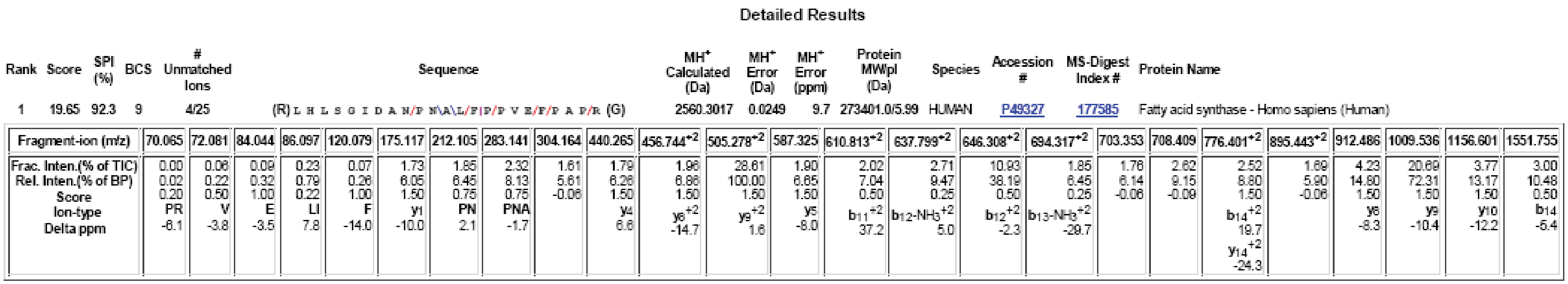
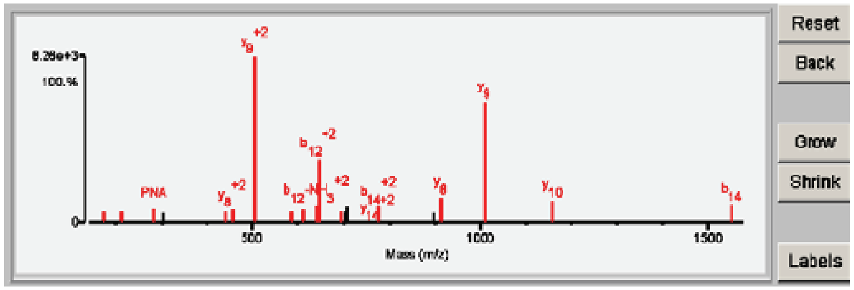


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.65	92.3	9	4/25	(R) L H L S G I D A N/P N\A\L/F|F/P V E/F/P A P/R (G)	2560.3017	0.0249	9.7	273401.0/5.99	HUMAN	P49327	177585	Fatty acid synthase - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	84.044	86.097	120.079	175.117	212.105	283.141	304.164	440.265	456.744^{+2}	505.278^{+2}	587.325
Frac. Inten.(% of TIC)	0.00	0.06	0.09	0.23	0.07	1.73	1.85	2.32	1.61	1.79	1.96	28.61	1.90
Rel. Inten.(% of BP)	0.02	0.22	0.32	0.79	0.26	6.05	6.45	8.13	5.61	6.26	6.86	100.00	6.65
Score	0.20	0.50	1.00	0.22	1.00	1.50	0.75	0.75	-0.06	1.50	1.50	1.50	1.50
Ion-type	PR	V	E	LI	F	y_1	PN	PNA		y_4	y_6^{+2}	y_9^{+2}	y_5
Delta ppm	-6.1	-3.8	-3.5	7.8	-14.0	-10.0	2.1	-1.7		6.6	-14.7	1.6	-8.0

Fragment-ion (m/z)	610.813^{+2}	637.799^{+2}	646.308^{+2}	694.317^{+2}	703.353	708.409	776.401^{+2}	895.443^{+2}	912.486	1009.536	1156.601	1551.755
Frac. Inten.(% of TIC)	2.02	2.71	10.93	1.85	1.76	2.62	2.52	1.69	4.23	20.69	3.77	3.00
Rel. Inten.(% of BP)	7.04	9.47	38.19	6.45	6.14	9.15	8.80	5.90	14.80	72.31	13.17	10.48
Score	0.50	0.25	0.50	0.25	-0.06	-0.09	1.50	-0.06	1.50	1.50	1.50	0.50
Ion-type	b_{11}^{+2}	$b_{12}\text{-NH}_3^{+2}$	b_{12}^{+2}	$b_{13}\text{-NH}_3^{+2}$			b_{14}^{+2} y_{14}^{+2}		y_8	y_9	y_{10}	b_{14}
Delta ppm	37.2	5.0	-2.3	-29.7			19.7 -24.3		-8.3	-10.4	-12.2	-5.4



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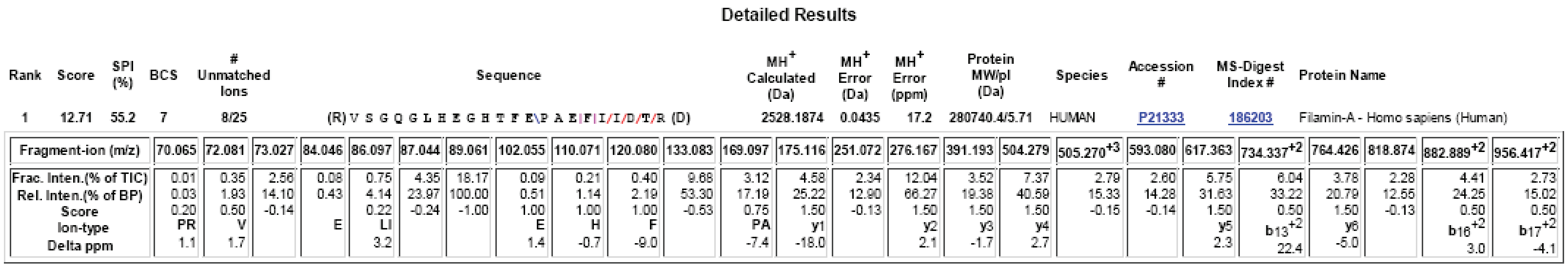
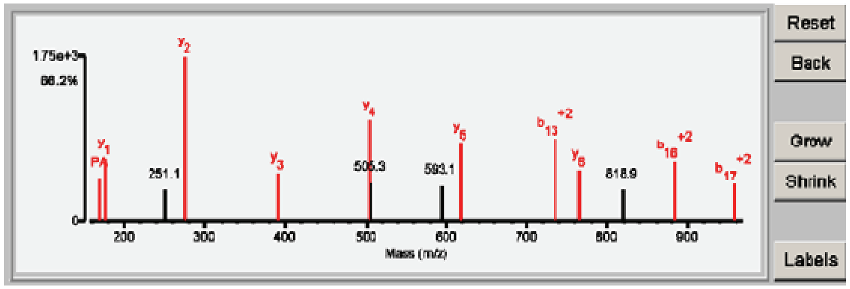


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.71	55.2	7	8/25	(R) V S G Q G L H E G H T F E\P A E|F|I/I/D/T/R (D)	2528.1874	0.0435	17.2	280740.4/5.71	HUMAN	P21333	186203	Filamin-A - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	73.027	84.046	86.097	87.044	89.061	102.055	110.071	120.080	133.083	169.097	175.116
Frac. Inten.(% of TIC)	0.01	0.35	2.56	0.08	0.75	4.35	18.17	0.09	0.21	0.40	9.68	3.12	4.58
Rel. Inten.(% of BP)	0.03	1.93	14.10	0.43	4.14	23.97	100.00	0.51	1.14	2.19	53.30	17.19	25.22
Score	0.20	0.50	-0.14		0.22	-0.24	-1.00	1.00	1.00	1.00	-0.53	0.75	1.50
Ion-type	PR	V		E	LI			E	H	F		PA	y_1
Delta ppm	1.1	1.7			3.2			1.4	-0.7	-9.0		-7.4	-18.0

Fragment-ion (m/z)	251.072	276.167	391.193	504.279	505.270^{+3}	593.080	617.363	734.337^{+2}	764.426	818.874	882.889^{+2}	956.417^{+2}
Frac. Inten.(% of TIC)	2.34	12.04	3.52	7.37	2.79	2.60	5.75	6.04	3.78	2.28	4.41	2.73
Rel. Inten.(% of BP)	12.90	66.27	19.38	40.59	15.33	14.28	31.63	33.22	20.79	12.55	24.25	15.02
Score	-0.13	1.50	1.50	1.50	-0.15	-0.14	1.50	0.50	1.50	-0.13	0.50	0.50
Ion-type		y_2	y_3	y_4			y_5	b_{13}^{+2}	y_6		b_{16}^{+2}	b_{17}^{+2}
Delta ppm		2.1	-1.7	2.7			2.3	22.4	-5.0		3.0	-4.1



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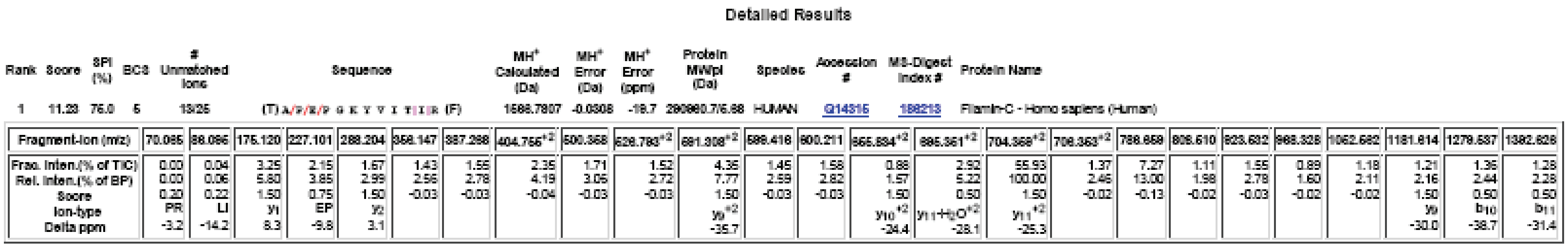
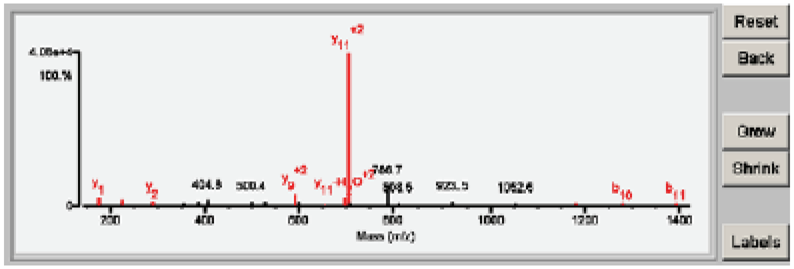


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.23	76.0	5	13/25	(T) A/P/E/P G K Y V I T|I|R (F)	1588.7807	-0.0308	-19.7	290880.7/6.88	HUMAN	Q14315	188213	Filamin-C - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	88.096	175.120	227.101	288.204	358.147	387.288	404.756^{+2}	500.368	528.783^{+2}	591.308^{+2}	599.416	600.211
Frac. Inten.(% of TIC)	0.00	0.04	3.25	2.15	1.67	1.43	1.55	2.35	1.71	1.52	4.36	1.45	1.58
Rel. Inten.(% of BP)	0.00	0.06	5.80	3.85	2.99	2.56	2.78	4.19	3.06	2.72	7.77	2.59	2.82
Score	0.20	0.22	1.50	0.75	1.50	-0.03	-0.03	-0.04	-0.03	-0.03	1.50	-0.03	-0.03
Ion-type	PR	LI	y_1	EP	y_2						y_9^{+2}		
Delta ppm	-3.2	-14.2	8.3	-9.8	3.1						-35.7		

Fragment-Ion (m/z)	665.834^{+2}	695.361^{+2}	704.368^{+2}	708.363^{+2}	788.859	808.610	923.632	968.328	1062.682	1181.814	1279.637	1382.628
Frac. Inten.(% of TIC)	0.88	2.92	55.93	1.37	7.27	1.11	1.55	0.89	1.18	1.21	1.36	1.28
Rel. Inten.(% of BP)	1.57	5.22	100.00	2.46	13.00	1.98	2.78	1.60	2.11	2.16	2.44	2.28
Score	1.50	0.50	1.50	-0.02	-0.13	-0.02	-0.03	-0.02	-0.02	1.50	0.50	0.50
Ion-type	y_{10}^{+2}	$y_{11}+H_2O^{+2}$	y_{11}^{+2}							y_9	b_{10}	b_{11}
Delta ppm	-24.4	-28.1	-25.3							-30.0	-38.7	-31.4



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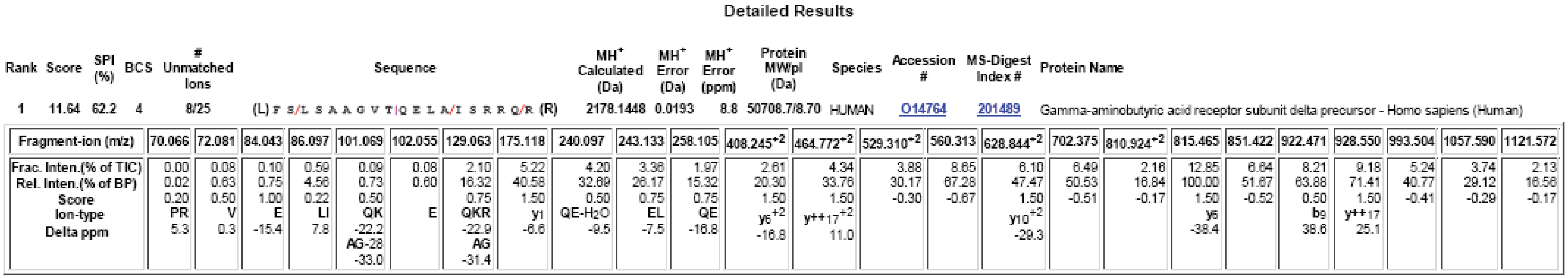
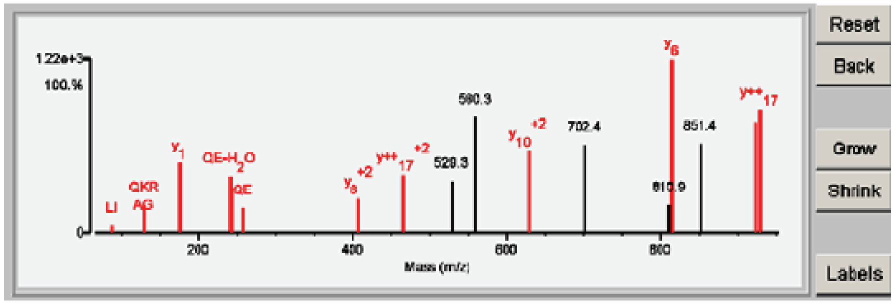


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.64	62.2	4	8/25	(L) F S/L S A A G V T|Q E L A/I S R R Q/R (R)	2178.1448	0.0193	8.8	50708.7/8.70	HUMAN	O14764	201489	Gamma-aminobutyric acid receptor subunit delta precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.043	86.097	101.069	102.055	129.063	175.118	240.097	243.133	258.105	408.245^{+2}	464.772^{+2}
Frac. Inten.(% of TIC)	0.00	0.08	0.10	0.59	0.09	0.08	2.10	5.22	4.20	3.36	1.97	2.61	4.34
Rel. Inten.(% of BP)	0.02	0.63	0.75	4.56	0.73	0.60	16.32	40.58	32.69	26.17	15.32	20.30	33.76
Score	0.20	0.50	1.00	0.22	0.50		0.75	1.50	0.50	0.75	0.75	1.50	1.50
Ion-type	PR	V	E	LI	QK	E	QKR	y_1	QE-H_2O	EL	QE	y_6^{+2}	$y{+}{+}_{17}^{+2}$
Delta ppm	5.3	0.3	-15.4	7.8	-22.2 AG-28 -33.0		-22.9 AG -31.4	-6.6	-9.5	-7.5	-16.8	-16.8	11.0

Fragment-ion (m/z)	529.310^{+2}	560.313	628.844^{+2}	702.375	810.924^{+2}	815.465	851.422	922.471	928.550	993.504	1057.590	1121.572
Frac. Inten.(% of TIC)	3.88	8.65	6.10	6.49	2.16	12.85	6.64	8.21	9.18	5.24	3.74	2.13
Rel. Inten.(% of BP)	30.17	67.28	47.47	50.53	16.84	100.00	51.67	63.88	71.41	40.77	29.12	16.56
Score	-0.30	-0.67	1.50	-0.51	-0.17	1.50	-0.52	0.50	1.50	-0.41	-0.29	-0.17
Ion-type			y_{10}^{+2}			y_6		b_9	$y{+}{+}_{17}$			
Delta ppm			-29.3			-38.4		38.6	25.1			



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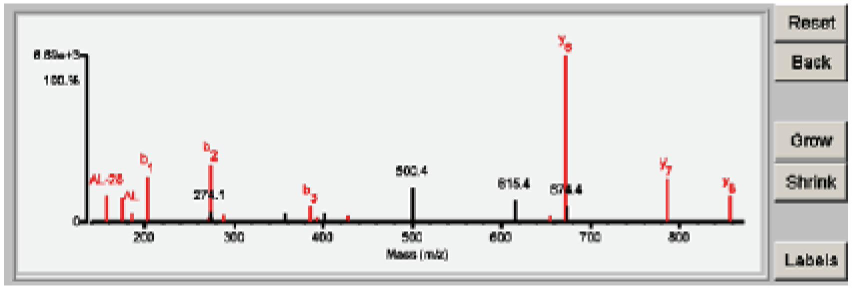
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.49	78.3	5	9/25	(L) L|A|L|L E A A/L/R (S)	1067.6074	0.0031	2.9	60509.7/5.88	HUMAN	Q6P531	208541	Gamma-glutamyltransferase 6 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	86.097	87.100	89.084	157.134	174.093	176.116	185.131	202.089	272.121	273.124	274.128	275.123	288.206
Frac. Inten.(% of TIC)	0.47	1.84	1.00	4.58	4.16	2.55	1.45	7.94	0.91	9.82	1.85	0.84	1.38
Rel. Inten.(% of BP)	1.67	6.50	3.54	16.22	14.73	9.02	5.15	28.08	3.22	34.76	6.54	2.99	4.89
Score	0.22	-0.06	-0.04	0.50	0.50	1.50	0.75	0.50	0.75	0.50	-0.07	-0.03	1.50
Ion-type	LI			AL-28	a_1	y_1	AL	b_1	EAA	b_2			y_2
Delta ppm	2.0			-7.2	-14.4	-20.3	8.4	-7.5	-15.4	-15.1			9.7

Fragment-ion (m/z)	367.179	386.207	393.245^{+2}	401.291	428.764^{+2}	600.364	616.379	654.394	672.400	674.406	785.483	856.518
Frac. Inten.(% of TIC)	1.48	2.71	0.93	1.52	1.09	5.81	3.69	1.18	28.26	2.70	7.31	4.51
Rel. Inten.(% of BP)	5.24	9.59	3.28	5.38	3.86	20.56	13.07	4.17	100.00	9.56	25.87	15.94
Score	-0.05	0.50	1.50	-0.05	1.50	-0.21	-0.13	0.50	1.50	-0.10	1.50	1.50
Ion-type		b_3	y_7^{+2}		y_8^{+2}			y_6-H_2O	y_6		y_7	y_8
Delta ppm		-11.9	-5.9		-4.2			0.3	-5.4		-6.3	-8.7



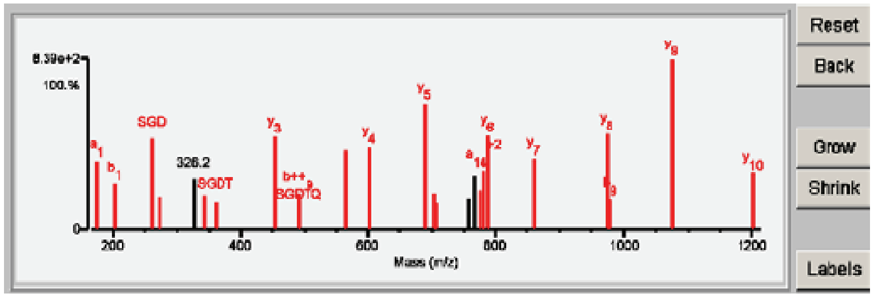
I46

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.71	91.5	10	3/25	(L) L\S G D T|Q/T/D/A|T/S/F/Y D/R (V)	1764.7381	0.0092	5.2	59425.8/4.33	HUMAN	P14314	216087	Glucosidase 2 subunit beta precursor - Homo sapiens (Human)

Fragment-ion (m/z)	174.094	175.120	202.092	260.089	271.109	326.189	343.119	361.136	453.211	489.191	562.214	600.273	687.309
Frac. Inten.(% of TIC)	4.36	3.84	2.86	5.72	2.09	3.19	2.12	1.75	5.80	2.21	5.02	5.16	7.92
Rel. Inten.(% of BP)	40.67	35.76	26.68	53.29	19.44	29.72	19.80	16.34	54.09	20.62	46.80	48.07	73.77
Score	0.50	1.50	0.50	0.75	0.25	-0.30	0.50	0.75	1.50	0.75	0.50	1.50	1.50
Ion-type	a_1	y_1	b_1	SGD	b_2-H_2O		SGDT-H_2O	SGDT	y_3	$b{++}_9$ SGDTQ	b_5	y_4	y_5
Delta ppm	-11.0	6.0	6.8	-1.2	-10.3		-19.0	-1.9	4.4	-14.9 -8.5	-8.1	-7.4	-1.3

Fragment-ion (m/z)	701.786^{+2}	705.259	756.284^{+2}	764.324^{+2}	773.312	781.796^{+2}	788.342	859.398	974.410	977.397	1075.464	1203.519
Frac. Inten.(% of TIC)	2.24	1.68	2.01	3.33	2.47	3.69	5.91	4.43	6.05	1.92	10.73	3.49
Rel. Inten.(% of BP)	20.92	15.68	18.73	30.99	23.01	34.38	55.08	41.25	56.42	17.89	100.00	32.50
Score	0.50	0.75	-0.19	-0.31	0.25	0.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	y_{12}-NH_3^{+2}	SGDTQTD			b_7-H_2O	a_{14}^{+2}	y_6	y_7	y_8	b_9	y_9	y_{10}
Delta ppm	-7.7	-15.3			-3.3	-30.3	-19.2	4.6	-11.3	7.8	-4.4	-6.9



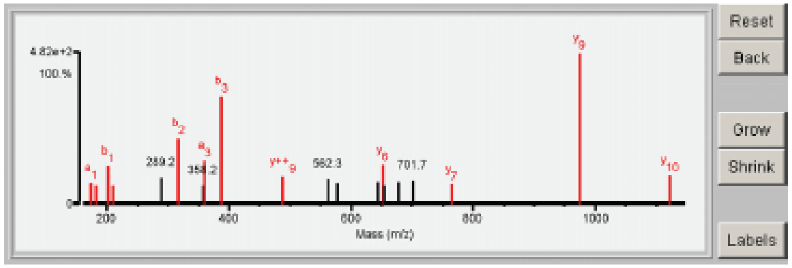
I47

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.66	68.3	6	11/25	(C) L\D\A|F/P L/L/S A Y V G R (L)	1509.7770	-0.0011	-0.7	23356.0/5.43	HUMAN	P09211	227826	Glutathione S-transferase P - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	86.076	88.093	102.084	136.073	174.089	183.149	202.087	211.146	289.168	317.114	358.182	360.168
Frac. Inten.(% of TIC)	0.00	2.22	5.35	2.93	0.06	2.46	2.22	4.52	2.25	3.18	7.74	2.24	5.10
Rel. Inten.(% of BP)	0.02	12.48	30.11	16.51	0.36	13.87	12.50	25.46	12.69	17.88	43.56	12.60	28.68
Score	0.20	-0.12	-0.30	-0.17	1.00	0.50	0.50	0.50	0.75	-0.18	0.50	-0.13	0.50
Ion-type	PR				Y	a_1	PL-28	b_1	PL		b_2		a_3
Delta ppm	-3.2				-19.0	-36.8	-9.8	-20.4	5.2		-11.2		-6.3

Fragment-ion (m/z)	388.160	488.280	562.327	578.336	643.298	652.342	653.334+2	677.314	701.723	765.402	975.558	1122.642
Frac. Inten.(% of TIC)	12.52	3.21	2.99	2.44	2.61	4.63	2.26	2.66	2.87	2.39	17.77	3.37
Rel. Inten.(% of BP)	70.43	18.06	16.84	13.73	14.68	26.04	12.71	14.99	16.13	13.43	100.00	18.96
Score	0.50	1.50	-0.17	-0.14	-0.15	1.50	-0.13	-0.15	-0.16	1.50	1.50	1.50
Ion-type	b_3	y^{++}_9				y_6				y_7	y_9	y_{10}
Delta ppm	-12.1	-9.1				0.3				-30.5	-6.0	10.0



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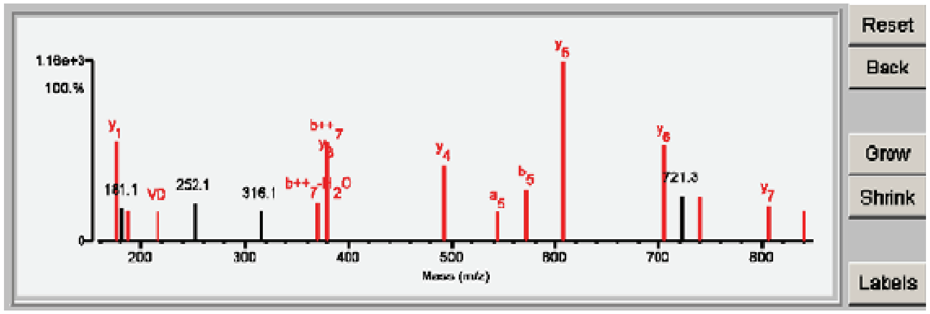
Detailed Results

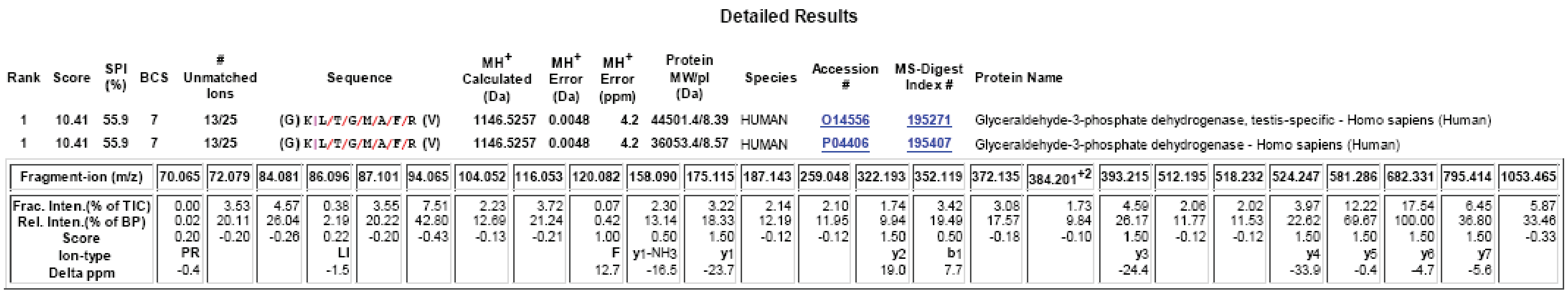
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.45	73.4	7	8/24	(R) V P T A N\V S|V/V/D/L/T C/R (L)	1561.7713	0.0170	10.9	36053.4/8.57	HUMAN	P04406	195407	Glyceraldehyde-3-phosphate dehydrogenase - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.095	94.067	110.070	120.082	136.075	175.120	181.095	187.111	215.100	252.134
Frac. Inten.(% of TIC)	0.01	0.89	0.60	3.17	5.27	2.84	2.73	8.56	2.82	2.57	2.46	3.26
Rel. Inten.(% of BP)	0.04	5.78	3.90	20.51	34.08	18.40	17.66	55.36	18.27	16.60	15.92	21.07
Score	0.20	0.50	0.22	-0.21	-0.34	-0.18	-0.18	1.50	-0.18	0.75	0.75	-0.21
Ion-type	PR	V	LI					y1		SV VD-28	VD	
Delta ppm	-1.8	-1.0	-11.9					4.3		10.6 10.6	-18.3	

Fragment-ion (m/z)	316.141	370.174	379.181	492.259	543.277	571.258	607.292	706.362	721.337	739.341	805.434	839.415
Frac. Inten.(% of TIC)	2.56	3.43	8.44	6.60	2.45	4.37	15.46	8.13	3.90	3.82	3.08	2.58
Rel. Inten.(% of BP)	16.57	22.19	54.62	42.70	15.86	28.25	100.00	52.56	25.22	24.72	19.91	16.70
Score	-0.17	0.25	1.50	1.50	0.50	0.50	1.50	1.50	-0.25	0.25	1.50	0.25
Ion-type		b^{++}_7-H_2O	b^{++}_7 y_3	y_4	a_5	b_5	y_5	y_6		b_7-H_2O	y_7	b_8-NH_3
Delta ppm		-5.6	-2.5 12.9	-1.6	29.4	3.8	8.7	9.3		-6.1	13.5	21.0



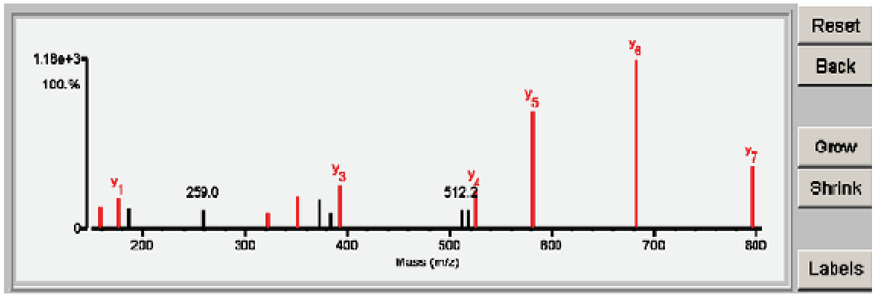
I49



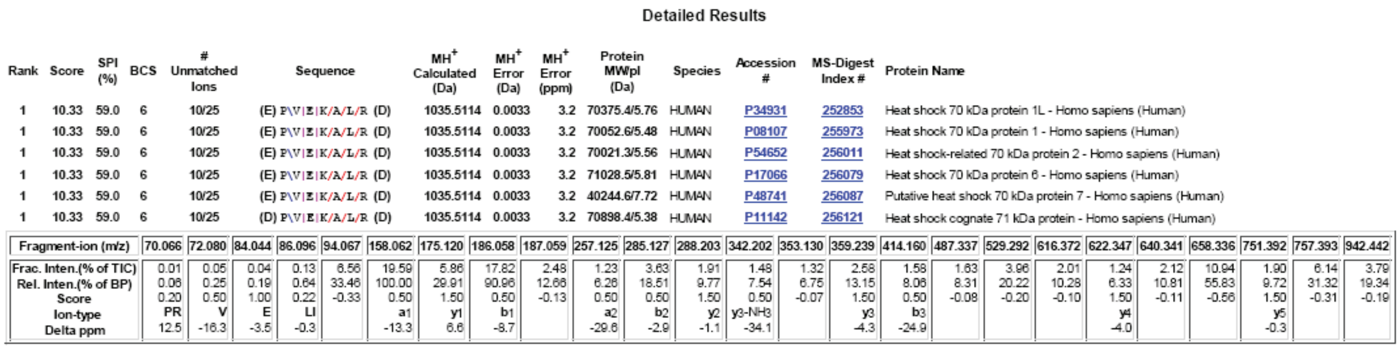
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.41	55.9	7	13/25	(G) K|L/T/G/M/A/F/R (V)	1146.5257	0.0048	4.2	44501.4/8.39	HUMAN	O14556	195271	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific - Homo sapiens (Human)
1	10.41	55.9	7	13/25	(G) K|L/T/G/M/A/F/R (V)	1146.5257	0.0048	4.2	36053.4/8.57	HUMAN	P04406	195407	Glyceraldehyde-3-phosphate dehydrogenase - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.079	84.081	86.096	87.101	94.065	104.052	116.053	120.082	158.090	175.115	187.143	259.048	322.193	352.119	372.135	384.201^{+2}	393.215	512.195	518.232	524.247	581.286	682.331	795.414	1053.465
Frac. Inten.(% of TIC)	0.00	3.53	4.57	0.38	3.55	7.51	2.23	3.72	0.07	2.30	3.22	2.14	2.10	1.74	3.42	3.08	1.73	4.59	2.06	2.02	3.97	12.22	17.54	6.45	5.87
Rel. Inten.(% of BP)	0.02	20.11	26.04	2.19	20.22	42.80	12.69	21.24	0.42	13.14	18.33	12.19	11.95	9.94	19.49	17.57	9.84	26.17	11.77	11.53	22.62	69.67	100.00	36.80	33.46
Score	0.20	-0.20	-0.26	0.22	-0.20	-0.43	-0.13	-0.21	1.00	0.50	1.50	-0.12	-0.12	1.50	0.50	-0.18	-0.10	1.50	-0.12	-0.12	1.50	1.50	1.50	1.50	-0.33
Ion-type	PR			LI					F	$y_1\text{-}NH_3$	y_1			y_2	b_1			y_3			y_4	y_5	y_6	y_7	
Delta ppm	-0.4			-1.5					12.7	-16.5	-23.7			19.0	7.7			-24.4			-33.9	-0.4	-4.7	-5.6	



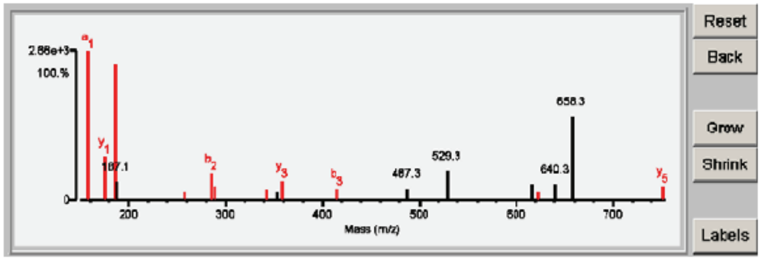
I50



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.33	59.0	6	10/25	(E) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	70375.4/5.76	HUMAN	P34931	252853	Heat shock 70 kDa protein 1L - Homo sapiens (Human)
1	10.33	59.0	6	10/25	(E) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	70052.6/5.48	HUMAN	P08107	255973	Heat shock 70 kDa protein 1 - Homo sapiens (Human)
1	10.33	59.0	6	10/25	(E) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	70021.3/5.56	HUMAN	P54652	256011	Heat shock-related 70 kDa protein 2 - Homo sapiens (Human)
1	10.33	59.0	6	10/25	(E) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	71028.5/5.81	HUMAN	P17066	256079	Heat shock 70 kDa protein 6 - Homo sapiens (Human)
1	10.33	59.0	6	10/25	(E) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	40244.6/7.72	HUMAN	P48741	256087	Putative heat shock 70 kDa protein 7 - Homo sapiens (Human)
1	10.33	59.0	6	10/25	(D) P\V|E|K/A/L/R (D)	1035.5114	0.0033	3.2	70898.4/5.38	HUMAN	P11142	256121	Heat shock cognate 71 kDa protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.080	84.044	86.096	94.067	158.062	175.120	186.058	187.059	257.125	285.127	288.203	342.202	353.130	359.239	414.160	487.337	529.292	616.372	622.347	640.341	658.336	751.392	757.393	942.442
Frac. Inten.(% of TIC)	0.01	0.05	0.04	0.13	6.56	19.59	5.86	17.82	2.48	1.23	3.63	1.91	1.48	1.32	2.58	1.58	1.63	3.96	2.01	1.24	2.12	10.94	1.90	6.14	3.79
Rel. Inten.(% of BP)	0.06	0.25	0.19	0.64	33.46	100.00	29.91	90.96	12.66	6.26	18.51	9.77	7.54	6.75	13.15	8.06	8.31	20.22	10.28	6.33	10.81	55.83	9.72	31.32	19.34
Score	0.20	0.50	1.00	0.22	-0.33	0.50	1.50	0.50	-0.13	0.50	0.50	1.50	0.50	-0.07	1.50	0.50	-0.08	-0.20	-0.10	1.50	-0.11	-0.56	1.50	-0.31	-0.19
Ion-type	PR	V	E	LI		a_1	y_1	b_1		a_2	b_2	y_2	$y_3\text{-}NH_3$		y_3	b_3				y_4			y_5		
Delta ppm	12.5	-16.3	-3.5	-0.3		-13.3	6.6	-8.7		-29.6	-2.9	-1.1	-34.1		-4.3	-24.9				-4.0			-0.3		



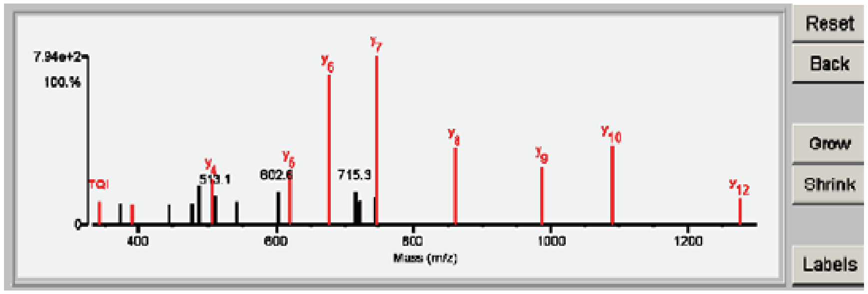
I51

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.06	62.2	10	14/25	(S) V M/D A/T/Q/I/A/G/L/N/C L/R (L)	1592.7593	0.0304	19.1	94300.5/5.18	HUMAN	P34932	256043	Heat shock 70 kDa protein 4 - Homo sapiens (Human)

Fragment-ion (m/z)	159.111	175.120	187.101	343.186	372.222	391.205	443.195^{+2}	477.214	486.209	505.255	513.094^{+2}	542.186
Frac. Inten.(% of TIC)	6.37	3.24	4.38	1.96	1.83	1.79	1.77	1.80	3.35	3.86	2.44	1.97
Rel. Inten.(% of BP)	45.38	23.05	31.18	13.95	13.05	12.76	12.57	12.85	23.83	27.48	17.41	14.02
Score	-0.45	1.50	-0.31	0.75	-0.13	1.50	-0.13	-0.13	-0.24	1.50	-0.17	-0.14
Ion-type		y_1		TQI		y_3				y_4		
Delta ppm		4.3		-38.2		-19.7				-0.8		

Fragment-ion (m/z)	602.641	618.322	675.357	715.308	715.708	720.251	721.078^{+2}	742.308	746.394	859.495	987.544	1088.593	1274.623
Frac. Inten.(% of TIC)	2.87	4.54	12.59	2.79	1.76	2.01	2.11	2.39	14.05	6.38	4.87	6.60	2.27
Rel. Inten.(% of BP)	20.45	32.34	89.62	19.84	12.52	14.31	15.05	16.99	100.00	45.45	34.70	47.02	16.16
Score	-0.20	1.50	1.50	-0.20	-0.13	-0.14	-0.15	-0.17	1.50	1.50	1.50	1.50	1.50
Ion-type		y_5	y_6						y_7	y_8	y_9	y_{10}	y_{12}
Delta ppm		-28.0	-5.7						-4.5	15.2	4.0	4.1	-23.2



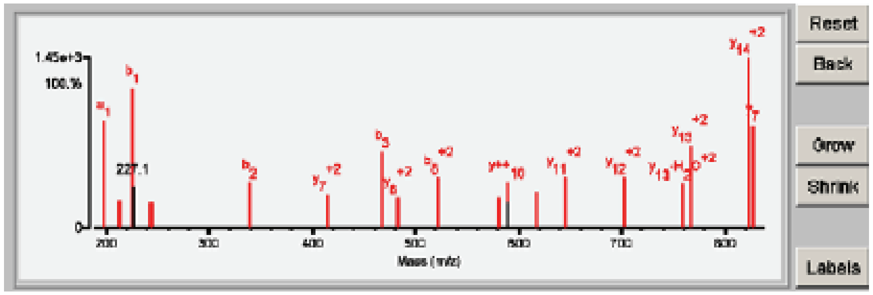
I52

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.48	90.2	8	4/25	(K) H|L|E|I|N/P D/H|P I/V E T L R (Q)	1870.9480	-0.0004	-0.2	83264.8/4.97	HUMAN	P08238	252911	Heat shock protein HSP 90-beta - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.096	110.070	120.081	183.146	198.070	213.092	226.085	227.086	243.137	339.149	414.266^{+2}	468.188
Frac. Inten.(% of TIC)	0.07	0.17	0.18	2.58	1.97	8.36	2.17	11.01	3.23	2.04	3.55	2.58	5.98
Rel. Inten.(% of BP)	0.51	1.28	1.35	19.37	14.77	62.66	16.23	82.48	24.19	15.31	26.60	19.32	44.80
Score	0.50	0.22	1.00	-0.19	-0.15	0.50	0.75	0.50	-0.24	0.75	0.50	1.50	0.50
Ion-type	V	LI	H			a_1	PD	b_1		EI	b_2	y_7^{+2}	b_3
Delta ppm	3.1	-13.1	-10.7			-5.3	20.3	-3.4		9.3	-1.9	4.3	-6.4

Fragment-ion (m/z)	482.778^{+2}	522.728^{+2}	581.276	588.821	589.320	617.361	646.848^{+2}	702.386^{+2}	767.887^{+2}	788.907^{+2}	823.466^{+2}	827.498
Frac. Inten.(% of TIC)	2.33	3.88	2.35	3.63	1.99	2.83	3.90	3.92	3.44	6.43	13.34	8.06
Rel. Inten.(% of BP)	17.46	29.10	17.65	27.21	14.88	21.24	29.23	29.35	25.75	48.21	100.00	60.43
Score	1.50	0.50	0.50	1.50	-0.15	1.50	1.50	1.50	0.50	1.50	1.50	1.50
Ion-type	y_8^{+2}	b_5^{+2}	b_4	y++10		y_5	y_{11}^{+2}	y_{12}^{+2}	$y_{13}\text{-}H_2O^{+2}$	y_{13}^{+2}	y_{14}^{+2}	y_7
Delta ppm	-9.9	-8.2	-1.0	-1.5		-16.8	-0.7	-0.6	-19.7	-0.5	7.5	-3.1

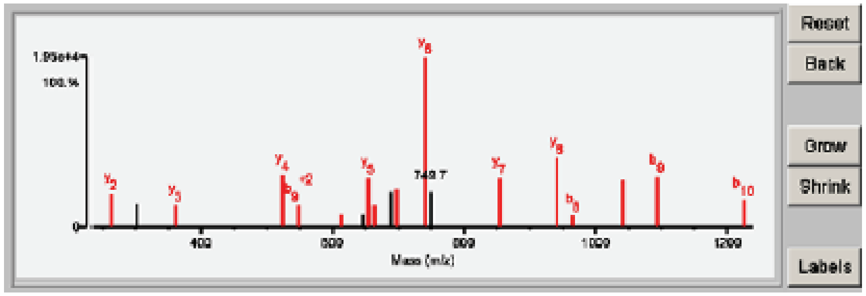


I53

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.44	78.7	10	8/24	(R) Y H T S Q S G D\E\M|T|S/L/S/E/Y/V/S R (M)	2284.9434	0.0130	6.7	83264.6/4.97	HUMAN	P08238	262911	Heat shock protein HSP 90-beta - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
74.060	1.52	7.75	-0.08		
86.097	0.18	0.90	0.22	LI	5.5
102.064	0.06	0.29	1.00	E	-13.3
104.062	6.33	32.22	-0.32		
136.076	0.05	0.25	1.00	Y	2.3
262.150	3.95	20.09	1.50	y_2	-3.0
301.130	2.73	13.88	-0.14		
361.223	2.66	13.52	1.50	y_3	9.2
524.283	6.07	30.90	1.50	y_4	1.1
547.197^{+2}	2.62	13.32	0.50	b_9^{+2}	-3.2
612.724^{+2}	1.52	7.73	0.50	b_{10}^{+2}	8.4
646.237^{+2}	1.58	8.03	-0.08		
653.323	5.77	29.37	1.50	y_5	-3.4
663.242^{+2}	2.66	13.54	0.50	b_{11}^{+2}	-0.6
688.760^{+2}	4.09	20.81	-0.21		
697.756^{+2}	4.43	22.53	0.25	$b_{12}\text{-}H_2O^{+2}$	1.4
740.357	19.65	100.00	1.50	y_6	-1.0
749.851	4.10	20.88	-0.21		
853.437	5.86	29.81	1.50	y_7	-4.7
940.471	8.08	41.10	1.50	y_8	-2.4
964.353	1.50	7.64	0.50	b_8	5.3
1041.520	5.52	28.08	1.50	y_9	-1.0
1093.382	5.90	30.02	0.50	b_9	-7.4
1224.431	3.20	16.28	0.50	b_{10}	0.5

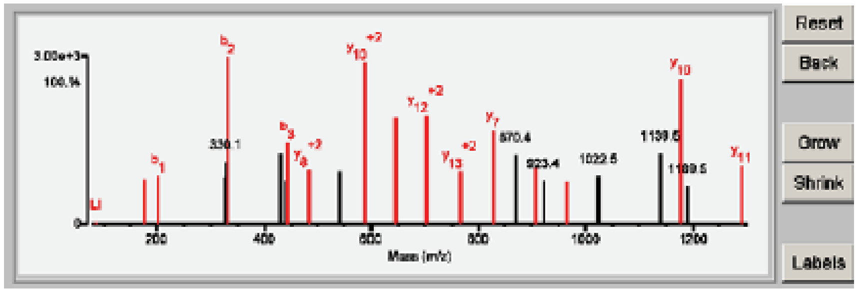


I54

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.86	69.1	7	10/26	(H) L|E|I|N/P D/H|P I V E T L/R (Q)	1733.8891	-0.0086	-4.9	83264.6/4.97	HUMAN	P08238	262911	Heat shock protein HSP 90-beta - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
86.096	0.11	1.15	0.22	LI	-9.6
175.113	2.56	26.99	1.50	y_1	-31.1
202.087	2.71	28.59	0.50	b_1	-20.9
327.164	2.63	27.74	-0.28		
330.144	3.53	37.26	-0.37		
331.131	9.48	100.00	0.50	b_2	-7.9
429.210	3.99	42.09	-0.42		
440.264	2.44	25.69	-0.26		
444.218	4.61	48.59	0.50	b_3	3.0
482.776^{+2}	3.05	32.12	1.50	y_8^{+2}	-4.9
542.286	2.97	31.33	-0.31		
588.818^{+2}	9.12	96.20	1.50	y_{10}^{+2}	-7.5
645.840^{+2}	6.06	63.88	1.50	y_{11}^{+2}	-6.0
702.376^{+2}	6.10	64.29	1.50	y_{12}^{+2}	-13.3
766.895^{+2}	2.93	30.91	1.50	y_{13}^{+2}	-29.2
827.491	5.22	55.03	1.50	y_7	-8.6
870.405	3.95	41.63	-0.42		
907.378	3.24	34.21	0.50	b_7	-23.3
923.400	2.50	26.33	-0.26		
964.544	2.39	25.25	1.50	y_8	-14.4
1022.488	2.73	28.79	-0.29		
1139.640	4.00	42.20	-0.42		
1176.638	8.19	86.40	1.50	y_{10}	0.6
1189.602	2.16	22.78	-0.23		
1290.670	3.31	34.92	1.50	y_{11}	-7.5



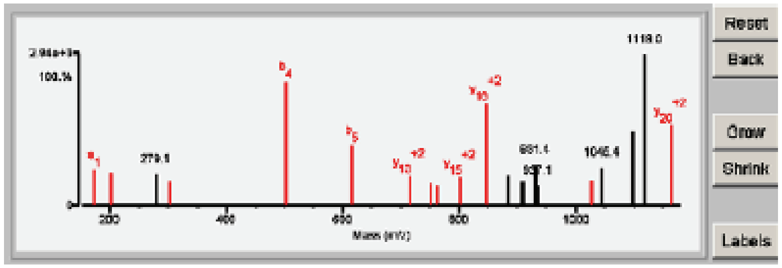
I55

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.66	56.1	9	10/25	(T) I\E D G\I|F\E/V K/S/T/A/G D T H L G G E D F D N R (M)	2945.2716	0.0209	7.1	70021.3/5.56	HUMAN	P54652	256011	Heat shock-related 70 kDa protein 2 - Homo sapiens (Human)
1	10.66	56.1	9	10/25	(T) I\E D G\I|F\E/V K/S/T/A/G D T H L G G E D F D N R (M)	2945.2716	0.0209	7.1	70898.4/5.38	HUMAN	P11142	256121	Heat shock cognate 71 kDa protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	86.095	102.055	174.094	202.088	279.134	302.104	503.181	616.259	716.808^{+2}	752.319^{+2}	763.384
Frac. Inten.(% of TIC)	0.00	0.12	0.06	3.40	3.19	3.07	2.98	11.91	5.74	2.78	2.01	1.92
Rel. Inten.(% of BP)	0.01	0.80	0.44	23.35	21.87	21.03	16.19	81.66	39.38	18.94	13.81	13.14
Score	0.20	0.22	1.00	0.50	0.50	-0.21	0.75	0.50	0.50	1.50	1.50	0.50
Ion-type	PR	LI	E	a1	b1		GED	b4	b5	$y13^{+2}$	$y14^{+2}$	b6
Delta ppm	5.3	-11.9	2.4	-10.4	-15.5		14.3	-1.2	-10.5	-0.2	-9.9	38.4

Fragment-ion (m/z)	802.849^{+2}	846.361^{+2}	884.380^{+3}	910.376^{+2}	931.403^{+2}	937.067^{+3}	1027.490^{+2}	1045.444^{+2}	1097.994^{+2}	1118.969^{+2}	1165.517^{+2}	1204.022^{+2}	1261.576^{+2}
Frac. Inten.(% of TIC)	2.71	9.80	2.89	2.32	3.94	1.91	2.44	3.74	7.03	14.58	7.66	2.00	2.43
Rel. Inten.(% of BP)	18.60	67.16	19.82	15.91	26.98	13.09	16.74	25.61	48.22	100.00	52.49	13.74	16.66
Score	1.50	1.50	-0.20	-0.16	-0.27	-0.13	1.50	-0.26	-0.48	-1.00	1.50	-0.14	-0.17
Ion-type	$y15^{+2}$	$y16^{+2}$					$y18^{+2}$				$y20^{+2}$		
Delta ppm	-1.4	-6.4					33.7				5.8		



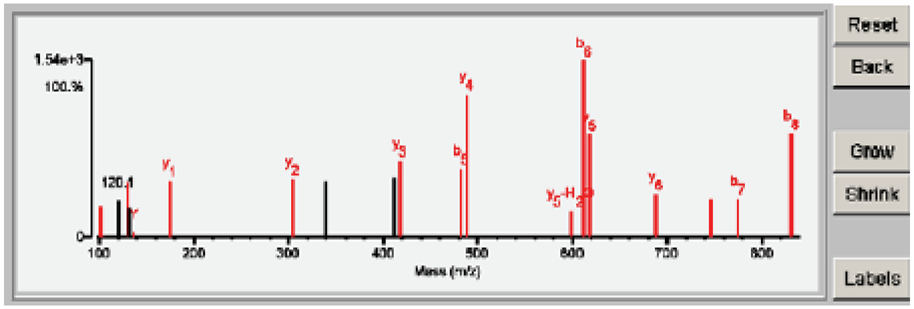
I56

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.18	79.7	9	6/26	(V) G A H A G\E\Y|G|A/E/A/L/E/R (M)	1618.6842	0.0186	12.2	16267.6/8.72	HUMAN	P69905	233416	Hemoglobin subunit alpha - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	86.097	94.066	101.073	102.054	110.070	120.080	129.066	131.084	136.075
Frac. Inten.(% of TIC)	0.00	3.84	0.25	2.52	2.44	0.22	0.07	2.82	4.30	2.24	0.45
Rel. Inten.(% of BP)	0.02	28.19	1.83	18.53	17.88	1.61	0.49	20.71	31.59	16.46	3.27
Score	0.20	-0.28	0.22	-0.19	0.50	1.00	1.00	-0.21	0.75	-0.16	1.00
Ion-type	PR		LI		GA-28	E	H		QKR GA		Y
Delta ppm	9.6		0.9		4.6	-11.3	-10.7		-8.9 -17.4		-7.3

Fragment-ion (m/z)	175.120	304.161	340.105	411.147	417.261	482.181	488.285	599.304	611.221	617.328	688.351	745.381	774.284	831.300
Frac. Inten.(% of TIC)	4.33	4.50	4.33	4.55	5.92	5.31	10.95	2.09	13.62	7.88	3.36	2.99	3.00	8.01
Rel. Inten.(% of BP)	31.82	33.04	31.82	33.44	43.49	38.97	80.36	15.37	100.00	57.87	24.69	21.98	22.01	58.77
Score	1.50	1.50	-0.32	-0.33	1.50	0.50	1.50	0.50	0.50	1.50	1.50	1.50	0.50	0.50
Ion-type	y1	y2			y3	b5	y4	y5-H2O	b6	y5	y6	y7	b7	b8
Delta ppm	5.4	-3.4			12.4	-3.0	4.5	-17.8	-7.6	4.2	-16.5	-3.7	-6.4	-12.4

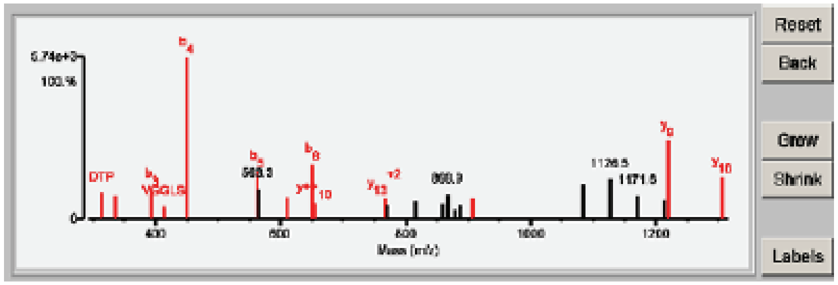


I57

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.04	70.0	8	11/26	(I) F V|G\G\L|S|P D T/P E E K I R (E)	1867.8717	0.0000	0.0	38434.4/7.61	HUMAN	Q14103	250125	Heterogeneous nuclear ribonucleoprotein D0 - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	314.123	336.141	382.168	414.232	448.181	562.269	583.274^{+2}	610.288^{+2}	648.298	653.806	767.369^{+2}	770.388^{+2}	816.412^{+2}	858.408^{+2}	866.844^{+2}	878.898^{+2}	888.461^{+2}	906.433	1084.654	1126.510	1171.588	1213.636	1219.587	1306.589
Frac. Inten.(% of TIC)	0.06	3.31	2.81	3.70	1.42	20.53	6.05	3.70	2.78	6.92	2.01	2.51	1.58	2.20	1.87	3.08	1.20	1.61	2.59	4.48	5.03	2.86	2.38	9.86	5.43
Rel. Inten.(% of BP)	0.32	16.13	13.69	18.00	6.93	100.00	29.49	18.02	13.56	33.72	9.77	12.21	7.72	10.71	9.12	15.02	5.84	7.86	12.62	21.84	24.52	13.92	11.59	48.05	26.43
Score	0.50	0.75	0.50	0.50	0.75	0.50	0.50	-0.18	1.50	0.50	1.50	1.50	-0.08	-0.11	-0.09	-0.15	-0.06	-0.08	1.50	-0.22	-0.25	-0.14	-0.12	1.50	1.50
Ion-type	V	DTP	b2	b3	VGGLS	b4	b5		y9^{+2}	b6	y++10	y13^{+2}							y8					y9	y10
Delta ppm	-14.9	-39.3	-7.7	9.8	-10.2	-11.2	-3.5		-11.2	-7.6	-5.4	-4.1							-18.6					-8.4	-8.1

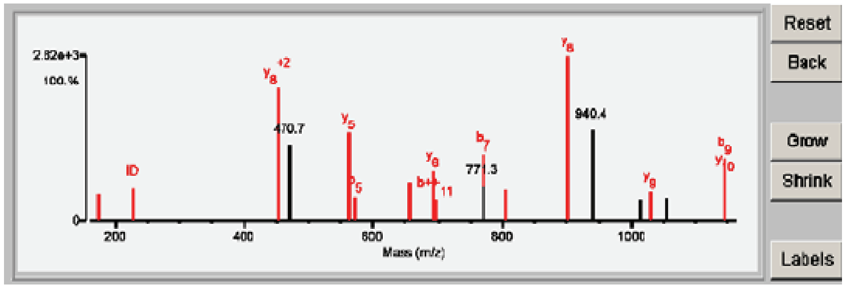


I58

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.55	64.2	10	10/25	(R) H E S G A\S\I\K I|D/E|P/L/E/G S E D/R (I)	2291.9907	0.0431	18.8	50976.5/5.39	HUMAN	P61978	250155	Heterogeneous nuclear ribonucleoprotein K - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	86.096	94.066	116.054	143.062	175.119	229.116	451.719^{+2}	470.691^{+2}	563.244	570.202	657.236	692.289	695.817	770.326	771.323^{+2}	805.379	902.433	940.383	1012.524	1031.473	1053.466	1146.507	1168.489	1297.527
Frac. Inten.(% of TIC)	0.00	0.27	2.02	2.74	5.28	2.29	2.69	11.01	6.20	7.27	2.01	3.26	4.13	1.82	5.58	2.83	2.58	13.65	7.55	1.85	2.36	1.97	5.24	2.25	3.13
Rel. Inten.(% of BP)	0.03	2.00	14.78	20.08	38.72	16.76	19.73	80.65	45.41	53.27	14.75	23.89	30.22	13.36	40.91	20.74	18.93	100.00	55.29	13.56	17.31	14.46	38.38	16.47	22.90
Score	0.20	0.22	-0.15	-0.20	-0.39	1.50	0.75	1.50	-0.45	1.50	0.50	0.50	1.50	0.50	0.50	-0.21	1.50	1.50	-0.55	-0.14	1.50	-0.14	1.50	-0.16	-0.23
Ion-type	PR	LI				y1	ID	y8^{+2}		y5	b5	b6	y6	b++11	b7		y7	y8			y9		b9 y10		
Delta ppm	-10.4	-3.8				0.8	-13.0	11.0		3.1	5.8	8.2	5.7	34.5	14.5		12.4	12.7			9.1		-0.7 14.4		



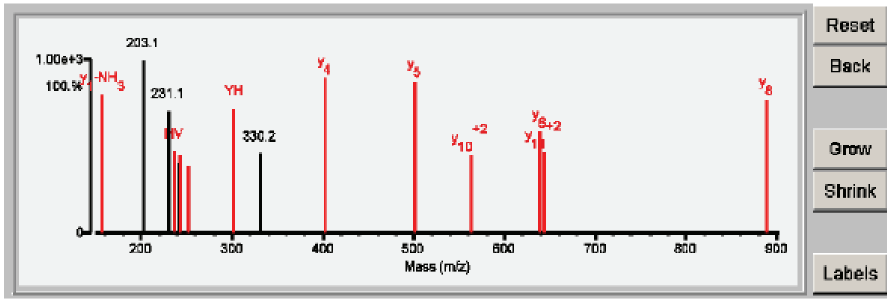
I59

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.12	63.7	6	6/24	(R) M V V N E G S D G G Q S V/Y/H V/H L/H/V/L G G R (Q)	2635.2504	0.0215	8.2	13802.0/6.43	HUMAN	P49773	241365	Histidine triad nucleotide-binding protein 1 - Homo sapiens (Human)

Fragment-ion (m/z)	60.045	70.066	72.081	84.045	86.096	102.054	104.055	110.071	136.077	158.097	203.120	231.116
Frac. Inten.(% of TIC)	5.71	0.00	0.61	0.27	0.21	0.30	7.61	0.61	0.11	7.13	8.96	6.32
Rel. Inten.(% of BP)	63.73	0.04	6.85	3.02	2.33	3.34	84.85	6.83	1.26	79.55	100.00	70.48
Score	-0.64	0.20	0.50		0.22	1.00	-0.85	1.00	1.00	0.50	-1.00	-0.70
Ion-type		PR	V	E	LI	E		H	Y	y1-NH3		
Delta ppm		8.2	0.3		-10.8	-9.4		-2.5	12.6	29.1		

Fragment-ion (m/z)	237.133	241.624	244.090	251.154	301.125	330.188	402.245	501.310	562.814^{+2}	638.373	644.348^{+2}	888.513
Frac. Inten.(% of TIC)	4.23	3.65	4.01	3.51	6.45	4.10	7.97	7.85	4.04	5.22	4.15	6.95
Rel. Inten.(% of BP)	47.18	40.71	44.77	39.18	72.01	45.75	88.96	87.54	45.11	58.29	46.29	77.58
Score	0.75	-0.41	0.75	1.50	0.75	-0.46	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	HV		NE	y++5 LH	YH		y4	y5	y10^{+2}	y6	y11^{+2}	y8
Delta ppm	-11.0		-16.0	-26.3 11.3	-20.0		-2.8	-8.1	-20.0	-0.7	-13.6	-3.2



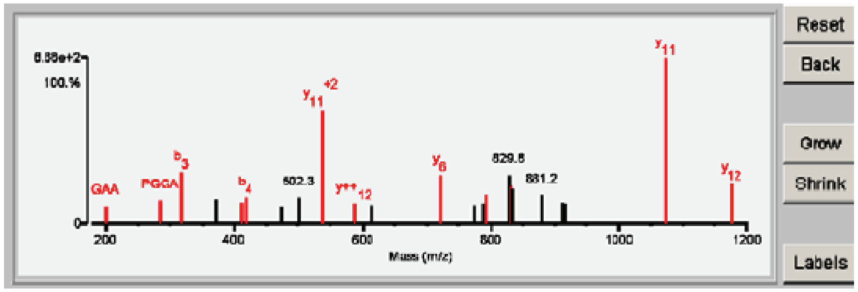
I60

Detailed Results

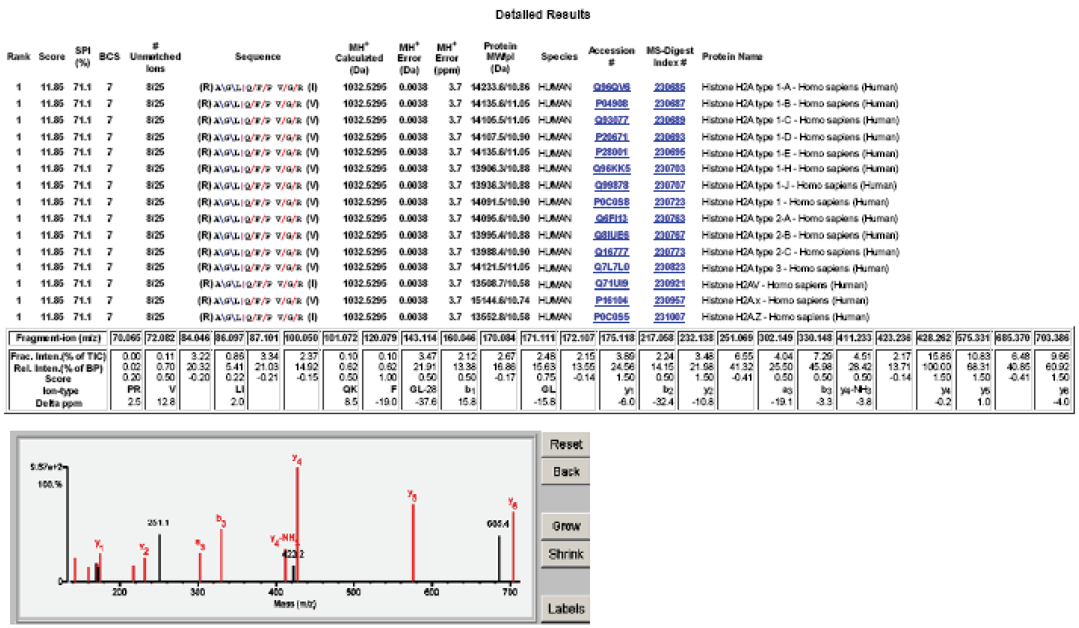
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.08	65.4	7	12/25	(A) A G V\T\D G N E V A K A Q Q A|T/P G G A/A/P T I/F S R (I)	2837.3345	0.0150	5.3	17161.8/9.20	HUMAN	Q9BX68	241377	Histidine triad nucleotide-binding protein 2 - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	200.100	283.132	316.128	373.199	409.224	417.189	471.268	502.252	537.287^{+2}	587.823	614.327	720.402
Frac. Inten.(% of TIC)	0.26	1.90	2.56	5.57	2.67	2.38	2.90	1.92	2.89	12.47	2.26	2.05	5.38
Rel. Inten.(% of BP)	1.43	10.56	14.24	30.94	14.84	13.23	16.11	10.67	16.07	69.25	12.53	11.38	29.85
Score	0.50	0.75	0.75	0.50	-0.15	1.50	0.50	-0.11	-0.16	1.50	1.50	-0.11	1.50
Ion-type	V	GAA	PGGA	b_3		y_3	b_4			y_{11}^{+2}	y^{++}_{12}		y_6
Delta ppm	1.7	-22.8	-31.7	-17.2		10.3	18.1			-6.8	15.5		-2.5

Fragment-ion (m/z)	774.742	788.342	791.439	829.784	832.334^{+2}	834.375	881.167	912.332	915.048^{+2}	1073.579	1174.611	1278.644
Frac. Inten.(% of TIC)	2.09	2.20	3.18	5.33	4.14	3.76	3.19	2.42	2.24	18.00	4.44	3.80
Rel. Inten.(% of BP)	11.61	12.23	17.64	29.58	22.97	20.89	17.71	13.45	12.44	100.00	24.68	21.10
Score	-0.12	-0.12	1.50	-0.30	0.50	-0.21	-0.18	-0.13	-0.12	1.50	1.50	-0.21
Ion-type			y_7		b_{15}^{+2}					y_{11}	y_{12}	
Delta ppm			-2.7		-36.8					4.8	-9.1	



I61



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (I)	1032.5295	0.0038	3.7	14233.6/10.86	HUMAN	Q96QV6	230685	Histone H2A type 1-A - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14135.6/11.05	HUMAN	P04908	230687	Histone H2A type 1-B - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14105.5/11.05	HUMAN	Q93077	230689	Histone H2A type 1-C - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14107.5/10.90	HUMAN	P20671	230693	Histone H2A type 1-D - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14135.6/11.05	HUMAN	P28001	230695	Histone H2A type 1-E - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	13906.3/10.88	HUMAN	Q96KK5	230703	Histone H2A type 1-H - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	13936.3/10.88	HUMAN	Q99878	230707	Histone H2A type 1-J - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14091.5/10.90	HUMAN	P0C0S8	230723	Histone H2A type 1 - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14095.6/10.90	HUMAN	Q6FI13	230763	Histone H2A type 2-A - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	13995.4/10.88	HUMAN	Q8IUE6	230767	Histone H2A type 2-B - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	13988.4/10.90	HUMAN	Q16777	230773	Histone H2A type 2-C - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	14121.5/11.05	HUMAN	Q7L7L0	230823	Histone H2A type 3 - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (I)	1032.5295	0.0038	3.7	13508.7/10.58	HUMAN	Q71UI9	230921	Histone H2AV - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (V)	1032.5295	0.0038	3.7	15144.6/10.74	HUMAN	P16104	230957	Histone H2A.x - Homo sapiens (Human)
1	11.85	71.1	7	8/25	(R)A\G\L|Q/F/P V/G/R (I)	1032.5295	0.0038	3.7	13552.8/10.58	HUMAN	P0C0S5	231007	Histone H2A.Z - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.082	84.046	86.097	87.101	100.050	101.072	120.079	143.114	160.046	170.084	171.111	172.107
Frac. Inten.(% of TIC)	0.00	0.11	3.22	0.86	3.34	2.37	0.10	0.10	3.47	2.12	2.67	2.48	2.15
Rel. Inten.(% of BP)	0.02	0.70	20.32	5.41	21.03	14.92	0.62	0.62	21.91	13.38	16.86	15.63	13.55
Score	0.20	0.50	-0.20	0.22	-0.21	-0.15	0.50	1.00	0.50	0.50	-0.17	0.75	-0.14
Ion-type	PR	V		LI			QK	F	GL-28	b_1		GL	
Delta ppm	2.5	12.8		2.0			8.5	-19.0	-37.6	15.8		-15.8	

Fragment-ion (m/z)	175.118	217.058	232.138	251.069	302.149	330.148	411.233	423.236	428.262	575.331	685.370	703.386
Frac. Inten.(% of TIC)	3.89	2.24	3.48	6.55	4.04	7.29	4.51	2.17	15.86	10.83	6.48	9.66
Rel. Inten.(% of BP)	24.56	14.15	21.98	41.32	25.50	45.98	28.42	13.71	100.00	68.31	40.85	60.92
Score	1.50	0.50	1.50	-0.41	0.50	0.50	0.50	-0.14	1.50	1.50	-0.41	1.50
Ion-type	y_1	b_2	y_2		a_3	b_3	y_4-NH_3		y_4	y_5		y_6
Delta ppm	-6.0	-32.4	-10.8		-19.1	-3.3	-3.8		-0.2	1.0		-4.0

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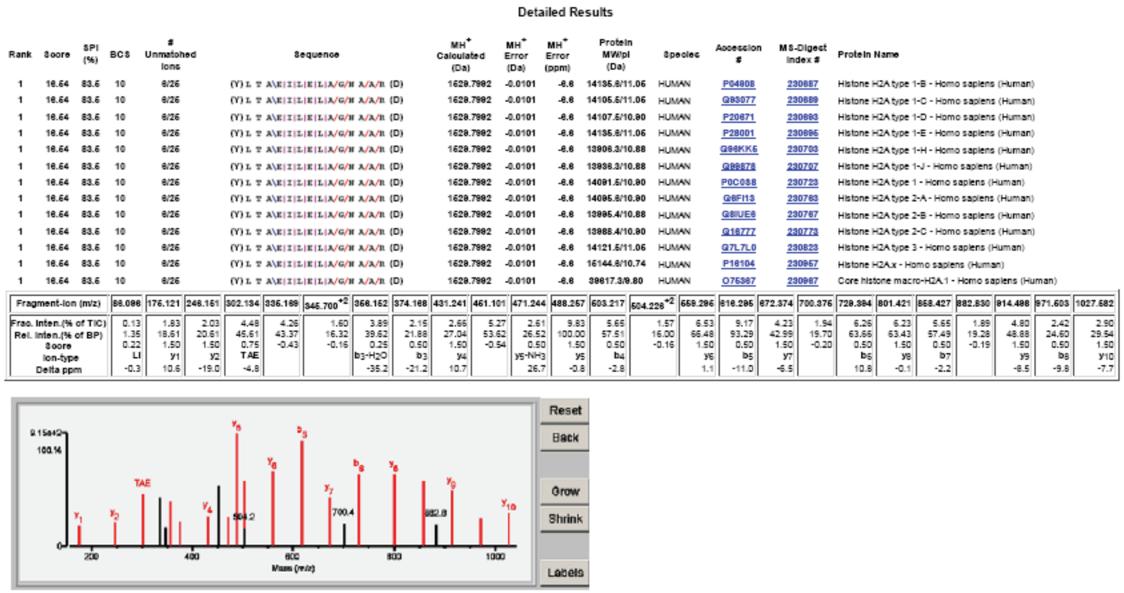

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14135.6/11.05	HUMAN	P04908	230687	Histone H2A type 1-B - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14105.5/11.05	HUMAN	Q93077	230689	Histone H2A type 1-C - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14107.5/10.90	HUMAN	P20671	230693	Histone H2A type 1-D - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14135.6/11.05	HUMAN	P28001	230695	Histone H2A type 1-E - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	13906.3/10.88	HUMAN	Q96KK5	230703	Histone H2A type 1-H - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	13936.3/10.88	HUMAN	Q99878	230707	Histone H2A type 1-J - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14091.5/10.90	HUMAN	P0C0S8	230723	Histone H2A type 1 - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14095.6/10.90	HUMAN	Q6FI13	230763	Histone H2A type 2-A - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	13995.4/10.88	HUMAN	Q8IUE6	230767	Histone H2A type 2-B - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	13988.4/10.90	HUMAN	Q16777	230773	Histone H2A type 2-C - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	14121.5/11.05	HUMAN	Q7L7L0	230823	Histone H2A type 3 - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	15144.6/10.74	HUMAN	P16104	230957	Histone H2A.x - Homo sapiens (Human)
1	16.64	83.6	10	6/26	(Y)L T A\E|I|L|E|L|A/G/N A/A/R (D)	1528.7992	-0.0101	-6.6	39617.3/9.80	HUMAN	O75367	230987	Core histone macro-H2A.1 - Homo sapiens (Human)

Fragment-ion (m/z)	86.096	175.121	246.151	302.134	336.169	345.700^{+2}	356.162	374.168	431.241	461.101	471.244	488.257	503.217
Frac. Inten.(% of TIC)	0.13	1.83	2.03	4.48	4.26	1.60	3.89	2.15	2.66	5.27	2.61	9.83	5.65
Rel. Inten.(% of BP)	1.35	18.61	20.61	45.61	43.37	16.32	39.62	21.88	27.04	53.62	26.52	100.00	57.51
Score	0.22	1.50	1.50	0.75	-0.43	-0.16	0.25	0.50	1.50	-0.54	0.50	1.50	0.50
Ion-type	LI	y_1	y_2	TAE			b_3-H_2O	b_3	y_4		y_5-NH_3	y_5	b_4
Delta ppm	-0.3	10.6	-19.0	-4.8			-35.2	-21.2	10.7		26.7	-0.8	-2.8

Fragment-ion (m/z)	504.226^{+2}	559.296	616.295	672.374	700.376	729.384	801.421	858.427	882.830	914.498	971.503	1027.582
Frac. Inten.(% of TIC)	1.57	6.53	9.17	4.23	1.94	6.26	6.23	5.65	1.89	4.80	2.42	2.90
Rel. Inten.(% of BP)	16.00	66.48	93.29	42.99	19.70	63.66	63.43	57.49	19.28	48.88	24.60	29.54
Score	-0.16	1.50	0.50	1.50	-0.20	0.50	1.50	0.50	-0.19	1.50	0.50	1.50
Ion-type		y_6	b_5	y_7		b_6	y_8	b_7		y_9	b_8	y_{10}
Delta ppm		1.1	-11.0	-6.5		10.8	-0.1	-2.2		-8.5	-9.8	-7.7

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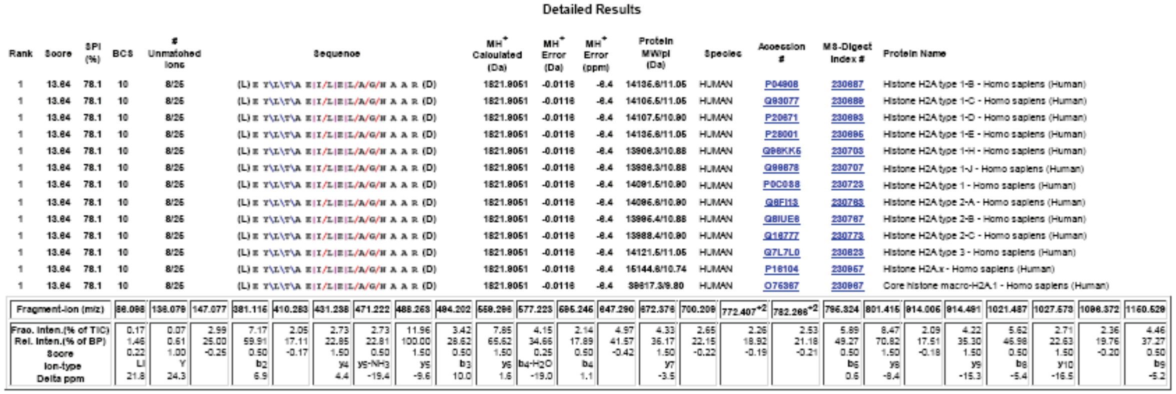
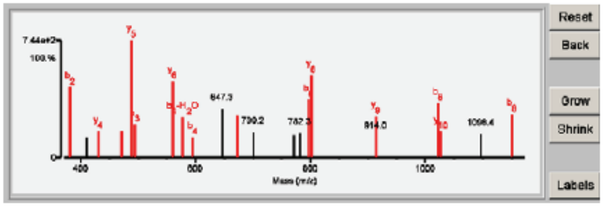


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14135.6/11.05	HUMAN	P04908	230687	Histone H2A type 1-B - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14106.5/11.05	HUMAN	Q93077	230689	Histone H2A type 1-C - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14107.5/10.90	HUMAN	P20671	230693	Histone H2A type 1-D - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14135.6/11.05	HUMAN	P28001	230695	Histone H2A type 1-E - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	13906.3/10.88	HUMAN	Q96KK5	230703	Histone H2A type 1-H - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	13936.3/10.88	HUMAN	Q99878	230707	Histone H2A type 1-J - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14091.5/10.90	HUMAN	P0C0S8	230723	Histone H2A type 1 - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14095.6/10.90	HUMAN	Q6FI13	230763	Histone H2A type 2-A - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	13995.4/10.88	HUMAN	Q8IUE6	230767	Histone H2A type 2-B - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	13988.4/10.90	HUMAN	Q16777	230773	Histone H2A type 2-C - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	14121.5/11.05	HUMAN	Q7L7L0	230823	Histone H2A type 3 - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	15144.6/10.74	HUMAN	P16104	230857	Histone H2A.x - Homo sapiens (Human)
1	13.84	78.1	10	8/25	(L) E Y\L\T\A E|I/L|E|L/A/G/N A A R (D)	1821.9051	-0.0116	-6.4	39617.3/9.80	HUMAN	O75367	230867	Core histone macro-H2A.1 - Homo sapiens (Human)

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
86.096	0.17	1.46	0.22	LI	21.8
136.076	0.07	0.61	1.00	Y	24.3
147.077	2.99	25.00	-0.25		
381.116	7.17	59.91	0.50	b_2	6.9
410.283	2.05	17.11	-0.17		
431.238	2.73	22.85	1.50	y_4	4.4
471.222	2.73	22.81	0.50	y_5-NH$_3$	-19.4
488.263	11.96	100.00	1.50	y_5	-9.6
494.202	3.42	28.62	0.50	b_3	10.0
559.296	7.85	65.62	1.50	y_6	1.6
577.223	4.15	34.66	0.25	b_4-H$_2$O	-19.0
595.246	2.14	17.89	0.50	b_4	1.1
647.290	4.97	41.57	-0.42		
672.376	4.33	36.17	1.50	y_7	-3.5
700.209	2.65	22.15	-0.22		
772.407^{+2}	2.26	18.92	-0.19		
782.266^{+2}	2.53	21.18	-0.21		
796.324	5.89	49.27	0.50	b_6	0.6
801.415	8.47	70.82	1.50	y_8	-8.4
814.006	2.09	17.51	-0.18		
814.491	4.22	35.30	1.50	y_9	-15.3
1021.487	5.62	46.98	0.50	b_8	-5.4
1027.573	2.71	22.63	1.50	y_{10}	-16.5
1096.372	2.36	19.76	-0.20		
1160.529	4.46	37.27	0.50	b_9	-5.2



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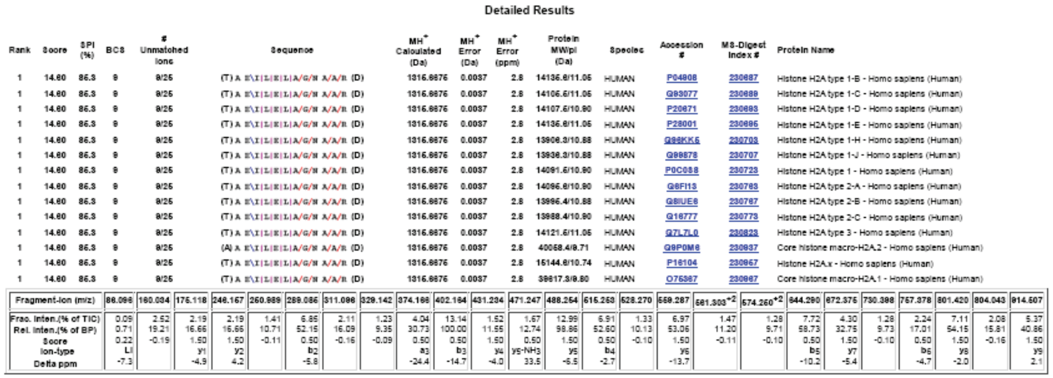
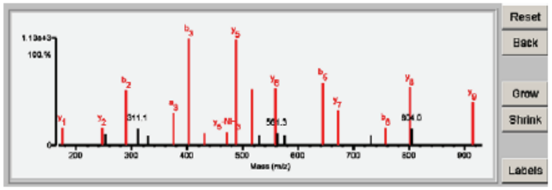


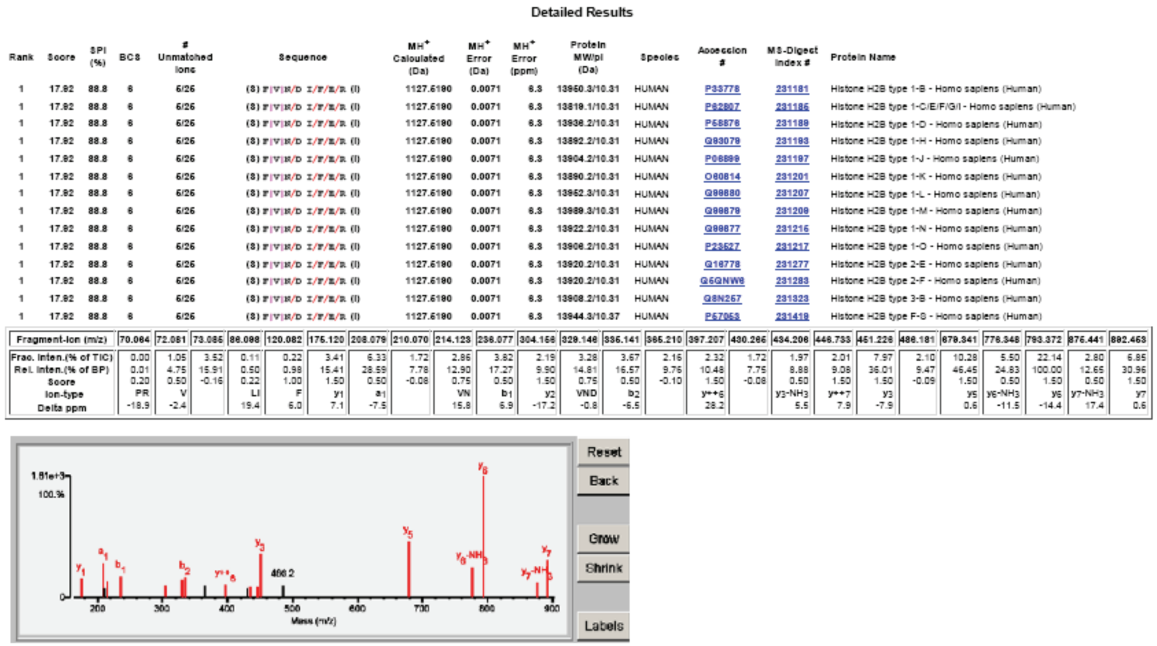
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14135.6/11.05	HUMAN	P04908	230687	Histone H2A type 1-B - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14106.5/11.05	HUMAN	Q93077	230689	Histone H2A type 1-C - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14107.5/10.90	HUMAN	P20671	230693	Histone H2A type 1-D - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14135.6/11.05	HUMAN	P28001	230695	Histone H2A type 1-E - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	13906.3/10.88	HUMAN	Q96KK5	230703	Histone H2A type 1-H - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	13936.3/10.88	HUMAN	Q99878	230707	Histone H2A type 1-J - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14091.5/10.90	HUMAN	P0C0S8	230723	Histone H2A type 1 - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14095.6/10.90	HUMAN	Q6FI13	230763	Histone H2A type 2-A - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	13995.4/10.88	HUMAN	Q8IUE6	230767	Histone H2A type 2-B - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	13988.4/10.90	HUMAN	Q16777	230773	Histone H2A type 2-C - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	14121.5/11.05	HUMAN	Q7L7L0	230823	Histone H2A type 3 - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(A) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	40058.4/9.71	HUMAN	Q9P0M6	230837	Core histone macro-H2A.2 - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	15144.6/10.74	HUMAN	P16104	230857	Histone H2A.x - Homo sapiens (Human)
1	14.60	86.3	9	9/25	(T) A E\I|L|E|L|A/G/N A/A/R (D)	1316.6876	0.0037	2.8	39617.3/9.80	HUMAN	O75367	230867	Core histone macro-H2A.1 - Homo sapiens (Human)

Fragment-ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
86.096	0.09	0.71	0.22	LI	-7.3
160.034	2.52	19.21	-0.19		
175.118	2.19	16.66	1.50	y_1	-4.9
246.167	2.19	16.66	1.50	y_2	4.2
260.989	1.41	10.71	-0.11		
289.086	6.85	52.15	0.50	b_2	-5.8
311.096	2.11	16.09	-0.16		
329.142	1.23	9.35	-0.09		
374.166	4.04	30.73	0.50	a_3	-24.4
402.164	13.14	100.00	0.50	b_3	-14.7
431.234	1.52	11.55	1.50	y_4	-4.0
471.247	1.67	12.74	0.50	y_5-NH$_3$	33.5
488.254	12.99	98.86	1.50	y_5	-6.5
515.263	6.91	52.60	0.50	b_4	-2.7
528.270	1.33	10.13	-0.10		
559.287	6.97	53.06	1.50	y_6	-13.7
561.303^{+2}	1.47	11.20	-0.11		
574.260^{+2}	1.28	9.71	-0.10		
644.290	7.72	58.73	0.50	b_5	-10.2
672.376	4.30	32.75	1.50	y_7	-5.4
730.398	1.28	9.73	-0.10		
757.378	2.24	17.01	0.50	b_6	-4.7
801.420	7.11	54.15	1.50	y_8	-2.0
804.043	2.08	15.81	-0.16		
914.507	5.37	40.86	1.50	y_9	2.1



I65

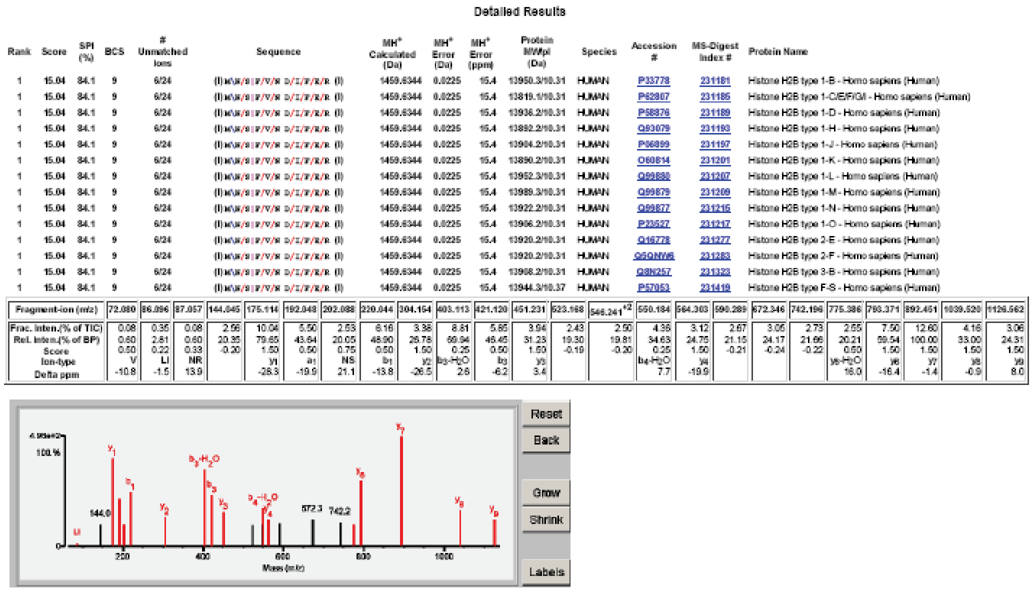


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13950.3/10.31	HUMAN	P33778	231181	Histone H2B type 1-B - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13819.1/10.31	HUMAN	P62807	231186	Histone H2B type 1-C/E/F/G/I - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13936.2/10.31	HUMAN	P58876	231189	Histone H2B type 1-D - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13892.2/10.31	HUMAN	Q93079	231193	Histone H2B type 1-H - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13904.2/10.31	HUMAN	P06899	231197	Histone H2B type 1-J - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13890.2/10.31	HUMAN	O60814	231201	Histone H2B type 1-K - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13952.3/10.31	HUMAN	Q99880	231207	Histone H2B type 1-L - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13989.3/10.31	HUMAN	Q99879	231209	Histone H2B type 1-M - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13922.2/10.31	HUMAN	Q99877	231216	Histone H2B type 1-N - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13906.2/10.31	HUMAN	P23527	231217	Histone H2B type 1-O - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13920.2/10.31	HUMAN	Q16778	231277	Histone H2B type 2-E - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13920.2/10.31	HUMAN	Q6QNW6	231283	Histone H2B type 2-F - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13908.2/10.31	HUMAN	Q8N257	231323	Histone H2B type 3-B - Homo sapiens (Human)
1	17.92	88.8	6	6/26	(S) F|V|N/D I/F/E/R (I)	1127.6190	0.0071	6.3	13944.3/10.37	HUMAN	P57053	231419	Histone H2B type F-S - Homo sapiens (Human)

Fragment-Ion (m/z)	70.064	72.081	73.085	86.098	120.082	175.120	208.079	210.070	214.123	236.077	304.166	329.146	336.141	365.210	397.207	430.266	434.206	446.733	451.226	486.181	679.341	776.348	793.372	876.441	892.463
Frac. Inten.(% of TIC)	0.00	1.05	3.52	0.11	0.22	3.41	6.33	1.72	2.86	3.82	2.19	3.28	3.67	2.16	2.32	1.72	1.97	2.01	7.97	2.10	10.28	5.50	22.14	2.80	6.85
Rel. Inten.(% of BP)	0.01	4.75	15.91	0.50	0.98	15.41	28.59	7.78	12.90	17.27	9.90	14.81	16.57	9.76	10.48	7.75	8.88	9.08	36.01	9.47	46.45	24.83	100.00	12.65	30.96
Score	0.20	0.50	-0.16	0.22	1.00	1.50	0.50	-0.08	0.75	0.50	1.50	0.75	0.50	-0.10	1.50	-0.08	0.50	1.50	1.50	-0.09	1.50	0.50	1.50	0.50	1.50
Ion-type	PR	V		LI	F	y_1	a_1		VN	b_1	y_2	VND	b_2		y^{++}_6		y_3-NH_3	y^{++}_7	y_3		y_5	y_6-NH_3	y_6	y_7-NH_3	y_7
Delta ppm	-18.9	-2.4		19.4	6.0	7.1	-7.5		15.8	6.9	-17.2	-0.8	-6.5		28.2		5.5	7.9	-7.9		0.6	-11.5	-14.4	17.4	0.6

I66

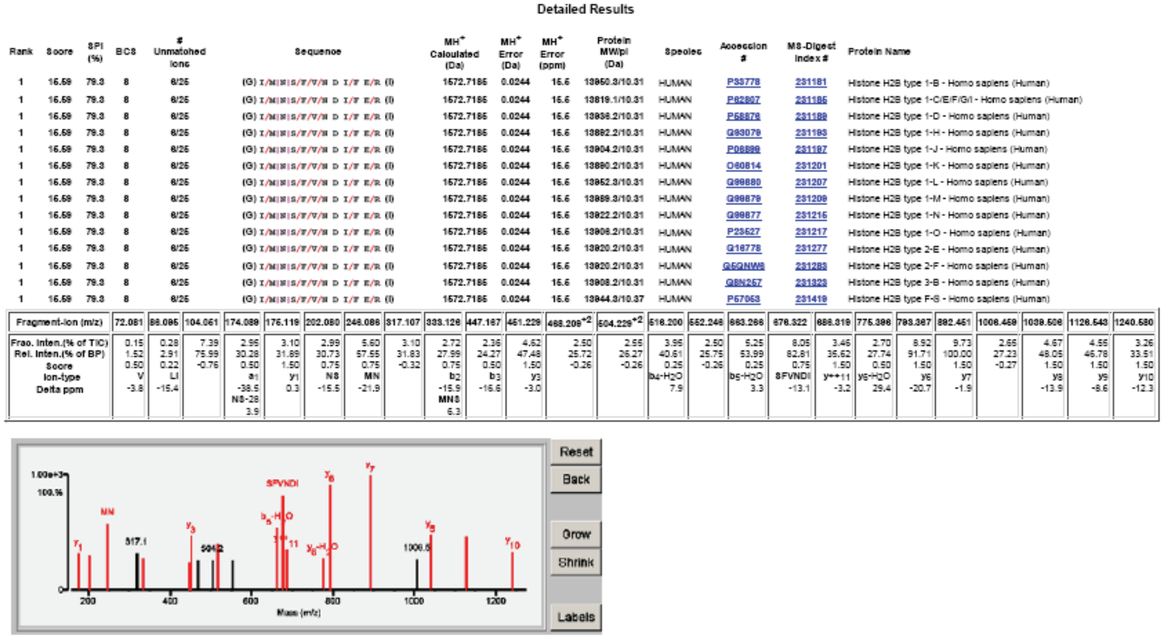


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13950.3/10.31	HUMAN	P33778	231181	Histone H2B type 1-B - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13819.1/10.31	HUMAN	P62807	231186	Histone H2B type 1-C/E/F/G/I - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13936.2/10.31	HUMAN	P58876	231189	Histone H2B type 1-D - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13892.2/10.31	HUMAN	Q93079	231193	Histone H2B type 1-H - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13904.2/10.31	HUMAN	P06899	231197	Histone H2B type 1-J - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13890.2/10.31	HUMAN	O60814	231201	Histone H2B type 1-K - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13952.3/10.31	HUMAN	Q99880	231207	Histone H2B type 1-L - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13989.3/10.31	HUMAN	Q99879	231209	Histone H2B type 1-M - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13922.2/10.31	HUMAN	Q99877	231216	Histone H2B type 1-N - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13906.2/10.31	HUMAN	P23527	231217	Histone H2B type 1-O - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13920.2/10.31	HUMAN	Q16778	231277	Histone H2B type 2-E - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13920.2/10.31	HUMAN	Q6QNW6	231283	Histone H2B type 2-F - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13908.2/10.31	HUMAN	Q8N257	231323	Histone H2B type 3-B - Homo sapiens (Human)
1	15.04	84.1	9	6/24	(I) M\N/S|F/V/N D/I/F/E/R (I)	1459.6344	0.0225	15.4	13944.3/10.37	HUMAN	P57053	231419	Histone H2B type F-S - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.096	87.057	144.045	175.114	192.048	202.088	220.044	304.154	403.113	421.120	451.231	523.168	546.241^{+2}	550.184	564.303	590.289	672.346	742.196	775.386	793.371	892.451	1039.520	1126.562
Frac. Inten.(% of TIC)	0.08	0.35	0.08	2.56	10.04	5.50	2.53	6.16	3.38	8.81	5.85	3.94	2.43	2.50	4.36	3.12	2.67	3.05	2.73	2.55	7.50	12.60	4.16	3.06
Rel. Inten.(% of BP)	0.60	2.81	0.60	20.35	79.65	43.64	20.05	48.90	26.78	69.94	46.45	31.23	19.30	19.81	34.63	24.75	21.15	24.17	21.66	20.21	59.54	100.00	33.00	24.31
Score	0.50	0.22	0.33	-0.20	1.50	0.50	0.75	0.50	1.50	0.25	0.50	1.50	-0.19	-0.20	0.25	1.50	-0.21	-0.24	-0.22	0.50	1.50	1.50	1.50	1.50
Ion-type	V	LI	NR		y_1	a_1	NS	b_1	y_2	b_3-H_2O	b_3	y_3			b_4-H_2O	y_4				y_6-H_2O	y_6	y_7	y_8	y_9
Delta ppm	-10.8	-1.5	13.9		-28.3	-19.9	21.1	-13.8	-26.5	2.6	-6.2	3.4			7.7	-19.9				16.0	-16.4	-1.4	-0.9	8.0

I67



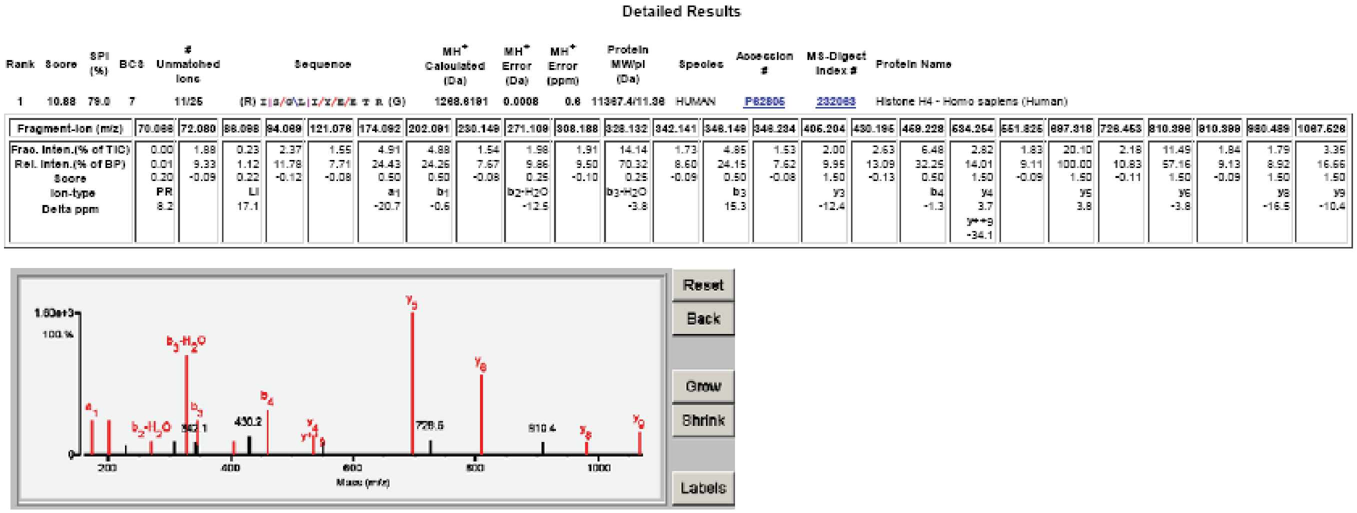
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13950.3/10.31	HUMAN	P33778	231181	Histone H2B type 1-B - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13819.1/10.31	HUMAN	P62807	231186	Histone H2B type 1-C/E/F/G/I - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13936.2/10.31	HUMAN	P58876	231189	Histone H2B type 1-D - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13892.2/10.31	HUMAN	Q93079	231193	Histone H2B type 1-H - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13904.2/10.31	HUMAN	P06899	231197	Histone H2B type 1-J - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13890.2/10.31	HUMAN	O60814	231201	Histone H2B type 1-K - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13952.3/10.31	HUMAN	Q99880	231207	Histone H2B type 1-L - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13989.3/10.31	HUMAN	Q99879	231209	Histone H2B type 1-M - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13922.2/10.31	HUMAN	Q99877	231216	Histone H2B type 1-N - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13906.2/10.31	HUMAN	P23527	231217	Histone H2B type 1-O - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13920.2/10.31	HUMAN	Q16778	231277	Histone H2B type 2-E - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13920.2/10.31	HUMAN	Q5QNW6	231283	Histone H2B type 2-F - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13908.2/10.31	HUMAN	Q8N257	231323	Histone H2B type 3-B - Homo sapiens (Human)
1	16.59	79.3	8	6/25	(G) I/M|N|S/F/V/N D I/F E/R (I)	1572.7185	0.0244	15.6	13944.3/10.37	HUMAN	P57053	231419	Histone H2B type F-S - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.095	104.061	174.089	175.119	202.080	246.086	317.107	333.126	447.167	451.229	468.209^{+2}
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.15 1.52 0.50 V -3.8	0.28 2.91 0.22 LI -15.4	7.39 75.99 -0.76	2.95 30.28 0.50 a_1 -38.5 NS-28 3.9	3.10 31.89 1.50 y_1 0.3	2.99 30.73 0.75 NS -15.5	5.60 57.55 0.75 MN -21.9	3.10 31.83 -0.32	2.72 27.99 0.75 b_2 -15.9 MNS 6.3	2.36 24.27 0.50 b_3 -16.6	4.62 47.48 1.50 y_3 -3.0	2.50 25.72 -0.26

Fragment-Ion (m/z)	504.229^{+2}	516.200	552.246	663.266	676.322	686.319	775.396	793.367	892.451	1006.459	1039.506	1126.543	1240.580
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	2.55 26.27 -0.26	3.95 40.61 0.25 b_4-H_2O 7.9	2.50 25.75 -0.26	5.25 53.99 0.25 b_5-H_2O 3.3	8.05 82.81 0.75 SFVNDI -13.1	3.46 35.62 1.50 y^{++}_{11} -3.2	2.70 27.74 0.50 y_6-H_2O 29.4	8.92 91.71 1.50 y_6 -20.7	9.73 100.00 1.50 y_7 -1.9	2.65 27.23 -0.27	4.67 48.05 1.50 y_8 -13.9	4.55 46.78 1.50 y_9 -8.6	3.26 33.51 1.50 y_{10} -12.3

I68



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.88	79.0	7	11/25	(R) I|S/G\L|I/Y/E/E T R (G)	1268.6181	0.0008	0.6	11367.4/11.36	HUMAN	P62805	232063	Histone H4 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.080	86.098	94.069	121.076	174.092	202.091	230.149	271.109	308.188	328.132	342.141	346.149
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.00 0.01 0.20 PR 8.2	1.88 9.33 -0.09	0.23 1.12 0.22 LI 17.1	2.37 11.78 -0.12	1.55 7.71 -0.08	4.91 24.43 0.50 a_1 -20.7	4.88 24.26 0.50 b_1 -0.6	1.54 7.67 -0.08	1.98 9.86 0.25 b_2-H_2O -12.5	1.91 9.50 -0.10	14.14 70.32 0.25 b_3-H_2O -3.8	1.73 8.60 -0.09	4.85 24.15 0.50 b_3 15.3

Fragment-Ion (m/z)	346.234	405.204	430.195	469.228	534.254	551.825	697.318	726.453	810.396	810.399	980.489	1067.528
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.53 7.62 -0.08	2.00 9.95 1.50 y_3 -12.4	2.63 13.09 -0.13	6.48 32.25 0.50 b_4 -1.3	2.82 14.01 1.50 y_4 3.7 y^{++}_9 -34.1	1.83 9.11 -0.09	20.10 100.00 1.50 y_5 3.8	2.18 10.83 -0.11	11.49 57.16 1.50 y_6 -3.8	1.84 9.13 -0.09	1.79 8.92 1.50 y_8 -16.5	3.35 16.66 1.50 y_9 -10.4

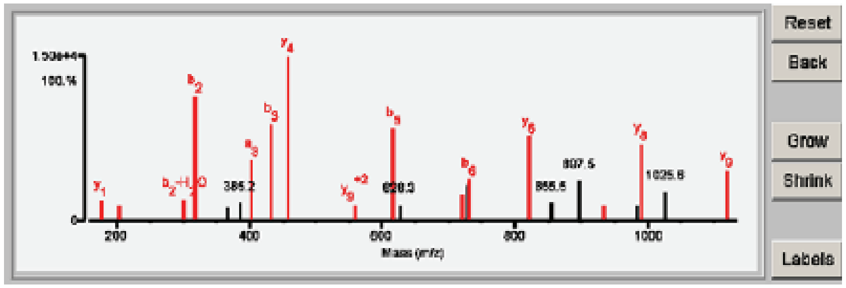
I69

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.67	83.0	9	8/25	(R) D\N\I|Q/G|I|T/K/P A I/R (R)	1548.7661	0.0018	1.2	11367.4/11.36	HUMAN	P62805	232083	Histone H4 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	87.066	176.120	204.033	300.082	318.076	367.113	385.152	403.164	431.161	456.283	559.812^{+2}	616.240
Frac. Inten.(% of TIC)	0.10	0.05	1.87	1.43	2.03	11.32	1.21	1.67	5.59	8.78	15.02	1.44	8.40
Rel. Inten.(% of BP)	0.66	0.31	12.48	9.52	13.51	75.32	8.04	11.10	37.20	58.45	100.00	9.56	55.91
Score	0.22	0.33	1.50	0.50	0.25	0.50	-0.08	-0.11	0.50	0.50	1.50	1.50	0.50
Ion-type	LI	NR	y_1	b_1	b_2-H_2O	b_2			a_3	b_3	y_4	y_9^{+2}	b_5
Delta ppm	6.7	-2.2	7.7	-3.4	-13.2	-0.4			-3.9	0.0	0.9	1.8	-0.7

Fragment-Ion (m/z)	626.339	719.403	727.391	729.324	820.449	856.638	897.495	933.633	983.593	990.557	1025.558	1118.811
Frac. Inten.(% of TIC)	1.48	2.41	3.29	3.79	7.61	1.64	3.61	1.48	1.50	7.04	2.63	4.62
Rel. Inten.(% of BP)	9.82	16.02	21.91	25.24	50.67	10.95	24.00	9.84	9.98	46.88	17.51	30.74
Score	-0.10	1.50	-0.22	0.50	1.50	-0.11	-0.24	1.50	-0.10	1.50	-0.18	1.50
Ion-type		y_5		b_6	y_6			y_7		y_8		y_9
Delta ppm		1.8		-1.5	-1.3			-1.0		2.0		-2.6



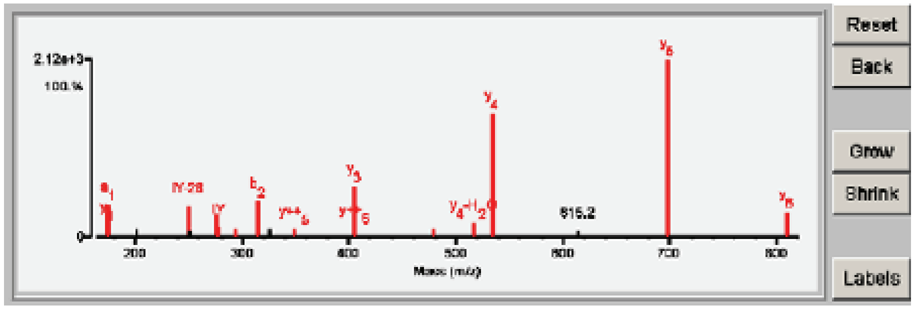
I70

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.86	89.8	6	8/25	(G) L/I|Y|E/E/T/R (R)	1011.4816	0.0016	1.6	11069.2/11.06	HUMAN	Q99525	231879	Histone H4-like protein type G - Homo sapiens (Human)
1	16.86	89.8	6	8/25	(G) L/I|Y|E/E/T/R (G)	1011.4816	0.0016	1.6	11367.4/11.36	HUMAN	P62805	232083	Histone H4 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	87.100	94.069	100.049	136.074	158.088	174.084	175.118	202.080	249.169	251.071	276.166	277.165
Frac. Inten.(% of TIC)	1.11	1.53	1.23	1.35	0.30	1.21	4.91	2.04	1.36	4.73	1.11	3.71	1.58
Rel. Inten.(% of BP)	4.05	5.61	4.50	4.93	1.10	4.43	18.01	7.49	5.00	17.35	4.08	13.60	5.78
Score	0.22	-0.06	-0.05	-0.05	1.00	-0.04	0.50	1.50	-0.05	0.50	-0.04	1.50	0.75
Ion-type	LI				Y		a_1	y_1		IY-28		y_2	IY
Delta ppm	2.0				-11.0		-11.0	-4.3		-6.2		-7.4	33.7

Fragment-Ion (m/z)	293.116	316.176	328.274	349.174	405.207	405.713	478.223	516.236	534.263	616.206	697.318	810.402
Frac. Inten.(% of TIC)	1.31	5.47	1.30	1.32	7.90	1.60	1.32	2.32	19.01	1.09	27.28	3.89
Rel. Inten.(% of BP)	4.81	20.03	4.76	4.85	28.96	5.86	4.85	8.51	69.69	4.01	100.00	14.25
Score	0.75	0.50	-0.05	1.50	1.50	1.50	0.50	0.50	1.50	-0.04	1.50	1.50
Ion-type	YE	b_2		y^{++}_5	y_3	y^{++}_6	b_3	y_4-H_2O	y_4		y_5	y_6
Delta ppm	1.0	1.0		36.6	-4.5	24.0	-32.0	-10.4	1.3		3.4	3.6



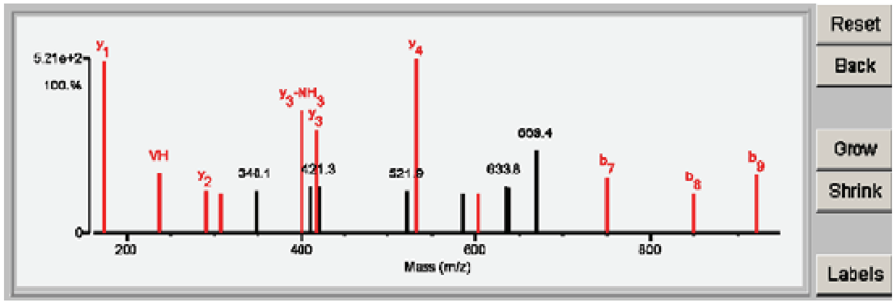
I71

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.70	66.5	6	9/25	(R) L A V H P S G\V|A|L/Q/D/R (V)	1450.7471	0.0072	5.0	17887.6/6.83	HUMAN	P05161	678667	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.080	86.097	101.074	110.072	175.117	237.130	290.150	308.167	348.132^{+2}	401.176	411.221	418.206
Frac. Inten.(% of TIC)	0.00	0.52	0.83	0.08	0.74	12.23	4.22	3.04	2.75	2.96	8.73	3.27	7.32
Rel. Inten.(% of BP)	0.03	4.24	6.74	0.67	6.02	99.23	34.24	24.63	22.34	24.05	70.82	26.53	59.40
Score	0.20	0.50	0.22	0.50	1.00	1.50	0.75	1.50	0.75	-0.24	0.50	-0.27	1.50
Ion-type	PR	V	LI	QK	H	y1	VH	y2	AVH		y3-NH3		y3
Delta ppm	13.9	-14.9	3.2	26.3	2.1	-8.9	-24.9	15.5	-19.8		-3.8		3.4

Fragment-ion (m/z)	421.254	521.862	531.289	584.278^{+2}	602.325	633.792	637.300	669.355^{+2}	750.357	849.424	920.463	1030.492
Frac. Inten.(% of TIC)	3.31	2.99	12.32	2.84	2.84	3.33	3.26	5.82	3.93	2.76	4.15	5.74
Rel. Inten.(% of BP)	26.90	24.27	100.00	23.04	23.05	27.03	26.42	47.26	31.91	22.40	33.68	46.59
Score	-0.27	-0.24	1.50	-0.23	1.50	-0.27	-0.26	-0.47	0.50	0.50	0.50	-0.47
Ion-type			y4		y5				b7	b8	b9	
Delta ppm			0.9		-0.6				-5.2	-6.5	-3.7	



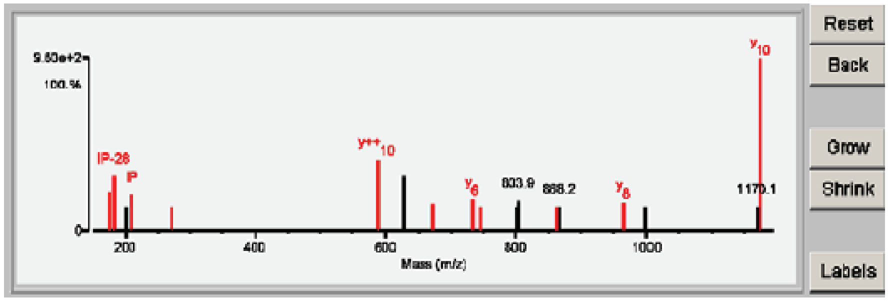
I72

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.47	74.3	7	7/25	(R) V T G N F K H A S P I L|P I/T/E/F/S D I/P/R (R)	2662.3156	0.0046	1.7	50670.5/9.39	HUMAN	P42167	297721	Lamina-associated polypeptide 2, isoforms beta/gamma - Homo sapiens (Human)

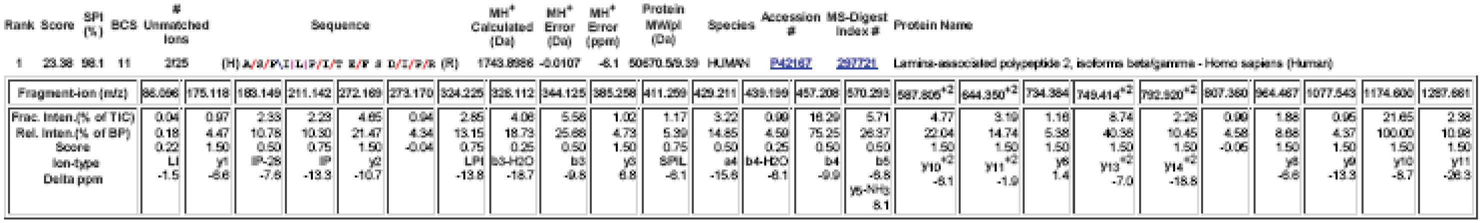
Fragment-ion (m/z)	70.067	72.081	84.046	86.097	101.070	120.084	175.120	183.147	201.108	211.140	272.168	587.296	587.811
Frac. Inten.(% of TIC)	0.01	0.17	0.09	0.33	0.10	0.14	4.90	6.89	3.05	4.48	2.94	7.01	8.91
Rel. Inten.(% of BP)	0.04	0.81	0.43	1.53	0.45	0.67	22.88	32.20	14.27	20.95	13.76	32.73	41.63
Score	0.20	0.50	1.00	0.22	0.50	1.00	1.50	0.50	-0.14	0.75	1.50	1.50	1.50
Ion-type	PR	V	E	LI	QK	F	y_1	IP-28		IP	y_2	y_5	y^{++}_{10}
Delta ppm	23.9	0.3	13.2	9.0	-14.2	26.9	6.0	-20.1		-23.2	-13.7	-31.2	3.8

Fragment-ion (m/z)	627.790^{+2}	674.326^{+2}	734.370	744.856^{+2}	802.569^{+3}	803.890^{+2}	863.421	868.207	964.475	999.484	1170.095^{+2}	1174.605
Frac. Inten.(% of TIC)	6.79	3.39	3.97	2.99	3.05	3.75	2.98	3.04	3.59	2.94	3.08	21.40
Rel. Inten.(% of BP)	31.73	15.84	18.57	13.95	14.24	17.52	13.94	14.22	16.78	13.73	14.41	100.00
Score	-0.32	0.50	1.50	0.50	-0.14	-0.18	1.50	-0.14	1.50	-0.14	-0.14	1.50
Ion-type		a_{11}^{+2}	y_6	b_{12}^{+2}			y_7		y_8			y_{10}
Delta ppm		7.1	-17.7	-6.7			-5.3		1.6			-4.7



I73

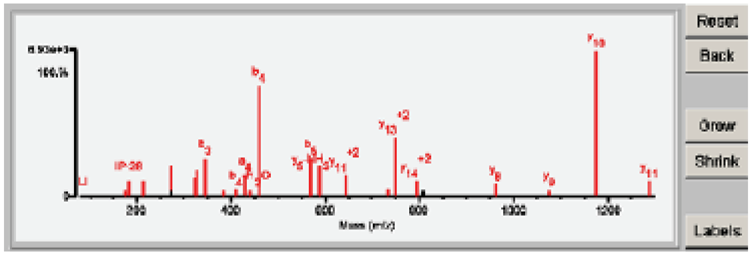
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.38	98.1	11	2/25	(H) A/S/P\I|L|P/I/T E/F S D/I/P/R (R)	1743.8986	-0.0107	-6.1	50670.5/9.39	HUMAN	P42167	297721	Lamina-associated polypeptide 2, isoforms beta/gamma - Homo sapiens (Human)

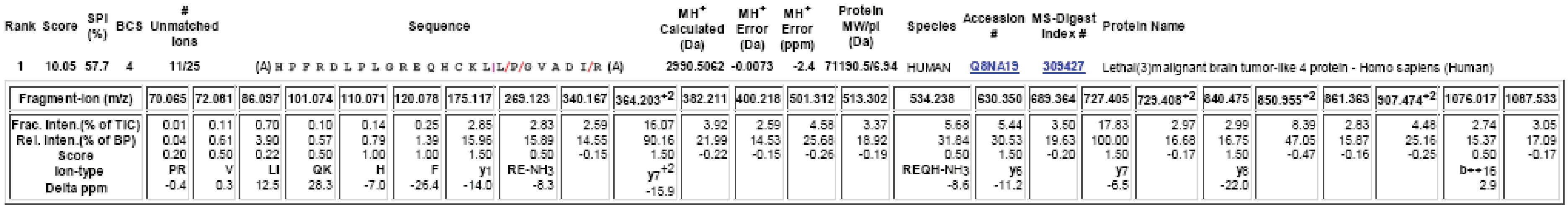
Fragment-ion (m/z)	86.096	175.118	183.149	211.142	272.169	273.170	324.225	328.112	344.125	385.258	411.259	429.211	439.199
Frac. Inten.(% of TIC)	0.04	0.97	2.33	2.23	4.65	0.94	2.85	4.06	5.58	1.02	1.17	3.22	0.99
Rel. Inten.(% of BP)	0.18	4.47	10.78	10.30	21.47	4.34	13.15	18.73	25.68	4.73	5.39	14.85	4.59
Score	0.22	1.50	0.50	0.75	1.50	-0.04	0.75	0.25	0.50	1.50	0.75	0.50	0.25
Ion-type	LI	y1	IP-28	IP	y2		LPI	b3-H2O	b3	y3	SPIL	a4	b4-H2O
Delta ppm	-1.5	-6.6	-7.6	-13.3	-10.7		-13.8	-18.7	-9.8	6.8	-6.1	-15.6	-6.1

Fragment-ion (m/z)	457.208	570.293	587.805^{+2}	644.350^{+2}	734.384	749.414^{+2}	792.920^{+2}	807.380	964.467	1077.543	1174.600	1287.681
Frac. Inten.(% of TIC)	16.29	5.71	4.77	3.19	1.16	8.74	2.28	0.99	1.88	0.95	21.65	2.38
Rel. Inten.(% of BP)	75.25	26.37	22.04	14.74	5.38	40.36	10.45	4.58	8.68	4.37	100.00	10.98
Score	0.50	0.50	1.50	1.50	1.50	1.50	1.50	-0.06	1.50	1.50	1.50	1.50
Ion-type	b4	b5 y5-NH$_3$	y10^{+2}	y11^{+2}	y6	y13^{+2}	y14^{+2}		y8	y9	y10	y11
Delta ppm	-9.9	-8.8 8.1	-6.1	-1.9	1.4	-7.0	-18.8		-6.6	-13.3	-8.7	-28.3



I74

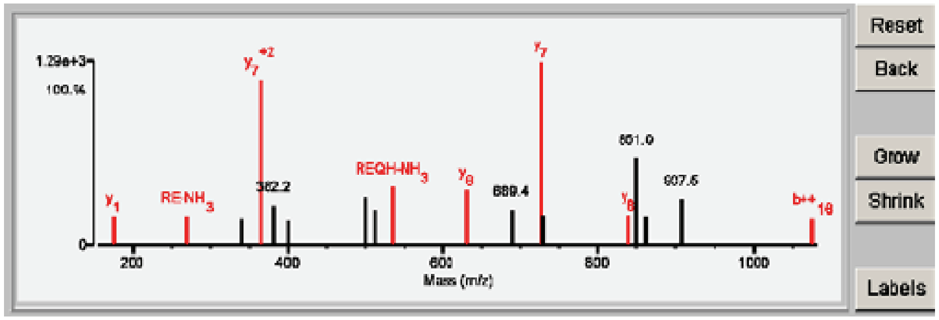
Detailed Results



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.05	57.7	4	11/25	(A) H P F R D L P L G R E Q H C K L|L/P/G V A D I/R (A)	2990.5062	-0.0073	-2.4	71190.5/6.94	HUMAN	Q8NA19	309427	Lethal(3)malignant brain tumor-like 4 protein - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.097	101.074	110.071	120.078	175.117	269.123	340.167	364.203^{+2}	382.211	400.218	501.312
Frac. Inten.(% of TIC)	0.01	0.11	0.70	0.10	0.14	0.25	2.85	2.83	2.59	16.07	3.92	2.59	4.58
Rel. Inten.(% of BP)	0.04	0.61	3.90	0.57	0.79	1.39	15.96	15.89	14.55	90.16	21.99	14.53	25.68
Score	0.20	0.50	0.22	0.50	1.00	1.00	1.50	0.50	-0.15	1.50	-0.22	-0.15	-0.26
Ion-type	PR	V	LI	QK	H	F	y1	RE-NH$_3$		y7^{+2}			
Delta ppm	-0.4	0.3	12.5	28.3	-7.0	-26.4	-14.0	-8.3		-15.9			

Fragment-ion (m/z)	513.302	534.238	630.350	689.364	727.405	729.408^{+2}	840.475	850.955^{+2}	861.363	907.474^{+2}	1076.017	1087.533
Frac. Inten.(% of TIC)	3.37	5.68	5.44	3.50	17.83	2.97	2.99	8.39	2.83	4.48	2.74	3.05
Rel. Inten.(% of BP)	16.92	31.84	30.53	19.63	100.00	16.68	16.75	47.05	15.87	25.16	15.37	17.09
Score	-0.19	0.50	1.50	-0.20	1.50	-0.17	1.50	-0.47	-0.16	-0.25	0.50	-0.17
Ion-type		REQH-NH$_3$	y6		y7		y8				b++16	
Delta ppm		-8.6	-11.2		-6.5		-22.0				2.9	

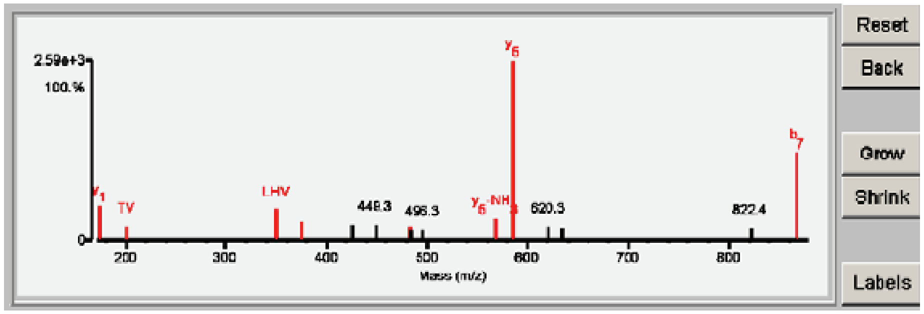


I75

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.07	72.0	5	10/25	(R) V L H V S E N\P\V/P L/T V/R (V)	1647.8887	0.0023	1.4	63473.3/8.55	HUMAN	Q8N1G4	314653	Leucine-rich repeat-containing protein 47 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.080	84.047	84.080	86.097	87.053	94.065	110.070	129.100	169.133	175.116	201.121	350.216	375.236	426.184	449.278	482.727	483.235	496.264^{+2}	568.349	585.368	620.292	634.291^{+2}	822.372	867.403
Frac. Inten.(% of TIC)	0.04	0.16	0.07	2.92	0.27	0.06	2.73	0.19	0.06	5.34	6.17	2.50	5.64	3.26	2.93	2.94	2.52	1.95	2.03	3.82	31.69	2.48	2.37	2.29	15.58
Rel. Inten.(% of BP)	0.12	0.49	0.21	9.20	0.85	0.19	8.61	0.61	0.19	16.86	19.46	7.88	17.80	10.30	9.25	9.27	7.94	6.15	6.39	12.07	100.00	7.82	7.47	7.23	49.16
Score	0.20	0.50	1.00	-0.09	0.22	0.33	-0.09	1.00	0.20	-0.17	1.50	0.75	0.75	1.50	-0.09	-0.09	0.50	-0.06	-0.06	0.50	1.50	-0.08	-0.07	-0.07	0.50
Ion-type	PR	V	E		LI	NR		H	RKQ		y1	TV	LHV	y3			b++8			y5-NH3	y5				b7
Delta ppm	-3.2	-10.8	35.8		11.3	-24.0		-9.8	-20.4		-16.9	-17.2	-11.6	2.8			-11.2			6.3	-6.6				-1.4

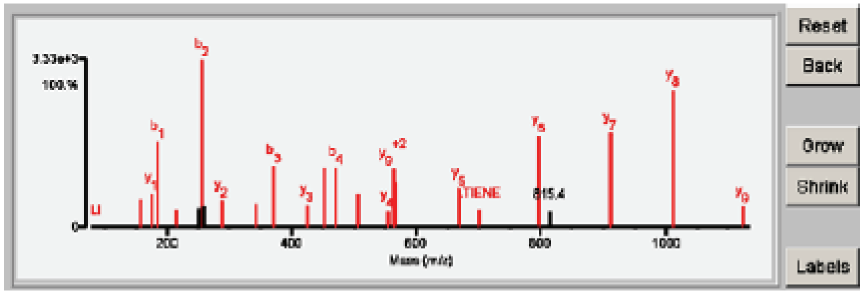


I76

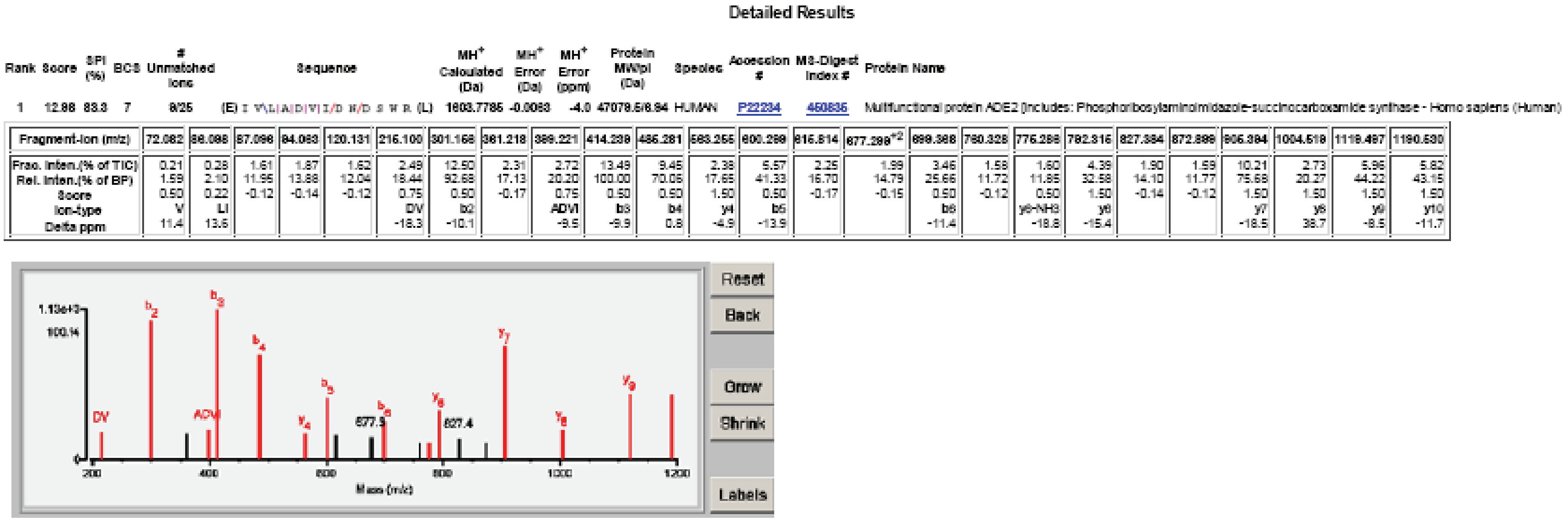
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.38	96.1	10	3/25	(S) P\A|L|T|I/E/N/E/N/I/R (A)	1380.6840	0.0001	0.1	113744.7/6.84	HUMAN	O00754	318636	Lysosomal alpha-mannosidase precursor - Homo sapiens (Human)

Fragment-ion (m/z)	86.098	168.063	176.120	186.058	216.138	251.081	257.085	268.087	288.201	342.181	370.181	426.258	463.214	471.228	506.269^{+2}	564.299	582.807^{+2}	588.303	688.360	700.375	787.389	816.393	910.476	1011.517	1124.588
Frac. Inten.(% of TIC)	0.09	2.30	2.83	7.13	1.46	1.68	14.07	1.79	2.19	1.97	5.15	1.92	4.95	4.96	2.82	1.36	4.92	3.73	3.18	1.45	7.61	1.40	7.82	11.54	1.70
Rel. Inten.(% of BP)	0.62	16.35	20.09	50.67	10.34	11.92	100.00	12.72	15.58	13.99	36.60	13.66	35.15	35.28	20.01	9.67	34.94	26.53	22.59	10.31	54.08	9.95	55.61	82.01	12.06
Score	0.22	0.50	1.50	0.50	0.75	-0.12	0.50	-0.13	1.50	0.50	0.50	1.50	0.25	0.50	1.50	1.50	1.50	0.25	1.50	0.75	1.50	-0.10	1.50	1.50	1.50
Ion-type	LI	a1	y1	b1	TI		b2		y2	a3	b3	y3	b4-H2O	b4	$y8^{+2}$	y4	$y9^{+2}$	b5-H2O	y5	LTIENE	y6		y7	y8	y9
Delta ppm	18.3	-12.1	4.3	-9.3	-7.5		-6.8		-8.0	-14.9	1.6	-13.2	-9.3	0.0	9.2	-10.0	0.8	2.0	4.0	32.1	-1.1		2.3	-5.1	-16.0



I77



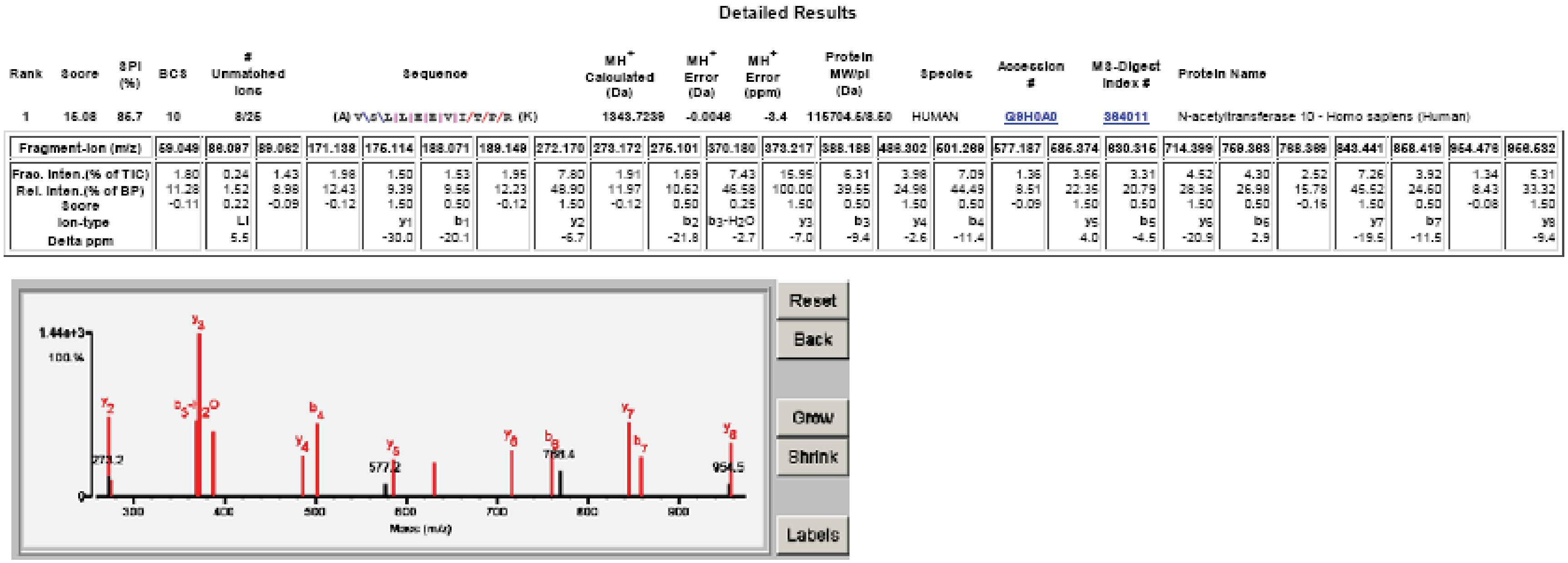
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.98	83.3	7	8/25	(E) I V\L|A|D|V|I/D H/D S W R (L)	1603.7785	-0.0063	-4.0	47078.5/6.94	HUMAN	P22234	450836	Multifunctional protein ADE2 (Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase - Homo sapiens (Human)

Fragment-Ion (m/z)	72.082	86.098	87.096	84.063	120.131	216.100	301.168	381.218	399.221	414.238	486.281	583.255	600.299
Frac. Inten.(% of TIC)	0.21	0.28	1.61	1.87	1.62	2.49	12.50	2.31	2.72	13.49	9.45	2.38	5.57
Rel. Inten.(% of BP)	1.59	2.10	11.95	13.88	12.04	18.44	92.68	17.13	20.20	100.00	70.05	17.65	41.33
Score	0.50	0.22	-0.12	-0.14	-0.12	0.75	0.50	-0.17	0.75	0.50	0.50	1.50	0.50
Ion-type	V	LI				DV	b2		ADVI	b3	b4	y4	b5
Delta ppm	11.4	13.6				-18.3	-10.1		-9.5	-9.9	0.8	-4.9	-13.9

Fragment-Ion (m/z)	616.814	677.299^{+2}	699.368	760.328	776.288	792.316	827.384	872.899	906.394	1004.519	1119.497	1190.530
Frac. Inten.(% of TIC)	2.25	1.99	3.46	1.58	1.60	4.39	1.90	1.59	10.21	2.73	5.96	5.82
Rel. Inten.(% of BP)	16.70	14.79	25.66	11.72	11.85	32.58	14.10	11.77	75.68	20.27	44.22	43.15
Score	-0.17	-0.15	0.50	-0.12	0.50	1.50	-0.14	-0.12	1.50	1.50	1.50	1.50
Ion-type			b6		y6-NH3	y6			y7	y8	y9	y10
Delta ppm			-11.4		-18.8	-15.4			-18.5	38.7	-8.5	-11.7

I78



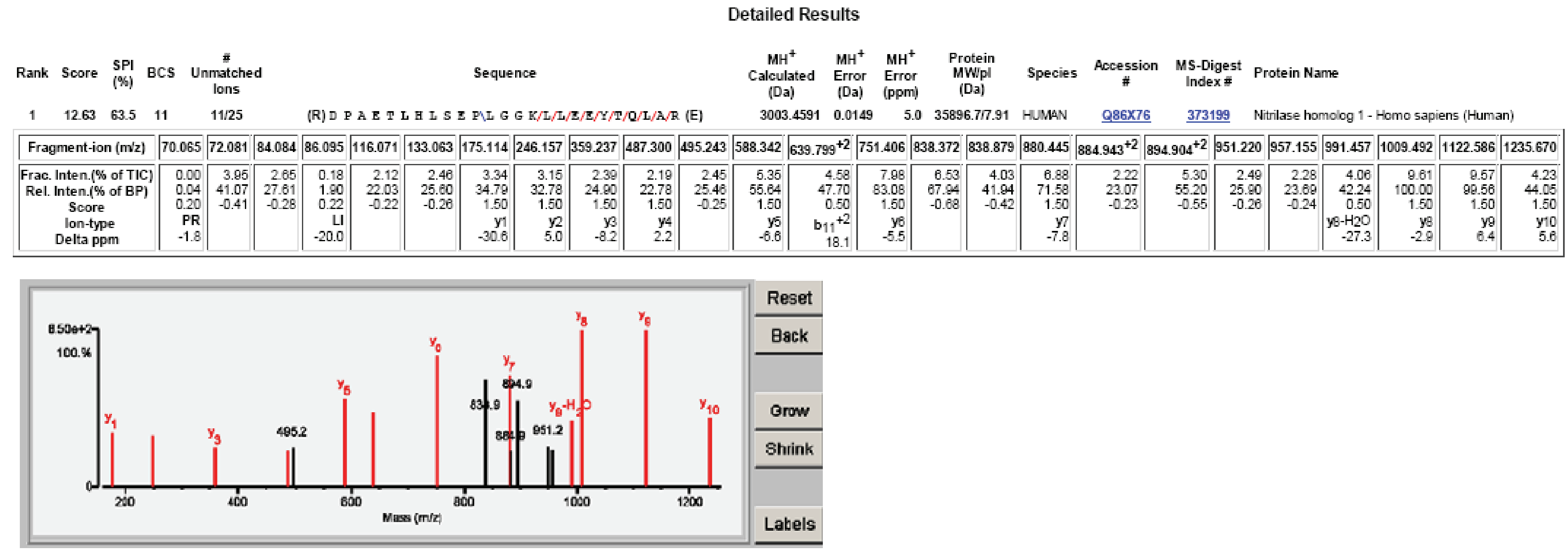
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.08	86.7	10	8/25	(A) V\S\L|L|E|E|V|I/T/P/R (K)	1343.7239	-0.0046	-3.4	115704.5/8.60	HUMAN	Q9H0A0	384011	N-acetyltransferase 10 - Homo sapiens (Human)

Fragment-Ion (m/z)	59.049	86.097	89.062	171.138	176.114	188.071	189.149	272.170	273.172	276.101	370.180	373.217	388.188
Frac. Inten.(% of TIC)	1.80	0.24	1.43	1.98	1.50	1.53	1.95	7.80	1.91	1.69	7.43	15.95	6.31
Rel. Inten.(% of BP)	11.28	1.52	8.98	12.43	9.39	9.56	12.23	48.90	11.97	10.62	46.58	100.00	39.55
Score	-0.11	0.22	-0.09	-0.12	1.50	0.50	-0.12	1.50	-0.12	0.50	0.25	1.50	0.50
Ion-type		LI			y1	b1		y2		b2	b3-H_2O	y3	b3
Delta ppm		5.5			-30.0	-20.1		-6.7		-21.8	-2.7	-7.0	-9.4

Fragment-Ion (m/z)	488.302	501.288	577.187	586.374	630.316	714.399	769.383	788.389	843.441	868.419	954.476	968.532
Frac. Inten.(% of TIC)	3.98	7.09	1.36	3.56	3.31	4.52	4.30	2.52	7.26	3.92	1.34	5.31
Rel. Inten.(% of BP)	24.98	44.49	8.51	22.35	20.79	28.36	26.98	15.78	45.52	24.60	8.43	33.32
Score	1.50	0.50	-0.09	1.50	0.50	1.50	0.50	-0.16	1.50	0.50	-0.08	1.50
Ion-type	y4	b4		y5	b5	y6	b6		y7	b7		y8
Delta ppm	-2.6	-11.4		4.0	-4.5	-20.9	2.9		-19.5	-11.5		-9.4

I79



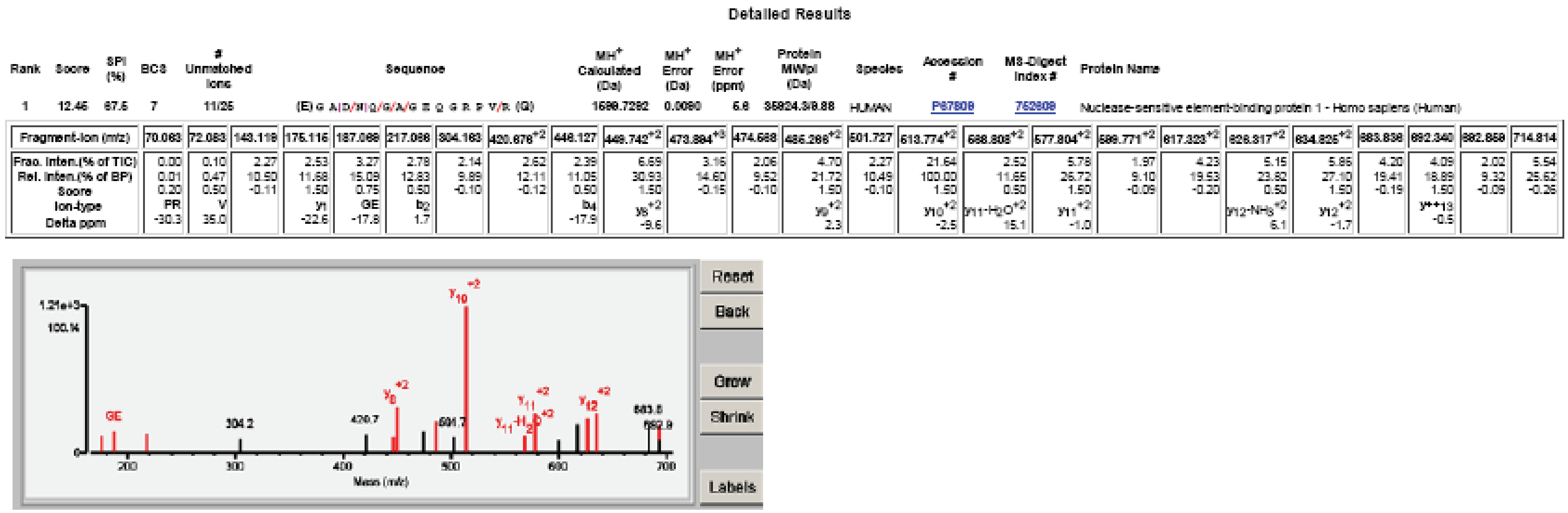
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.63	63.5	11	11/25	(R) D P A E T L H L S E P\L G G K/L/L/E/E/Y/T/Q/L/A/R (E)	3003.4591	0.0149	5.0	35896.7/7.91	HUMAN	Q86X76	373199	Nitrilase homolog 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	84.084	86.095	116.071	133.063	175.114	246.157	359.237	487.300	495.243	588.342	639.799^{+2}
Frac. Inten.(% of TIC)	0.00	3.95	2.65	0.18	2.12	2.46	3.34	3.15	2.39	2.19	2.45	5.35	4.58
Rel. Inten.(% of BP)	0.04	41.07	27.61	1.90	22.03	25.60	34.79	32.78	24.90	22.78	25.46	55.64	47.70
Score	0.20	-0.41	-0.28	0.22	-0.22	-0.26	1.50	1.50	1.50	1.50	-0.25	1.50	0.50
Ion-type	PR			LI			y1	y2	y3	y4		y5	b_{11}^{+2}
Delta ppm	-1.8			-20.0			-30.6	5.0	-8.2	2.2		-6.6	18.1

Fragment-ion (m/z)	751.406	838.372	838.879	880.445	884.943^{+2}	894.904^{+2}	951.220	957.155	991.457	1009.492	1122.586	1235.670
Frac. Inten.(% of TIC)	7.98	6.53	4.03	6.88	2.22	5.30	2.49	2.28	4.06	9.61	9.57	4.23
Rel. Inten.(% of BP)	83.08	67.94	41.94	71.58	23.07	55.20	25.90	23.69	42.24	100.00	99.56	44.05
Score	1.50	-0.68	-0.42	1.50	-0.23	-0.55	-0.26	-0.24	0.50	1.50	1.50	1.50
Ion-type	y6			y7					y8-H2O	y8	y9	y10
Delta ppm	-5.5			-7.8					-27.3	-2.9	6.4	5.6

I80



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.46	67.5	7	11/25	(E) G A|D/N|Q/G/A/G E Q G R P V/R (G)	1698.7292	0.0090	6.8	35924.3/9.88	HUMAN	P67809	752809	Nuclease-sensitive element-binding protein 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.063	72.083	143.119	175.116	187.068	217.088	304.163	420.678^{+2}	448.127	449.742^{+2}	473.894^{+3}	474.688	486.288^{+2}
Frac. Inten.(% of TIC)	0.00	0.10	2.27	2.53	3.27	2.78	2.14	2.62	2.39	6.69	3.16	2.06	4.70
Rel. Inten.(% of BP)	0.01	0.47	10.50	11.68	15.09	12.83	9.89	12.11	11.05	30.93	14.60	9.52	21.72
Score	0.20	0.50	-0.11	1.50	0.75	0.50	-0.10	-0.12	0.50	1.50	-0.15	-0.10	1.50
Ion-type	PR	V		y1	GE	b_2			b_4	y_8^{+2}			y_9^{+2}
Delta ppm	-30.3	35.0		-22.6	-17.8	1.7			-17.9	-9.6			2.3

Fragment-ion (m/z)	501.727	513.774^{+2}	568.808^{+2}	577.804^{+2}	589.771^{+2}	617.323^{+2}	626.317^{+2}	634.825^{+2}	683.838	692.340	692.858	714.814
Frac. Inten.(% of TIC)	2.27	21.64	2.52	5.78	1.97	4.23	5.15	5.86	4.20	4.09	2.02	5.54
Rel. Inten.(% of BP)	10.49	100.00	11.65	26.72	9.10	19.53	23.82	27.10	19.41	18.89	9.32	25.62
Score	-0.10	1.50	0.50	1.50	-0.09	-0.20	0.50	1.50	-0.19	1.50	-0.09	-0.26
Ion-type		y_{10}^{+2}	$y_{11}\text{-}H_2O^{+2}$	y_{11}^{+2}			$y_{12}\text{-}NH_3^{+2}$	y_{12}^{+2}		y++13		
Delta ppm		-2.5	15.1	-1.0			6.1	-1.7		-0.5		

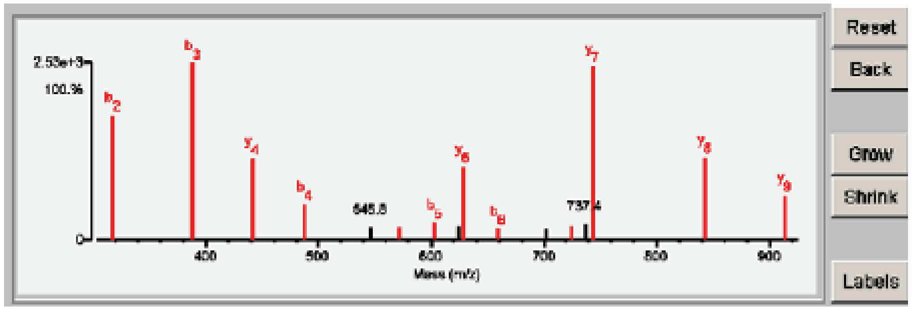
I81

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.02	84.2	6	10/25	(F) D I|A|V|D|G|E/P L G R (V)	1228.6831	-0.0006	-0.4	18012.6/7.68	HUMAN	P62937	428898	Peptidyl-prolyl cis-trans isomerase A - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.081	86.097	94.066	104.060	120.083	136.074	143.116	176.082	317.115	388.154	442.276
Frac. Inten.(% of TIC)	0.00	0.09	0.43	1.77	1.25	2.50	1.92	1.96	1.13	12.29	17.50	7.93
Rel. Inten.(% of BP)	0.01	0.54	2.45	10.11	7.15	14.31	10.95	11.19	6.44	70.22	100.00	45.33
Score	0.20	0.50	0.22	-0.10	-0.07	-0.14	-0.11	-0.11	-0.06	0.50	0.50	1.50
Ion-type	PR	V	LI							b_2	b_3	y_4
Delta ppm	-4.6	1.7	7.8							-10.0	-2.8	-4.2

Fragment-Ion (m/z)	487.220	546.758	571.323	602.249	624.271	628.334	659.270	701.310	726.366	737.370	743.363	842.436	913.474
Frac. Inten.(% of TIC)	3.49	1.23	1.23	1.77	1.41	7.29	1.17	1.06	1.39	1.55	17.14	8.08	4.42
Rel. Inten.(% of BP)	19.93	7.02	7.01	10.11	8.08	41.66	6.66	5.98	7.94	8.86	97.94	46.17	25.27
Score	0.50	-0.07	1.50	0.50	-0.08	1.50	0.50	-0.06	0.50	-0.09	1.50	1.50	1.50
Ion-type	b_4		y_5	b_5		y_6	b_6		y_7-H_2O		y_7	y_8	y_9
Delta ppm	-5.7		5.7	-1.4		-11.6	-2.0		-4.1		-6.9	-1.5	0.0



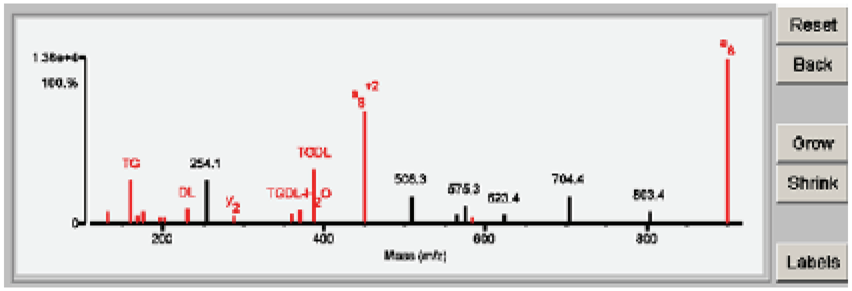
I82

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.24	70.8	3	8/25	(K) R T V P T G D L/A/L/R (P)	1286.6885	-0.0092	-7.2	155004.6/7.56	HUMAN	Q9BXM0	431723	Periaxin - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.080	86.096	131.080	159.076	169.131	176.118	197.128	201.126	229.117	254.150	288.199	359.241
Frac. Inten.(% of TIC)	0.00	0.05	0.39	1.73	6.33	1.10	1.84	0.98	0.99	2.15	6.51	1.24	1.66
Rel. Inten.(% of BP)	0.01	0.20	1.58	7.03	25.71	4.48	7.48	3.97	4.03	8.73	26.42	5.05	6.73
Score	0.20	0.50	0.22	0.50	0.75	0.50	1.50	0.75	0.75	0.75	-0.26	1.50	1.50
Ion-type	PR	V	LI	TG-28	TG	VP-28	y_1	VP	TV	DL		y_2	y_3
Delta ppm	-1.8	-6.6	-1.5	-19.1	-11.4	-20.9	-6.6	-18.0	8.1 DL-28 8.1	-8.6		-12.9	2.4

Fragment-Ion (m/z)	369.188	387.186	460.762^{+2}	508.283^{+2}	584.814^{+2}	575.328	683.314	623.359	704.389	803.440	900.483	1016.521
Frac. Inten.(% of TIC)	1.95	8.18	16.68	4.10	1.39	2.70	0.97	1.27	4.10	1.88	24.63	7.17
Rel. Inten.(% of BP)	7.94	33.22	67.73	16.64	5.65	10.94	3.93	5.17	16.65	7.62	100.00	29.12
Score	0.50	0.75	0.50	-0.17	-0.06	-0.11	0.75	-0.05	-0.17	-0.08	0.50	-0.29
Ion-type	TGDL-H_2O	TGDL	a_8^{+2}				VPTGDL				a_8	
Delta ppm	-25.1	-10.4	39.2				7.9				34.8	



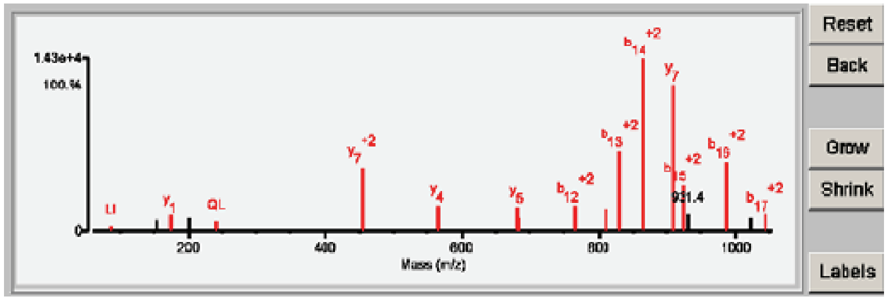
I83

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.36	93.3	11	4/25	(R) D Q H D T F F L R D\P A\E\A\L\Q\L|P/M/D/Y V Q/R (V)	2993.3920	0.0405	13.5	57563.9/7.31	HUMAN	Q9Y285	619389	Phenylalanyl-tRNA synthetase alpha chain - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.043	86.097	101.071	110.072	136.074	153.102	175.118	201.106	242.150	454.723^{+2}	565.313
Frac. Inten.(% of TIC)	0.01	0.06	0.11	0.56	0.10	0.07	0.04	1.40	2.03	1.56	1.29	8.00	3.17
Rel. Inten.(% of BP)	0.02	0.26	0.52	2.57	0.47	0.32	0.19	6.46	9.36	7.20	5.97	36.90	14.61
Score	0.20	0.50	1.00	0.22	0.50	1.00	1.00	-0.06	1.50	-0.07	0.75	1.50	1.50
Ion-type	PR	V	E	LI	QK	H	Y		y_1		QL	y_7^{+2}	y_4
Delta ppm	6.8	10.0	-10.6	4.3	3.6	2.1	-11.0		-7.1		-4.6	9.3	6.4

Fragment-ion (m/z)	680.347	682.298^{+2}	766.334^{+2}	811.376	830.863^{+2}	866.380^{+2}	908.429	922.923^{+2}	931.440^{+2}	986.952^{+2}	1021.512^{+2}	1043.508^{+2}
Frac. Inten.(% of TIC)	3.14	1.57	3.16	2.83	10.07	21.69	18.51	5.80	2.14	8.89	1.57	2.22
Rel. Inten.(% of BP)	14.49	7.23	14.58	13.04	46.43	100.00	85.33	26.76	9.88	40.98	7.24	10.23
Score	1.50	0.50	0.50	1.50	0.50	0.50	1.50	0.50	-0.10	0.50	-0.07	0.50
Ion-type	y_5	b_{10}^{+2}	b_{12}^{+2}	y_6	b_{13}^{+2}	b_{14}^{+2}	y_7	b_{15}^{+2}		b_{16}^{+2}		b_{17}^{+2}
Delta ppm	15.3	10.2	-2.8	-0.7	6.7	4.8	-0.4	5.9		4.9		18.6



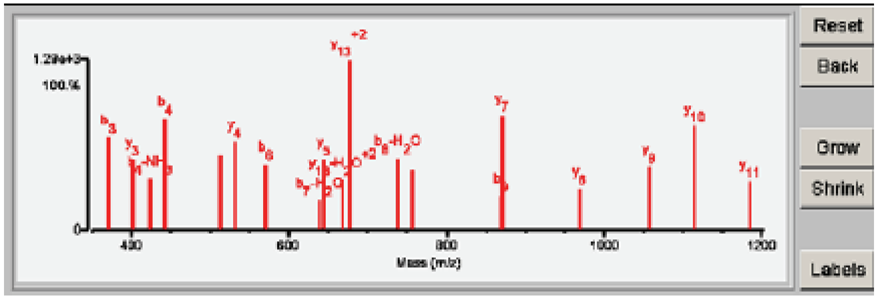
I84

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.30	97.7	11	1/25	(C) A N|F\A|A|G|S/V/I|L/L/E/N L R (F)	1625.8880	-0.0028	-1.7	44615.0/8.30	HUMAN	P00558	413803	Phosphoglycerate kinase 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	86.098	87.066	274.087	283.108	371.142	402.247	426.143	442.177	513.216	531.282	570.223
Frac. Inten.(% of TIC)	0.00	0.06	0.15	0.06	2.01	2.32	6.28	4.73	3.44	7.53	5.09	5.93	4.43
Rel. Inten.(% of BP)	0.02	0.53	1.32	0.52	17.50	20.19	54.61	41.19	29.92	65.52	44.28	51.63	38.57
Score	0.20	0.50	0.22	0.33	0.50	-0.20	0.50	1.50	0.25	0.50	0.50	1.50	0.50
Ion-type	PR	V	LI	NR	b_2		b_3	y_3	b_4-NH_3	b_4	b_5	y_4	b_6
Delta ppm	5.3	19.8	19.4	1.3	1.8		6.3	2.4	-16.8	0.0	5.1	-11.6	-20.4

Fragment-ion (m/z)	638.251	644.376	667.898^{+2}	678.908^{+2}	738.321	767.471	869.428	870.532	969.806	1068.842	1113.841	1184.707
Frac. Inten.(% of TIC)	2.05	4.76	3.37	11.49	4.83	4.03	2.31	7.70	2.80	4.25	7.03	3.33
Rel. Inten.(% of BP)	17.80	41.40	29.28	100.00	42.05	35.10	20.09	67.00	24.37	37.00	61.20	28.98
Score	0.25	1.50	0.50	1.50	0.25	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	b_7-H_2O	y_5	y_{13}-H_2O^{+2}	y_{13}^{+2}	b_8-H_2O	y_6	b_9	y_7	y_8	y_9	y_{10}	y_{11}
Delta ppm	-8.3	6.1	4.5	14.1	-5.5	18.3	7.6	-10.3	-3.9	0.9	-19.2	5.8

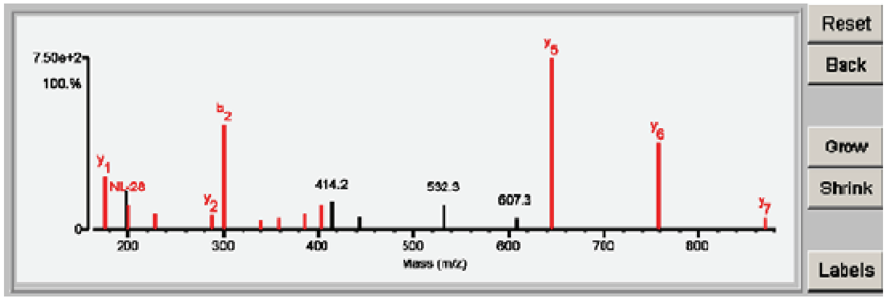


I85

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.23	77.9	6	9/25	(S) V/I|L/L E/N/L/R (F)	1057.6074	0.0007	0.7	44615.0/8.30	HUMAN	P00558	413803	Phosphoglycerate kinase 1 - Homo sapiens (Human)
1	13.23	77.9	6	9/25	(S) V/I|L/L E/N/L/R (F)	1057.6074	0.0007	0.7	44796.4/8.74	HUMAN	P07205	413827	Phosphoglycerate kinase 2 - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.097	117.100	129.144	147.085	155.112	158.089	160.075	175.120	199.184	200.137	228.131	288.201	301.154	339.168	357.171	385.216	402.245	414.238+2	443.262+2	532.283	607.314	644.369	757.460	870.518
Frac. Inten.(% of TIC)	0.06	1.42	1.52	1.58	1.88	1.45	2.22	2.16	6.88	5.05	3.39	2.24	1.99	13.67	1.41	1.64	2.26	3.35	3.67	1.83	3.43	1.70	22.30	11.33	1.56
Rel. Inten.(% of BP)	0.27	6.38	6.83	7.09	8.42	6.49	9.97	9.68	30.85	22.64	15.22	10.06	8.94	61.31	6.34	7.34	10.13	15.03	16.46	8.22	15.36	7.62	100.00	50.81	7.01
Score	0.50	0.22	-0.07	-0.07	-0.08	-0.06	0.50	0.50	1.50	-0.23	0.50	0.75	1.50	0.50	0.50	0.75	0.50	1.50	-0.16	-0.08	-0.15	-0.08	1.50	1.50	1.50
Ion-type	V	LI					y1-NH3	a1	y1		NL-28	NL	y2	b2	ENL-H2O	ENL	y3-NH3	y3					y5	y6	y7
Delta ppm	-13.5	4.3					-21.5	-29.7	8.3		-17.2	-21.3	-5.6	-18.1	3.0	-20.3	-9.1	-3.1					-5.7	3.7	-26.0

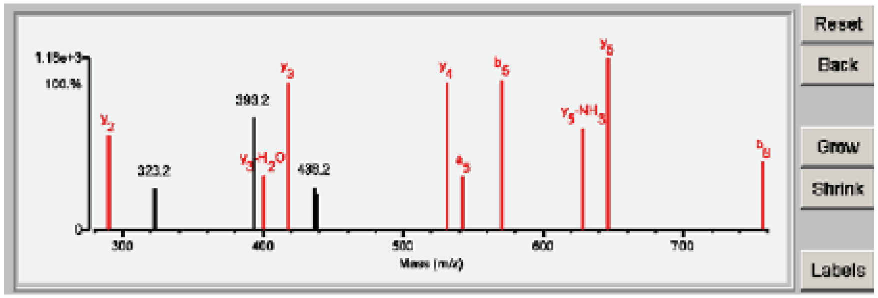


I86

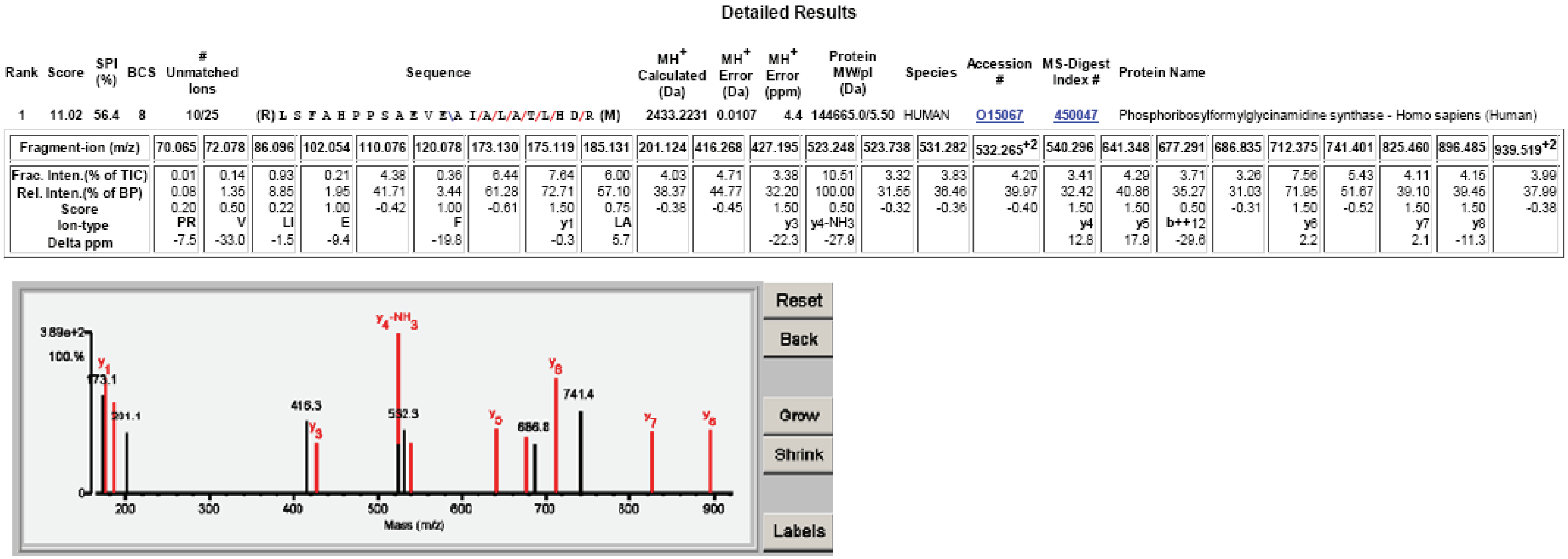
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.73	67.5	6	8/25	(R) H G E S A\W|N/L/E/N/R (F)	1400.6012	0.0127	9.0	28804.1/6.68	HUMAN	P18669	413507	Phosphoglycerate mutase 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.044	86.096	87.055	101.069	110.071	130.064	159.091	175.116	187.090	195.087	289.162	323.153	393.151	400.188	418.200	436.186	439.178	531.289	542.212	570.198	628.308	645.330	756.283
Frac. Inten.(% of TIC)	0.00	7.96	0.07	0.36	0.06	2.02	0.16	0.18	0.53	4.09	4.90	2.93	5.96	2.58	7.02	3.40	9.25	2.73	2.33	9.20	3.35	9.44	6.39	10.75	4.29
Rel. Inten.(% of BP)	0.03	74.24	0.64	3.49	0.71	18.75	1.52	1.66	4.93	38.03	45.57	27.23	55.40	23.96	65.28	31.65	86.00	25.43	21.66	85.61	31.15	87.85	59.42	100.00	39.91
Score	0.20	-0.74	1.00	0.22	0.33	-0.19	1.00		2.00	1.50	-0.46	-0.27	1.50	-0.24	-0.65	0.50	1.50	-0.25	-0.22	1.50	0.50	0.50	0.50	1.50	0.50
Ion-type	PR		E	LI	NR		H	W	W	y1			y2			y3-H2O	y3			y4	a5	b5	y5-NH3	y5	b6
Delta ppm	5.3		-3.5	-6.1	0.1		-0.7		-4.9	-16.9			1.5			-14.0	-11.9			1.8	15.0	-1.7	4.9	-1.6	6.0



I87



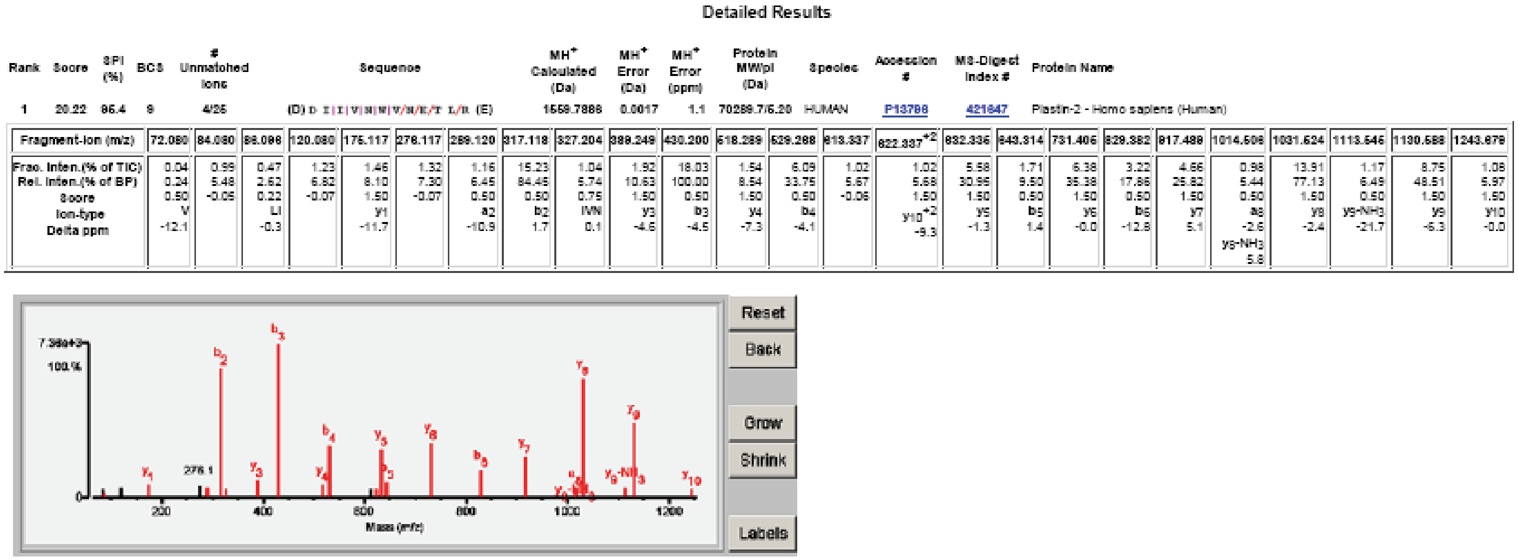
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.02	56.4	8	10/25	(R) L S F A H P P S A E V E\A I/A/L/A/T/L/H D/R (M)	2433.2231	0.0107	4.4	144665.0/5.50	HUMAN	O15067	450047	Phosphoribosylformylglycinamidine synthase - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.078	86.096	102.054	110.076	120.078	173.130	175.119	185.131	201.124	416.268	427.195
Frac. Inten.(% of TIC)	0.01	0.14	0.93	0.21	4.38	0.36	6.44	7.64	6.00	4.03	4.71	3.38
Rel. Inten.(% of BP)	0.08	1.35	8.85	1.95	41.71	3.44	61.28	72.71	57.10	38.37	44.77	32.20
Score	0.20	0.50	0.22	1.00	-0.42	1.00	-0.61	1.50	0.75	-0.38	-0.45	1.50
Ion-type	PR	V	LI	E		F		y1	LA			y3
Delta ppm	-7.5	-33.0	-1.5	-9.4		-19.8		-0.3	5.7			-22.3

Fragment-ion (m/z)	523.248	523.738	531.282	532.265^{+2}	540.296	641.348	677.291	686.835	712.375	741.401	825.460	896.485	939.519^{+2}
Frac. Inten.(% of TIC)	10.51	3.32	3.83	4.20	3.41	4.29	3.71	3.26	7.56	5.43	4.11	4.15	3.99
Rel. Inten.(% of BP)	100.00	31.55	36.46	39.97	32.42	40.86	35.27	31.03	71.95	51.67	39.10	39.45	37.99
Score	0.50	-0.32	-0.36	-0.40	1.50	1.50	0.50	-0.31	1.50	-0.52	1.50	1.50	-0.38
Ion-type	y4-NH3				y4	y5	b++12		y6		y7	y8	
Delta ppm	-27.9				12.8	17.9	-29.6		2.2		2.1	-11.3	

I88



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.22	86.4	9	4/25	(D) D I|I|V|N|W|V/N/E/T L/R (E)	1559.7888	0.0017	1.1	70289.7/6.20	HUMAN	P13796	421647	Plastin-2 - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	84.080	86.096	120.080	175.117	276.117	289.120	317.118	327.204	389.249	430.200	518.289	529.268	613.337
Frac. Inten.(% of TIC)	0.04	0.99	0.47	1.23	1.46	1.32	1.16	15.23	1.04	1.92	18.03	1.54	6.09	1.02
Rel. Inten.(% of BP)	0.24	5.48	2.62	6.82	8.10	7.30	6.45	84.45	5.74	10.63	100.00	8.54	33.75	5.67
Score	0.50	-0.05	0.22	-0.07	1.50	-0.07	0.50	0.50	0.75	1.50	0.50	1.50	0.50	-0.06
Ion-type	V		LI		y1		a2	b2	IVN	y3	b3	y4	b4	
Delta ppm	-12.1		-0.3		-11.7		-10.9	1.7	0.1	-4.6	-4.5	-7.3	-4.1	

Fragment-ion (m/z)	622.337^{+2}	632.336	643.314	731.406	829.382	917.488	1014.506	1031.524	1113.546	1130.588	1243.679
Frac. Inten.(% of TIC)	1.02	5.58	1.71	6.38	3.22	4.66	0.98	13.91	1.17	8.75	1.08
Rel. Inten.(% of BP)	5.68	30.96	9.50	35.38	17.86	25.82	5.44	77.13	6.49	48.51	5.97
Score	1.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	y10^{+2}	y5	b5	y6	b6	y7	a8 y9-NH3	y8	y9-NH3	y9	y10
Delta ppm	-9.3	-1.3	1.4	-0.0	-12.8	5.1	-2.6 5.8	-2.4	-21.7	-6.3	-0.0

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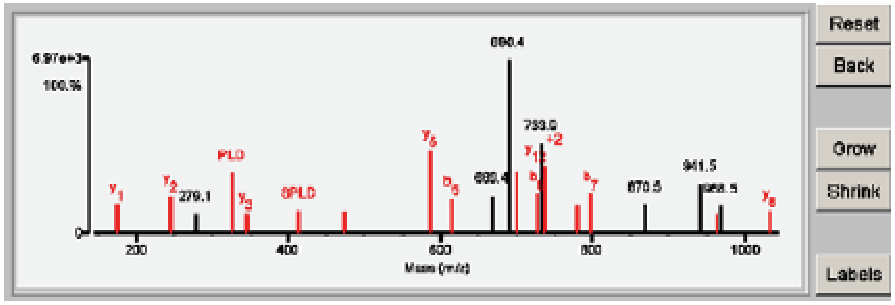
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.48	68.0	11	7/26	(T) I/S/P L D\L|A|K/L/N/Q/V/A/R (Q)	1760.9188	-0.0269	-14.7	37498.0/6.66	HUMAN	Q15365	404801	Poly(rC)-binding protein 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.079	86.095	175.115	246.151	279.130	326.188	345.218	413.196	473.273	587.317	614.280	669.385^{+2}
Frac. Inten.(% of TIC)	0.00	0.06	0.20	2.88	3.69	2.04	5.88	2.00	2.21	2.05	8.08	3.50	3.66
Rel. Inten.(% of BP)	0.01	0.36	1.15	16.84	21.61	11.92	34.39	11.70	12.95	12.01	47.28	20.51	21.43
Score	0.20	0.50	0.22	1.50	1.50	-0.12	0.75	1.50	0.75	1.50	1.50	0.50	-0.21
Ion-type	PR	V	LI	y_1	y_2		PLD	y_3	SPLD	y_4	y_5	b_5	
Delta ppm	13.9	-17.7	-18.9	-20.3	-19.4		-19.1	-19.9	-19.5	-20.6	-15.3	-10.0	

Fragment-ion (m/z)	690.368^{+2}	700.398	727.380	733.883^{+2}	738.883^{+2}	780.408^{+2}	798.388	870.451	941.486	963.494	968.454	1034.540
Frac. Inten.(% of TIC)	17.08	6.02	3.91	8.78	6.64	2.74	3.88	2.87	4.88	1.93	2.70	2.32
Rel. Inten.(% of BP)	100.00	35.23	22.91	51.38	38.88	16.04	22.69	16.82	28.55	11.27	15.83	13.57
Score	-1.00	1.50	0.50	-0.51	1.50	1.50	0.50	-0.17	-0.29	1.50	-0.16	1.50
Ion-type		y_6	b_6		y_{12}^{+2}	y_{13}^{+2}	b_7			y_7		y_8
Delta ppm		-16.6	-15.0		-16.9	-17.4	-24.3			-26.7		-16.3



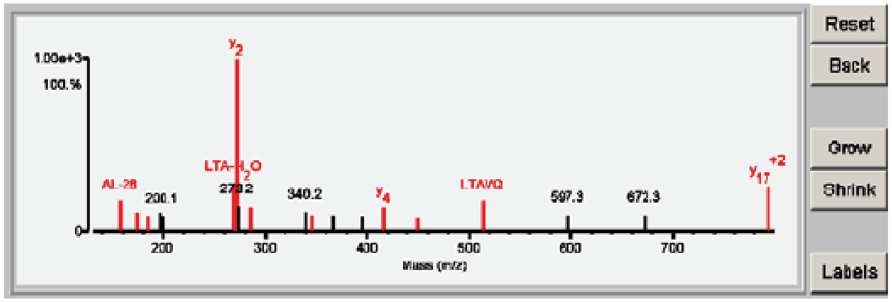
I90

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MWpI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.23	68.3	5	11/25	(P) G D A P R A E L\V A L/T A V Q S E Q G E A G G G/G S/P/R (R)	2768.3268	0.0262	9.5	77092.2/9.60	HUMAN	P56696	286441	Potassium voltage-gated channel subfamily KQT member 4 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	86.096	157.132	175.115	185.131	197.130	200.132	268.163	272.173	273.173	286.178	340.188
Frac. Inten.(% of TIC)	0.01	0.23	0.35	4.58	2.78	2.28	2.82	2.46	7.40	26.52	3.89	3.84	3.07
Rel. Inten.(% of BP)	0.03	0.88	1.31	17.27	10.49	8.61	10.63	9.26	27.90	100.00	14.67	14.49	11.56
Score	0.20	0.50	0.22	0.50	1.50	0.75	-0.11	-0.09	0.50	1.50	-0.15	0.75	-0.12
Ion-type	PR	V	LI	AL-28	y_1	AL			LTA-H_2O	y_2		LTA	
Delta ppm	-3.2	-3.8	-3.8	-15.5	-24.9	10.0			-13.7	6.6		1.6	

Fragment-ion (m/z)	345.140	367.229	395.230	416.231	449.694	513.317	597.319	672.296^{+2}	794.345^{+2}	812.870^{+2}	843.853	1039.429
Frac. Inten.(% of TIC)	2.72	2.55	2.41	3.74	2.24	4.64	2.59	2.52	6.95	4.33	2.44	2.62
Rel. Inten.(% of BP)	10.24	9.61	9.10	14.10	8.46	17.48	9.78	9.52	26.22	16.34	9.19	9.89
Score	0.75	-0.10	-0.09	1.50	0.50	0.75	-0.10	-0.10	1.50	-0.16	-0.09	-0.10
Ion-type	SEQ			y_4	$b{+}{+}_8$	LTAVQ			y_{17}^{+2}			
Delta ppm	-3.7			13.9	-31.5	23.9			-33.0			

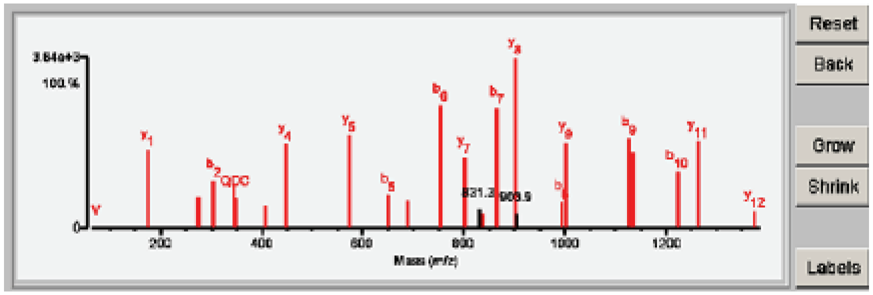


I91

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.68	97.8	16	2/26	(G) D V\C\Q D\C|I|Q|M|V|T/D/I/Q/T/A/V/R (T)	2126.8386	0.0058	2.7	68113.1/5.07	HUMAN	P07602	683787	Proactivator polypeptide precursor [Contains: Saposin-A - Homo sapiens (Human)

Fragment-Ion (m/z)	72.079	175.119	274.190	303.100	346.226	347.101	408.113	446.267	574.329	649.199	687.410	752.202	802.437	831.288	837.300	866.289	903.484	908.913	993.330	1002.651	1124.387	1133.590	1223.454	1261.661	1374.722
Frac. Inten.(% of TIC)	0.04	5.39	2.15	3.25	3.04	2.05	1.53	5.72	6.34	2.23	1.82	8.41	4.89	1.27	0.98	8.28	11.69	0.92	1.73	5.86	6.18	5.22	3.89	5.94	1.17
Rel. Inten.(% of BP)	0.37	46.07	18.37	27.79	26.02	17.54	13.05	48.89	54.21	19.09	15.60	71.95	41.84	10.88	8.34	70.76	100.00	7.88	14.80	50.11	52.82	44.65	33.30	50.76	10.01
Score	0.50	1.50	1.50	0.50	1.50	0.75	0.50	1.50	1.50	0.50	1.50	0.50	1.50	-0.11	0.50	0.50	1.50	-0.08	0.50	1.50	0.50	1.50	0.50	1.50	1.50
Ion-type	V	y_1	y_2	b_2	y_3	QDC	b_3	y_4	y_5	b_5	y_6	b_6	y_7		a_7	b_7	y_8		b_8	y_9	b_9	y_{10}	b_{10}	y_{11}	y_{12}
Delta ppm	-27.4	-1.4	8.9	-5.3	4.4	-4.5	4.7	-10.4	-3.7	3.2	-7.0	-5.7	-5.4		5.7	-1.4	-6.6		-19.2	-6.5	-1.7	-7.3	-2.8	-4.9	-13.9

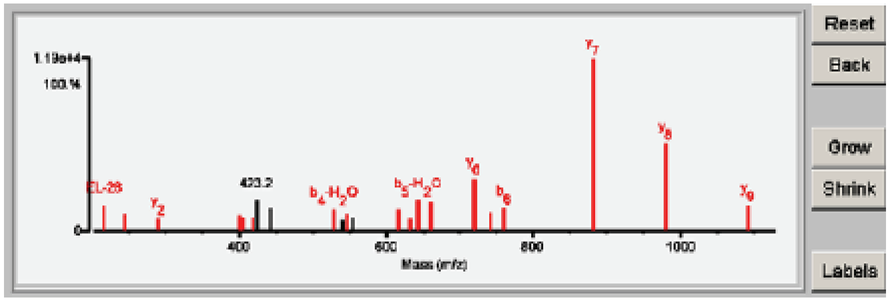


I92

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.82	84.6	8	6/25	(R) E L S\E|L|V|Y/T/D V/L/D R (S)	1639.7884	-0.0010	-0.6	20694.6/5.37	HUMAN	Q8WU39	399501	Proapoptotic caspase adapter protein precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	199.074	215.138	243.134	290.143	400.152	403.223	418.158	423.185	441.195	528.193	540.278	547.204	564.282	617.319	632.288	642.278	660.290	718.368	741.346	759.360	881.433	980.502	1093.587	1397.864
Frac. Inten.(% of TIC)	0.10	2.06	3.54	2.32	1.65	2.22	1.99	1.91	4.26	3.16	2.98	1.61	2.35	1.93	2.90	1.83	4.28	3.93	7.18	2.48	3.21	23.91	12.15	3.52	2.52
Rel. Inten.(% of BP)	0.42	8.62	14.78	9.68	6.88	9.30	8.32	7.98	17.81	13.21	12.47	6.72	9.84	8.07	12.14	7.64	17.92	16.43	30.03	10.39	13.42	100.00	50.79	14.73	10.56
Score	0.22	-0.09	0.50	0.75	1.50	0.25	1.50	0.50	-0.18	-0.13	0.25	-0.07	0.50	-0.08	1.50	0.50	0.25	0.50	1.50	0.25	0.50	1.50	1.50	1.50	-0.11
Ion-type	LI		EL-28	EL	y_2	b_3-H_2O	y_3	b_3			b_4-H_2O		b_4		y_5	a_5	b_5-H_2O	b_5	y_6	b_6-H_2O	b_6	y_7	y_8	y_9	
Delta ppm	-2.6		-8.9	-3.8	-11.0	-7.2	-17.5	-17.6			-9.2		-6.8		-10.1	-15.0	-3.5	-3.6	-7.2	-4.5	-13.2	-3.3	-2.4	-1.6	



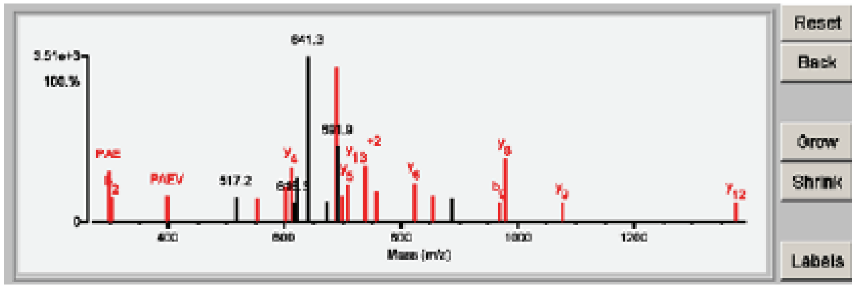
I93

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.83	63.8	8	8/26	(N) I/T|P A E|V|G\V|L|V/G K D R (S)	1676.8499	0.0043	2.5	15054.3/8.44	HUMAN	P07737	436225	Profilin-1 - Homo sapiens (Human)

Fragment-Ion (m/z)	74.058	298.141	303.145	397.206	517.218	553.296	600.273	610.282	616.282	620.367^{+2}	641.336^{+2}	670.874^{+2}	687.862^{+2}
Frac. Inten.(% of TIC)	2.39	4.72	2.26	2.36	2.23	2.08	3.26	4.97	1.75	4.07	14.95	1.84	13.97
Rel. Inten.(% of BP)	15.99	31.57	15.14	15.76	14.94	13.91	21.82	33.27	11.68	27.23	100.00	12.32	93.45
Score	-0.16	0.75	0.50	0.75	-0.15	0.75	0.50	1.50	-0.12	-0.27	-1.00	-0.12	1.50
Ion-type		PAE	b_2	PAEV		PAEVGV	b_5	y_4					y_{12}^{+2}
Delta ppm		1.5	22.8	-8.0		-5.5	2.9	8.2					-1.7

Fragment-Ion (m/z)	691.858^{+2}	699.331	709.345	738.390^{+2}	756.364	822.431	855.422	886.466	968.507	978.526	1077.573	1374.720
Frac. Inten.(% of TIC)	6.87	2.35	3.36	5.02	2.70	3.56	2.30	2.09	1.69	5.66	1.79	1.77
Rel. Inten.(% of BP)	45.95	15.69	22.47	33.57	18.07	23.78	15.41	14.00	11.28	37.86	11.95	11.83
Score	-0.46	0.50	1.50	1.50	0.50	1.50	0.50	-0.14	0.50	1.50	1.50	1.50
Ion-type		b_6	y_5	y_{13}^{+2}	b_7	y_6	b_8		b_9	y_8	y_9	y_{12}
Delta ppm		-12.3	-0.1	3.7	4.4	2.7	-8.0		-7.7	7.3	-12.1	0.5



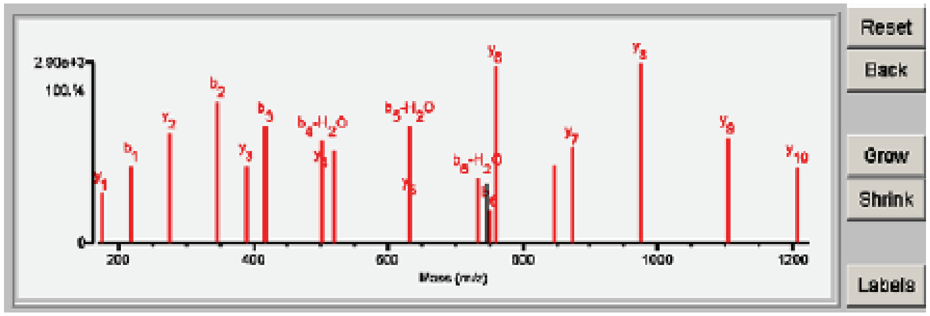
I94

Detailed Results

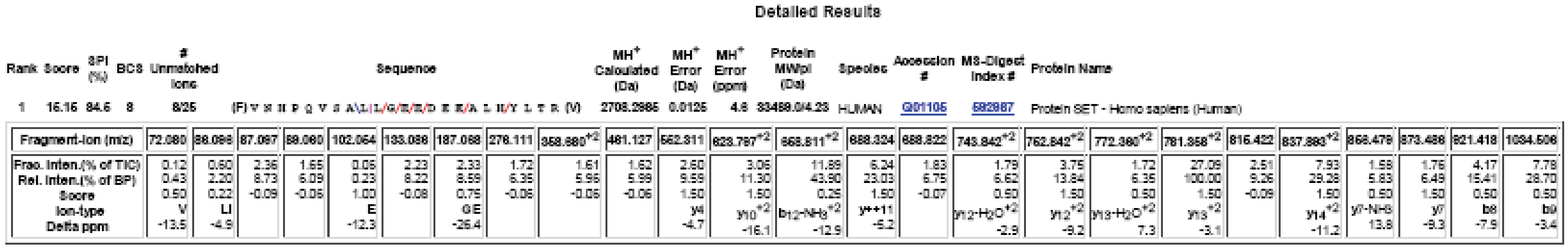
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.13	88.4	12	6/26	(H) E\E\A|T|M/T|I/E/E/L/L/T/R (Y)	1623.7604	-0.0009	-0.6	59271.8/4.27	HUMAN	O15355	428583	Protein phosphatase 1G - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.096	120.079	136.076	166.084	175.117	218.048	276.164	347.091	389.250	418.127	501.167	502.339
Frac. Inten.(% of TIC)	4.37	0.25	2.13	2.59	1.62	2.38	3.67	5.24	6.78	3.72	5.62	4.88	3.41
Rel. Inten.(% of BP)	51.19	2.94	24.89	30.34	19.00	27.86	42.91	61.41	79.39	43.56	65.79	57.16	39.90
Score	-0.51	0.22	-0.25	-0.30	-0.19	1.50	0.50	1.50	0.50	1.50	0.50	0.25	1.50
Ion-type		LI				y_1	b_1	y_2	b_2	y_3	b_3	b_4-H_2O	y_4
Delta ppm		-2.6				-13.4	-2.5	-8.1	-3.0	-1.3	-5.6	1.3	8.4

Fragment-Ion (m/z)	519.177	631.367	632.196	733.243	746.388	751.259	760.413	846.338	873.499	974.553	1105.591	1206.622
Frac. Inten.(% of TIC)	4.39	2.08	5.56	3.11	2.87	1.57	8.34	3.74	4.52	8.54	4.99	3.63
Rel. Inten.(% of BP)	51.44	24.41	65.06	36.36	33.57	18.41	97.60	43.81	52.94	100.00	58.43	42.45
Score	0.50	1.50	0.25	0.25	-0.34	0.50	1.50	0.25	1.50	1.50	1.50	1.50
Ion-type	b_4	y_5	b_5-H_2O	b_6-H_2O		b_6	y_6	b_7-H_2O	y_7	y_8	y_9	y_{10}
Delta ppm	-0.3	-16.9	-17.0	-14.9		-7.7	-9.3	-0.8	-6.0	1.4	-0.8	-14.4



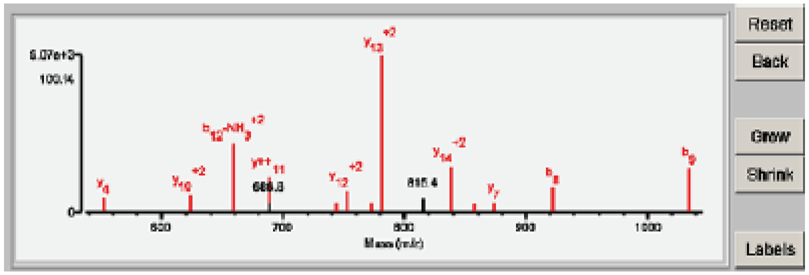
I95



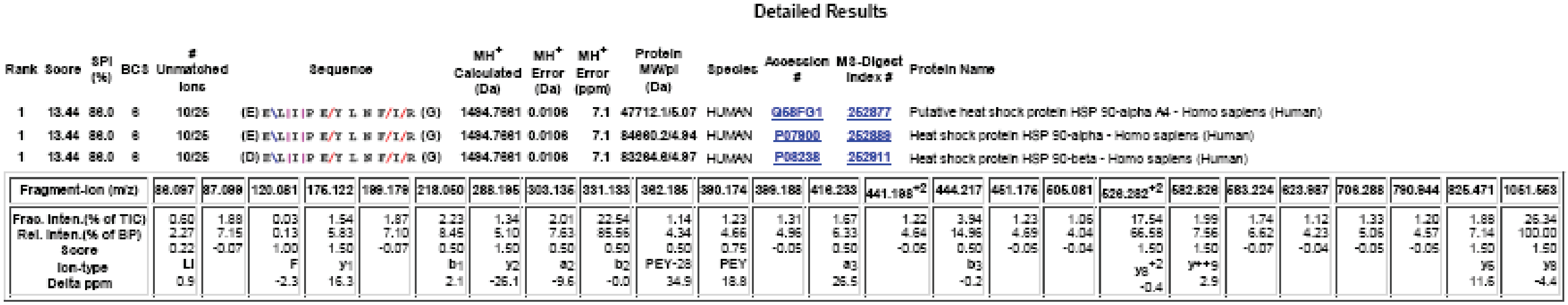
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.16	84.6	8	8/25	(F) V N H P Q V S A\L|L/G/E/E/D E E/A L H/Y L T R (V)	2708.2985	0.0125	4.6	33489.0/4.23	HUMAN	Q01105	692987	Protein SET - Homo sapiens (Human)

Fragment-Ion (m/z)	72.080	86.096	87.097	89.060	102.064	133.098	187.068	278.111	358.680^{+2}	481.127	562.311	623.797^{+2}	668.811^{+2}	688.324	688.822	743.842^{+2}	762.842^{+2}	772.360^{+2}	781.358^{+2}	816.422	837.883^{+2}	868.479	873.488	921.418	1034.506
Frac. Inten.(% of TIC)	0.12	0.60	2.36	1.65	0.06	2.23	2.33	1.72	1.61	1.62	2.60	3.06	11.89	6.24	1.83	1.79	3.75	1.72	27.09	2.51	7.93	1.58	1.76	4.17	7.78
Rel. Inten.(% of BP)	0.43	2.20	8.73	6.09	0.23	8.22	8.59	6.35	5.96	5.99	9.59	11.30	43.90	23.03	6.75	6.62	13.84	6.35	100.00	9.26	29.28	5.83	6.49	15.41	28.70
Score	0.50	0.22	-0.09	-0.06	1.00	-0.08	0.75	-0.06	-0.06	-0.06	1.50	1.50	0.25	1.50	-0.07	0.50	1.50	0.50	1.50	-0.09	1.50	0.50	1.50	0.50	0.50
Ion-type	V	LI			E		GE				y_4	y_{10}^{+2}	b_{12}-NH$_3^{+2}$	y++11		y_{12}-H$_2$O^{+2}	y_{12}^{+2}	y_{13}-H$_2$O^{+2}	y_{13}^{+2}		y_{14}^{+2}	y_7-NH$_3$	y_7	b_8	b_9
Delta ppm	-13.5	-4.9			-12.3		-26.4				-4.7	-16.1	-12.9	-5.2		-2.9	-9.2	7.3	-3.1		-11.2	13.8	-9.3	-7.9	-3.4



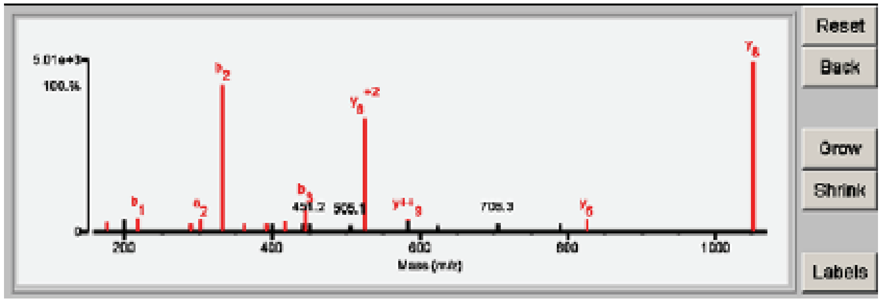
I96



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.44	88.0	6	10/25	(E) E\L|I|P E/Y L N F/I/R (G)	1494.7881	0.0106	7.1	47712.1/5.07	HUMAN	Q58FG1	252877	Putative heat shock protein HSP 90-alpha A4 - Homo sapiens (Human)
1	13.44	88.0	6	10/25	(E) E\L|I|P E/Y L N F/I/R (G)	1494.7881	0.0106	7.1	84660.2/4.94	HUMAN	P07900	252889	Heat shock protein HSP 90-alpha - Homo sapiens (Human)
1	13.44	88.0	6	10/25	(D) E\L|I|P E/Y L N F/I/R (G)	1494.7881	0.0106	7.1	83264.8/4.97	HUMAN	P08238	252811	Heat shock protein HSP 90-beta - Homo sapiens (Human)

Fragment-Ion (m/z)	86.097	87.099	120.081	176.122	199.179	218.050	288.185	303.136	331.133	382.185	390.174	399.188	416.233	441.198^{+2}	444.217	461.176	505.081	528.282^{+2}	582.826	583.224	623.887	706.288	790.944	825.471	1051.563
Frac. Inten.(% of TIC)	0.60	1.88	0.03	1.54	1.87	2.23	1.34	2.01	22.54	1.14	1.23	1.31	1.67	1.22	3.94	1.23	1.06	17.54	1.99	1.74	1.12	1.33	1.20	1.88	26.34
Rel. Inten.(% of BP)	2.27	7.15	0.13	5.83	7.10	8.45	5.10	7.63	85.56	4.34	4.66	4.96	6.33	4.64	14.96	4.69	4.04	66.58	7.56	6.62	4.23	5.06	4.57	7.14	100.00
Score	0.22	-0.07	1.00	1.50	-0.07	0.50	1.50	0.50	0.50	0.50	0.75	-0.05	0.50	-0.05	0.50	-0.05	-0.04	1.50	1.50	-0.07	-0.04	-0.05	-0.05	1.50	1.50
Ion-type	LI		F	y_1		b_1	y_2	a_2	b_2	PEY-28	PEY		a_3		b_3			y_8^{+2}	y++9					y_6	y_8
Delta ppm	0.9		-2.3	16.3		2.1	-26.1	-9.6	-0.0	34.9	18.8		26.5		-0.2			-0.4	2.9					11.6	-4.4



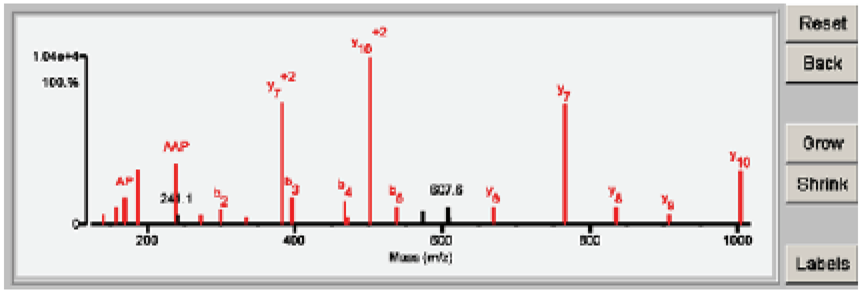
I97

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.13	84.2	7	4/26	(G) P\L|P|A|A|P/P V/A P E R (Q)	1302.6875	-0.0033	-2.6	129932.0/4.43	HUMAN	Q9NQC3	675907	Reticulon-4 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	86.097	141.103	158.061	169.094	186.058	240.132	241.134	271.142	299.139	334.691^{+2}	383.216^{+2}	396.193
Frac. Inten.(% of TIC)	0.00	0.03	1.35	2.16	3.10	6.54	7.32	1.09	1.09	1.80	0.95	14.60	3.08
Rel. Inten.(% of BP)	0.01	0.16	6.74	10.79	15.48	32.65	36.56	5.43	5.43	9.02	4.75	72.96	15.40
Score	0.20	0.22	0.50	0.50	0.75	0.50	0.75	-0.05	0.50	0.50	1.50	1.50	0.50
Ion-type	PR	LI	AP-28	a_1	AP	b_1	AAP		a_2	b_2	y_6^{+2}	y_7^{+2}	b_3
Delta ppm	8.2	9.0	-5.2	-19.7	-24.0	-7.6	-11.9		-22.4	-14.3	2.3	-0.6	-8.2

Fragment-Ion (m/z)	467.232	472.248	502.782^{+2}	538.263	573.786^{+2}	607.667	608.967	668.369	765.422	836.469	907.490	1004.546
Frac. Inten.(% of TIC)	2.79	0.87	20.01	2.09	1.64	2.17	0.87	2.13	14.35	2.20	1.31	6.46
Rel. Inten.(% of BP)	13.94	4.33	100.00	10.46	8.20	10.82	4.36	10.64	71.72	11.01	6.53	32.26
Score	0.50	1.50	1.50	0.50	-0.08	-0.11	-0.04	1.50	1.50	1.50	1.50	1.50
Ion-type	b_4	y_4	y_{10}^{+2}	b_5				y_6	y_7	y_8	y_9	y_{10}
Delta ppm	-2.1	-6.2	4.5	-13.3				-5.2	-4.0	7.4	-10.2	-7.6



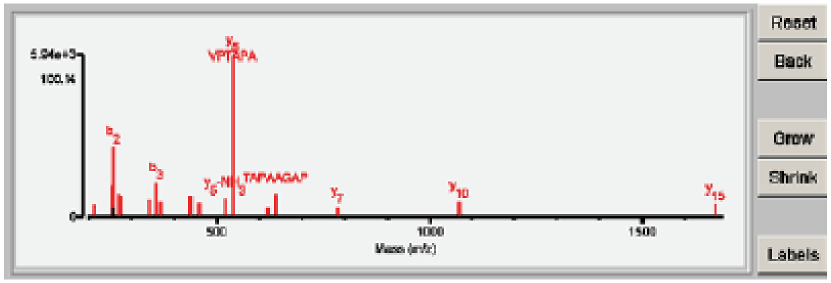
I98

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.08	80.6	7	3/25	(A) A P\V\P T A P A A G A/P L M D F/G N D/F V/P P A/P R (G)	2664.2949	0.0048	1.8	129932.0/4.43	HUMAN	Q9NQC3	675907	Reticulon-4 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.066	72.080	86.096	120.081	128.060	169.128	211.143	252.133	257.094	258.099	269.161	270.161	272.170
Frac. Inten.(% of TIC)	0.02	0.12	0.23	0.12	2.85	4.87	1.94	5.40	11.96	1.74	3.84	2.26	3.57
Rel. Inten.(% of BP)	0.06	0.44	0.82	0.43	10.26	17.58	6.98	19.50	43.14	6.29	13.86	8.16	12.89
Score	0.20	0.50	0.22	1.00	-0.10	-0.18	0.75	0.50	0.50	-0.06	1.50	0.75	1.50
Ion-type	PR	V	LI	F			PL	TAP-H_2O	b_2		y^{++}_5	TAP	y_2
Delta ppm	8.2	-16.3	-2.6	5.2			-9.5	-10.2	-7.9		1.8	19.5	-6.7

Fragment-Ion (m/z)	340.194	356.163	368.193	439.224	457.212	520.286	537.313	619.318	637.333	783.450	1089.525	1672.806
Frac. Inten.(% of TIC)	2.92	5.76	2.66	3.74	2.43	3.25	27.72	1.76	3.92	1.87	2.81	2.24
Rel. Inten.(% of BP)	10.53	20.78	9.60	13.48	8.76	11.72	100.00	6.34	14.14	6.73	10.15	8.09
Score	0.50	0.50	0.75	0.75	0.75	0.50	1.50	0.50	0.75	1.50	1.50	1.50
Ion-type	AAGAP-28	b_3	AAGAP	APAAGA	PLMD	y_5-NH_3	y_5 -3.3 VPTAPA	TAPAAGAP-H_2O	TAPAAGAP	y_7	y_{10}	y_{15}
Delta ppm	-11.3	-6.6	1.2	-16.1	-0.9	-5.8	15.6	-5.1	2.5	-1.0	-16.0	-5.2



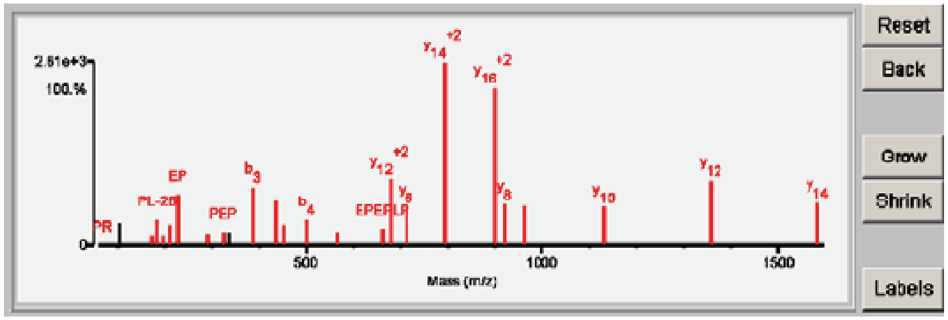
I99

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.51	96.6	9	2/25	(L) A/M|P\L|P E/P E/P L/P L/P L E V V/R (G)	2085.1123	0.0116	5.6	50414.3/9.65	HUMAN	Q9BTD8	470709	RNA-binding protein 42 - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	104.054	175.115	183.150	199.103	211.140	227.103	291.081	324.154	337.198	388.135	437.234	453.187
Frac. Inten.(% of TIC)	0.00	2.18	0.94	2.56	0.92	2.10	4.97	1.17	1.32	1.26	5.68	4.36	2.11
Rel. Inten.(% of BP)	0.02	12.27	5.27	14.39	5.17	11.81	28.00	6.60	7.42	7.12	31.97	24.57	11.90
Score	0.20	-0.12	1.50	0.50	0.50	0.75	0.75	0.50	0.75	-0.07	0.50	0.75	0.75
Ion-type	PR		y_1	PL-28	EP-28	PL	EP	b_2	PEP		b_3	EPLP	EPEP
Delta ppm	28.2		-22.6	-3.8	-28.2	-27.0	-3.7	-12.6	-9.2		-5.2	-14.5	-27.1

Fragment-ion (m/z)	501.204	566.843	663.332	679.905^{+2}	712.435	792.956^{+2}	898.020^{+2}	922.581	963.551^{+2}	1132.713	1358.786	1584.893
Frac. Inten.(% of TIC)	2.52	1.27	1.63	6.39	3.66	17.76	15.19	4.00	3.89	3.66	6.24	4.22
Rel. Inten.(% of BP)	14.22	7.16	9.16	35.95	20.60	100.00	85.51	22.53	21.88	20.62	35.11	23.78
Score	0.50	1.50	0.75	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50
Ion-type	b_4	$y{+}{+}_{10}$	EPEPLP	y_{12}^{+2}	y_6	y_{14}^{+2}	y_{16}^{+2}	y_8	y_{17}^{+2}	y_{10}	y_{12}	y_{14}
Delta ppm	-33.3	-26.0	-6.5	-0.5	0.1	3.6	-1.7	9.3	9.0	3.5	-13.8	-4.4



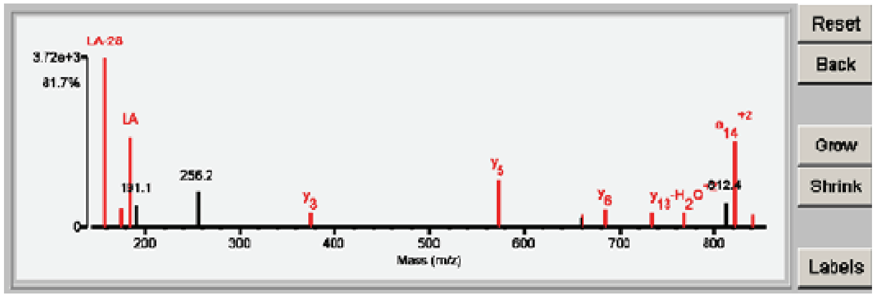
I100

Detailed Results

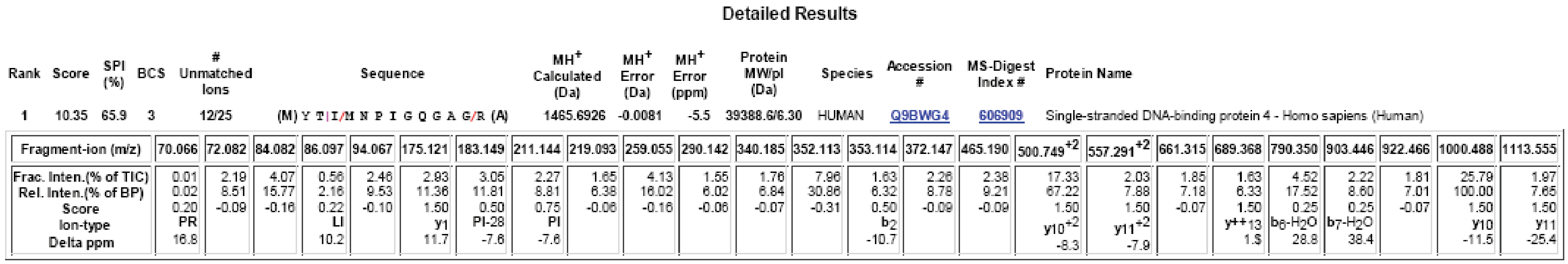
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.53	54.3	6	7/25	(M) A L A F S/E Q E E/H E/L/P V/L S/R (Q)	2042.9852	0.0355	17.4	41595.7/5.18	HUMAN	O75995	584219	SAM and SH3 domain-containing protein 3 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	86.097	101.069	110.072	120.081	157.133	175.119	185.128	191.118	256.165	375.241	571.366
Frac. Inten.(% of TIC)	0.00	0.04	0.49	0.04	0.07	0.11	17.39	2.07	9.34	2.32	3.65	1.57	4.96
Rel. Inten.(% of BP)	0.01	0.21	2.31	0.18	0.32	0.50	81.72	9.74	43.88	10.90	17.16	7.36	23.29
Score	0.20	0.50	0.22	0.50	1.00	1.00	0.50	1.50	0.75	-0.11	-0.17	1.50	1.50
Ion-type	PR	V	LI	QK	H	F	LA-28	y_1	LA			y_3	y_5
Delta ppm	5.3	4.5	6.7	-16.2	4.8	-0.6	-11.7	0.8	-7.3			16.4	16.4

Fragment-ion (m/z)	659.358	660.340^{+2}	684.443	733.365^{+2}	767.891^{+2}	811.886	812.379	820.890^{+2}	841.420^{+2}	894.426^{+2}	929.946^{+2}	950.544
Frac. Inten.(% of TIC)	1.19	1.40	1.84	1.54	1.49	1.65	2.58	8.79	1.41	13.01	21.28	1.79
Rel. Inten.(% of BP)	5.57	6.58	8.66	7.23	6.99	7.76	12.12	41.29	6.63	61.12	100.00	8.43
Score	-0.06	0.50	1.50	1.50	0.50	-0.08	-0.12	0.50	0.50	-0.61	-1.00	1.50
Ion-type		$y_{11}\text{-}NH_3^{+2}$	y_6	y_{12}^{+2}	$y_{13}\text{-}H_2O^{+2}$			a_{14}^{+2}	$y_{14}\text{-}H_2O^{+2}$			y_8
Delta ppm		10.2	4.3	-3.6	16.4			5.0	9.3			2.1



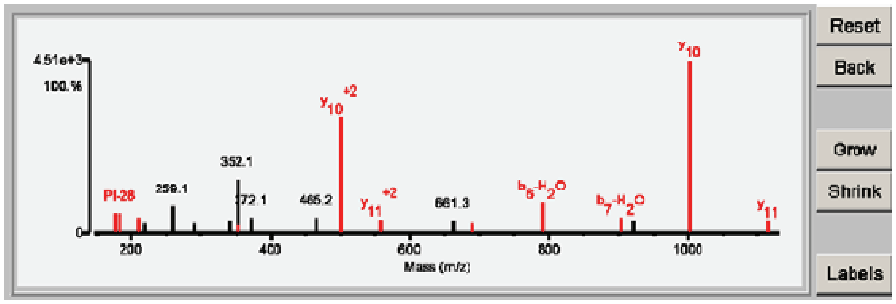
I101



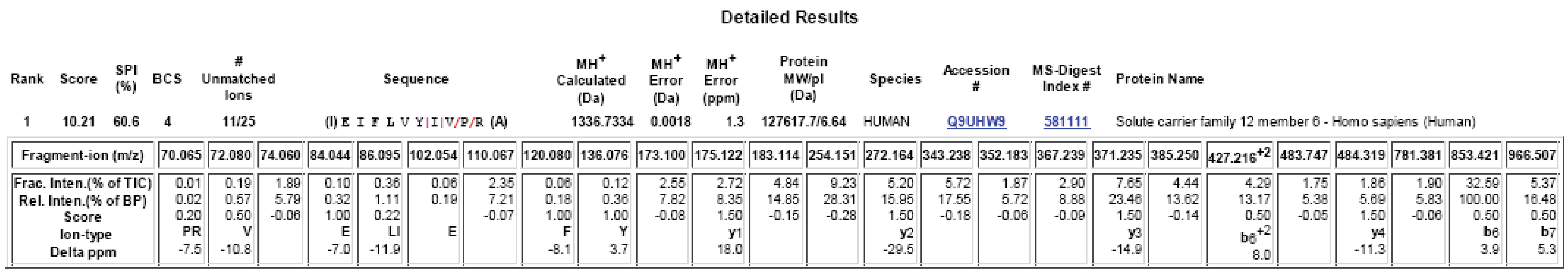
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.35	65.9	3	12/25	(M) Y T|I/M N P I G Q G A G/R (A)	1465.6926	-0.0081	-5.5	39388.6/6.30	HUMAN	Q9BWG4	606909	Single-stranded DNA-binding protein 4 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.082	86.097	94.067	175.121	183.149	211.144	219.093	259.055	290.142	340.185	352.113	353.114	372.147	465.190	500.749^{+2}	557.291^{+2}	661.315	689.368	790.350	903.446	922.466	1000.488	1113.555
Frac. Inten.(% of TIC)	0.01	2.19	4.07	0.56	2.46	2.93	3.05	2.27	1.65	4.13	1.55	1.76	7.96	1.63	2.26	2.38	17.33	2.03	1.85	1.63	4.52	2.22	1.81	25.79	1.97
Rel. Inten.(% of BP)	0.02	8.51	15.77	2.16	9.53	11.36	11.81	8.81	6.38	16.02	6.02	6.84	30.86	6.32	8.78	9.21	67.22	7.88	7.18	6.33	17.52	8.60	7.01	100.00	7.65
Score	0.20	-0.09	-0.16	0.22	-0.10	1.50	0.50	0.75	-0.06	-0.16	-0.06	-0.07	-0.31	0.50	-0.09	-0.09	1.50	1.50	-0.07	1.50	0.25	0.25	-0.07	1.50	1.50
Ion-type	PR			LI		y1	PI-28	PI						b_2			$y10^{+2}$	$y11^{+2}$		y^{++}_{13}	b_6-H_2O	b_7-H_2O		y10	y11
Delta ppm	16.8			10.2		11.7	-7.6	-7.6						-10.7			-8.3	-7.9		1.$	28.8	38.4		-11.5	-25.4



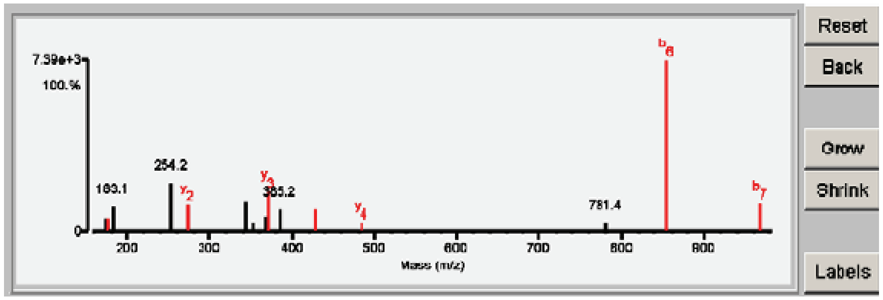
I102



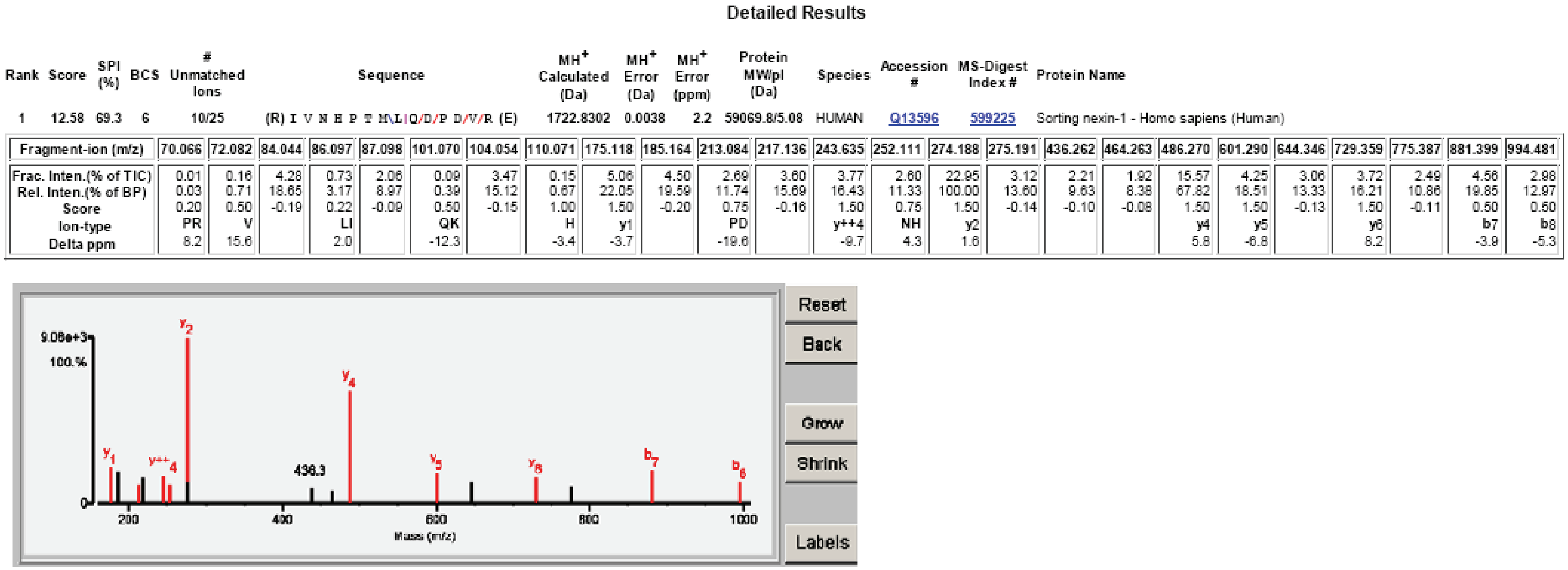
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.21	60.6	4	11/25	(I) E I F L V Y|I|V/P/R (A)	1336.7334	0.0018	1.3	127617.7/6.64	HUMAN	Q9UHW9	581111	Solute carrier family 12 member 6 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.080	74.060	84.044	86.095	102.054	110.067	120.080	136.076	173.100	175.122	183.114	254.151	272.164	343.238	352.183	367.239	371.235	385.250	427.216^{+2}	483.747	484.319	781.381	853.421	966.507
Frac. Inten.(% of TIC)	0.01	0.19	1.89	0.10	0.36	0.06	2.35	0.06	0.12	2.55	2.72	4.84	9.23	5.20	5.72	1.87	2.90	7.65	4.44	4.29	1.75	1.86	1.90	32.59	5.37
Rel. Inten.(% of BP)	0.02	0.57	5.79	0.32	1.11	0.19	7.21	0.18	0.36	7.82	8.35	14.85	28.31	15.95	17.55	5.72	8.88	23.46	13.62	13.17	5.38	5.69	5.83	100.00	16.48
Score	0.20	0.50	-0.06	1.00	0.22		-0.07	1.00	1.00	-0.08	1.50	-0.15	-0.28	1.50	-0.18	-0.06	-0.09	1.50	-0.14	0.50	-0.05	1.50	-0.06	0.50	0.50
Ion-type	PR	V		E	LI	E		F	Y		y1			y2				y3		$b6^{+2}$		y4		b6	b7
Delta ppm	-7.5	-10.8		-7.0	-11.9			-8.1	3.7		18.0			-29.5				-14.9		8.0		-11.3		3.9	5.3



I103



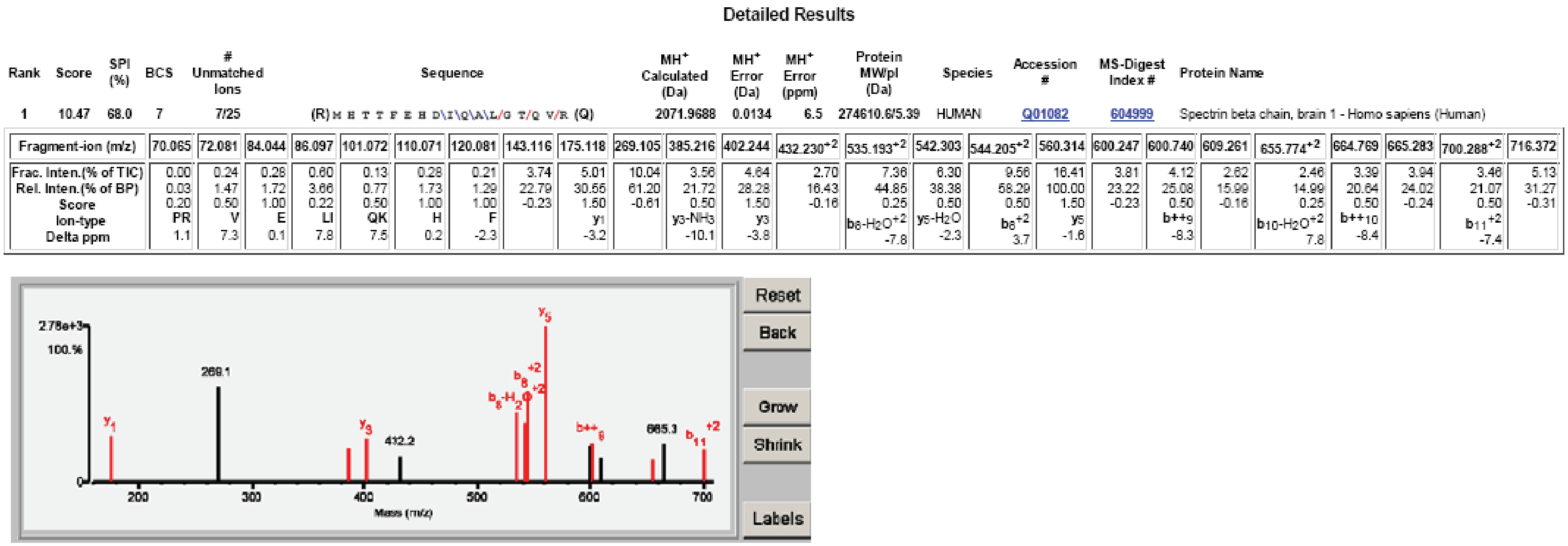
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.58	69.3	6	10/25	(R) I V N E P T M\L|Q/D/P D/V/R (E)	1722.8302	0.0038	2.2	59069.8/5.08	HUMAN	Q13596	599225	Sorting nexin-1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.044	86.097	87.098	101.070	104.054	110.071	175.118	185.164	213.084	217.136
Frac. Inten.(% of TIC)	0.01	0.16	4.28	0.73	2.06	0.09	3.47	0.15	5.06	4.50	2.69	3.60
Rel. Inten.(% of BP)	0.03	0.71	18.65	3.17	8.97	0.39	15.12	0.67	22.05	19.59	11.74	15.69
Score	0.20	0.50	-0.19	0.22	-0.09	0.50	-0.15	1.00	1.50	-0.20	0.75	-0.16
Ion-type	PR	V		LI		QK		H	y1		PD	
Delta ppm	8.2	15.6		2.0		-12.3		-3.4	-3.7		-19.6	

Fragment-ion (m/z)	243.635	252.111	274.188	275.191	436.262	464.263	486.270	601.290	644.346	729.359	775.387	881.399	994.481
Frac. Inten.(% of TIC)	3.77	2.60	22.95	3.12	2.21	1.92	15.57	4.25	3.06	3.72	2.49	4.56	2.98
Rel. Inten.(% of BP)	16.43	11.33	100.00	13.60	9.63	8.38	67.82	18.51	13.33	16.21	10.86	19.85	12.97
Score	1.50	0.75	1.50	-0.14	-0.10	-0.08	1.50	1.50	-0.13	1.50	-0.11	0.50	0.50
Ion-type	y++4	NH	y2				y4	y5		y6		b7	b8
Delta ppm	-9.7	4.3	1.6				5.8	-6.8		8.2		-3.9	-5.3

I104



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.47	68.0	7	7/25	(R) M E T T F E H D\I\Q\A\L/G T/Q V/R (Q)	2071.9688	0.0134	6.5	274610.6/5.39	HUMAN	Q01082	604999	Spectrin beta chain, brain 1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.081	84.044	86.097	101.072	110.071	120.081	143.116	175.118	269.105	385.216	402.244	432.230^{+2}
Frac. Inten.(% of TIC)	0.00	0.24	0.28	0.60	0.13	0.28	0.21	3.74	5.01	10.04	3.56	4.64	2.70
Rel. Inten.(% of BP)	0.03	1.47	1.72	3.66	0.77	1.73	1.29	22.79	30.55	61.20	21.72	28.28	16.43
Score	0.20	0.50	1.00	0.22	0.50	1.00	1.00	-0.23	1.50	-0.61	0.50	1.50	-0.16
Ion-type	PR	V	E	LI	QK	H	F		y_1		y_3-NH_3	y_3	
Delta ppm	1.1	7.3	0.1	7.8	7.5	0.2	-2.3		-3.2		-10.1	-3.8	

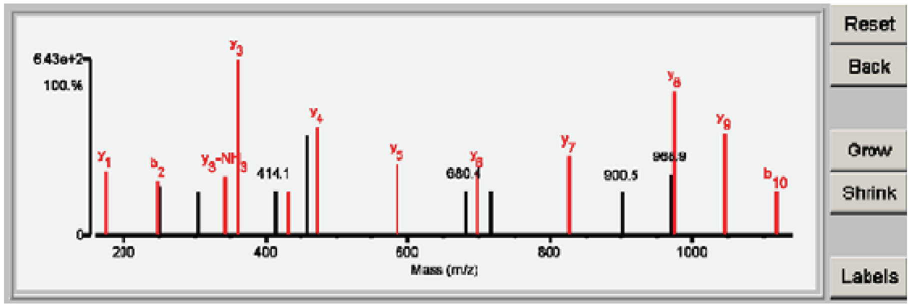
Fragment-ion (m/z)	535.193^{+2}	542.303	544.205^{+2}	560.314	600.247	600.740	609.261	655.774^{+2}	664.769	665.283	700.288^{+2}	716.372
Frac. Inten.(% of TIC)	7.36	6.30	9.56	16.41	3.81	4.12	2.62	2.46	3.39	3.94	3.46	5.13
Rel. Inten.(% of BP)	44.85	38.38	58.29	100.00	23.22	25.08	15.99	14.99	20.64	24.02	21.07	31.27
Score	0.25	0.50	0.50	1.50	-0.23	0.50	-0.16	0.25	0.50	-0.24	0.50	-0.31
Ion-type	b_8-H_2O^{+2}	y_5-H_2O	b_8^{+2}	y_5		b^{++}_9		b_{10}-H_2O^{+2}	b^{++}_{10}		b_{11}^{+2}	
Delta ppm	-7.8	-2.3	3.7	-1.6		-8.3		7.8	-8.4		-7.4	

I105

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.10	63.6	9	10/25	(R) A S\G Q|A/F/E/L/I/L|S P/R (S)	1476.7515	0.0020	1.4	17302.6/5.76	HUMAN	P16949	610899	Stathmin - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.081	86.095	110.069	120.081	175.119	247.081	251.067	304.144	342.190	359.204	414.125	432.166	457.254	472.285	585.376	680.373	698.463	716.309^{+2}	827.501	900.451	968.900	974.571	1045.618	1118.560
Frac. Inten.(% of TIC)	0.01	5.13	0.38	4.44	0.14	4.00	3.40	3.15	2.65	3.67	10.98	2.79	2.72	6.28	6.73	4.46	2.81	3.98	2.76	4.95	2.65	3.77	9.00	6.36	2.78
Rel. Inten.(% of BP)	0.07	46.70	3.50	40.46	1.25	36.45	30.97	28.65	24.17	33.38	100.00	25.38	24.77	57.21	61.33	40.63	25.63	36.24	25.16	45.08	24.17	34.36	81.96	57.87	25.29
Score	0.20	-0.47	0.22	-0.40	1.00	1.50	0.50	-0.29	-0.24	0.50	1.50	-0.25	0.50	-0.57	1.50	1.50	-0.26	1.50	-0.25	1.50	-0.24	-0.34	1.50	1.50	0.50
Ion-type	PR		LI		F	y1	b2			y3-NH3	y3		b4		y4	y5		y6		y7			y8	y9	b10
Delta ppm	-13.2		-14.2		-2.3	1.4	19.0			36.3	0.7		23.7		-6.6	7.1		9.7		2.9			4.5	13.3	3.4

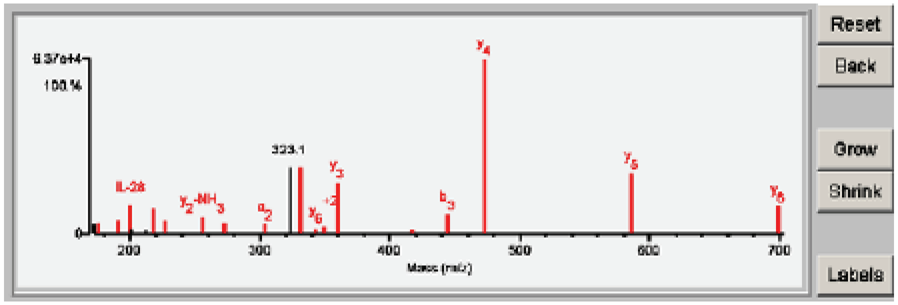


I106

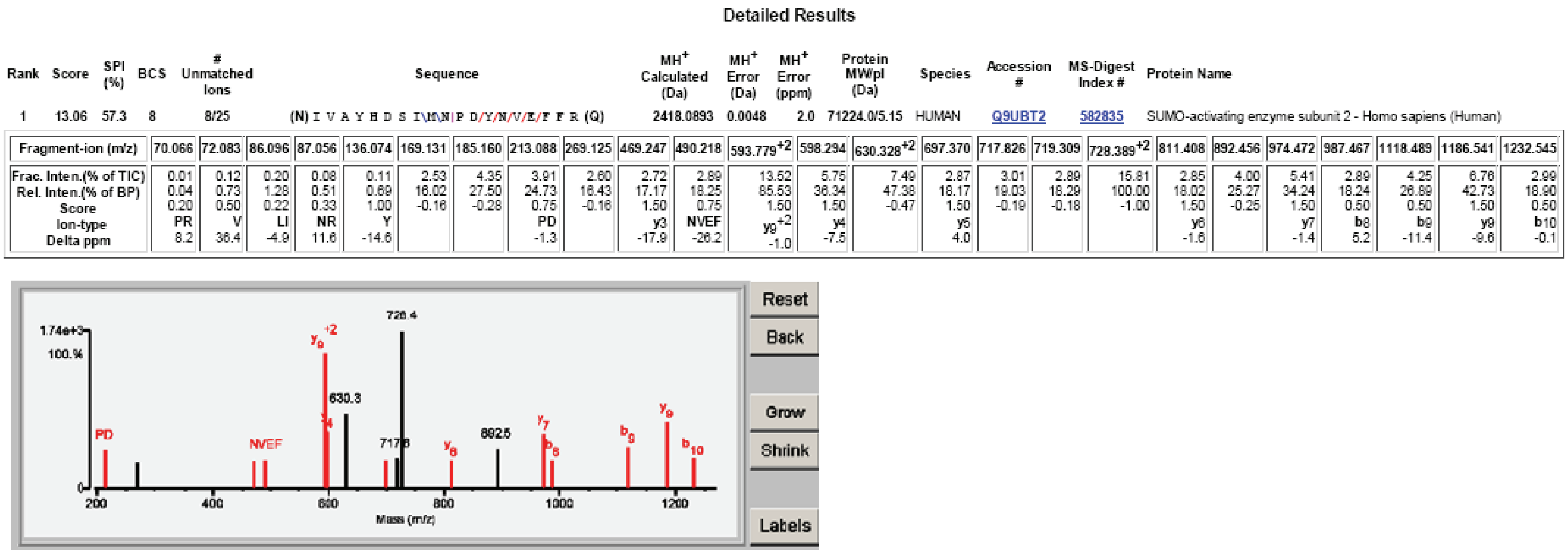
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.80	84.7	6	6/25	(F) E|L|I|L/S/P/R (S)	916.4988	0.0169	17.4	17302.6/5.76	HUMAN	P16949	610899	Stathmin - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	86.097	87.100	106.033	172.045	176.120	190.063	199.182	200.186	212.163	218.050	227.176	255.146	272.173	303.138	323.089	331.135	342.182	349.730^{+2}	359.206	416.221	444.220	472.290	586.374	698.462
Frac. Inten.(% of TIC)	0.00	0.82	1.68	0.68	1.46	1.69	2.13	4.51	0.69	0.64	3.95	1.93	2.58	1.75	1.39	10.14	10.09	0.88	1.01	7.94	0.63	3.17	26.75	9.35	4.16
Rel. Inten.(% of BP)	0.00	3.06	6.30	2.53	5.46	6.30	7.95	16.86	2.59	2.37	14.75	7.20	9.66	6.53	5.18	37.89	37.72	3.30	3.76	29.69	2.37	11.84	100.00	34.96	15.54
Score	0.20	0.22	-0.06	-0.03	-0.05	1.50	0.50	0.50	-0.03	-0.02	0.50	0.75	0.50	1.50	0.50	-0.38	0.50	0.50	1.50	1.50	0.50	0.50	1.50	1.50	1.50
Ion-type	PR	LI				y1	a1	IL-28			b1	IL	y2-NH3	y2	a2		b2	y3-NH3	$y6^{+2}$	y3	a3	b3	y4	y5	y6
Delta ppm	12.5	7.8				6.0	-4.9	0.6			4.3	-2.2	3.3	6.6	-2.6		4.8	14.3	-4.3	6.0	-4.2	6.1	5.1	3.8	8.3



I107

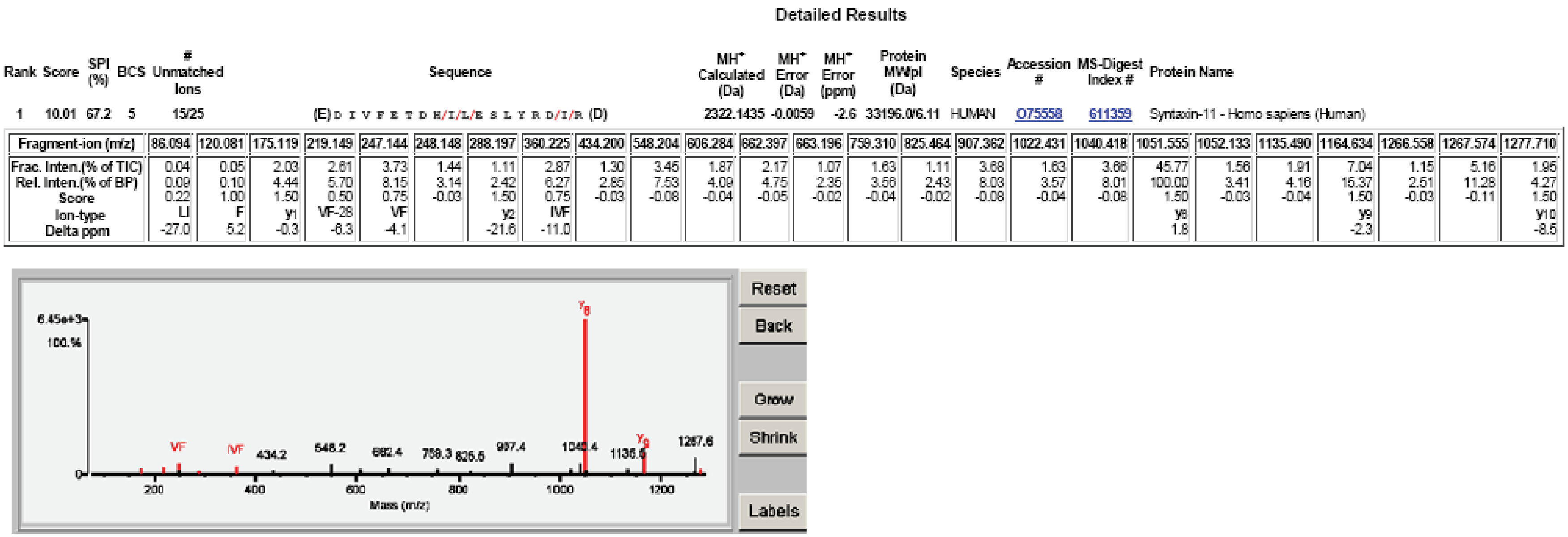


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.06	57.3	8	8/25	(N) I V A Y H D S I\M\N|P D/Y/N/V/E/F F R (Q)	2418.0893	0.0048	2.0	71224.0/5.15	HUMAN	Q9UBT2	582835	SUMO-activating enzyme subunit 2 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.083	86.096	87.056	136.074	169.131	185.160	213.088	269.125	469.247	490.218	593.779^{+2}	598.294	630.328^{+2}	697.370	717.826	719.309	728.389^{+2}	811.408	892.456	974.472	987.467	1118.489	1186.541	1232.545
Frac. Inten.(% of TIC)	0.01	0.12	0.20	0.08	0.11	2.53	4.35	3.91	2.60	2.72	2.89	13.52	5.75	7.49	2.87	3.01	2.89	15.81	2.85	4.00	5.41	2.89	4.25	6.76	2.99
Rel. Inten.(% of BP)	0.04	0.73	1.28	0.51	0.69	16.02	27.50	24.73	16.43	17.17	18.25	85.53	36.34	47.38	18.17	19.03	18.29	100.00	18.02	25.27	34.24	18.24	26.89	42.73	18.90
Score	0.20	0.50	0.22	0.33	1.00	-0.16	-0.28	0.75	-0.16	1.50	0.75	1.50	1.50	-0.47	1.50	-0.19	-0.18	-1.00	1.50	-0.25	1.50	0.50	0.50	1.50	0.50
Ion-type	PR	V	LI	NR	Y			PD		y3	NVEF	$y9^{+2}$	y4		y5				y6		y7	b8	b9	y9	b10
Delta ppm	8.2	36.4	-4.9	11.6	-14.6			-1.3		-17.9	-26.2	-1.0	-7.5		4.0				-1.6		-1.4	5.2	-11.4	-9.6	-0.1

I108



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.01	67.2	5	15/25	(E) D I V F E T D H/I/L/E S L Y R D/I/R (D)	2322.1435	-0.0059	-2.6	33196.0/6.11	HUMAN	O75558	611359	Syntaxin-11 - Homo sapiens (Human)

Fragment-ion (m/z)	86.094	120.081	175.119	219.149	247.144	248.148	288.197	360.225	434.200	548.204	606.284	662.397	663.196	759.310	825.464	907.362	1022.431	1040.418	1051.555	1052.133	1135.490	1164.634	1266.558	1267.574	1277.710
Frac. Inten.(% of TIC)	0.04	0.05	2.03	2.61	3.73	1.44	1.11	2.87	1.30	3.45	1.87	2.17	1.07	1.63	1.11	3.68	1.63	3.66	45.77	1.56	1.91	7.04	1.15	5.16	1.95
Rel. Inten.(% of BP)	0.09	0.10	4.44	5.70	8.15	3.14	2.42	6.27	2.85	7.53	4.09	4.75	2.35	3.56	2.43	8.03	3.57	8.01	100.00	3.41	4.16	15.37	2.51	11.28	4.27
Score	0.22	1.00	1.50	0.50	0.75	-0.03	1.50	0.75	-0.03	-0.08	-0.04	-0.05	-0.02	-0.04	-0.02	-0.08	-0.04	-0.08	1.50	-0.03	-0.04	1.50	-0.03	-0.11	1.50
Ion-type	LI	F	y1	VF-28	VF		y2	IVF											y8			y9			y10
Delta ppm	-27.0	5.2	-0.3	-6.3	-4.1		-21.6	-11.0											1.8			-2.3			-8.5

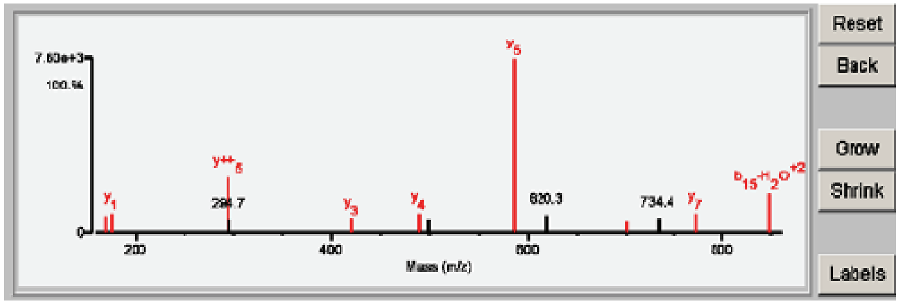
I109

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.71	64.9	6	11/25	(R) V G K V E H G S V/A/L/P/A/I M/R (S)	1886.9438	0.0124	6.6	269768.5/5.78	HUMAN	Q9Y490	650651	Talin-1 - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	72.082	86.097	94.065	110.070	141.102	143.068	157.098	169.096	175.118	294.173	294.669	419.241
Frac. Inten.(% of TIC)	0.01	0.58	0.44	7.28	0.13	2.04	2.00	1.96	2.70	3.35	9.19	2.10	2.44
Rel. Inten.(% of BP)	0.02	2.02	1.54	25.24	0.44	7.06	6.92	6.78	9.37	11.60	31.84	7.29	8.45
Score	0.20	0.50	0.22	-0.25	1.00	0.50	-0.07	-0.07	0.75	1.50	1.50	-0.07	1.50
Ion-type	PR	V	LI		H	PA-28			PA	y_1	y^{++}_5		y_3
Delta ppm	3.9	12.8	5.5		-8.8	-10.9			-14.5	-8.3	8.4		-6.9

Fragment-Ion (m/z)	490.277	498.214^{+2}	587.333	620.326^{+2}	700.407	734.373^{+2}	771.450	847.920^{+2}	897.445^{+2}	1094.475	1102.566	1207.562
Frac. Inten.(% of TIC)	3.37	2.06	28.85	2.77	1.93	2.22	3.39	6.54	3.76	5.66	2.87	2.37
Rel. Inten.(% of BP)	11.68	7.14	100.00	9.59	6.67	7.71	11.75	22.65	13.03	19.64	9.96	8.22
Score	1.50	-0.07	1.50	-0.10	1.50	-0.08	1.50	0.25	-0.13	-0.20	-0.10	-0.08
Ion-type	y_4		y_5		y_6		y_7	b_{15}-H_2O^{+2}				
Delta ppm	-6.4		-0.5		-14.9		-5.9	5.5				



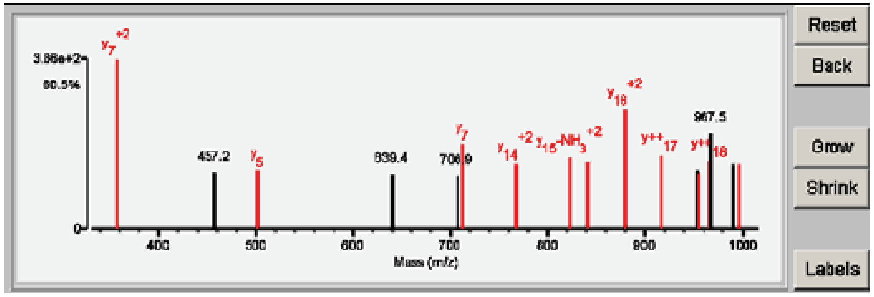
I110

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.63	54.1	9	9/25	(R) E G I S/Q E A L H T Q M L/T/A/V Q/E I S H L/I/E/P L/A N A A R (A)	3458.7407	0.0187	5.4	269768.5/5.78	HUMAN	Q9Y490	650651	Talin-1 - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	84.044	86.096	110.070	356.708^{+2}	457.241	502.274	639.352^{+2}	706.889	712.394	767.452^{+2}	822.930^{+2}
Frac. Inten.(% of TIC)	0.00	0.16	0.19	0.62	0.10	9.94	3.27	3.41	3.16	3.15	5.02	3.83	4.19
Rel. Inten.(% of BP)	0.02	0.98	1.15	3.79	0.61	60.46	19.87	20.73	19.22	19.16	30.55	23.31	25.46
Score	0.20	0.50	1.00	0.22	1.00	1.50	-0.20	1.50	-0.19	-0.19	1.50	1.50	0.50
Ion-type	PR	V	E	LI	H	y_7^{+2}		y_5			y_7	y_{14}^{+2}	y_{15}-NH_3^{+2}
Delta ppm	11.1	18.4	1.3	-1.5	-7.9	-2.4		1.4			-22.8	37.7	-10.3

Fragment-ion (m/z)	841.454	880.989^{+2}	916.509	952.830	953.185	954.553	967.037	967.483	990.543^{+3}	995.529^{+3}	1053.887^{+3}	1058.531^{+2}
Frac. Inten.(% of TIC)	3.99	7.05	4.38	3.48	3.48	3.26	4.05	5.55	3.88	3.86	16.44	3.55
Rel. Inten.(% of BP)	24.29	42.90	26.66	21.16	21.16	19.82	24.67	33.79	23.61	23.51	100.00	21.57
Score	1.50	1.50	1.50	-0.21	-0.21	1.50	1.50	-0.34	-0.24	1.50	-1.00	-0.22
Ion-type	y_8	y_{16}^{+2}	y^{++}_{17}			y_9	y^{++}_{18}			y_{27}^{+3}		
Delta ppm	1.4	3.2	4.3			16.9	8.3			3.3		

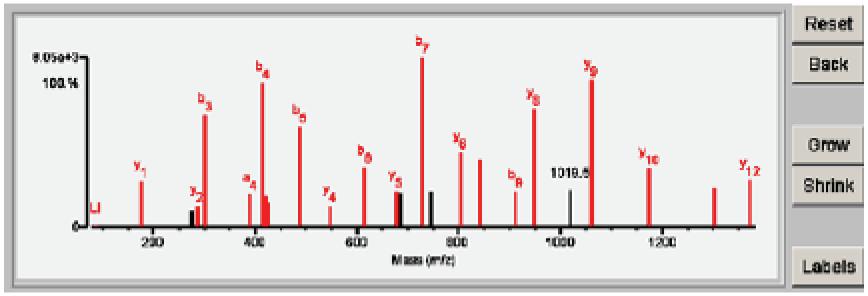


I111

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.75	91.8	13	4/26	(M) V G G\I|A|Q|I|I|A\A/Q/E/E/M/L/R (K)	1788.9190	-0.0073	-4.1	269768.5/6.78	HUMAN	Q9Y490	850651	Talin-1 - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	176.117	276.113	288.201	302.116	387.204	415.200	419.242	426.272	486.236	548.279	614.288	677.323	684.403	727.380	744.789⁺²	806.378	840.461	911.502	947.456	1019.614	1060.645	1173.629	1301.671	1372.708
Frac. Inten.(% of TIC)	0.14	3.02	1.14	1.36	7.46	2.21	9.51	2.11	1.56	6.66	1.38	3.99	2.37	2.26	11.23	2.32	4.98	4.46	2.32	7.78	2.44	9.76	3.85	2.55	3.14
Rel. Inten.(% of BP)	1.28	26.87	10.13	12.15	66.48	19.65	84.75	18.76	13.93	59.32	12.34	35.51	21.14	20.11	100.00	20.71	44.36	39.72	20.63	69.26	21.75	86.96	34.27	22.74	27.94
Score	0.22	1.50	-0.10	1.50	0.50	0.50	0.50	1.50	0.75	0.50	1.50	0.50	1.50	-0.20	0.50	-0.21	1.50	0.50	0.50	1.50	-0.22	1.50	1.50	1.50	1.50
Ion-type	LI	y1		y2	b3	a4	b4	y3	QIIA	b5	y4	b6	y5		b7		y6	b8	b9	y8		y9	y10	y11	y12
Delta ppm	-6.1	-12.9		-8.4	-7.9	-9.4	-5.2	-3.3	0.7	-7.8	-12.4	0.1	-8.8		-2.8		-11.4	-5.7	-0.7	-5.5		-0.5	-0.8	-13.2	-12.3

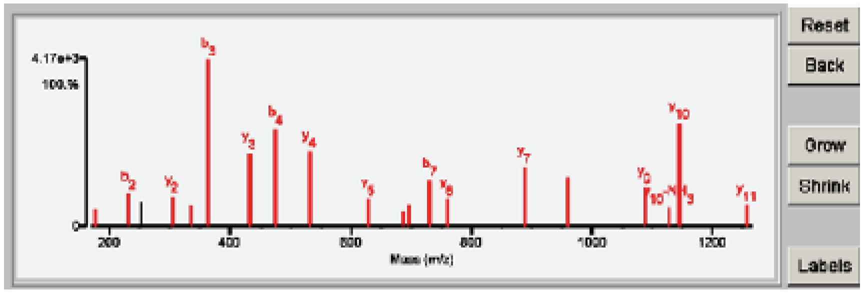


I112

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	23.54	93.8	12	2/25	(E) A A|M|L|G/Q/A|E/E/V/V/Q/E/R (I)	1618.7584	-0.0016	-1.0	60343.9/5.80	HUMAN	P17987	839987	T-complex protein 1 subunit alpha - Homo sapiens (Human)

Fragment-Ion (m/z)	70.064	72.078	86.096	104.061	176.118	231.080	261.066	304.156	334.116	362.119	432.220	475.203	631.288	628.311⁺²	630.348	686.848⁺²	694.861⁺²	731.313	759.394	888.438	959.476	1087.626	1127.619	1144.560	1267.631
Frac. Inten.(% of TIC)	0.00	0.07	0.11	3.86	1.71	3.29	2.38	2.97	1.94	16.20	7.20	9.48	7.31	1.62	2.65	1.40	2.21	4.54	2.68	5.77	4.79	3.75	1.81	10.09	2.19
Rel. Inten.(% of BP)	0.01	0.41	0.65	23.83	10.53	20.28	14.67	18.30	11.98	100.00	44.43	58.49	45.14	9.97	16.38	8.62	13.61	28.02	16.53	35.62	29.57	23.14	11.18	62.24	13.49
Score	0.20	0.50	0.22	-0.24	1.50	0.50	-0.15	1.50	0.50	0.50	1.50	0.50	1.50	1.50	1.50	0.50	1.50	0.50	1.50	1.50	1.50	1.50	0.50	1.50	1.50
Ion-type	PR	V	LI		y1	b2		y2	a3	b3	y3	b4	y4	y11⁺²	y5	y12-H2O⁺²	y12⁺²	b7	y6	y7	y8	y9	y10-NH3	y10	y11
Delta ppm	-14.6	-38.5	-14.2		-5.4	-4.3		-17.6	-32.5	-7.4	0.2	-4.7	-1.8	-22.1	-12.1	11.3	7.7	-13.5	-7.3	-4.8	-3.2	-11.7	-12.5	1.0	-10.1



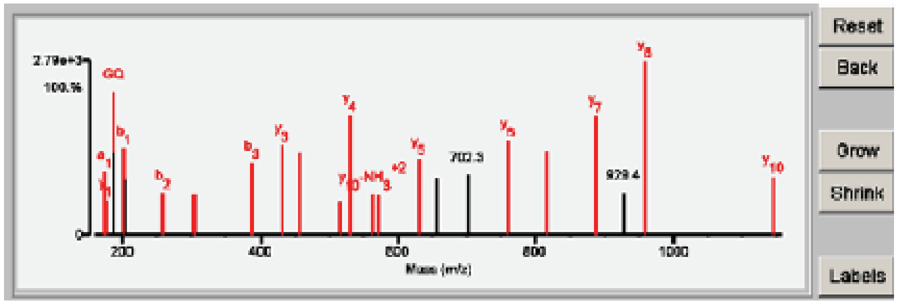
I113

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.50	83.3	10	5/25	(M) L|G\Q|A|E/E/V|V/Q/E/R (I)	1345.6418	0.0001	0.1	60343.9/5.80	HUMAN	P17987	638887	T-complex protein 1 subunit alpha - Homo sapiens (Human)

Fragment-Ion (m/z)	86.096	174.094	175.116	186.088	188.071	202.088	206.098	259.108	304.165	387.170	432.218	458.208	515.199
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.09 0.95 0.22 LI -4.9	3.49 36.05 0.50 a_1 -12.7	1.95 20.15 1.50 y_1 -16.9	7.98 82.51 0.75 GQ -2.8	4.57 47.27 -0.47	4.80 49.67 0.50 b_1 -13.0	3.11 32.15 -0.32	2.34 24.20 0.50 b_2 -14.2	2.31 23.86 1.50 y_2 10.7	4.03 41.65 0.50 b_3 -0.9	5.04 52.07 1.50 y_3 -5.6	4.58 47.31 0.50 b_4 0.5	1.90 19.64 0.75 GQAEE -21.8

Fragment-Ion (m/z)	531.281	564.257^{+2}	572.801^{+2}	630.356	657.291^{+2}	702.287	759.394	815.368	888.442	929.413	959.475	1144.540
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	6.64 68.60 1.50 y_4 -14.8	2.26 23.37 0.50 $y_{10}\text{-NH}_3^{+2}$ -22.9	2.17 22.42 1.50 y_{10}^{+2} 30.1	4.25 43.97 1.50 y_5 -1.7	3.21 33.17 -0.33	3.38 34.92 -0.35	5.26 54.43 1.50 y_6 -7.8	4.68 48.43 0.50 b_7 8.5	6.61 68.34 1.50 y_7 -0.0	2.38 24.65 -0.25	9.67 100.00 1.50 y_8 -4.5	3.30 34.10 1.50 y_{10} -17.3



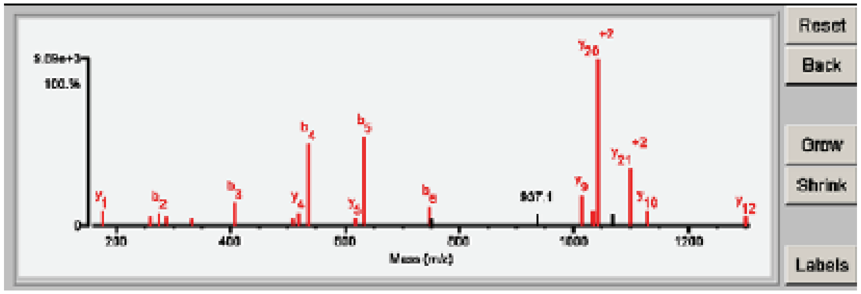
I114

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.89	91.5	12	5/25	(A) D A\M\E\V|I|P S T L A E N A/G L/N/P I S T/V/T E/L/R (N)	2828.4009	0.0058	2.0	57924.6/7.96	HUMAN	P50991	638723	T-complex protein 1 subunit delta - Homo sapiens (Human)

Fragment-Ion (m/z)	72.081	86.097	104.054	120.081	175.118	261.088	275.066	288.199	332.124	406.102	508.294^{+2}	518.293	535.150
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	0.05 0.18 0.50 V 5.9	0.09 0.37 0.22 LI 4.3	2.13 8.31 -0.08	1.54 6.02 -0.06	2.25 8.76 1.50 y_1 -6.0	1.53 5.96 0.75 ME -12.1	2.03 7.89 0.50 b_2 -20.4	1.50 5.83 1.50 y_2 -14.6	1.30 5.06 0.75 AME -15.0	3.65 14.24 0.50 b_3 -23.1	1.29 5.01 1.50 y_9^{+2} 2.1	2.13 8.31 1.50 y_4 0.0	12.60 49.13 0.50 b_4 -6.2

Fragment-Ion (m/z)	617.348	634.221	747.298	749.316^{+2}	937.074^{+3}	1015.583	1033.528^{+2}	1042.067^{+2}	1068.628	1098.598^{+2}	1129.619	1299.717
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta ppm	1.21 4.71 1.50 y_5 -21.2	13.64 53.15 0.50 b_5 -1.1	3.03 11.82 0.50 b_6 -18.2	1.15 4.47 -0.04	1.91 7.46 -0.07	4.62 18.02 1.50 y_9 5.0	2.39 9.33 0.50 $y_{20}\text{-NH}_3^{+2}$ -22.6	25.66 100.00 1.50 y_{20}^{+2} 2.1	1.78 6.92 -0.07	8.82 34.36 1.50 y_{21}^{+2} -10.3	2.21 8.61 1.50 y_{10} -2.1	1.49 5.82 1.50 y_{12} -7.1



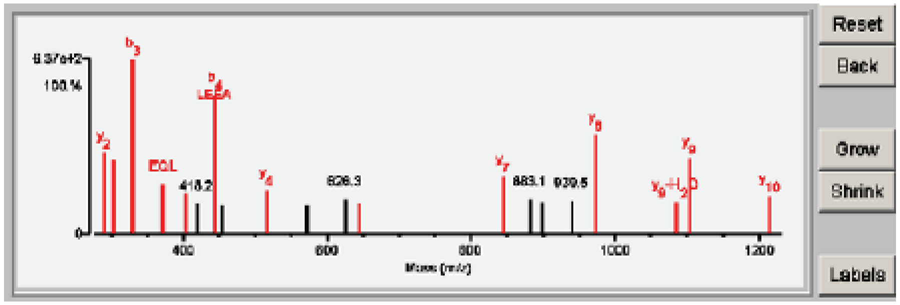
I115

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.40	74.8	8	10/24	(A) G A L|L|E/E/A E/Q/L/L/D R (G)	1644.7625	-0.0002	-0.1	59671.4/6.46	HUMAN	P48643	838751	T-complex protein 1 subunit epsilon - Homo sapiens (Human)

Fragment-Ion (m/z)	86.098	87.087	120.078	175.110	280.143	302.163	330.148	371.205	403.228	418.176	443.227	453.174^{+2}
Frac. Inten.(% of TIC)	0.38	2.26	2.90	2.20	6.51	5.88	13.86	3.97	3.25	2.47	11.05	2.32
Rel. Inten.(% of BP)	2.72	16.30	20.94	15.91	47.00	42.42	100.00	28.67	23.44	17.81	79.74	16.71
Score	0.22	-0.16	-0.21	-0.16	1.50	0.50	0.50	0.75	1.50	-0.18	0.75	-0.17
Ion-type	LI				y_2	a_3	b_3	EQL	y_3		b_4 LEEA	
Delta ppm	13.6				-11.4	-5.9	-3.3	31.2	-5.6		-14.8 27.2	

Fragment-Ion (m/z)	516.311	672.342	828.308	844.382	844.443	883.106	898.457	939.471	973.478	1084.568	1102.525	1216.603
Frac. Inten.(% of TIC)	3.45	2.26	2.73	2.39	4.59	2.79	2.57	2.69	7.84	2.60	6.04	2.98
Rel. Inten.(% of BP)	24.88	16.28	19.70	17.27	33.10	20.15	18.55	19.41	56.59	18.78	43.57	21.47
Score	1.50	-0.16	-0.20	1.50	1.50	-0.20	-0.19	-0.19	1.50	0.50	1.50	1.50
Ion-type	y_4			y_5	y_7				y_8	y_9-H_2O	y_9	y_{10}
Delta ppm	-5.9			14.6	-10.9				-17.5	26.4	-11.0	-15.5



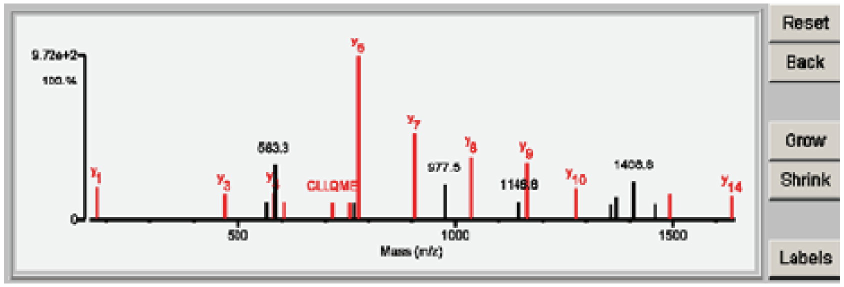
I116

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.11	65.6	10	12/25	(R) G L D P S L P S P L P N L G P Q G P A L T P E Q E N I L H T T Q T D C Y N N L/A A/C L/L/Q/M/E/P V/N/Y E/R (V)	5860.7965	0.0312	5.3	20012.7/9.02	HUMAN	Q8N5M4	669669	Tetratricopeptide repeat protein 9C - Homo sapiens (Human)

Fragment-Ion (m/z)	175.117	467.218	565.286	581.255	583.300	606.308	718.316	759.361	767.391	777.392	906.440	977.519	1037.474
Frac. Inten.(% of TIC)	3.56	2.89	2.15	3.10	6.13	2.07	1.95	1.67	1.86	18.15	9.56	4.01	7.02
Rel. Inten.(% of BP)	19.73	15.92	11.84	17.06	33.78	11.41	10.73	10.33	10.34	100.00	52.67	22.08	38.69
Score	1.50	1.50	-0.12	1.50	-0.34	0.75	0.75	0.50	-0.10	1.50	1.50	-0.22	1.50
Ion-type	y_1	y_3		y_4		PSPLPN	CLLQME	y_6-H_2O		y_6	y_7		y_8
Delta ppm	-10.0	-14.3		-21.9		-29.0	-15.6	-23.1		3.6	9.2		1.7

Fragment-Ion (m/z)	1146.562	1165.543	1278.622	1359.755	1370.714^{+2}	1408.785	1409.321	1410.056^{+4}	1459.475	1494.709	1636.812	1652.810^{+3}
Frac. Inten.(% of TIC)	2.16	6.41	3.42	1.60	2.53	4.23	1.82	3.77	1.72	2.89	2.71	2.35
Rel. Inten.(% of BP)	11.92	35.33	18.84	8.81	13.95	23.33	10.05	20.75	9.49	15.95	14.94	12.95
Score	-0.12	1.50	1.50	-0.09	-0.14	-0.23	-0.10	-0.21	-0.09	1.50	1.50	-0.13
Ion-type		y_9	y_{10}							y_{12}	y_{14}	
Delta ppm		10.6	5.6							0.4	16.0	

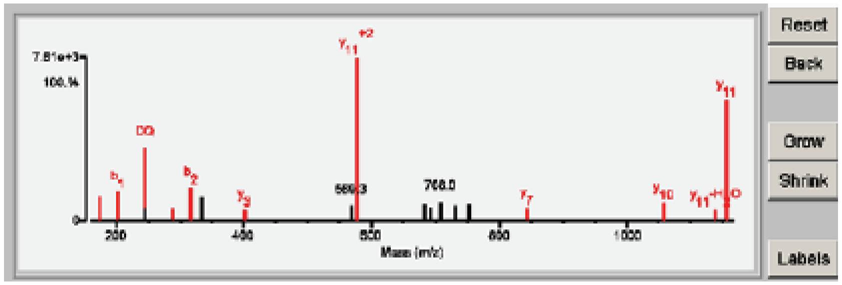


I117

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.60	73.4	8	11/26	(S) I\D\Q/F/G G T/L D L T/L/I/R (A)	1689.8411	-0.0101	-6.3	88560.2/6.62	HUMAN	Q13263	847887	Transcription intermediary factor 1-beta - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
70.086	0.00	0.01	0.20	PR	-0.4
98.096	0.21	0.91	0.22	LI	-20.0
133.059	4.02	17.65	-0.18		
174.092	3.33	14.64	0.50	a_1	-22.5
176.117	2.92	12.83	1.50	y_1	-13.4
202.088	4.03	17.71	0.50	b_1	-15.9
244.093	10.31	45.30	0.75	DQ	-4.1
246.099	1.59	6.97	-0.07		
288.201	1.60	7.01	1.50	y_2	-7.3
317.118	4.58	20.13	0.50	b_2	0.1
334.140	3.30	14.49	-0.14		
401.280	1.45	6.38	1.50	y_3	-18.1
588.333	2.01	8.84	-0.09		
678.340^{+2}	22.76	100.00	1.50	y_{11}^{+2}	-0.6
682.368^{+2}	2.30	10.12	-0.10		
691.319^{+2}	1.75	7.70	-0.08		
707.706	2.62	11.52	-0.12		
708.036	2.65	11.65	-0.12		
708.384	2.06	9.05	-0.09		
730.433^{+2}	2.01	8.84	-0.09		
752.338	2.26	9.91	-0.10		
843.630	1.61	7.07	1.50	y_7	0.1
1058.810	2.45	10.78	1.50	y_{10}	-10.0
1137.850	1.45	6.35	0.50	y_{11}-H_2O	-10.8
1155.885	16.74	73.54	1.50	y_{11}	-7.5

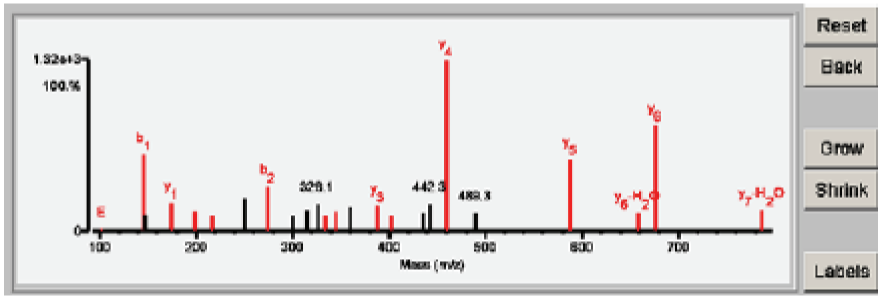


I118

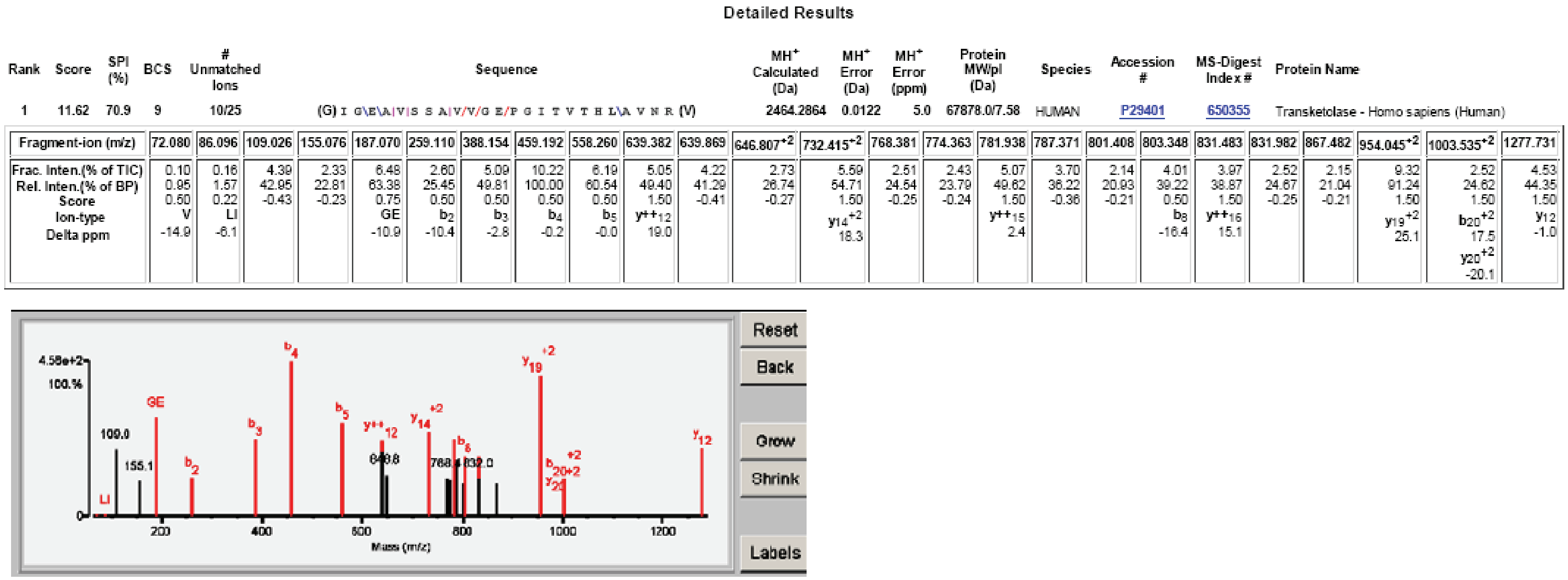
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.57	78.7	7	9/26	(F) G\E|S/E/A/N/V/R (E)	949.4044	0.0070	7.3	89322.3/6.14	HUMAN	P55072	841186	Transitional endoplasmic reticulum ATPase - Homo sapiens (Human)

Fragment-Ion (m/z)	Frac. Inten.(% of TIC)	Rel. Inten.(% of BP)	Score	Ion-type	Delta ppm
102.064	0.26	1.31	1.00	E	-11.3
146.030	8.83	44.81	0.50	b_1	12.2
147.035	1.98	10.04	-0.10		
175.117	3.31	16.81	1.50	y_1	-13.4
199.071	2.29	11.59	0.50	SE-H_2O	-6.7
217.084	1.79	9.10	0.75	SE	3.7
261.073	3.81	19.34	-0.19		
274.188	1.84	9.31	1.50	y_2	-6.1
275.077	5.06	25.67	0.50	b_2	23.6
300.106	1.84	9.31	-0.09		
316.092	2.45	12.44	-0.12		
326.079	3.19	16.20	-0.16		
334.114	1.83	9.31	0.50	a_3	17.3
344.098	2.20	11.17	0.25	b_3-H_2O	10.8
360.086	2.74	13.91	-0.14		
388.220	2.98	15.10	1.50	y_3	-26.3
402.173	1.76	8.94	0.75	SEAN	25.3
435.407	2.15	10.92	-0.11		
442.260^{+2}	3.10	15.71	-0.16		
469.288	19.71	100.00	1.50	y_4	-2.6
489.297	2.02	10.27	-0.10		
588.313	8.28	42.00	1.50	y_5	5.3
657.357	2.03	10.28	0.50	y_6-H_2O	38.7
675.338	12.14	61.61	1.50	y_6	-6.6
788.380	2.41	12.21	0.50	y_7-H_2O	8.2



I119



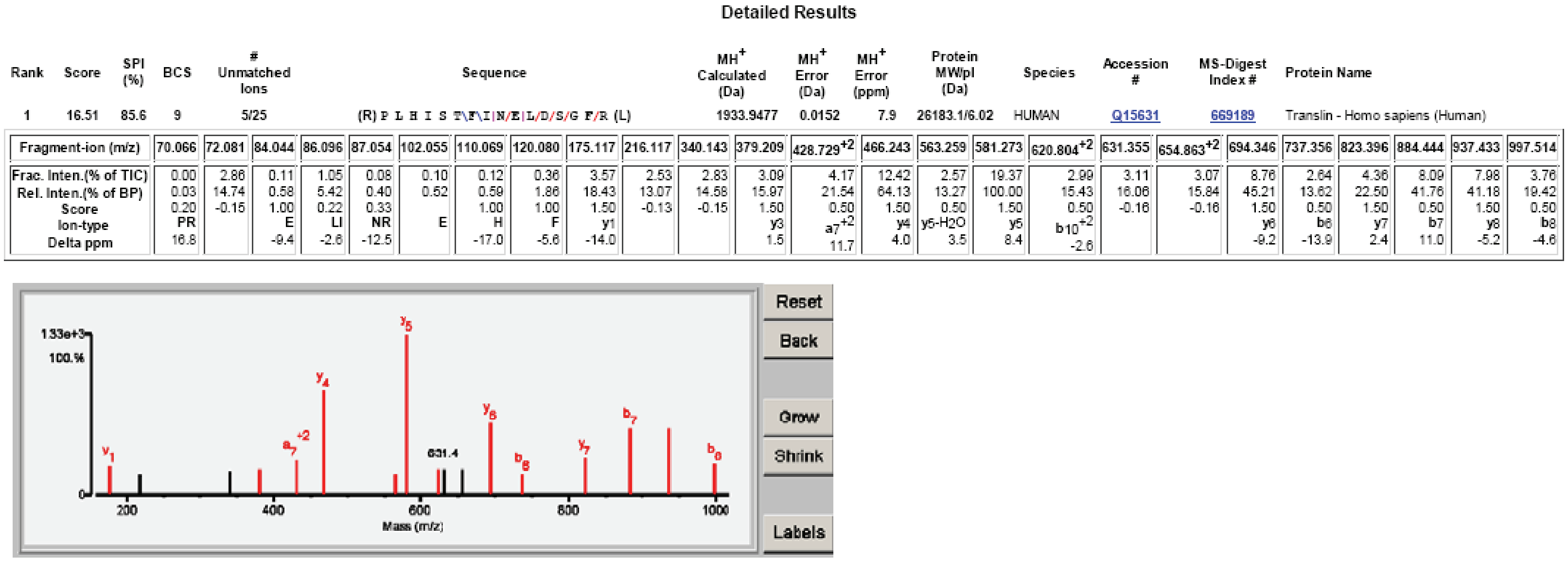
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.62	70.9	9	10/25	(G) I G\E\A|V|S S A|V/V/G E/P G I T V T H L\A V N R (V)	2464.2864	0.0122	5.0	67878.0/7.58	HUMAN	P29401	650355	Transketolase - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.096	109.026	155.076	187.070	259.110	388.154	459.192	558.260	639.382	639.869	646.807^{+2}	732.415^{+2}
Frac. Inten.(% of TIC)	0.10	0.16	4.39	2.33	6.48	2.60	5.09	10.22	6.19	5.05	4.22	2.73	5.59
Rel. Inten.(% of BP)	0.95	1.57	42.95	22.81	63.38	25.45	49.81	100.00	60.54	49.40	41.29	26.74	54.71
Score	0.50	0.22	-0.43	-0.23	0.75	0.50	0.50	0.50	0.50	1.50	-0.41	-0.27	1.50
Ion-type	V	LI			GE	b_2	b_3	b_4	b_5	y++$_{12}$			y_{14}^{+2}
Delta ppm	-14.9	-6.1			-10.9	-10.4	-2.8	-0.2	-0.0	19.0			18.3

Fragment-ion (m/z)	768.381	774.363	781.938	787.371	801.408	803.348	831.483	831.982	867.482	954.045^{+2}	1003.535^{+2}	1277.731
Frac. Inten.(% of TIC)	2.51	2.43	5.07	3.70	2.14	4.01	3.97	2.52	2.15	9.32	2.52	4.53
Rel. Inten.(% of BP)	24.54	23.79	49.62	36.22	20.93	39.22	38.87	24.67	21.04	91.24	24.62	44.35
Score	-0.25	-0.24	1.50	-0.36	-0.21	0.50	1.50	-0.25	-0.21	1.50	1.50	1.50
Ion-type			y++$_{15}$			b_8	y++$_{16}$			y_{19}^{+2}	b_{20}^{+2} y_{20}^{+2}	y_{12}
Delta ppm			2.4			-16.4	15.1			25.1	17.5 -20.1	-1.0

I120



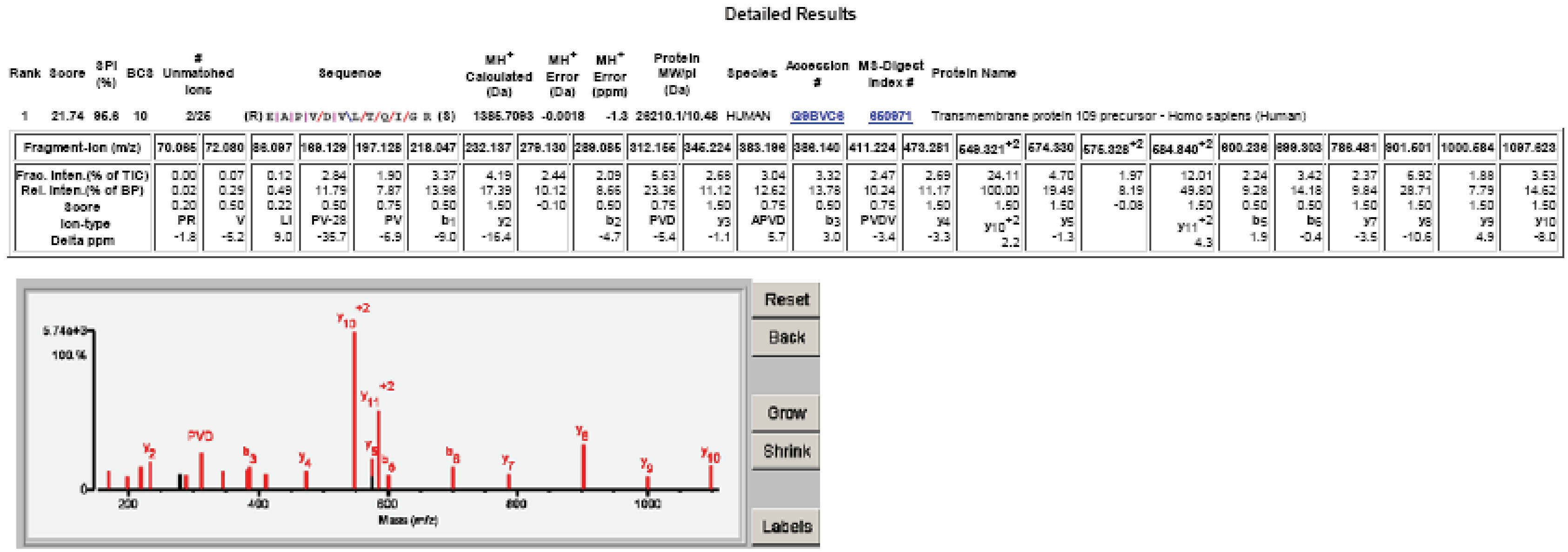
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.51	85.6	9	5/25	(R) P L H I S T\F\I|N/E|L/D/S/G F/R (L)	1933.9477	0.0152	7.9	26183.1/6.02	HUMAN	Q15631	669189	Translin - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.044	86.096	87.054	102.055	110.069	120.080	175.117	216.117	340.143	379.209	428.729^{+2}
Frac. Inten.(% of TIC)	0.00	2.86	0.11	1.05	0.08	0.10	0.12	0.36	3.57	2.53	2.83	3.09	4.17
Rel. Inten.(% of BP)	0.03	14.74	0.58	5.42	0.40	0.52	0.59	1.86	18.43	13.07	14.58	15.97	21.54
Score	0.20	-0.15	1.00	0.22	0.33		1.00	1.00	1.50	-0.13	-0.15	1.50	0.50
Ion-type	PR		E	LI	NR	E	H	F	y1			y3	a_7^{+2}
Delta ppm	16.8		-9.4	-2.6	-12.5		-17.0	-5.6	-14.0			1.5	11.7

Fragment-ion (m/z)	466.243	563.259	581.273	620.804^{+2}	631.355	654.863^{+2}	694.346	737.356	823.396	884.444	937.433	997.514
Frac. Inten.(% of TIC)	12.42	2.57	19.37	2.99	3.11	3.07	8.76	2.64	4.36	8.09	7.98	3.76
Rel. Inten.(% of BP)	64.13	13.27	100.00	15.43	16.06	15.84	45.21	13.62	22.50	41.76	41.18	19.42
Score	1.50	0.50	1.50	0.50	-0.16	-0.16	1.50	0.50	1.50	0.50	1.50	0.50
Ion-type	y4	y5-H2O	y5	b_{10}^{+2}			y6	b6	y7	b7	y8	b8
Delta ppm	4.0	3.5	8.4	-2.6			-9.2	-13.9	2.4	11.0	-5.2	-4.6

I121

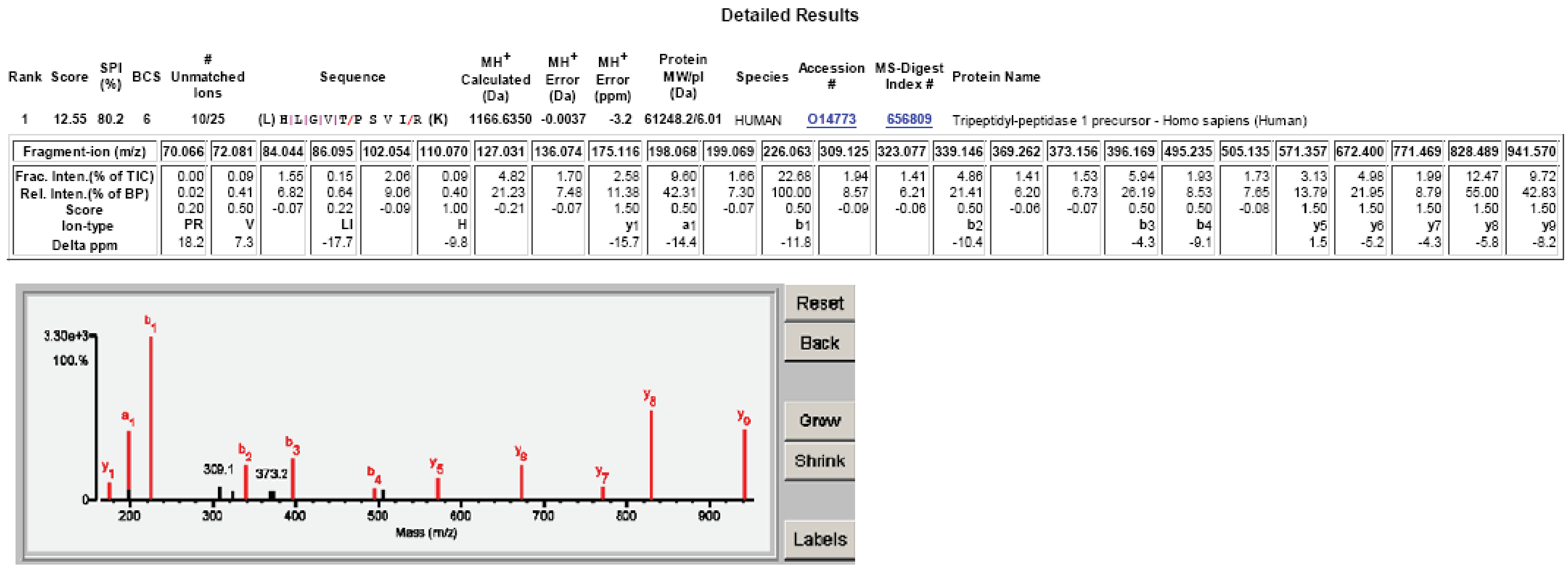


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	21.74	96.8	10	2/26	(R) E|A|P|V/D|V\L/T/Q/I/G R (S)	1385.7093	-0.0018	-1.3	26210.1/10.48	HUMAN	Q9BVC6	860871	Transmembrane protein 109 precursor - Homo sapiens (Human)

Fragment-Ion (m/z)	70.065	72.080	86.097	169.129	197.128	218.047	232.137	279.130	289.085	312.166	345.224	383.196	386.140	411.224	473.281	549.321^{+2}	574.330	575.328^{+2}	584.840^{+2}	600.238	699.303	786.481	901.501	1000.584	1097.623
Frac. Inten.(% of TIC)	0.00	0.07	0.12	2.84	1.90	3.37	4.19	2.44	2.09	5.63	2.68	3.04	3.32	2.47	2.69	24.11	4.70	1.97	12.01	2.24	3.42	2.37	6.92	1.88	3.53
Rel. Inten.(% of BP)	0.02	0.29	0.49	11.79	7.87	13.98	17.39	10.12	8.66	23.36	11.12	12.62	13.78	10.24	11.17	100.00	19.49	8.19	49.80	9.28	14.18	9.84	28.71	7.79	14.62
Score	0.20	0.50	0.22	0.50	0.75	0.50	1.50	-0.10	0.50	0.75	1.50	0.75	0.50	0.75	1.50	1.50	1.50	-0.08	1.50	0.50	0.50	1.50	1.50	1.50	1.50
Ion-type	PR	V	LI	PV-28	PV	b1	y2		b2	PVD	y3	APVD	b3	PVDV	y4	y10^{+2}	y5		y11^{+2}	b5	b6	y7	y8	y9	y10
Delta ppm	-1.8	-5.2	9.0	-35.7	-6.9	-9.0	-16.4		-4.7	-5.4	-1.1	5.7	3.0	-3.4	-3.3	2.2	-1.3		4.3	1.9	-0.4	-3.5	-10.6	4.9	-8.0

I122



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.55	80.2	6	10/25	(L) H|L|G|V|T/P S V I/R (K)	1166.6350	-0.0037	-3.2	61248.2/6.01	HUMAN	O14773	656809	Tripeptidyl-peptidase 1 precursor - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.044	86.095	102.054	110.070	127.031	136.074	175.116	198.068	199.069	226.063	309.125	323.077	339.146	369.262	373.156	396.169	495.235	505.135	571.357	672.400	771.469	828.489	941.570
Frac. Inten.(% of TIC)	0.00	0.09	1.55	0.15	2.06	0.09	4.82	1.70	2.58	9.60	1.66	22.68	1.94	1.41	4.86	1.41	1.53	5.94	1.93	1.73	3.13	4.98	1.99	12.47	9.72
Rel. Inten.(% of BP)	0.02	0.41	6.82	0.64	9.06	0.40	21.23	7.48	11.38	42.31	7.30	100.00	8.57	6.21	21.41	6.20	6.73	26.19	8.53	7.65	13.79	21.95	8.79	55.00	42.83
Score	0.20	0.50	-0.07	0.22	-0.09	1.00	-0.21	-0.07	1.50	0.50	-0.07	0.50	-0.09	-0.06	0.50	-0.06	-0.07	0.50	0.50	-0.08	1.50	1.50	1.50	1.50	1.50
Ion-type	PR	V		LI		H			y1	a1		b1			b2			b3	b4		y5	y6	y7	y8	y9
Delta ppm	18.2	7.3		-17.7		-9.8			-15.7	-14.4		-11.8			-10.4			-4.3	-9.1		1.5	-5.2	-4.3	-5.8	-8.2

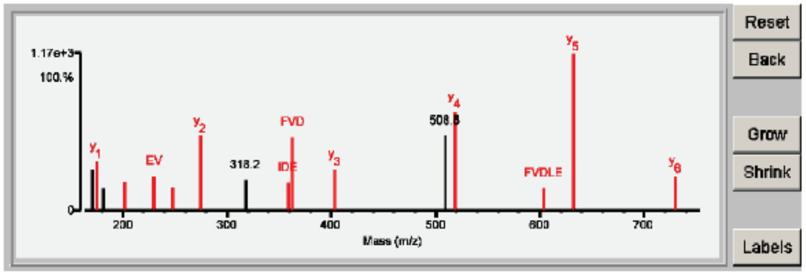
I123

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.96	63.7	6	7/24	(R) A V F V D L E P T/V/I/D/E/V/R (T)	1789.9041	0.0105	5.9	50135.9/4.94	HUMAN	Q71U36	637677	Tubulin alpha-1A chain - Homo sapiens (Human)
1	13.96	63.7	6	7/24	(R) A V F V D L E P T/V/I/D/E/V/R (T)	1789.9041	0.0105	5.9	50151.9/4.94	HUMAN	P68363	637689	Tubulin alpha-1B chain - Homo sapiens (Human)
1	13.96	63.7	6	7/24	(R) A V F V D L E P T/V/I/D/E/V/R (T)	1789.9041	0.0105	5.9	49895.6/4.96	HUMAN	Q9BQE3	637707	Tubulin alpha-1C chain - Homo sapiens (Human)

Fragment-ion (m/z)	70.065	72.082	86.096	102.055	120.081	143.118	171.107	175.115	181.098	201.125	229.118	247.143
Frac. Inten.(% of TIC)	0.01	0.55	0.34	0.07	0.36	10.83	3.81	4.66	2.11	2.69	3.27	2.16
Rel. Inten.(% of BP)	0.05	3.70	2.30	0.48	2.41	73.38	25.80	31.58	14.28	18.23	22.14	14.62
Score	0.20	0.50	0.22	1.00	1.00	-0.73	-0.26	1.50	-0.14	0.75	0.75	0.75
Ion-type	PR	V	LI	E	F			y1		TV EV-28	EV	FV
Delta ppm	2.5	10.0	-2.6	3.4	-1.5			-22.0		5.1 5.1	-6.5	-10.9

Fragment-ion (m/z)	274.187	318.183	358.164	362.168	403.224	508.758^{+2}	518.258	604.292	631.338	730.407	774.411	1016.505
Frac. Inten.(% of TIC)	7.01	2.86	2.58	6.86	3.85	7.03	9.27	2.05	14.76	3.21	2.54	7.15
Rel. Inten.(% of BP)	47.50	19.35	17.45	46.48	26.07	47.66	62.80	13.92	100.00	21.78	17.18	48.44
Score	1.50	-0.19	0.75	0.75	1.50	-0.48	1.50	0.75	1.50	1.50	-0.17	-0.48
Ion-type	y2		IDE	FVD	y3		y4	FVDLE	y5	y6		
Delta ppm	-2.1		6.5	-11.2	-15.5		2.3	-10.6	-4.5	-3.3		



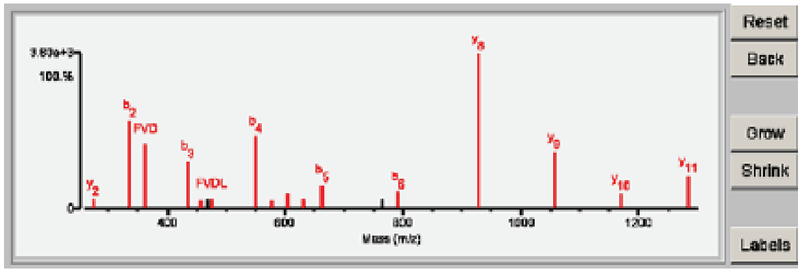
I124

Detailed Results

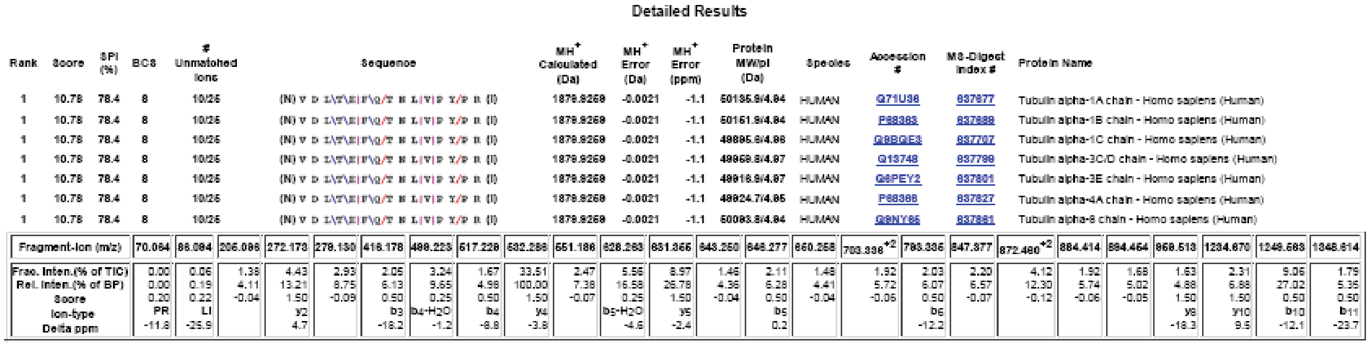
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.87	82.2	8	5/26	(A) V F\V|D|L|E|P T V/I D E/V/R (T)	1718.8670	-0.0084	-3.7	50135.9/4.94	HUMAN	Q71U36	637677	Tubulin alpha-1A chain - Homo sapiens (Human)
1	17.87	82.2	8	5/26	(A) V F\V|D|L|E|P T V/I D E/V/R (T)	1718.8670	-0.0084	-3.7	50151.9/4.94	HUMAN	P68363	637689	Tubulin alpha-1B chain - Homo sapiens (Human)
1	17.87	82.2	8	5/26	(A) V F\V|D|L|E|P T V/I D E/V/R (T)	1718.8670	-0.0084	-3.7	49895.6/4.96	HUMAN	Q9BQE3	637707	Tubulin alpha-1C chain - Homo sapiens (Human)

Fragment-ion (m/z)	72.080	86.097	120.081	175.124	182.083	200.101	274.191	335.141	362.171	434.212	457.213	468.262	475.248
Frac. Inten.(% of TIC)	0.05	0.13	0.17	1.39	1.56	2.08	1.34	12.57	9.15	6.74	1.31	1.42	1.51
Rel. Inten.(% of BP)	0.24	0.59	0.77	6.28	7.05	9.37	6.07	56.70	41.29	30.42	5.89	6.40	6.84
Score	0.50	0.22	1.00	1.50	-0.07	-0.09	1.50	0.50	0.75	0.50	0.75	-0.06	0.75
Ion-type	V	LI	F	y_1			y_2	b_2	FVD	b_3	IDEV		FVDL
Delta ppm	-12.1	3.2	4.4	30.0			14.3	-6.2	-2.3	-0.2	-37.6		-21.9

Fragment-ion (m/z)	549.234	577.306^{+2}	604.288	631.331	662.319	764.811	791.367	928.506	1057.546	1170.643	1285.667	1308.581
Frac. Inten.(% of TIC)	10.38	1.22	2.18	1.44	3.32	1.50	2.37	22.16	8.09	2.13	4.58	1.22
Rel. Inten.(% of BP)	46.84	5.49	9.85	6.48	15.00	6.75	10.70	100.00	36.50	9.61	20.65	5.49
Score	0.50	0.50	0.75	1.50	0.50	-0.07	0.50	1.50	1.50	1.50	1.50	-0.05
Ion-type	b_4	y_{10}-NH_3^{+2}	FVDLE	y_5	b_5		b_6	y_8	y_9	y_{10}	y_{11}	
Delta ppm	-9.5	-6.4	-21.0	-15.8	-5.4		-11.0	-4.9	-5.8	5.7	2.4	



I125

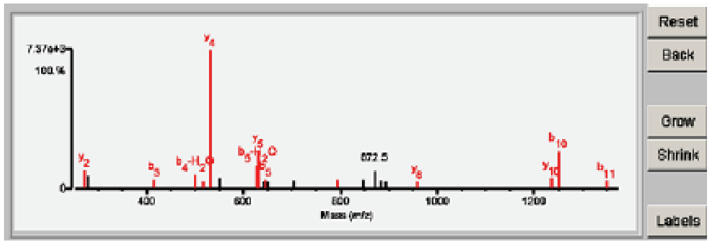


Detailed Results

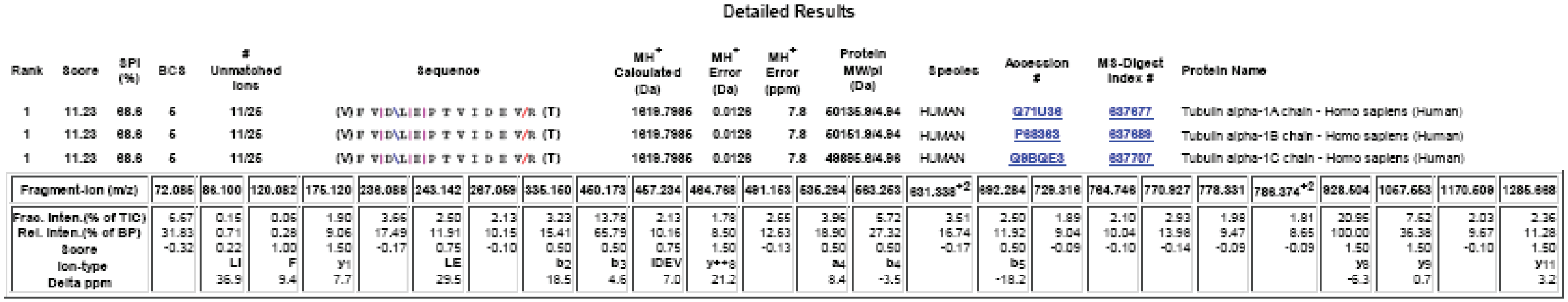
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	50135.9/4.94	HUMAN	Q71U36	837677	Tubulin alpha-1A chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	50151.9/4.94	HUMAN	P68363	837689	Tubulin alpha-1B chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	49895.6/4.96	HUMAN	Q9BQE3	837707	Tubulin alpha-1C chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	49959.8/4.97	HUMAN	Q13748	837799	Tubulin alpha-3C/D chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	49915.9/4.97	HUMAN	Q6PEY2	837801	Tubulin alpha-3E chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	49924.7/4.95	HUMAN	P68366	837827	Tubulin alpha-4A chain - Homo sapiens (Human)
1	10.78	78.4	8	10/26	(N) V D L\T\E|F\Q/T N L|V|P Y/P R (I)	1879.9269	-0.0021	-1.1	50093.9/4.94	HUMAN	Q9NY65	837881	Tubulin alpha-8 chain - Homo sapiens (Human)

Fragment-Ion (m/z)	70.064	86.094	206.086	272.173	278.130	416.178	499.223	517.228	532.288	551.186	628.263	631.366	643.260
Frac. Inten.(% of TIC)	0.00	0.06	1.38	4.43	2.93	2.05	3.24	1.67	33.51	2.47	5.56	8.97	1.46
Rel. Inten.(% of BP)	0.00	0.19	4.11	13.21	8.75	6.13	9.65	4.98	100.00	7.38	16.58	26.78	4.36
Score	0.20	0.22	-0.04	1.50	-0.09	0.50	0.25	0.50	1.50	-0.07	0.25	1.50	-0.04
Ion-type	PR	LI		y_2		b_3	b_4-H_2O	b_4	y_4		b_5-H_2O	y_5	
Delta ppm	-11.8	-25.9		4.7		-18.2	-1.2	-8.8	-3.8		-4.6	-2.4	

Fragment-Ion (m/z)	646.277	660.258	703.338^{+2}	793.336	847.877	872.480^{+2}	884.414	894.464	959.513	1234.670	1248.663	1348.614
Frac. Inten.(% of TIC)	2.11	1.48	1.92	2.03	2.20	4.12	1.92	1.68	1.63	2.31	9.06	1.79
Rel. Inten.(% of BP)	6.28	4.41	5.72	6.07	6.57	12.30	5.74	5.02	4.88	6.88	27.02	5.35
Score	0.50	-0.04	-0.06	0.50	-0.07	-0.12	-0.06	-0.05	1.50	1.50	0.50	0.50
Ion-type	b_5			b_6					y_8	y_{10}	b_{10}	b_{11}
Delta ppm	0.2			-12.2					-18.3	9.5	-12.1	-23.7



I126

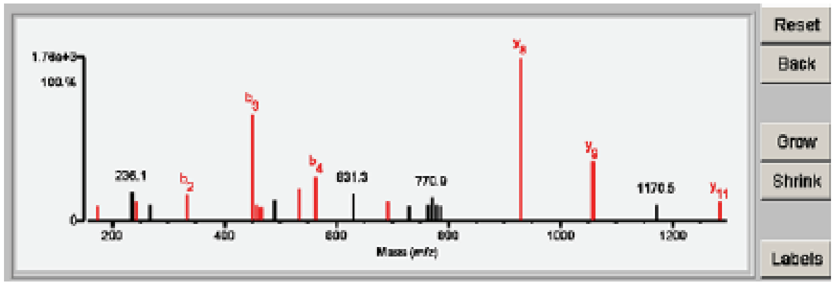


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.23	68.8	6	11/26	(V) F V|D\L|E|P T V I D E V/R (T)	1619.7986	0.0126	7.8	50135.9/4.94	HUMAN	Q71U36	837677	Tubulin alpha-1A chain - Homo sapiens (Human)
1	11.23	68.8	6	11/26	(V) F V|D\L|E|P T V I D E V/R (T)	1619.7986	0.0126	7.8	50151.9/4.94	HUMAN	P68363	837689	Tubulin alpha-1B chain - Homo sapiens (Human)
1	11.23	68.8	6	11/26	(V) F V|D\L|E|P T V I D E V/R (T)	1619.7986	0.0126	7.8	49895.6/4.96	HUMAN	Q9BQE3	837707	Tubulin alpha-1C chain - Homo sapiens (Human)

Fragment-Ion (m/z)	72.086	86.100	120.082	175.120	238.088	243.142	287.059	335.160	450.173	457.234	464.768	491.163	535.264
Frac. Inten.(% of TIC)	6.67	0.15	0.06	1.90	3.66	2.50	2.13	3.23	13.78	2.13	1.78	2.65	3.96
Rel. Inten.(% of BP)	31.83	0.71	0.28	9.06	17.49	11.91	10.15	15.41	65.79	10.16	8.50	12.63	18.90
Score	-0.32	0.22	1.00	1.50	-0.17	0.75	-0.10	0.50	0.50	0.75	1.50	-0.13	0.50
Ion-type		LI	F	y_1		LE		b_2	b_3	IDEV	y^{++}_8		a_4
Delta ppm		36.9	9.4	7.7		29.5		18.5	4.6	7.0	21.2		8.4

Fragment-Ion (m/z)	563.263	631.338^{+2}	692.284	729.316	764.746	770.927	778.331	788.374^{+2}	928.504	1057.653	1170.608	1285.668
Frac. Inten.(% of TIC)	5.72	3.51	2.50	1.89	2.10	2.93	1.98	1.81	20.96	7.62	2.03	2.36
Rel. Inten.(% of BP)	27.32	16.74	11.92	9.04	10.04	13.98	9.47	8.65	100.00	36.38	9.67	11.28
Score	0.50	-0.17	0.50	-0.09	-0.10	-0.14	-0.09	-0.09	1.50	1.50	-0.10	1.50
Ion-type	b_4		b_5						y_8	y_9		y_{11}
Delta ppm	-3.5		-18.2						-6.3	0.7		3.2

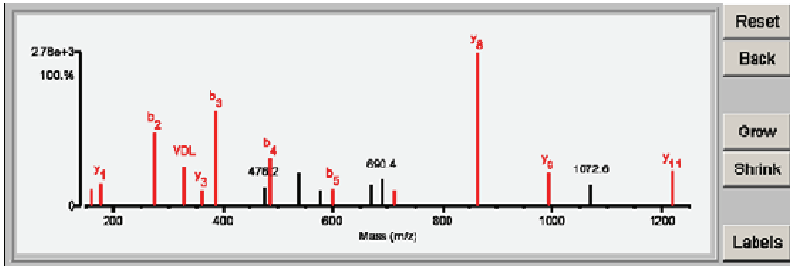


I127

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.90	71.2	8	10/25	(R) A I\L\V|D\L|E/P G T M D/S V/R (S)	1703.8343	-0.0177	-10.4	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	10.90	71.2	8	10/25	(R) A I\L\V|D\L|E/P G T M D/S V/R (S)	1703.8343	-0.0177	-10.4	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	10.90	71.2	8	10/25	(R) A I\L\V|D\L|E/P G T M D/S V/R (S)	1703.8343	-0.0177	-10.4	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	10.90	71.2	8	10/25	(R) A I\L\V|D\L|E/P G T M D/S V/R (S)	1703.8343	-0.0177	-10.4	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.082	86.098	94.065	110.071	120.079	136.076	159.077	175.122	273.128	328.180	361.216	386.212	476.199	485.277	536.793^{+2}	577.314	600.315	669.294	690.356	713.378	862.405	991.448	1072.581	1219.551
Frac. Inten.(% of TIC)	0.00	0.10	0.49	2.27	2.19	3.55	3.61	2.16	2.92	9.13	4.95	2.06	11.74	2.34	5.92	4.14	2.02	2.12	2.61	3.40	2.02	19.01	4.19	2.73	4.34
Rel. Inten.(% of BP)	0.03	0.52	2.60	11.92	11.50	18.66	19.01	11.35	15.36	48.03	26.02	10.81	61.77	12.32	31.15	21.77	10.62	11.15	13.73	17.87	10.64	100.00	22.03	14.35	22.86
Score	0.20	0.50	0.22	-0.12	-0.12	-0.19	-0.19	0.75	1.50	0.50	0.75	1.50	0.50	-0.12	0.50	-0.22	-0.11	0.50	-0.14	-0.18	0.50	1.50	1.50	-0.14	1.50
Ion-type	PR	V	LI					GT	y_1	b_2	VDL	y_3	b_3		b_4			b_5			b_6	y_8	y_9		y_{11}
Delta ppm	6.8	14.2	13.6					-3.2	14.5	-0.5	-23.1	-10.5	0.5		-6.0			12.6			-18.1	-4.1	-3.7		-9.5

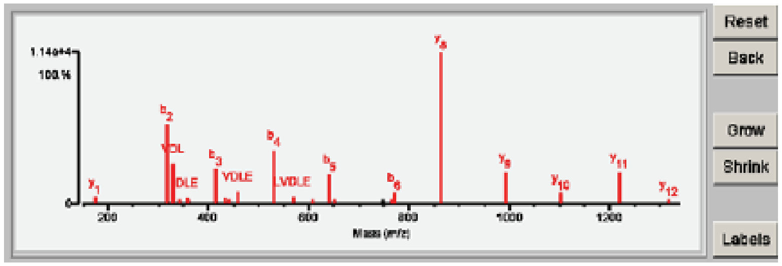


I128

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.84	98.1	9	1/26	(A) I L|V|D|L|E|P/G T/M D/S V/R (S)	1632.7872	-0.0020	-1.2	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	22.84	98.1	9	1/26	(A) I L|V|D|L|E|P/G T/M D/S V/R (S)	1632.7872	-0.0020	-1.2	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	22.84	98.1	9	1/26	(A) I L|V|D|L|E|P/G T/M D/S V/R (S)	1632.7872	-0.0020	-1.2	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	22.84	98.1	9	1/26	(A) I L|V|D|L|E|P/G T/M D/S V/R (S)	1632.7872	-0.0020	-1.2	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	72.081	86.096	175.118	316.176	328.187	343.208	358.166	361.215	414.240	431.708^{+2}	441.258	457.229	529.288	570.302	607.284	642.348	661.306^{+2}	746.410	765.348	771.383	862.405	991.448	1104.643	1219.580	1318.621
Frac. Inten.(% of TIC)	0.05	0.22	1.19	14.46	7.24	0.79	1.12	0.91	6.16	1.09	0.90	2.21	9.79	1.29	0.93	5.35	0.85	0.87	0.83	2.03	27.50	5.73	2.03	5.67	0.81
Rel. Inten.(% of BP)	0.18	0.79	4.32	52.57	26.32	2.87	4.07	3.32	22.41	3.96	3.27	8.02	35.58	4.69	3.37	19.47	3.10	3.15	3.01	7.37	100.00	20.83	7.38	20.63	2.93
Score	0.50	0.22	1.50	0.50	0.75	0.50	0.75	1.50	0.50	1.50	0.75	0.75	0.50	0.75	1.50	0.50	0.50	-0.03	1.50	0.50	1.50	1.50	1.50	1.50	1.50
Ion-type	V	LI	y_1	b_2	VDL	y_3-H_2O	DLE	y_3	b_3	y_8^{+2}	LVDL	VDLE	b_4	LVDLE	y_5	b_5	y_{12}-NH_3^{+2}		y_7	b_6	y_8	y_9	y_{10}	y_{11}	y_{12}
Delta ppm	4.5	-3.8	-6.0	0.0	-3.0	-3.3	9.8	-12.4	-7.5	-0.7	-31.9	-2.2	-4.2	-22.2	-4.6	-9.7	-0.8		-10.9	-18.4	-3.7	-3.4	6.4	-1.8	-7.2

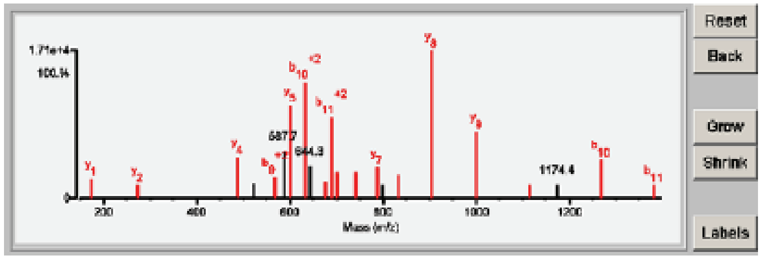


I129

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.00	84.8	10	8/26	(W) A K G H Y T E G A\E|L|V|D/S/V/L/D V/V/R (K)	2381.1284	0.0276	11.6	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	17.00	84.8	10	8/26	(W) A K G H Y T E G A\E|L|V|D/S/V/L/D V/V/R (K)	2381.1284	0.0276	11.6	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	17.00	84.8	10	8/26	(W) A K G H Y T E G A\E|L|V|D/S/V/L/D V/V/R (K)	2381.1284	0.0276	11.6	49831.3/4.79	HUMAN	P68371	638067	Tubulin beta-2C chain - Homo sapiens (Human)
1	17.00	84.8	10	8/26	(W) A K G H Y T E G A\E|L|V|D/S/V/L/D V/V/R (K)	2381.1284	0.0276	11.6	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	17.00	84.8	10	8/26	(W) A K G H Y T E G A\E|L|V|D/S/V/L/D V/V/R (K)	2381.1284	0.0276	11.6	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	72.082	86.098	94.067	175.120	274.186	488.290	523.199^{+2}	569.741^{+2}	587.721^{+2}	601.373	634.266^{+2}	644.271^{+2}	676.787^{+2}	690.786^{+2}	700.443	740.338	787.470	798.362	832.358^{+2}	902.503	1001.567	1114.660	1174.460	1267.607	1380.672
Frac. Inten.(% of TIC)	0.12	0.30	2.56	2.12	1.41	4.38	1.58	2.22	5.01	9.90	12.49	3.40	1.74	8.75	2.77	2.75	3.31	1.40	2.46	15.82	7.11	1.41	1.42	4.09	1.49
Rel. Inten.(% of BP)	0.78	1.87	16.19	13.40	8.89	27.67	10.02	14.04	31.66	62.60	78.99	21.47	11.01	55.30	17.49	17.36	20.92	8.84	15.58	100.00	44.93	8.89	9.00	25.84	9.39
Score	0.50	0.22	-0.16	1.50	1.50	1.50	-0.10	0.50	-0.32	1.50	0.50	-0.21	0.50	0.50	1.50	0.50	1.50	-0.09	0.25	1.50	1.50	1.50	-0.09	0.50	0.50
Ion-type	V	LI		y1	y2	y4		b_9^{+2}		y5	b_{10}^{+2}		a_{11}^{+2}	b_{11}^{+2}	y6	b++12	y7		b_{14}-H_2O^{+2}	y8	y9	y10		b_{10}	b_{11}
Delta ppm	17.0	19.4		8.3	-6.6	14.9		25.6		10.2	12.1		7.6	12.4	11.0	15.9	3.9		8.8	10.2	3.9	12.2		15.3	-0.1

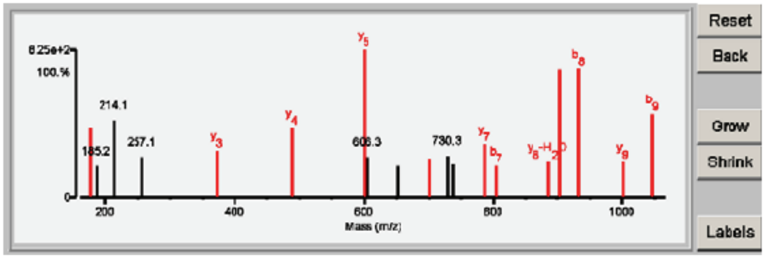


I130

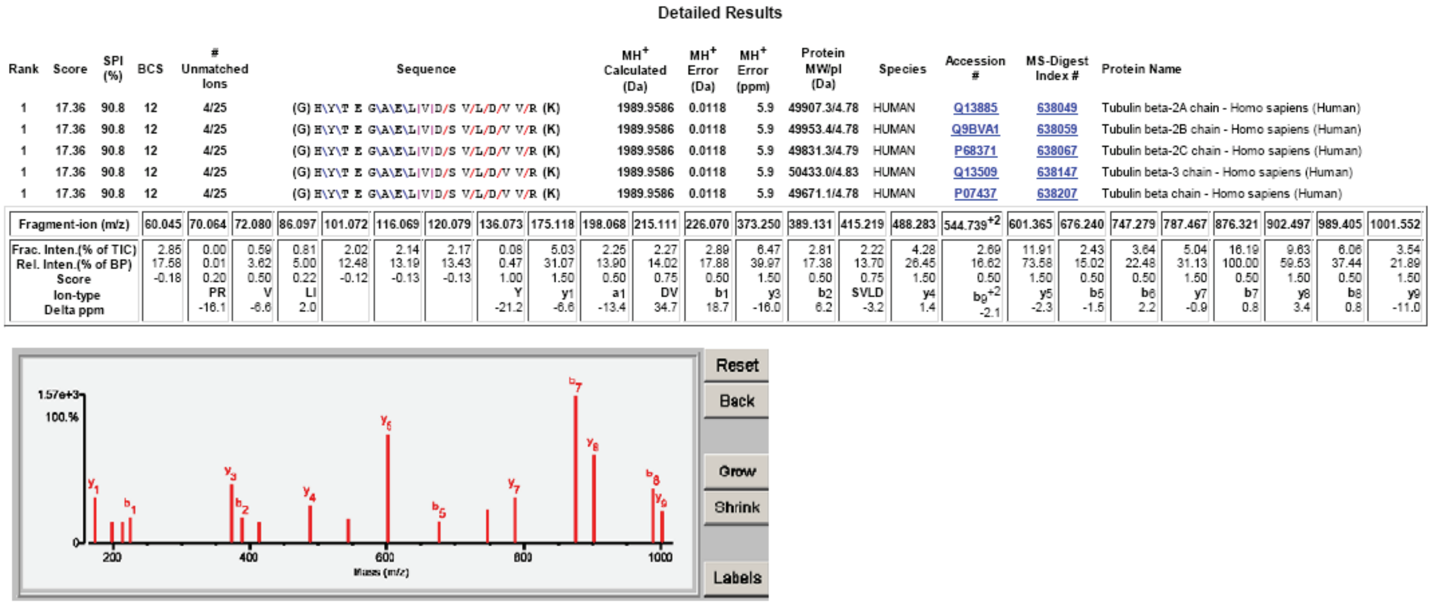
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.31	69.9	10	8/25	(K) G H Y T E G A\E\L|V/D/S/V/L/D/V V/R (K)	2046.9801	0.0021	1.0	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	14.31	69.9	10	8/25	(K) G H Y T E G A\E\L|V/D/S/V/L/D/V V/R (K)	2046.9801	0.0021	1.0	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	14.31	69.9	10	8/25	(K) G H Y T E G A\E\L|V/D/S/V/L/D/V V/R (K)	2046.9801	0.0021	1.0	49831.3/4.79	HUMAN	P68371	638067	Tubulin beta-2C chain - Homo sapiens (Human)
1	14.31	69.9	10	8/25	(K) G H Y T E G A\E\L|V/D/S/V/L/D/V V/R (K)	2046.9801	0.0021	1.0	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	14.31	69.9	10	8/25	(K) G H Y T E G A\E\L|V/D/S/V/L/D/V V/R (K)	2046.9801	0.0021	1.0	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	70.067	72.081	86.096	94.066	110.070	136.075	175.119	185.162	214.101	257.127	373.252	488.276	601.366	606.277	650.837^{+2}	700.445	730.283^{+2}	737.379	787.469	804.276	884.481	902.487	933.350	1001.551	1046.423
Frac. Inten.(% of TIC)	0.00	0.52	0.83	6.84	0.12	0.29	5.44	2.47	6.04	3.16	3.66	5.48	11.50	3.18	2.54	3.06	3.28	2.58	4.18	2.55	2.76	10.03	10.12	2.84	6.51
Rel. Inten.(% of BP)	0.02	4.52	7.23	59.48	1.01	2.50	47.33	21.49	52.50	27.48	31.83	47.66	100.00	27.66	22.12	26.63	28.48	22.44	36.34	22.21	24.04	87.18	87.98	24.69	56.62
Score	0.20	0.50	0.22	-0.59	1.00	1.00	1.50	-0.21	-0.52	-0.27	1.50	1.50	1.50	-0.28	-0.22	1.50	-0.28	-0.22	1.50	0.50	0.50	1.50	0.50	1.50	0.50
Ion-type	PR	V	LI		H	Y	y1				y3	y4	y5			y6			y7	b7	y8-H_2O	y8	b8	y9	b9
Delta ppm	28.2	0.3	-0.3		-8.8	-5.1	-1.4				-9.9	-14.6	-1.8			14.3			1.7	-28.7	-3.1	-7.4	9.2	-11.9	-2.6



I131

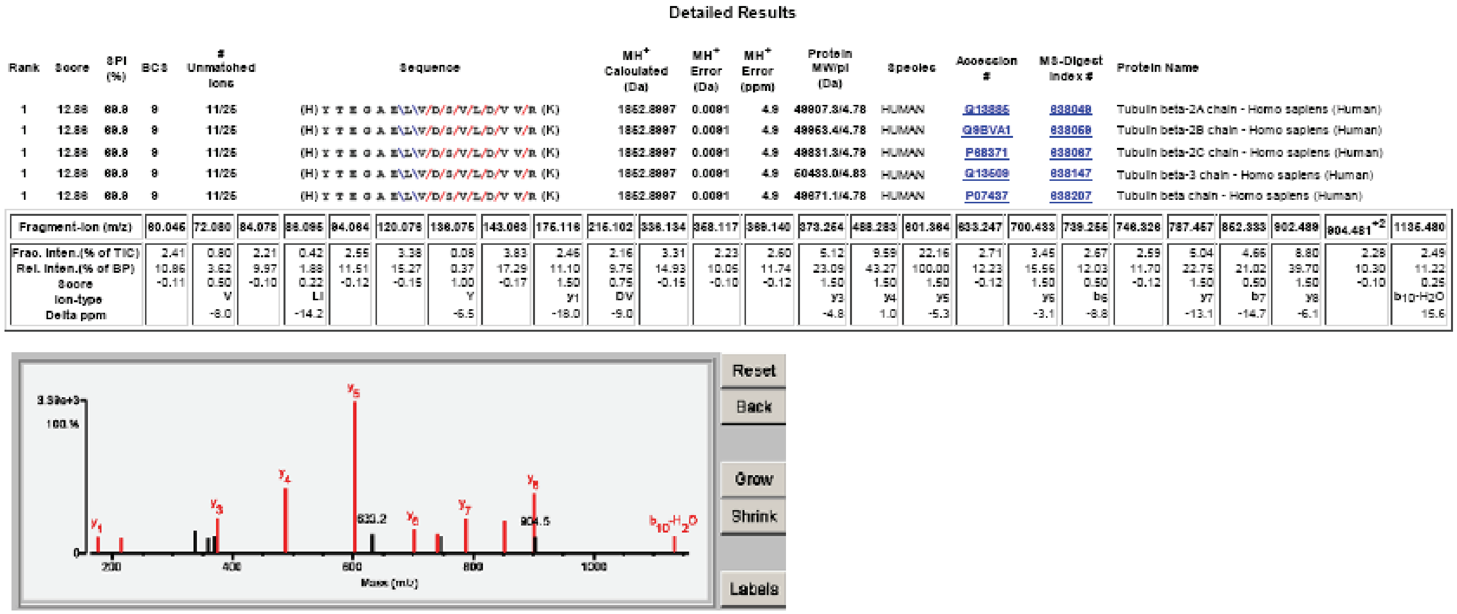


Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.36	90.8	12	4/25	(G) H\Y\T E G\A\E\L|V|D/S V/L/D/V V/R (K)	1989.9586	0.0118	5.9	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	17.36	90.8	12	4/25	(G) H\Y\T E G\A\E\L|V|D/S V/L/D/V V/R (K)	1989.9586	0.0118	5.9	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	17.36	90.8	12	4/25	(G) H\Y\T E G\A\E\L|V|D/S V/L/D/V V/R (K)	1989.9586	0.0118	5.9	49831.3/4.79	HUMAN	P68371	638067	Tubulin beta-2C chain - Homo sapiens (Human)
1	17.36	90.8	12	4/25	(G) H\Y\T E G\A\E\L|V|D/S V/L/D/V V/R (K)	1989.9586	0.0118	5.9	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	17.36	90.8	12	4/25	(G) H\Y\T E G\A\E\L|V|D/S V/L/D/V V/R (K)	1989.9586	0.0118	5.9	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	60.045	70.064	72.080	86.097	101.072	116.069	120.079	136.073	175.118	198.068	215.111	226.070	373.250	389.131	415.219	488.283	544.739^{+2}	601.365	676.240	747.279	787.467	876.321	902.497	989.405	1001.552
Frac. Inten.(% of TIC)	2.85	0.00	0.59	0.81	2.02	2.14	2.17	0.08	5.03	2.25	2.27	2.89	6.47	2.81	2.22	4.28	2.69	11.91	2.43	3.64	5.04	16.19	9.63	6.06	3.54
Rel. Inten.(% of BP)	17.58	0.01	3.62	5.00	12.48	13.19	13.43	0.47	31.07	13.90	14.02	17.88	39.97	17.38	13.70	26.45	16.62	73.58	15.02	22.48	31.13	100.00	59.53	37.44	21.89
Score	-0.18	0.20	0.50	0.22	-0.12	-0.13	-0.13	1.00	1.50	0.50	0.75	0.50	1.50	0.50	0.75	1.50	0.50	1.50	0.50	0.50	1.50	0.50	1.50	0.50	1.50
Ion-type		PR	V	LI				Y	y_1	a_1	DV	b_1	y_3	b_2	SVLD	y_4	b_9^{+2}	y_5	b_5	b_6	y_7	b_7	y_8	b_8	y_9
Delta ppm		-16.1	-6.6	2.0				-21.2	-6.6	-13.4	34.7	18.7	-16.0	6.2	-3.2	1.4	-2.1	-2.3	-1.5	2.2	-0.9	0.8	3.4	0.8	-11.0

I132



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.88	68.8	8	11/25	(H) Y T E G A E\L\V/D/S/V/L/D/V V/R (K)	1852.8997	0.0091	4.9	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	12.88	68.8	8	11/25	(H) Y T E G A E\L\V/D/S/V/L/D/V V/R (K)	1852.8997	0.0091	4.9	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	12.88	68.8	8	11/25	(H) Y T E G A E\L\V/D/S/V/L/D/V V/R (K)	1852.8997	0.0091	4.9	49831.3/4.79	HUMAN	P68371	638067	Tubulin beta-2C chain - Homo sapiens (Human)
1	12.88	68.8	8	11/25	(H) Y T E G A E\L\V/D/S/V/L/D/V V/R (K)	1852.8997	0.0091	4.9	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	12.88	68.8	8	11/25	(H) Y T E G A E\L\V/D/S/V/L/D/V V/R (K)	1852.8997	0.0091	4.9	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	60.046	72.080	84.078	86.096	94.064	120.076	136.075	143.083	175.116	215.102	336.134	368.117	369.140	373.254	488.283	601.364	633.247	700.433	739.266	748.326	787.457	862.333	902.489	904.481^{+2}	1136.480
Frac. Inten.(% of TIC)	2.41	0.80	2.21	0.42	2.55	3.38	0.08	3.83	2.46	2.16	3.31	2.23	2.60	5.12	9.59	22.16	2.71	3.45	2.67	2.59	5.04	4.66	8.80	2.28	2.49
Rel. Inten.(% of BP)	10.86	3.62	9.97	1.88	11.51	15.27	0.37	17.29	11.10	9.75	14.93	10.05	11.74	23.09	43.27	100.00	12.23	15.56	12.03	11.70	22.75	21.02	39.70	10.30	11.22
Score	-0.11	0.50	-0.10	0.22	-0.12	-0.15	1.00	-0.17	1.50	0.75	-0.15	-0.10	-0.12	1.50	1.50	1.50	-0.12	1.50	0.50	-0.12	1.50	0.50	1.50	-0.10	0.25
Ion-type		V		LI			Y		y_1	DV				y_3	y_4	y_5		y_6	b_6		y_7	b_7	y_8		b_{10}-H_2O
Delta ppm		-8.0		-14.2			-6.5		-18.0	-9.0				-4.8	1.0	-5.3		-3.1	-8.8		-13.1	-14.7	-6.1		15.6

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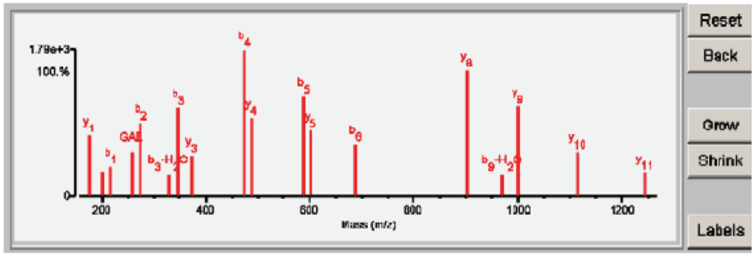
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.08	95.9	11	2/25	(T) E\G\A|E|L|V|D S V/L/D/V/V/R (K)	1588.7887	-0.0014	-0.9	49907.3/4.78	HUMAN	Q13885	638049	Tubulin beta-2A chain - Homo sapiens (Human)
1	20.08	95.9	11	2/25	(T) E\G\A|E|L|V|D S V/L/D/V/V/R (K)	1588.7887	-0.0014	-0.9	49953.4/4.78	HUMAN	Q9BVA1	638059	Tubulin beta-2B chain - Homo sapiens (Human)
1	20.08	95.9	11	2/25	(T) E\G\A|E|L|V|D S V/L/D/V/V/R (K)	1588.7887	-0.0014	-0.9	49831.3/4.79	HUMAN	P68371	638067	Tubulin beta-2C chain - Homo sapiens (Human)
1	20.08	95.9	11	2/25	(T) E\G\A|E|L|V|D S V/L/D/V/V/R (K)	1588.7887	-0.0014	-0.9	50433.0/4.83	HUMAN	Q13509	638147	Tubulin beta-3 chain - Homo sapiens (Human)
1	20.08	95.9	11	2/25	(T) E\G\A|E|L|V|D S V/L/D/V/V/R (K)	1588.7887	-0.0014	-0.9	49671.1/4.78	HUMAN	P07437	638207	Tubulin beta chain - Homo sapiens (Human)

Fragment-ion (m/z)	70.066	72.081	84.041	86.097	120.081	136.075	175.118	201.084	218.055	258.109	274.184	275.069	328.092
Frac. Inten.(% of TIC)	0.00	0.09	0.06	0.22	2.34	1.78	5.02	1.99	2.44	3.71	1.73	6.04	1.81
Rel. Inten.(% of BP)	0.03	0.71	0.51	1.85	19.28	14.68	41.34	16.35	20.08	30.56	14.27	49.72	14.93
Score	0.20	0.50	1.00	0.22	-0.19	-0.15	1.50	0.75	0.50	0.75	1.50	0.50	0.25
Ion-type	PR	V	E	LI			y1	AE	b1	GAE	y2	b2	b3-H2O
Delta ppm	5.3	-2.4	-35.6	3.2			-4.9	-19.3	26.8	-3.7	-11.2	-5.1	-17.6

Fragment-ion (m/z)	346.109	373.253	475.153	488.281	588.235	601.361	687.305	902.503	970.427	1001.568	1114.641	1243.665
Frac. Inten.(% of TIC)	7.34	3.42	12.14	6.50	8.27	5.46	4.32	10.44	1.78	7.47	3.69	1.95
Rel. Inten.(% of BP)	60.44	28.12	100.00	53.50	68.13	44.94	35.55	85.95	14.63	61.48	30.38	16.02
Score	0.50	1.50	0.50	1.50	0.50	1.50	0.50	1.50	0.25	1.50	1.50	1.50
Ion-type	b3	y3	b4	y4	b5	y5	b6	y8	b9-H2O	y9	y10	y11
Delta ppm	4.0	-7.4	5.2	-4.6	0.2	-10.5	2.9	10.2	7.7	5.8	-5.4	-19.3



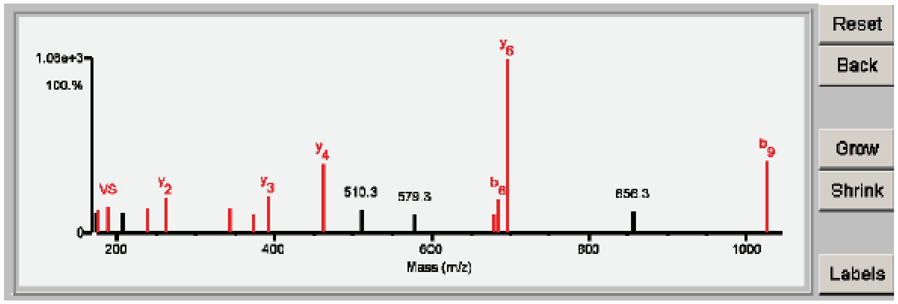
I134

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.50	77.3	7	8/24	(R) A V T H T S\P E D\V/S F/A/E/S/R (R)	1820.8120	0.0074	4.1	132528.6/5.83	HUMAN	Q9BTW9	638633	Tubulin-specific chaperone D - Homo sapiens (Human)

Fragment-ion (m/z)	60.043	70.066	72.082	110.072	115.089	120.080	144.116	173.128	175.118	187.107	207.110	239.118
Frac. Inten.(% of TIC)	2.79	0.00	0.70	0.08	2.74	0.39	3.03	2.74	3.24	3.63	2.85	3.41
Rel. Inten.(% of BP)	11.70	0.01	2.92	0.35	11.51	1.65	12.74	11.49	13.61	15.25	11.97	14.34
Score	-0.12	0.20	0.50	1.00	-0.12	1.00	-0.13	-0.11	1.50	0.75	-0.12	0.75
Ion-type		PR	V	H		F			y1	VS		HT
Delta ppm		13.9	17.0	7.5		-4.0			-6.0	-9.7		14.4

Fragment-ion (m/z)	262.149	342.125	373.173	391.192	462.226	510.259	579.288	678.317	685.293	696.327	856.310	1026.417
Frac. Inten.(% of TIC)	4.73	3.29	2.62	5.02	9.54	3.14	2.48	2.53	4.53	23.81	2.92	9.78
Rel. Inten.(% of BP)	19.87	13.82	11.01	21.10	40.06	13.17	10.43	10.64	19.03	100.00	12.25	41.07
Score	1.50	0.75	0.50	1.50	1.50	-0.13	-0.10	0.50	0.50	1.50	-0.12	0.50
Ion-type	y2	PED	y3-H2O	y3	y4			y6-H2O	b6	y6		b9
Delta ppm	-7.6	-17.2	-27.4	-3.8	-10.8			-5.7	-8.3	-5.5		-3.8

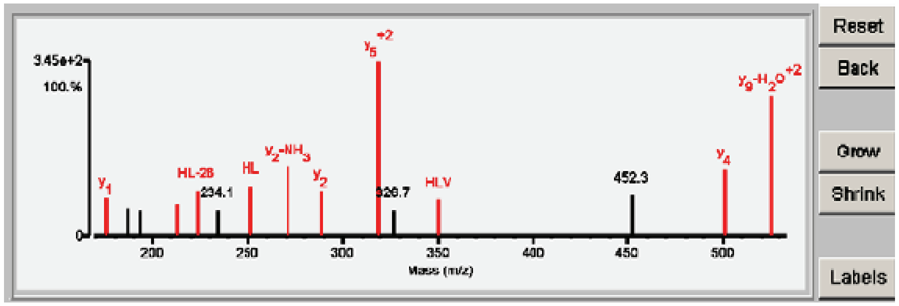


I135

Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.65	66.8	4	10/25	(K) E S T L/H/L V/L/R (L)	1155.6191	0.0076	6.6	8564.9/6.56	HUMAN	P62988	677557	Ubiquitin - Homo sapiens (Human)

Fragment-ion (m/z)	61.011	70.066	72.082	74.058	84.047	86.056	86.097	110.070	153.065	160.113	175.122	187.141	193.143	213.157	223.150	234.122	251.145	271.180	288.205	319.216^{+2}	326.717	350.214	452.265	500.344	525.315^{+2}
Frac. Inten.(% of TIC)	6.68	0.01	0.10	2.55	0.23	3.97	0.51	0.23	2.98	3.04	3.65	2.63	2.52	2.96	4.30	2.53	4.65	6.52	4.27	16.44	2.45	3.48	3.86	6.27	13.18
Rel. Inten.(% of BP)	40.60	0.03	0.59	15.49	1.40	24.13	3.11	1.37	18.10	18.47	22.19	16.01	15.34	17.98	26.16	15.37	28.25	39.68	25.99	100.00	14.88	21.17	23.49	38.14	80.16
Score	-0.41	0.20	0.50	-0.15	1.00	-0.24	0.22	1.00	-0.18	-0.18	1.50	-0.16	-0.15	0.75	0.50	-0.15	0.75	0.50	1.50	1.50	-0.15	0.75	-0.23	1.50	0.50
Ion-type		PR	V		E		LI	H			y1			VL	HL-28		HL	y2-NH3	y2	$y5^{+2}$		HLV		y4	$y9\text{-}H_2O^{+2}$
Delta ppm		18.2	10.0		31.1		7.8	-10.7			16.3			-17.6	-30.6		-24.9	13.4	6.2	14.9		-15.0		-22.2	1.8

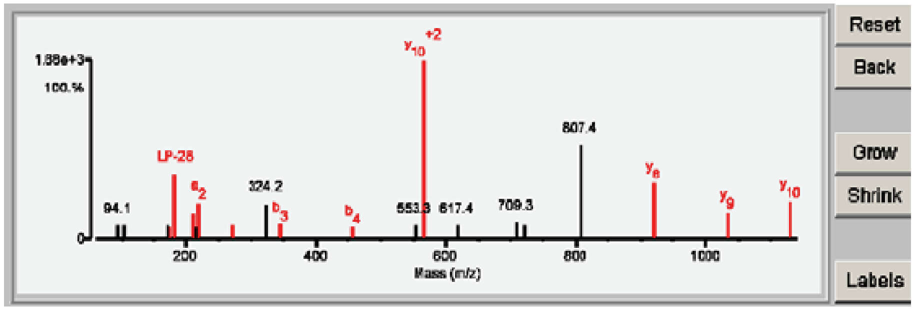


I136

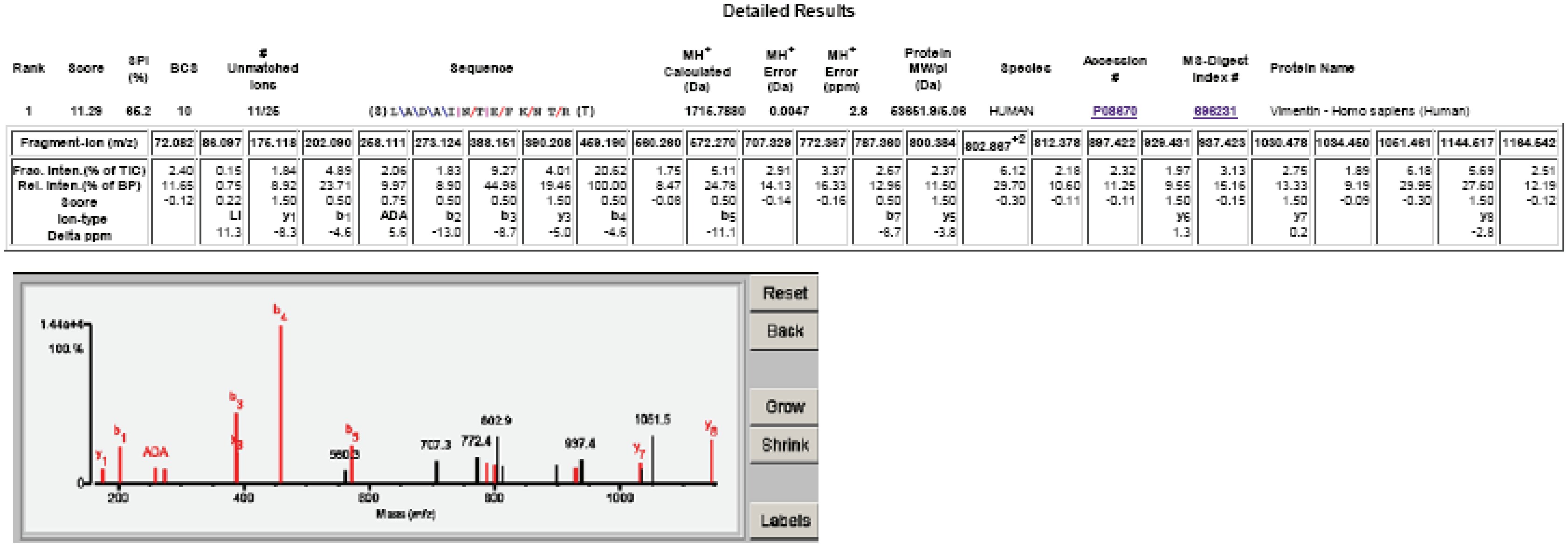
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.36	67.0	5	10/25	(A) A S/P|L|P E E P P V/P/R (P)	1376.6879	0.0093	6.7	35187.1/8.54	HUMAN	A8MZF0	765589	Uncharacterized protein LOC728008 - Homo sapiens (Human)

Fragment-ion (m/z)	70.064	72.081	86.097	94.066	102.054	104.050	171.072	175.113	183.150	211.147	215.143	219.079	272.174	324.223	344.131	457.215	553.255	565.817^{+2}	617.364	709.271	720.399	807.406	920.483	1033.579	1130.628
Frac. Inten.(% of TIC)	0.01	0.06	0.20	1.86	0.05	1.79	1.84	1.59	9.23	3.50	1.53	5.00	1.91	4.92	1.95	1.60	1.76	25.16	1.88	2.29	1.86	13.23	7.82	3.70	5.26
Rel. Inten.(% of BP)	0.02	0.26	0.80	7.38	0.20	7.12	7.32	6.33	36.68	13.92	6.07	19.86	7.58	19.58	7.74	6.38	7.01	100.00	7.46	9.09	7.41	52.58	31.07	14.71	20.91
Score	0.20	0.50	0.22	-0.07	1.00	-0.07	-0.07	1.50	0.50	0.75	-0.06	0.50	1.50	-0.20	0.50	0.50	-0.07	1.50	-0.07	-0.09	-0.07	-0.53	1.50	1.50	1.50
Ion-type	PR	V	LI		E			y1	LP-28	LP		a2	y2		b3	b4		$y10^{+2}$					y8	y9	y10
Delta ppm	-17.5	4.5	4.3		-9.4			-34.0	-2.7	6.1		-8.6	9.5		7.1	5.6		5.7					-0.4	10.6	6.8



I137



Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.29	86.2	10	11/25	(S) L\A\D\A\I|N/T|E/F K/N T/R (T)	1716.7880	0.0047	2.8	53651.9/5.06	HUMAN	P08670	896231	Vimentin - Homo sapiens (Human)

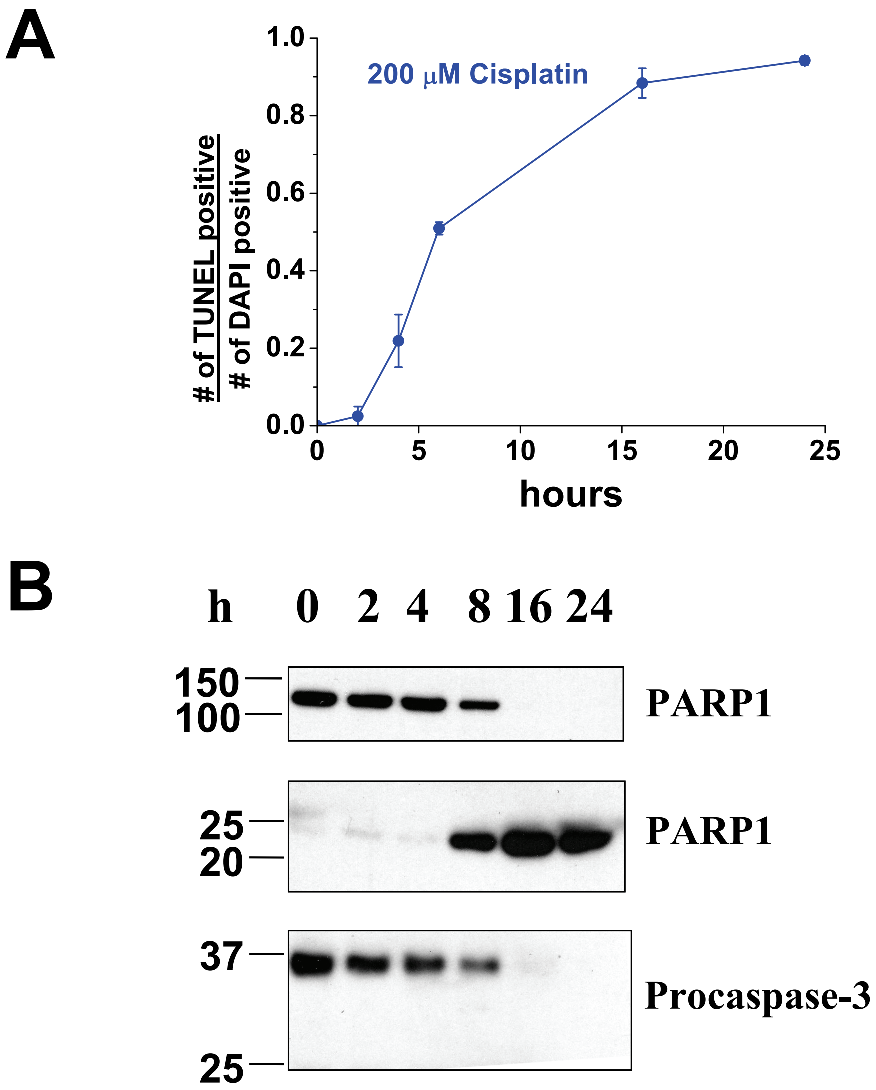
Fragment-Ion (m/z)	72.082	86.097	176.118	202.090	268.111	273.124	388.151	390.208	469.190	560.280	572.270	707.328
Frac. Inten.(% of TIC)	2.40	0.15	1.84	4.89	2.06	1.83	9.27	4.01	20.62	1.75	5.11	2.91
Rel. Inten.(% of BP)	11.65	0.75	8.92	23.71	9.97	8.90	44.98	19.46	100.00	8.47	24.78	14.13
Score	-0.12	0.22	1.50	0.50	0.75	0.50	0.50	1.50	0.50	-0.08	0.50	-0.14
Ion-type		LI	y1	b1	ADA	b2	b3	y3	b4		b5	
Delta ppm		11.3	-8.3	-4.6	5.6	-13.0	-8.7	-5.0	-4.6		-11.1	

Fragment-Ion (m/z)	772.367	787.360	800.384	802.887⁺²	812.378	897.422	929.431	937.423	1030.478	1034.450	1051.461	1144.617	1164.542
Frac. Inten.(% of TIC)	3.37	2.67	2.37	6.12	2.18	2.32	1.97	3.13	2.75	1.89	6.18	5.69	2.51
Rel. Inten.(% of BP)	16.33	12.96	11.50	29.70	10.60	11.25	9.55	15.16	13.33	9.19	29.95	27.60	12.19
Score	-0.16	0.50	1.50	-0.30	-0.11	-0.11	1.50	-0.15	1.50	-0.09	-0.30	1.50	-0.12
Ion-type		b7	y5				y6		y7			y8	
Delta ppm		-8.7	-3.8				1.3		0.2			-2.8	

Fig. S5. Time course of cisplatin-induced apoptosis in Jurkat T-cells.

(*A*) The fraction of cells with terminal deoxynucleotide transferase dUTP nick end labeling (TUNEL) positive signal was measured. The total number of cells was established by staining with 4[prime]-6-diamidino-2-phenylindole (DAPI). The time course was measured after treatment with 200 μM cisplatin.

(*B*) Western blot analysis of apoptotic markers after cisplatin (200 μM) treatment. More than 50% of nuclear enzyme poly(ADPribose) polymerase-1 (PARP1) and procaspase-3 were cleaved after 8 h cisplatin treatment. Both are completely abolished after 16 h of treatment. The band at approximately 22 kDa is the PARP1 fragment generated after the caspase cleavage of Asp-214.


A
200 μM Cisplatin
# of TUNEL positive / # of DAPI positive
1.0
0.8
0.6
0.4
0.2
0.0
0
5
10
15
20
25
hours
B
h
0
2
4
8
16
24
150
100
PARP1
25
20
PARP1
37
25
Procaspase-3