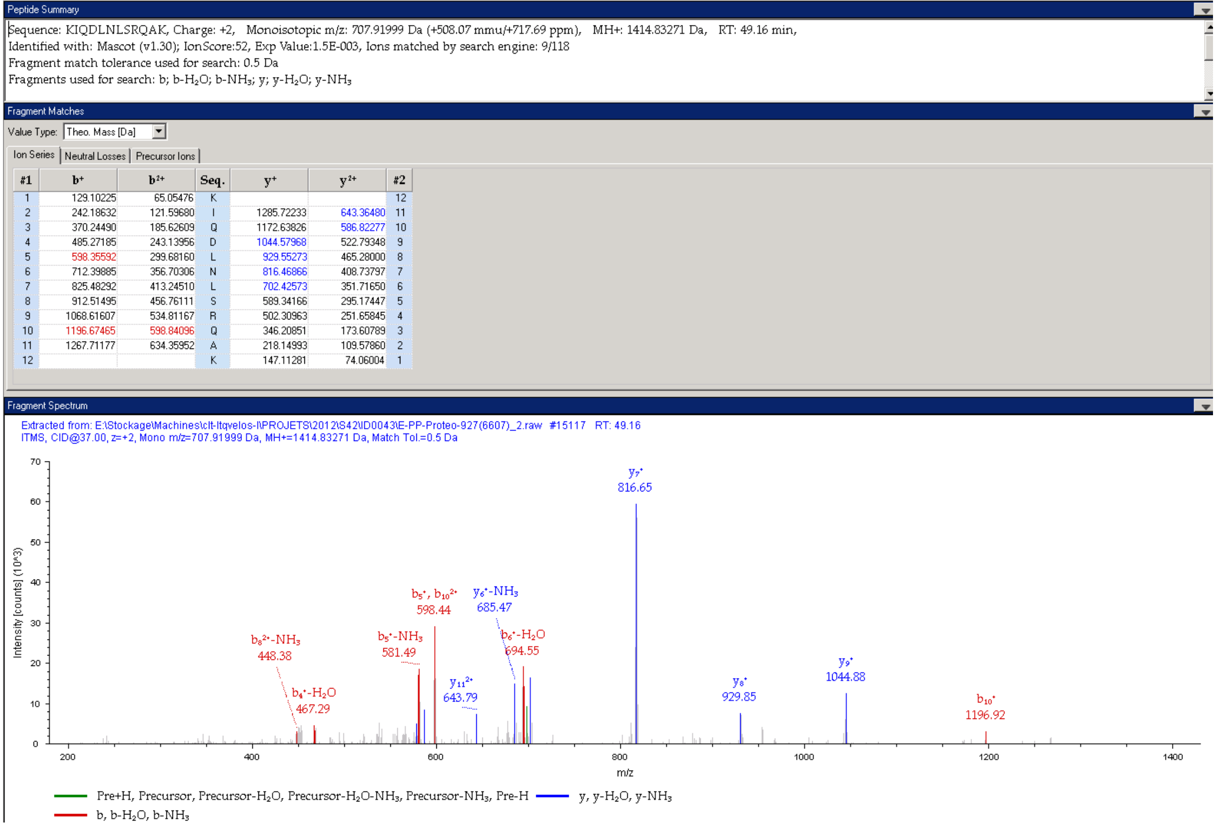
Protein references (1):

- Laminin subunit beta-4 OS=Homo sapiens GN=LAMB4 PE=2 SV=1 - [LAMB4_HUMAN]



Peptide Summary

Sequence: KIQDLNLSRQAK, Charge: +2, Monoisotopic m/z: 707.91999 Da (+508.07 mmu/+717.69 ppm), MH+: 1414.83271 Da, RT: 49.16 min,
Identified with: Mascot (v1.30); IonScore:52, Exp Value:1.5E-003, Ions matched by search engine: 9/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

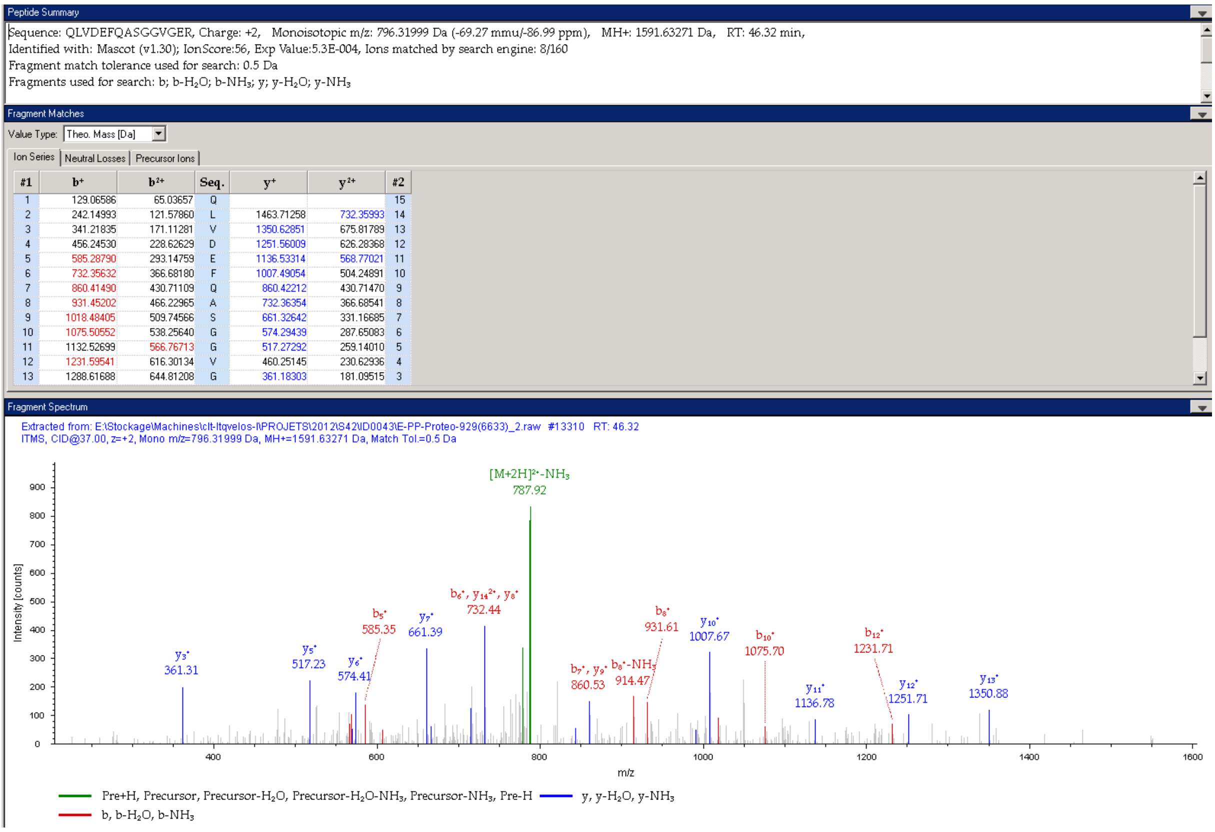
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.10225	65.05476	K			12
2	242.18632	121.59680	I	1285.72233	643.36480	11
3	370.24490	185.62609	Q	1172.63826	586.82277	10
4	485.27185	243.13956	D	1044.57968	522.79348	9
5	598.35592	299.68160	L	929.55273	465.28000	8
6	712.39885	356.70306	N	816.46866	408.73797	7
7	825.48292	413.24510	L	702.42573	351.71650	6
8	912.51495	456.76111	S	589.34166	295.17447	5
9	1068.61607	534.81167	R	502.30963	251.65845	4
10	1196.67465	598.84096	Q	346.20851	173.60789	3
11	1267.71177	634.35952	A	218.14993	109.57860	2
12			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #15117 RT: 49.16
ITMS, CID@37.00, z=+2, Mono m/z=707.91999 Da, MH+=1414.83271 Da, Match Tol.=0.5 Da

Protein references (1):

- Carnitine O-acetyltransferase OS=Homo sapiens GN=CRAT PE=1 SV=5 - [CACP_HUMAN]



Peptide Summary

Sequence: QLVDEFQASGGVGER, Charge: +2, Monoisotopic m/z: 796.31999 Da (-69.27 mmu/-86.99 ppm), MH+: 1591.63271 Da, RT: 46.32 min,
Identified with: Mascot (v1.30); IonScore:56, Exp Value:5.3E-004, Ions matched by search engine: 8/160
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

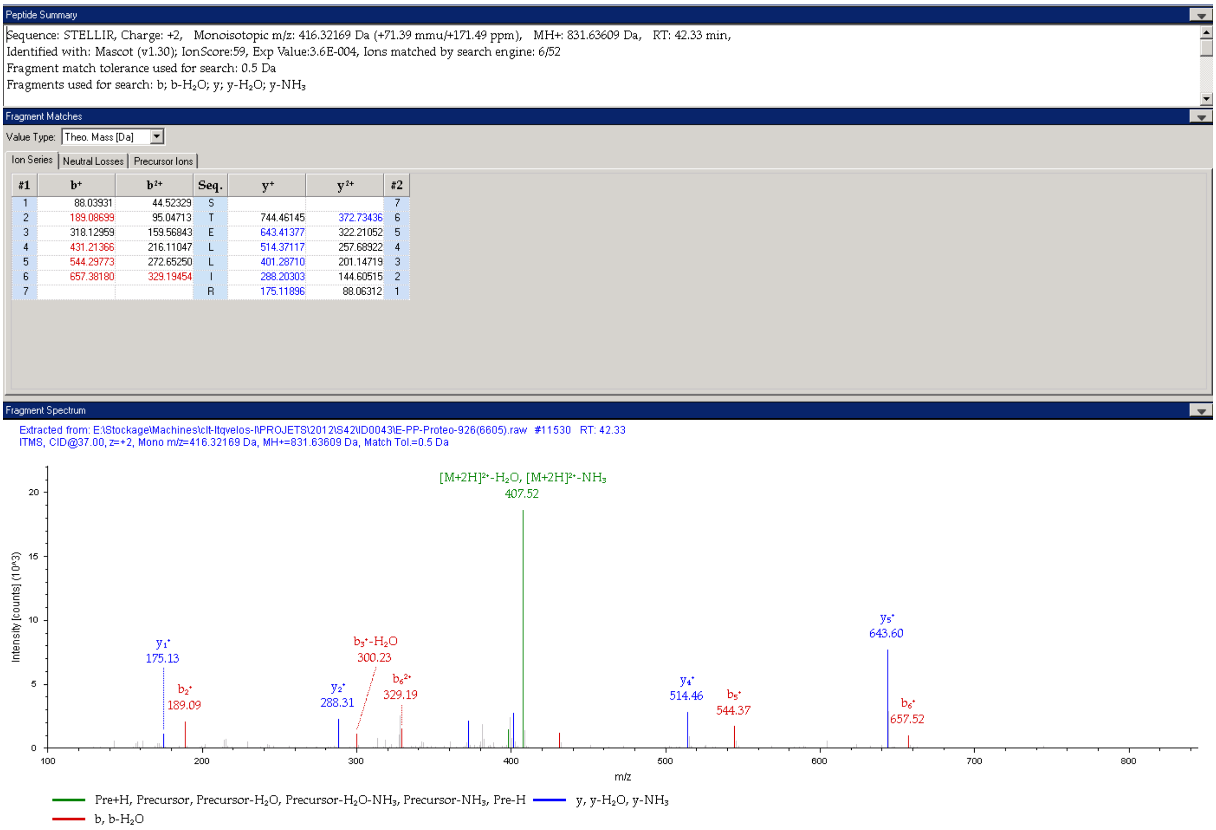
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			15
2	242.14993	121.57860	L	1463.71258	732.35993	14
3	341.21835	171.11281	V	1350.62851	675.81789	13
4	456.24530	228.62629	D	1251.56009	626.28368	12
5	585.28790	293.14759	E	1136.53314	568.77021	11
6	732.35632	366.68180	F	1007.49054	504.24891	10
7	860.41490	430.71109	Q	860.42212	430.71470	9
8	931.45202	466.22965	A	732.36354	366.68541	8
9	1018.48405	509.74566	S	661.32642	331.16685	7
10	1075.50552	538.25640	G	574.29439	287.65083	6
11	1132.52699	566.76713	G	517.27292	259.14010	5
12	1231.59541	616.30134	V	460.25145	230.62936	4
13	1288.61688	644.81208	G	361.18303	181.09515	3

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #13310 RT: 46.32
ITMS, CID@37.00, z=+2, Mono m/z=796.31999 Da, MH+=1591.63271 Da, Match Tol.=0.5 Da

Protein references (5):

- Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]
- Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3 - [H31T_HUMAN]



Peptide Summary

Sequence: STELLIR, Charge: +2, Monoisotopic m/z: 416.32169 Da (+71.39 mmu/+171.49 ppm), MH+: 831.63609 Da, RT: 42.33 min,
Identified with: Mascot (v1.30); IonScore:59, Exp Value:3.6E-004, Ions matched by search engine: 6/52
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

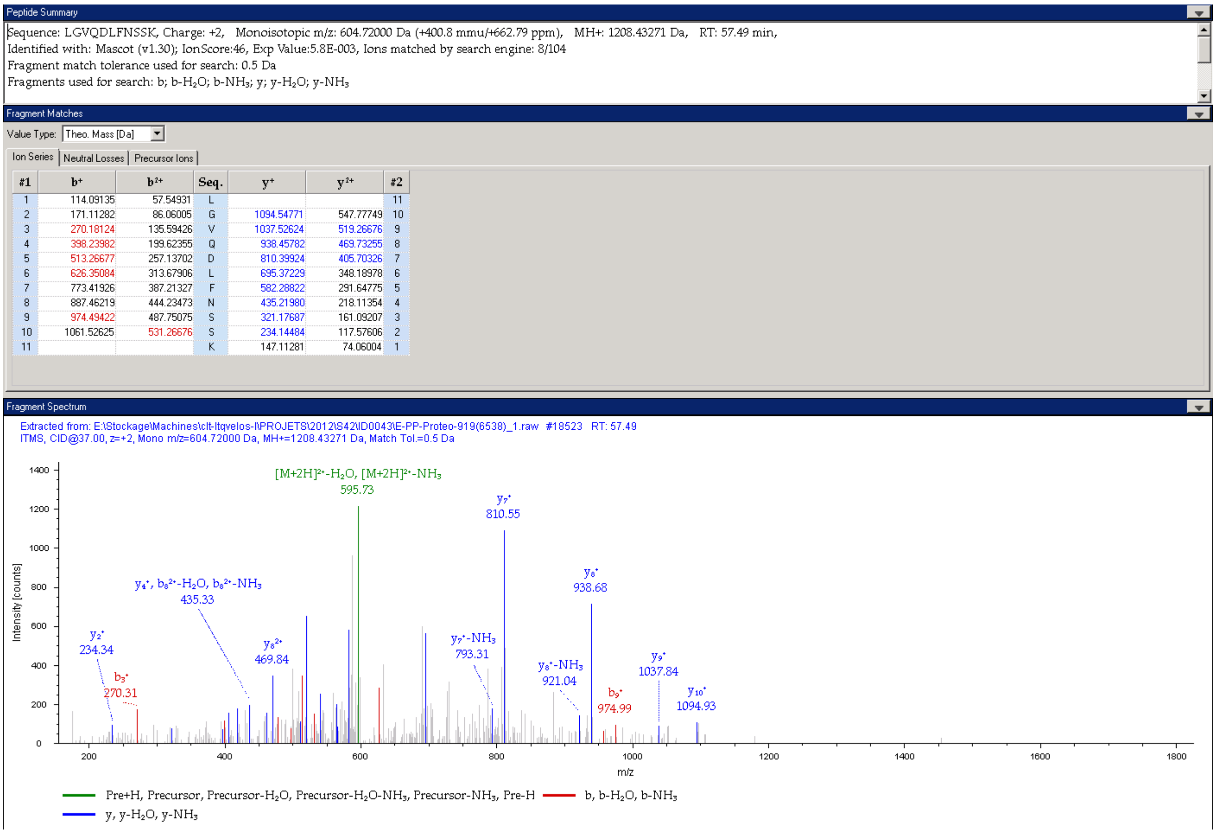
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			7
2	189.08699	95.04713	T	744.46145	372.73436	6
3	318.12959	159.56843	E	643.41377	322.21052	5
4	431.21366	216.11047	L	514.37117	257.68922	4
5	544.29773	272.65250	L	401.28710	201.14719	3
6	657.38180	329.19454	I	288.20303	144.60515	2
7			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605).raw #11530 RT: 42.33
ITMS, CID@37.00, z=+2, Mono m/z=416.32169 Da, MH+=831.63609 Da, Match Tol.=0.5 Da

Protein references (1):
- Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1 - [ILEU_HUMAN]



Sequence: LGVQDLFNSSK, Charge: +2, Monoisotopic m/z: 604.72000 Da (+400.8 mmu/+662.79 ppm), MH+: 1208.43271 Da, RT: 57.49 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:5.8E-003, Ions matched by search engine: 8/104
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

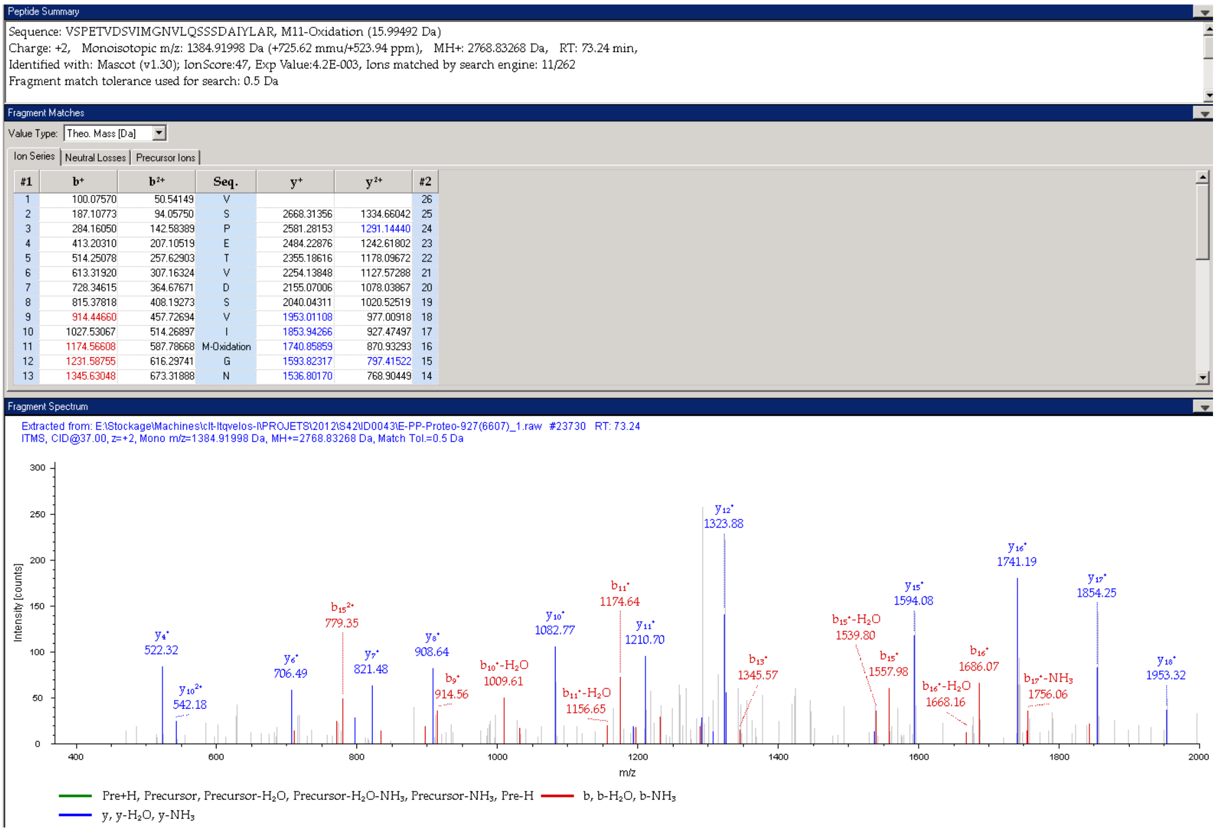
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			11
2	171.11282	86.06005	G	1094.54771	547.77749	10
3	270.18124	135.59426	V	1037.52624	519.26676	9
4	398.23982	199.62355	Q	938.45782	469.73255	8
5	513.26677	257.13702	D	810.39924	405.70326	7
6	626.35084	313.67906	L	695.37229	348.18978	6
7	773.41926	387.21327	F	582.28822	291.64775	5
8	887.46219	444.23473	N	435.21980	218.11354	4
9	974.49422	487.75075	S	321.17687	161.09207	3
10	1061.52625	531.26676	S	234.14484	117.57606	2
11			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_1.raw #18523 RT: 57.49
ITMS, CID@37.00, z=+2, Mono m/z=604.72000 Da, MH+=1208.43271 Da, Match Tol.=0.5 Da

Protein references (1):

- 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]



Peptide Summary

Sequence: VSPETVDSVIMGNVLQSSSDAIYLAR, M11-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 1384.91998 Da (+725.62 mmu/+523.94 ppm), MH+: 2768.83268 Da, RT: 73.24 min,
Identified with: Mascot (v1.30); IonScore:47, Exp Value:4.2E-003, Ions matched by search engine: 11/262
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

Value Type: Theo. Mass [Da]

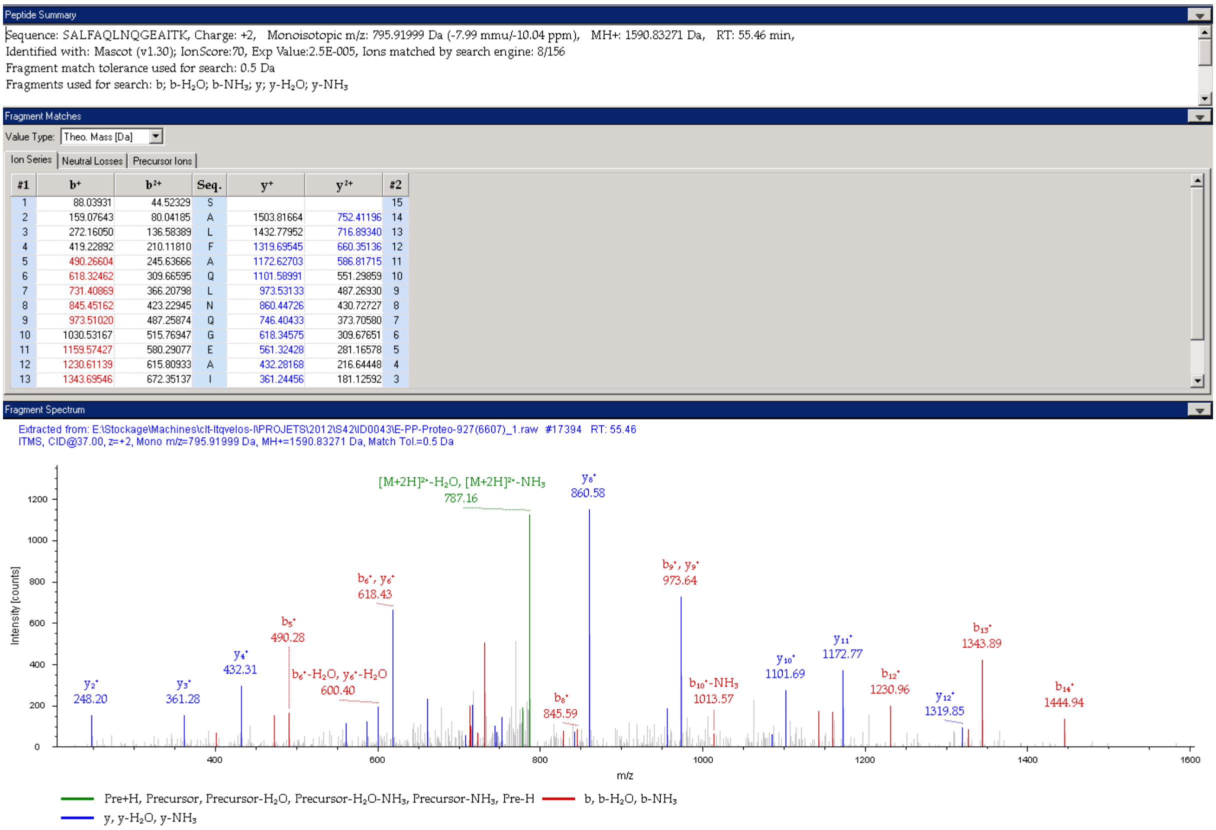
#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	100.07570	50.54149	V			26
2	187.10773	94.05750	S	2668.31356	1334.66042	25
3	284.16050	142.58389	P	2581.28153	1291.14440	24
4	413.20310	207.10519	E	2484.22876	1242.61802	23
5	514.25078	257.62903	T	2355.18616	1178.09672	22
6	613.31920	307.16324	V	2254.13848	1127.57288	21
7	728.34615	364.67671	D	2155.07006	1078.03867	20
8	815.37818	408.19273	S	2040.04311	1020.52519	19
9	914.44660	457.72694	V	1953.01108	977.00918	18
10	1027.53067	514.26897	I	1853.94266	927.47497	17
11	1174.56608	587.78668	M-Oxidation	1740.85859	870.93293	16
12	1231.58755	616.29741	G	1593.82317	797.41522	15
13	1345.63048	673.31888	N	1536.80170	768.90449	14

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #23730 RT: 73.24
ITMS, CID@37.00, z=+2, Mono m/z=1384.91998 Da, MH+=2768.83268 Da, Match Tol.=0.5 Da

Protein references (1):

- Adenylyl cyclase-associated protein 2 OS=Homo sapiens GN=CAP2 PE=1 SV=1 - [CAP2_HUMAN]



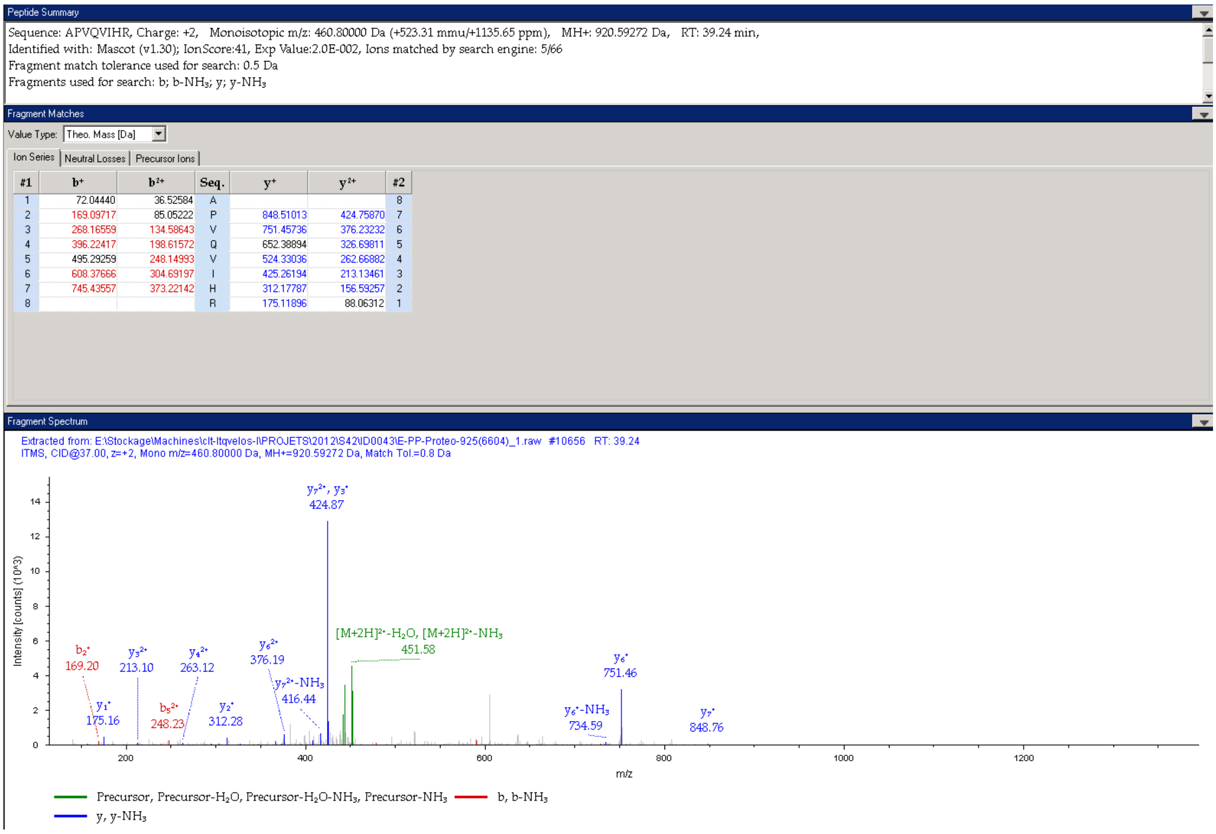
Sequence: SALFAQLNQGEAITK, Charge: +2, Monoisotopic m/z: 795.91999 Da (-7.99 mmu/-10.04 ppm), MH+: 1590.83271 Da, RT: 55.46 min,
Identified with: Mascot (v1.30); IonScore:70, Exp Value:2.5E-005, Ions matched by search engine: 8/156
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			15
2	159.07643	80.04185	A	1503.81664	752.41196	14
3	272.16050	136.58389	L	1432.77952	716.89340	13
4	419.22892	210.11810	F	1319.69545	660.35136	12
5	490.26604	245.63666	A	1172.62703	586.81715	11
6	618.32462	309.66595	Q	1101.58991	551.29859	10
7	731.40869	366.20798	L	973.53133	487.26930	9
8	845.45162	423.22945	N	860.44726	430.72727	8
9	973.51020	487.25874	Q	746.40433	373.70580	7
10	1030.53167	515.76947	G	618.34575	309.67651	6
11	1159.57427	580.29077	E	561.32428	281.16578	5
12	1230.61139	615.80933	A	432.28168	216.64448	4
13	1343.69546	672.35137	I	361.24456	181.12592	3

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #17394 RT: 55.46
ITMS, CID@37.00, z=+2, Mono m/z=795.91999 Da, MH+=1590.83271 Da, Match Tol.=0.5 Da

Protein references (1):
- Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2 - [PAAF1_HUMAN]



Peptide Summary

Sequence: APVQVIHR, Charge: +2, Monoisotopic m/z: 460.80000 Da (+523.31 mmu/+1135.65 ppm), MH+: 920.59272 Da, RT: 39.24 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 5/66
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-NH_3; y; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

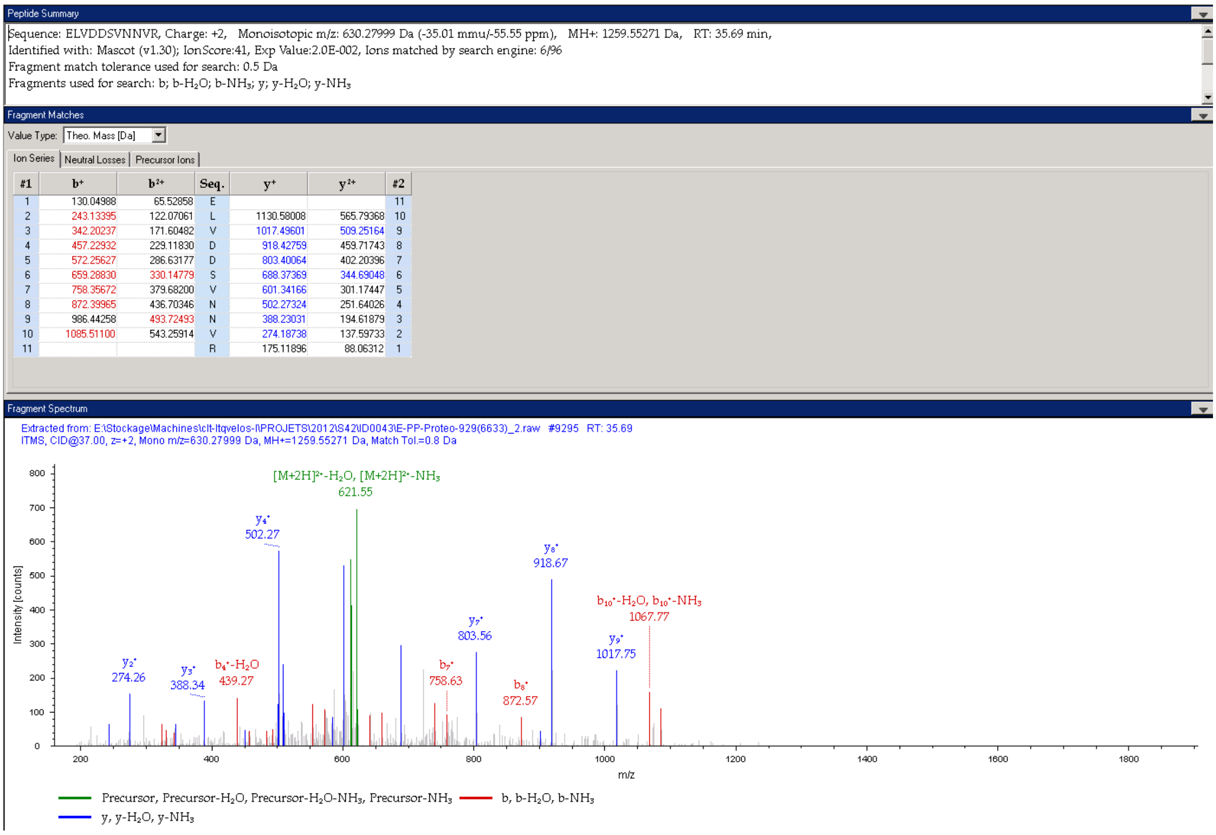
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			8
2	169.09717	85.05222	P	848.51013	424.75870	7
3	268.16559	134.58643	V	751.45736	376.23232	6
4	396.22417	198.61572	Q	652.38894	326.69811	5
5	495.29259	248.14993	V	524.33036	262.66882	4
6	608.37666	304.69197	I	425.26194	213.13461	3
7	745.43557	373.22142	H	312.17787	156.59257	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #10656 RT: 39.24
ITMS, CID@37.00, z=+2, Mono m/z=460.80000 Da, MH+=920.59272 Da, Match Tol.=0.8 Da

Protein references (1):

- Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PIMT_HUMAN]



Peptide Summary

Sequence: ELVDDSVNNVR, Charge: +2, Monoisotopic m/z: 630.27999 Da (-35.01 mmu/-55.55 ppm), MH+: 1259.55271 Da, RT: 35.69 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 6/96
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

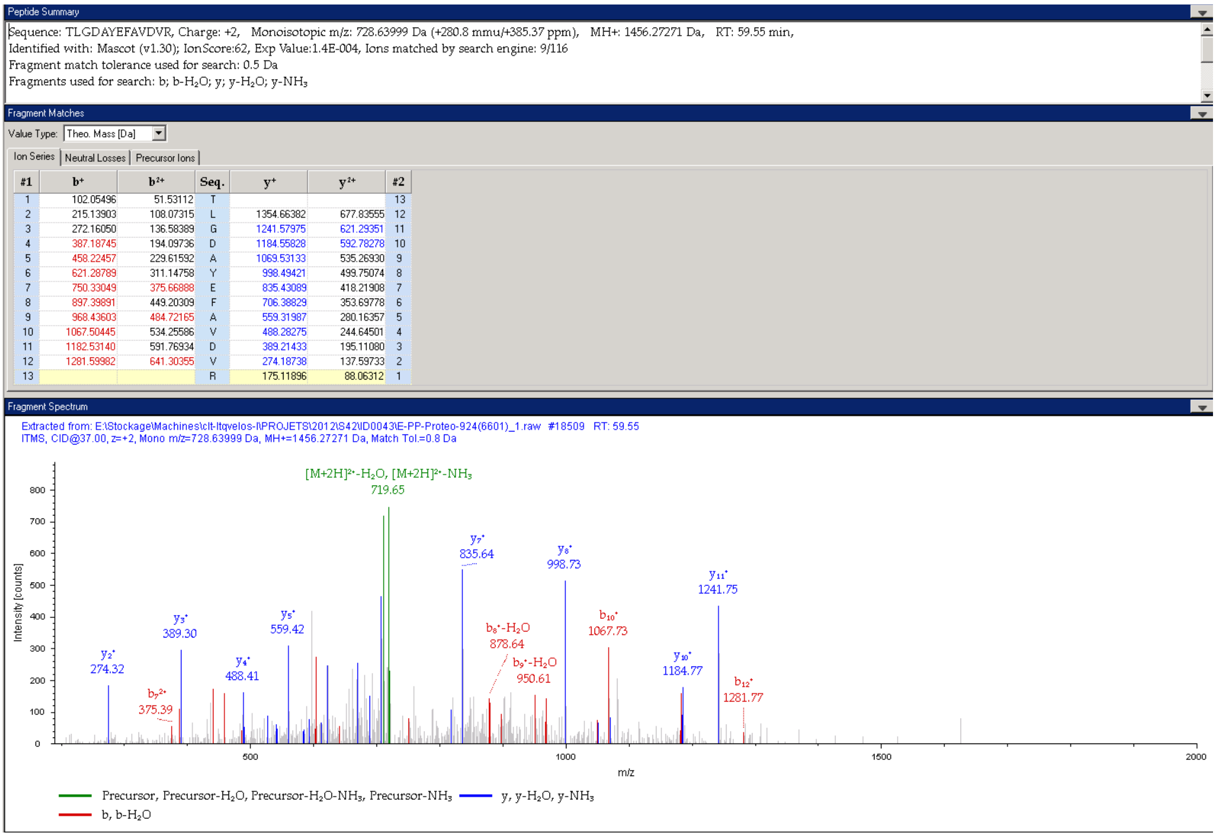
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			11
2	243.13395	122.07061	L	1130.58008	565.79368	10
3	342.20237	171.60482	V	1017.49601	509.25164	9
4	457.22932	229.11830	D	918.42759	459.71743	8
5	572.25627	286.63177	D	803.40064	402.20396	7
6	659.28830	330.14779	S	688.37369	344.69048	6
7	758.35672	379.68200	V	601.34166	301.17447	5
8	872.39965	436.70346	N	502.27324	251.64026	4
9	986.44258	493.72493	N	388.23031	194.61879	3
10	1085.51100	543.25914	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #9295 RT: 35.69
ITMS, CID@37.00, z=+2, Mono m/z=630.27999 Da, MH+=1259.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- Heat shock protein beta-7 OS=Homo sapiens GN=HSPB7 PE=1 SV=1 - [HSPB7_HUMAN]



Peptide Summary

Sequence: TLGDAYEFAVDVR, Charge: +2, Monoisotopic m/z: 728.63999 Da (+280.8 mmu/+385.37 ppm), MH+: 1456.27271 Da, RT: 59.55 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.4E-004, Ions matched by search engine: 9/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

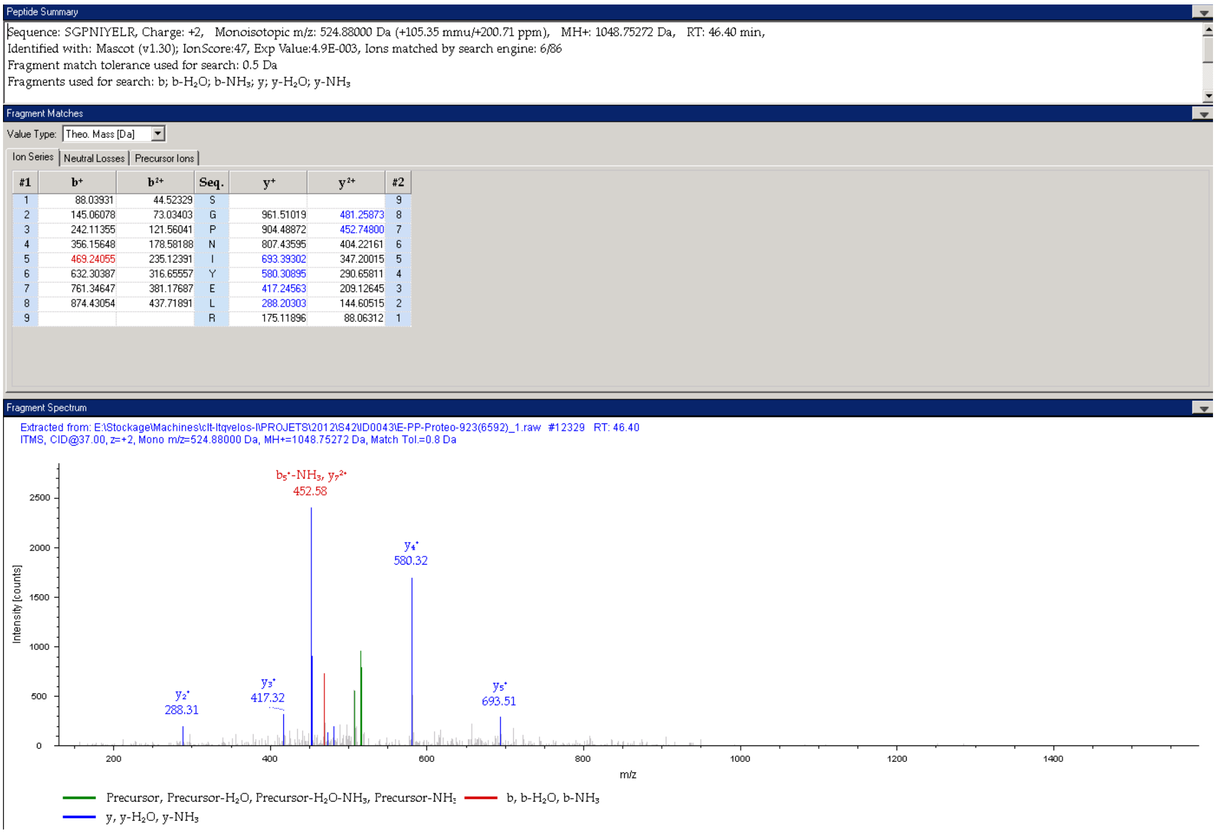
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			13
2	215.13903	108.07315	L	1354.66382	677.83555	12
3	272.16050	136.58389	G	1241.57975	621.29351	11
4	387.18745	194.09736	D	1184.55828	592.78278	10
5	458.22457	229.61592	A	1069.53133	535.26930	9
6	621.28789	311.14758	Y	998.49421	499.75074	8
7	750.33049	375.66888	E	835.43089	418.21908	7
8	897.39891	449.20309	F	706.38829	353.69778	6
9	968.43603	484.72165	A	559.31987	280.16357	5
10	1067.50445	534.25586	V	488.28275	244.64501	4
11	1182.53140	591.76934	D	389.21433	195.11080	3
12	1281.59982	641.30355	V	274.18738	137.59733	2
13			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_1.raw #18509 RT: 59.55
ITMS, CID@37.00, z=+2, Mono m/z=728.63999 Da, MH+=1456.27271 Da, Match Tol.=0.8 Da

━ Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3 ━ y, y-H_2O, y-NH_3
━ b, b-H_2O

Protein references (1):
- Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1 - [NIPS2_HUMAN]



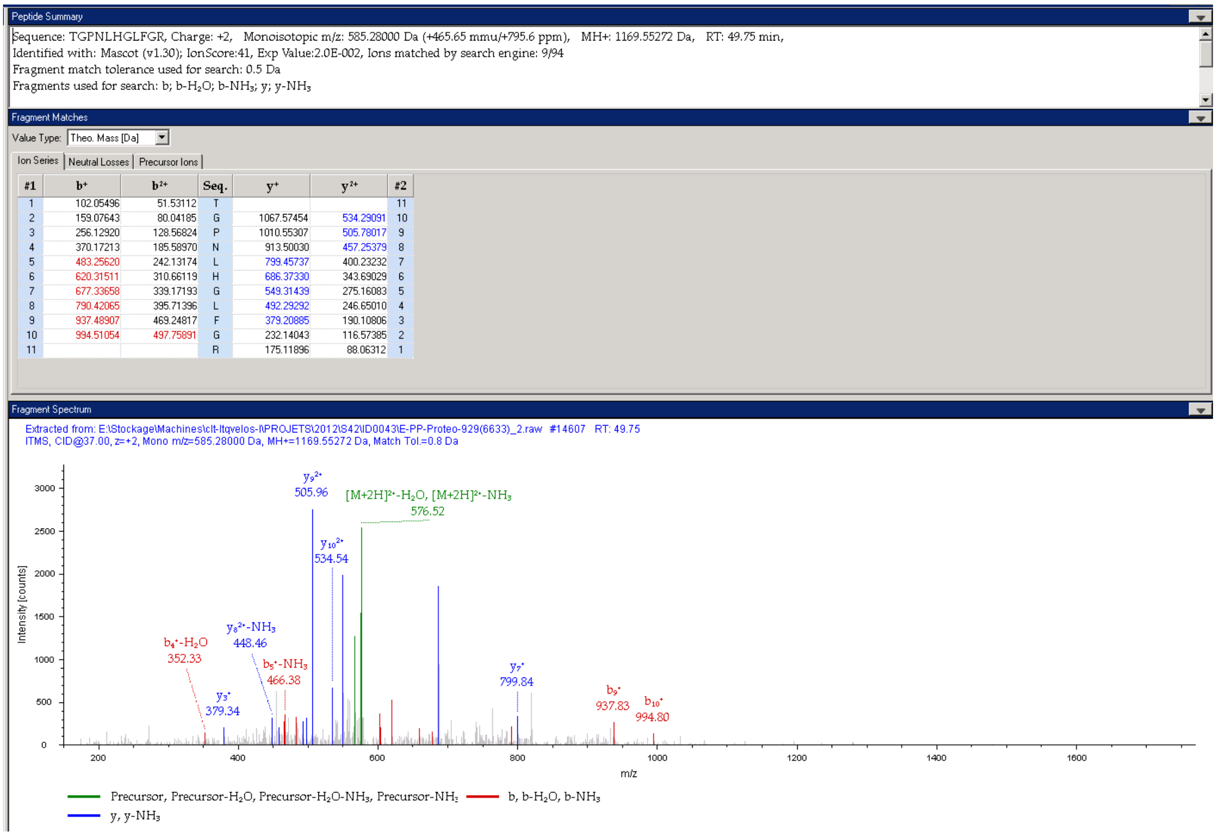
Sequence: SGPNIYELR, Charge: +2, Monoisotopic m/z: 524.88000 Da (+105.35 mmu/+200.71 ppm), MH+: 1048.75272 Da, RT: 46.40 min,
Identified with: Mascot (v1.30); IonScore:47, Exp Value:4.9E-003, Ions matched by search engine: 6/86
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			9
2	145.06078	73.03403	G	961.51019	481.25873	8
3	242.11355	121.56041	P	904.48872	452.74800	7
4	356.15648	178.58188	N	807.43595	404.22161	6
5	469.24055	235.12391	I	693.39302	347.20015	5
6	632.30387	316.65557	Y	580.30895	290.65811	4
7	761.34647	381.17687	E	417.24563	209.12645	3
8	874.43054	437.71891	L	288.20303	144.60515	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw #12329 RT: 46.40
ITMS, CID@37.00, z=+2, Mono m/z=524.88000 Da, MH+=1048.75272 Da, Match Tol.=0.8 Da

Protein references (1):

- Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2 - [CYC_HUMAN]



Peptide Summary

Sequence: TGPNLHGLFGR, Charge: +2,   Monoisotopic m/z: 585.28000 Da (+465.65 mmu/+795.6 ppm),   MH+: 1169.55272 Da,   RT: 49.75 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 9/94
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

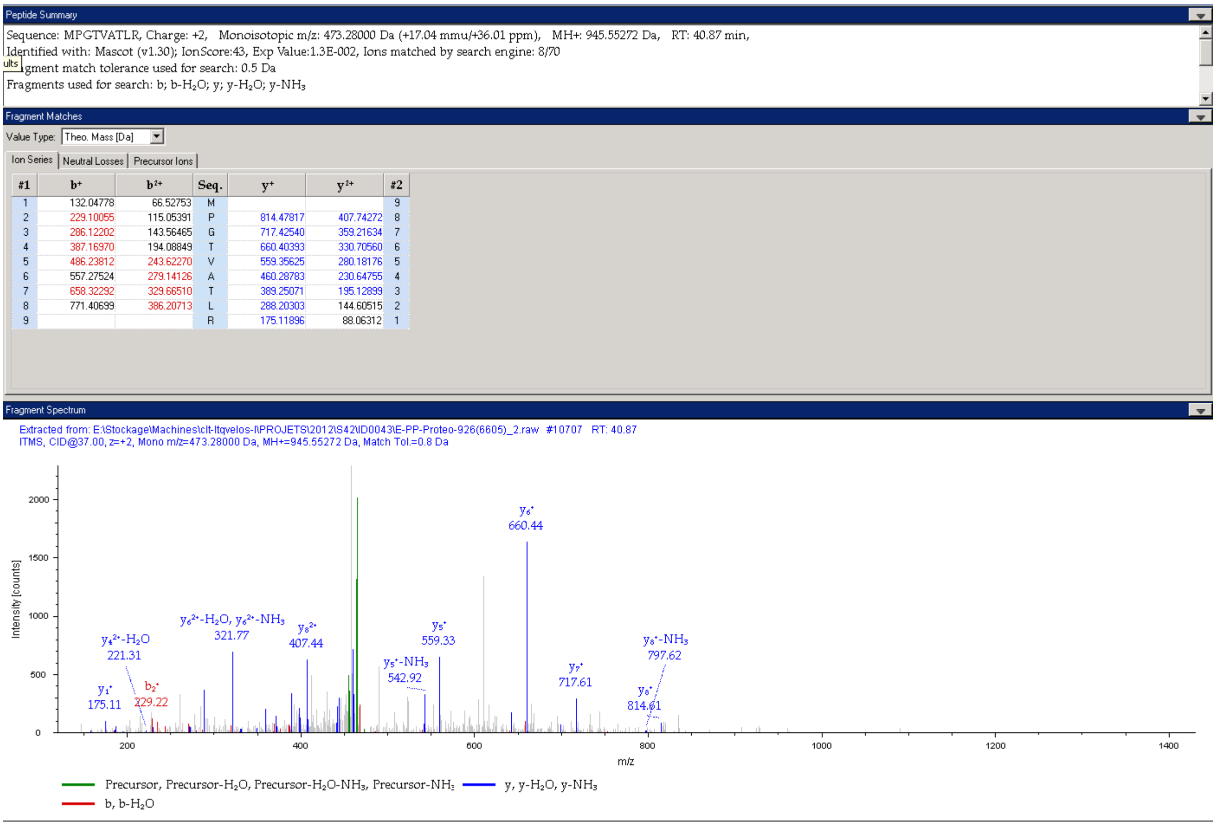
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			11
2	159.07643	80.04185	G	1067.57454	534.29091	10
3	256.12920	128.56824	P	1010.55307	505.78017	9
4	370.17213	185.58970	N	913.50030	457.25379	8
5	483.25620	242.13174	L	799.45737	400.23232	7
6	620.31511	310.66119	H	686.37330	343.69029	6
7	677.33658	339.17193	G	549.31439	275.16083	5
8	790.42065	395.71396	L	492.29292	246.65010	4
9	937.48907	469.24817	F	379.20885	190.10806	3
10	994.51054	497.75891	G	232.14043	116.57385	2
11			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #14607 RT: 49.75
ITMS, CID@37.00, z=+2, Mono m/z=585.28000 Da, MH+=1169.55272 Da, Match Tol.=0.8 Da

Protein references (1):

- Transmembrane protein 198 OS=Homo sapiens GN=TMEM198 PE=1 SV=1 - [TM198_HUMAN]



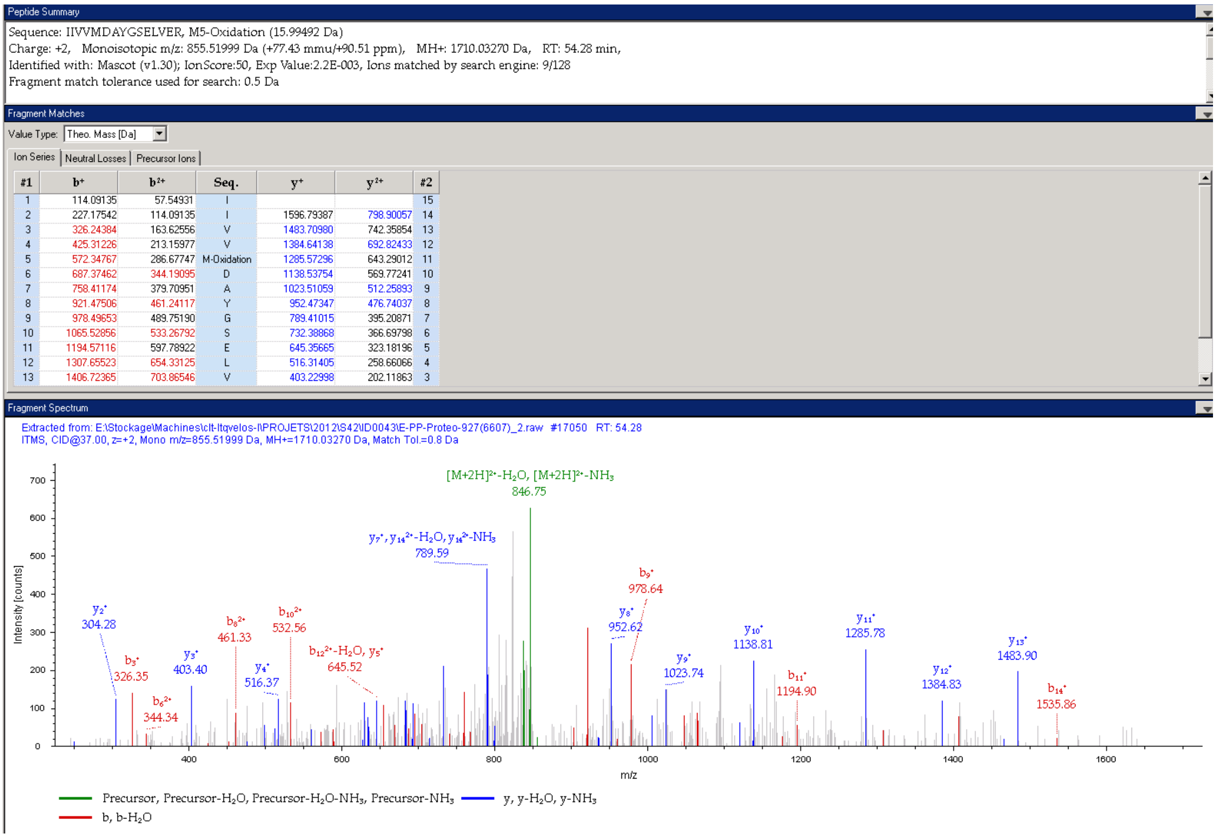
Sequence: MPGTVATLR, Charge: +2, Monoisotopic m/z: 473.28000 Da (+17.04 mmu/+36.01 ppm), MH+: 945.55272 Da, RT: 40.87 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.3E-002, Ions matched by search engine: 8/70
gment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	132.04778	66.52753	M			9
2	229.10055	115.05391	P	814.47817	407.74272	8
3	286.12202	143.56465	G	717.42540	359.21634	7
4	387.16970	194.08849	T	660.40393	330.70560	6
5	486.23812	243.62270	V	559.35625	280.18176	5
6	557.27524	279.14126	A	460.28783	230.64755	4
7	658.32292	329.66510	T	389.25071	195.12899	3
8	771.40699	386.20713	L	288.20303	144.60515	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_2.raw #10707 RT: 40.87
ITMS, CID@37.00, z=+2, Mono m/z=473.28000 Da, MH+=945.55272 Da, Match Tol.=0.8 Da

Protein references (1):
- Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]



Sequence: IIVVMDAYGSELVER, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 855.51999 Da (+77.43 mmu/+90.51 ppm), MH+: 1710.03270 Da, RT: 54.28 min,
Identified with: Mascot (v1.30); IonScore:50, Exp Value:2.2E-003, Ions matched by search engine: 9/128
Fragment match tolerance used for search: 0.5 Da

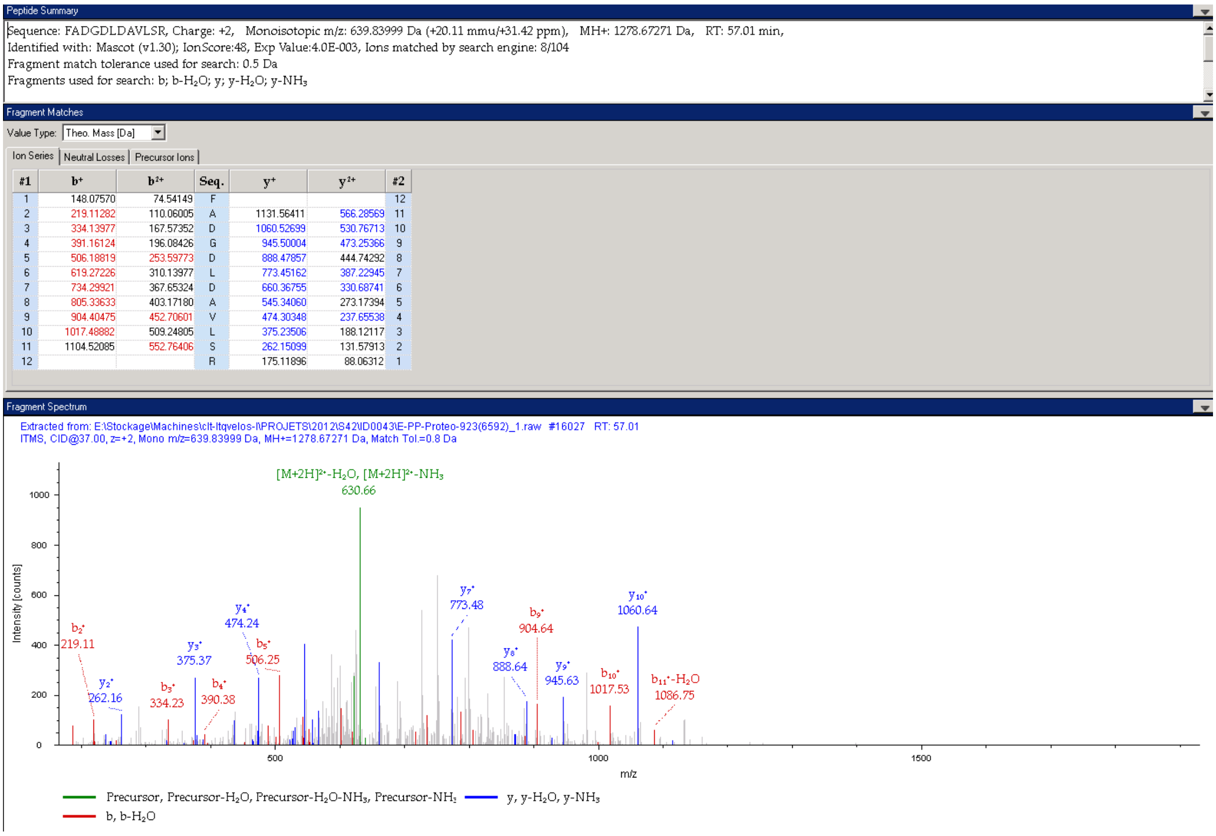
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			15
2	227.17542	114.09135	I	1596.79387	798.90057	14
3	326.24384	163.62556	V	1483.70980	742.35854	13
4	425.31226	213.15977	V	1384.64138	692.82433	12
5	572.34767	286.67747	M-Oxidation	1285.57296	643.29012	11
6	687.37462	344.19095	D	1138.53754	569.77241	10
7	758.41174	379.70951	A	1023.51059	512.25893	9
8	921.47506	461.24117	Y	952.47347	476.74037	8
9	978.49653	489.75190	G	789.41015	395.20871	7
10	1065.52856	533.26792	S	732.38868	366.69798	6
11	1194.57116	597.78922	E	645.35665	323.18196	5
12	1307.65523	654.33125	L	516.31405	258.66066	4
13	1406.72365	703.86546	V	403.22998	202.11863	3

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #17050 RT: 54.28
ITMS, CID@37.00, z=+2, Mono m/z=855.51999 Da, MH+=1710.03270 Da, Match Tol.=0.8 Da

Protein references (1):

- Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]



Peptide Summary

Sequence: FADGDLDAVLSR, Charge: +2, Monoisotopic m/z: 639.83999 Da (+20.11 mmu/+31.42 ppm), MH+: 1278.67271 Da, RT: 57.01 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:4.0E-003, Ions matched by search engine: 8/104
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

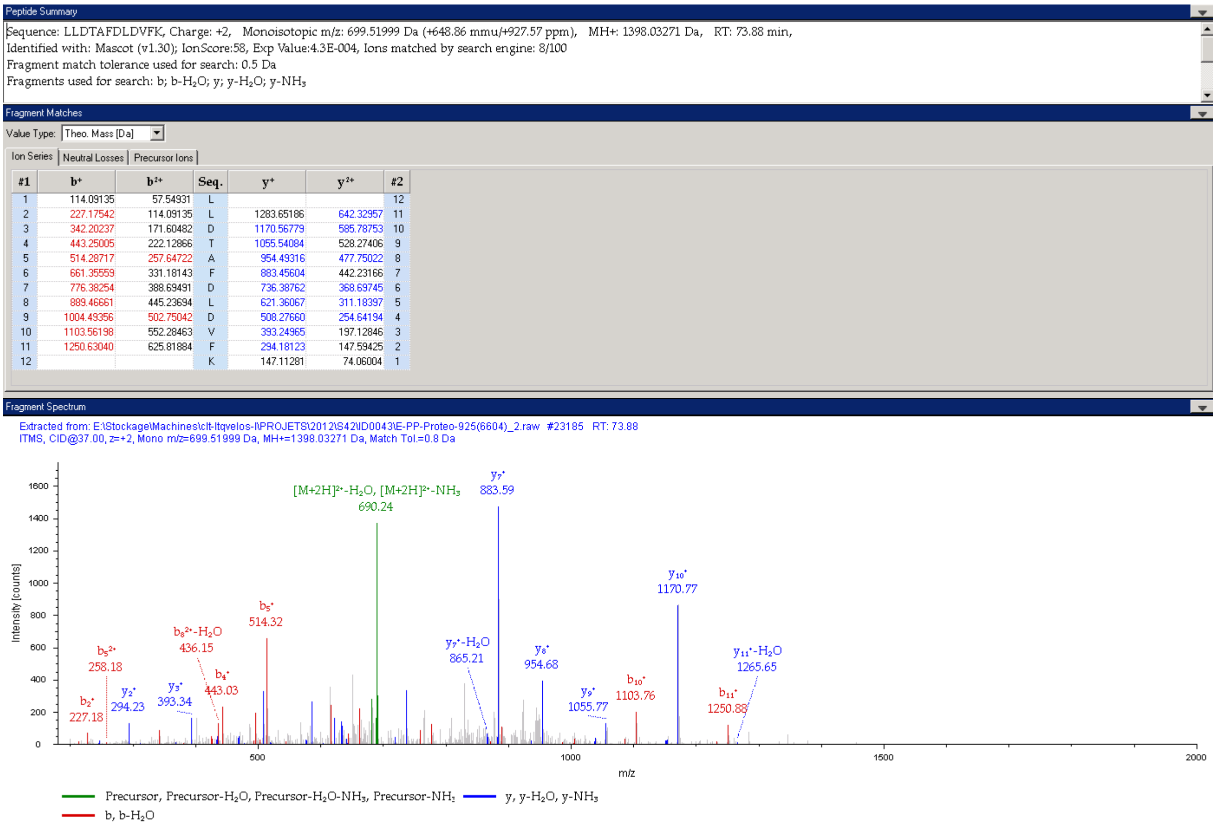
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			12
2	219.11282	110.06005	A	1131.56411	566.28569	11
3	334.13977	167.57352	D	1060.52699	530.76713	10
4	391.16124	196.08426	G	945.50004	473.25366	9
5	506.18819	253.59773	D	888.47857	444.74292	8
6	619.27226	310.13977	L	773.45162	387.22945	7
7	734.29921	367.65324	D	660.36755	330.68741	6
8	805.33633	403.17180	A	545.34060	273.17394	5
9	904.40475	452.70601	V	474.30348	237.65538	4
10	1017.48882	509.24805	L	375.23506	188.12117	3
11	1104.52085	552.76406	S	262.15099	131.57913	2
12			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw #16027 RT: 57.01
ITMS, CID@37.00, z=+2, Mono m/z=639.83999 Da, MH+=1278.67271 Da, Match Tol.=0.8 Da

Protein references (1):

- 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 - [ODO1_HUMAN]

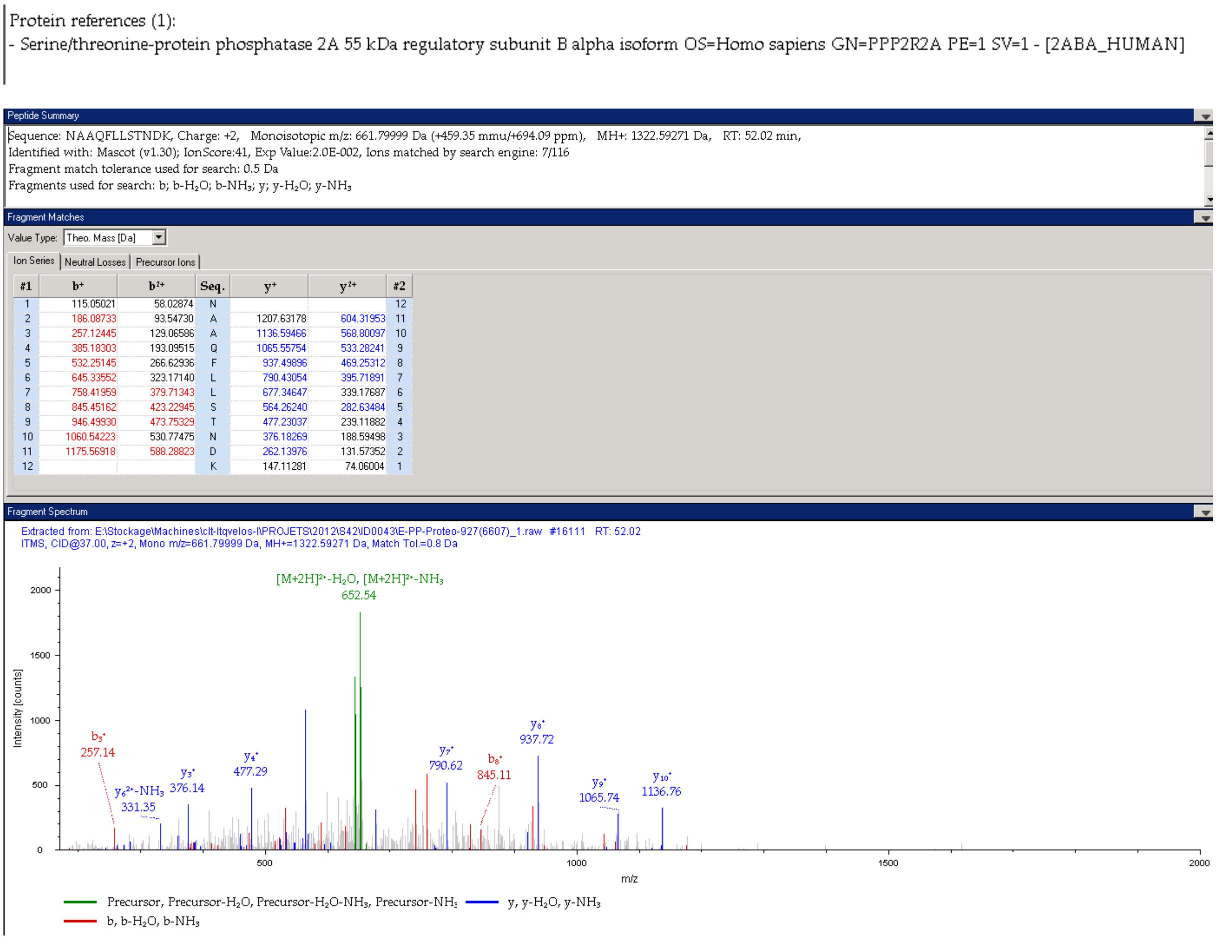


Sequence: LLDTAFDLDVFK, Charge: +2, Monoisotopic m/z: 699.51999 Da (+648.86 mmu/+927.57 ppm), MH+: 1398.03271 Da, RT: 73.88 min,
Identified with: Mascot (v1.30); IonScore:58, Exp Value:4.3E-004, Ions matched by search engine: 8/100
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			12
2	227.17542	114.09135	L	1283.65186	642.32957	11
3	342.20237	171.60482	D	1170.56779	585.78753	10
4	443.25005	222.12866	T	1055.54084	528.27406	9
5	514.28717	257.64722	A	954.49316	477.75022	8
6	661.35559	331.18143	F	883.45604	442.23166	7
7	776.38254	388.69491	D	736.38762	368.69745	6
8	889.46661	445.23694	L	621.36067	311.18397	5
9	1004.49356	502.75042	D	508.27660	254.64194	4
10	1103.56198	552.28463	V	393.24965	197.12846	3
11	1250.63040	625.81884	F	294.18123	147.59425	2
12			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #23185 RT: 73.88
ITMS, CID@37.00, z=+2, Mono m/z=699.51999 Da, MH+=1398.03271 Da, Match Tol.=0.8 Da



Protein references (1):
- Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 - [2ABA_HUMAN]

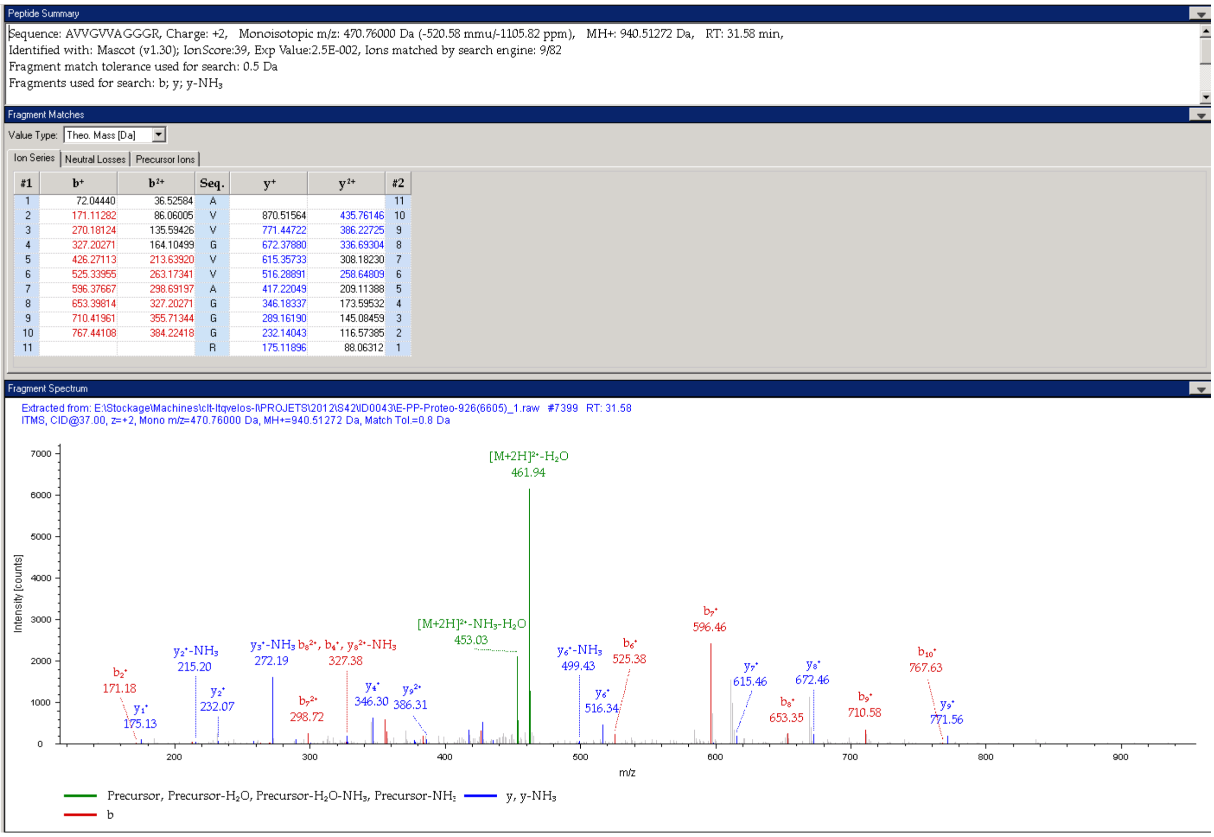
Sequence: NAAQFLLSTNDK, Charge: +2, Monoisotopic m/z: 661.79999 Da (+459.35 mmu/+694.09 ppm), MH+: 1322.59271 Da, RT: 52.02 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 7/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			12
2	186.08733	93.54730	A	1207.63178	604.31953	11
3	257.12445	129.06586	A	1136.59466	568.80097	10
4	385.18303	193.09515	Q	1065.55754	533.28241	9
5	532.25145	266.62936	F	937.49896	469.25312	8
6	645.33552	323.17140	L	790.43054	395.71891	7
7	758.41959	379.71343	L	677.34647	339.17687	6
8	845.45162	423.22945	S	564.26240	282.63484	5
9	946.49930	473.75329	T	477.23037	239.11882	4
10	1060.54223	530.77475	N	376.18269	188.59498	3
11	1175.56918	588.28823	D	262.13976	131.57352	2
12			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #16111 RT: 52.02
ITMS, CID@37.00, z=+2, Mono m/z=661.79999 Da, MH+=1322.59271 Da, Match Tol.=0.8 Da

Protein references (1):
- 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]

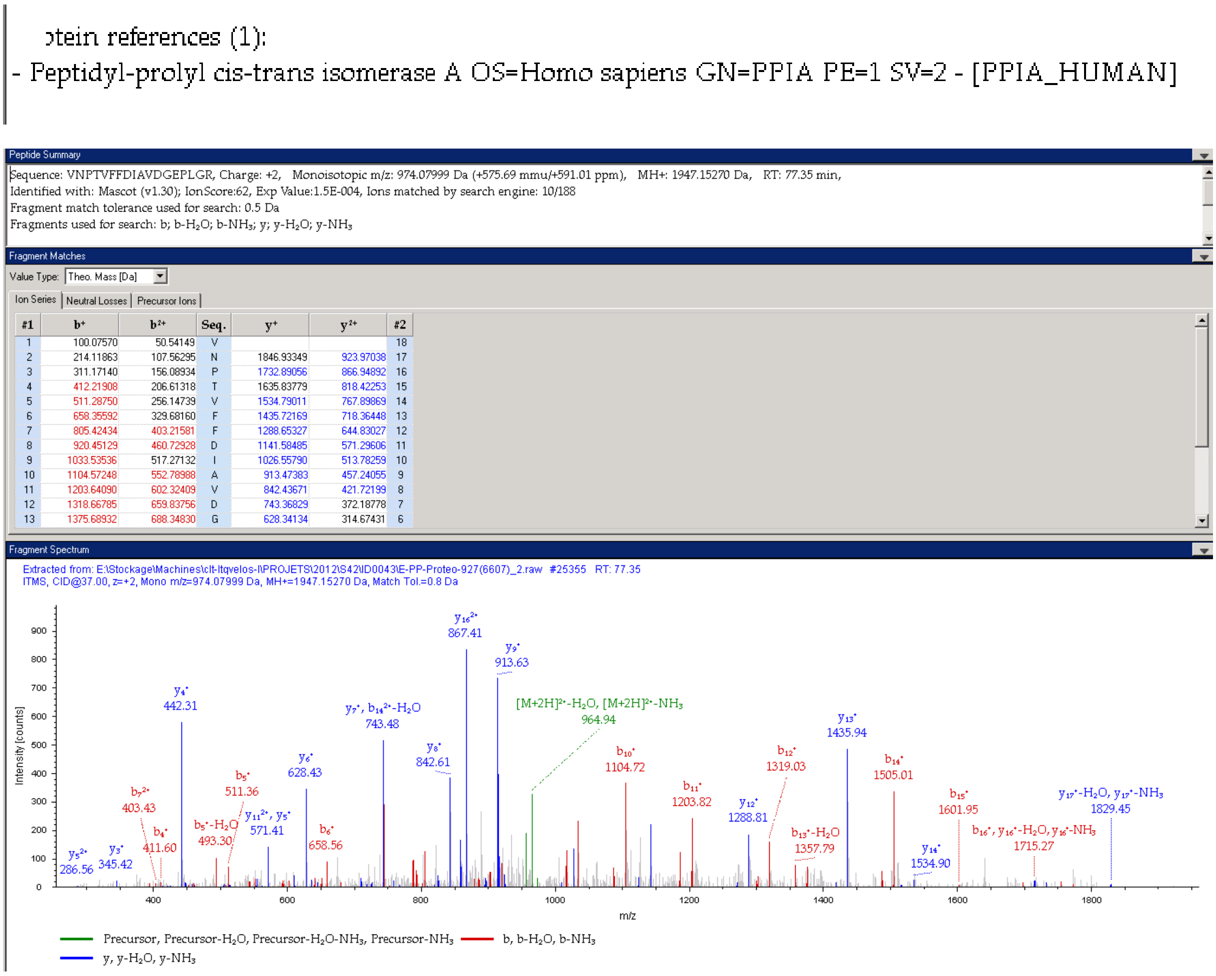


Sequence: AVVGVVAGGGR, Charge: +2, Monoisotopic m/z: 470.76000 Da (-520.58 mmu/-1105.82 ppm), MH+: 940.51272 Da, RT: 31.58 min,
Identified with: Mascot (v1.30); IonScore:39, Exp Value:2.5E-002, Ions matched by search engine: 9/82
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; y; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			11
2	171.11282	86.06005	V	870.51564	435.76146	10
3	270.18124	135.59426	V	771.44722	386.22725	9
4	327.20271	164.10499	G	672.37880	336.69304	8
5	426.27113	213.63920	V	615.35733	308.18230	7
6	525.33955	263.17341	V	516.28891	258.64809	6
7	596.37667	298.69197	A	417.22049	209.11388	5
8	653.39814	327.20271	G	346.18337	173.59532	4
9	710.41961	355.71344	G	289.16190	145.08459	3
10	767.44108	384.22418	G	232.14043	116.57385	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #7399 RT: 31.58
ITMS, CID@37.00, z=+2, Mono m/z=470.76000 Da, MH+=940.51272 Da, Match Tol.=0.8 Da



otein references (1):

- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

Peptide Summary

Sequence: VNPTVFFDIAVDGEPLGR, Charge: +2, Monoisotopic m/z: 974.07999 Da (+575.69 mmu/+591.01 ppm), MH+: 1947.15270 Da, RT: 77.35 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.5E-004, Ions matched by search engine: 10/188
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

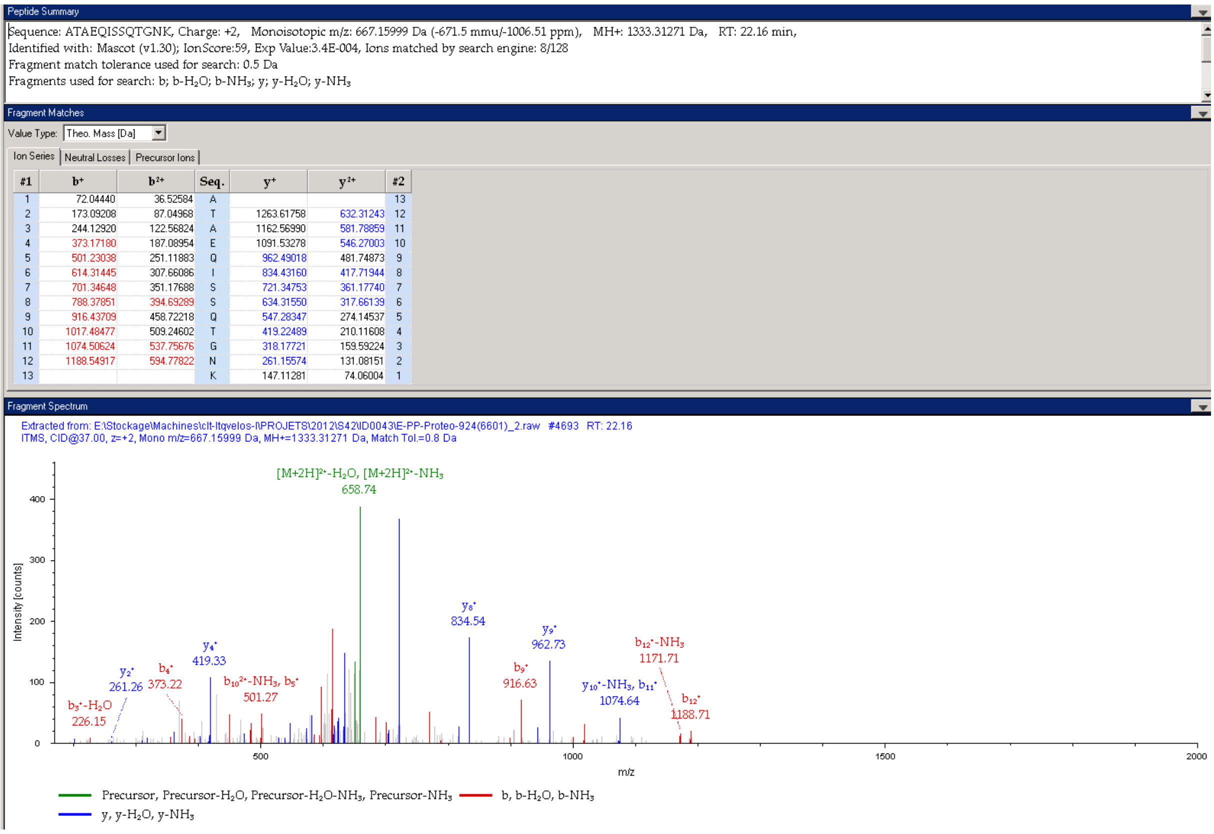
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			18
2	214.11863	107.56295	N	1846.93349	923.97038	17
3	311.17140	156.08934	P	1732.89056	866.94892	16
4	412.21908	206.61318	T	1635.83779	818.42253	15
5	511.28750	256.14739	V	1534.79011	767.89869	14
6	658.35592	329.68160	F	1435.72169	718.36448	13
7	805.42434	403.21581	F	1288.65327	644.83027	12
8	920.45129	460.72928	D	1141.58485	571.29606	11
9	1033.53536	517.27132	I	1026.55790	513.78259	10
10	1104.57248	552.78988	A	913.47383	457.24055	9
11	1203.64090	602.32409	V	842.43671	421.72199	8
12	1318.66785	659.83756	D	743.36829	372.18778	7
13	1375.68932	688.34830	G	628.34134	314.67431	6

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #25355 RT: 77.35
ITMS, CID@37.00, z=+2, Mono m/z=974.07999 Da, MH+=1947.15270 Da, Match Tol.=0.8 Da

Protein references (1):

- 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]



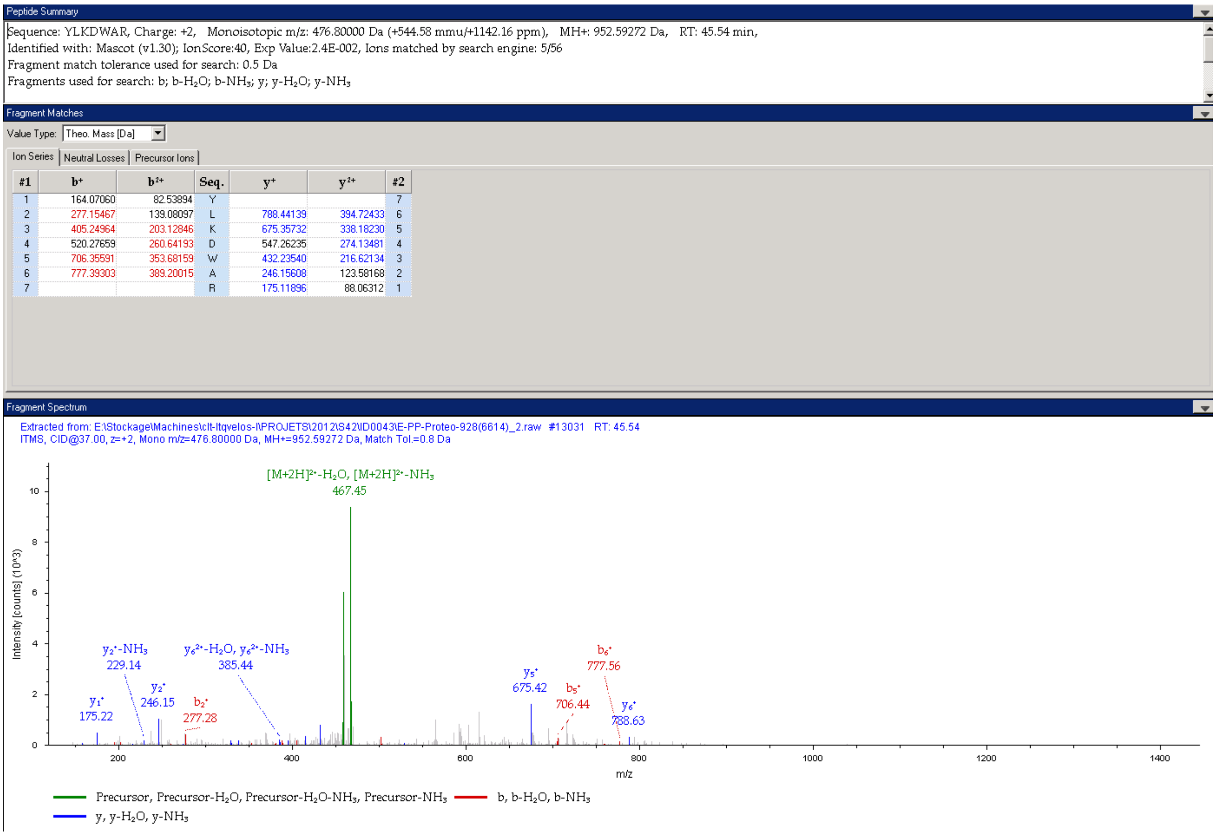
Sequence: ATAEQISSQTGNK, Charge: +2, Monoisotopic m/z: 667.15999 Da (-671.5 mmu/-1006.51 ppm), MH+: 1333.31271 Da, RT: 22.16 min,
Identified with: Mascot (v1.30); IonScore:59, Exp Value:3.4E-004, Ions matched by search engine: 8/128
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	173.09208	87.04968	T	1263.61758	632.31243	12
3	244.12920	122.56824	A	1162.56990	581.78859	11
4	373.17180	187.08954	E	1091.53278	546.27003	10
5	501.23038	251.11883	Q	962.49018	481.74873	9
6	614.31445	307.66086	I	834.43160	417.71944	8
7	701.34648	351.17688	S	721.34753	361.17740	7
8	788.37851	394.69289	S	634.31550	317.66139	6
9	916.43709	458.72218	Q	547.28347	274.14537	5
10	1017.48477	509.24602	T	419.22489	210.11608	4
11	1074.50624	537.75676	G	318.17721	159.59224	3
12	1188.54917	594.77822	N	261.15574	131.08151	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #4693 RT: 22.16
ITMS, CID@37.00, z=+2, Mono m/z=667.15999 Da, MH+=1333.31271 Da, Match Tol.=0.8 Da

Protein references (1):
- LYR motif-containing protein 2 OS=Homo sapiens GN=LYRM2 PE=1 SV=1 - [LYRM2_HUMAN]



Peptide Summary

Sequence: YLKDWAR, Charge: +2, Monoisotopic m/z: 476.80000 Da (+544.58 mmu/+1142.16 ppm), MH+: 952.59272 Da, RT: 45.54 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.4E-002, Ions matched by search engine: 5/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

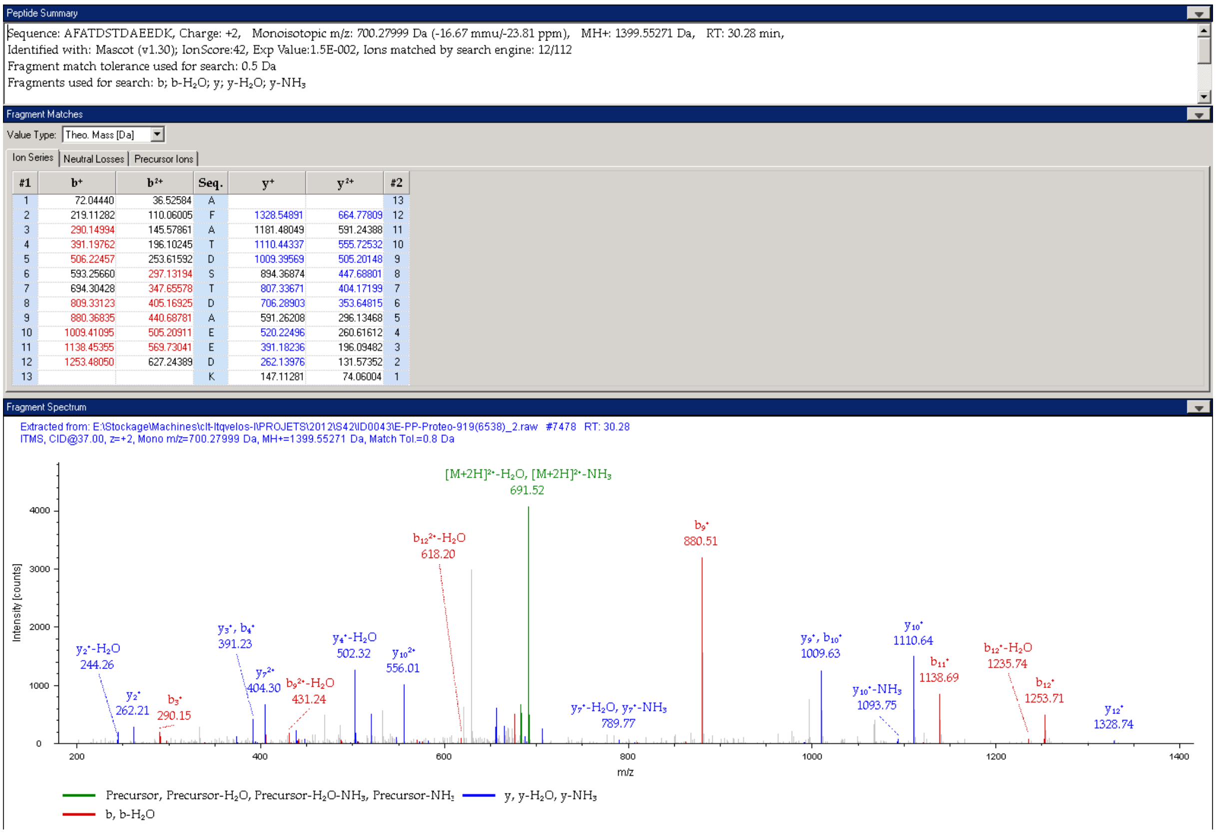
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	164.07060	82.53894	Y			7
2	277.15467	139.08097	L	788.44139	394.72433	6
3	405.24964	203.12846	K	675.35732	338.18230	5
4	520.27659	260.64193	D	547.26235	274.13481	4
5	706.35591	353.68159	W	432.23540	216.62134	3
6	777.39303	389.20015	A	246.15608	123.58168	2
7			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_2.raw #13031 RT: 45.54
ITMS, CID@37.00, z=+2, Mono m/z=476.80000 Da, MH+=952.59272 Da, Match Tol.=0.8 Da

Protein references (1):

- S-arrestin OS=Homo sapiens GN=SAG PE=2 SV=3 - [ARRS_HUMAN]



Sequence: AFATDSTDAEEDK, Charge: +2, Monoisotopic m/z: 700.27999 Da (-16.67 mmu/-23.81 ppm), MH+: 1399.55271 Da, RT: 30.28 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.5E-002, Ions matched by search engine: 12/112
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

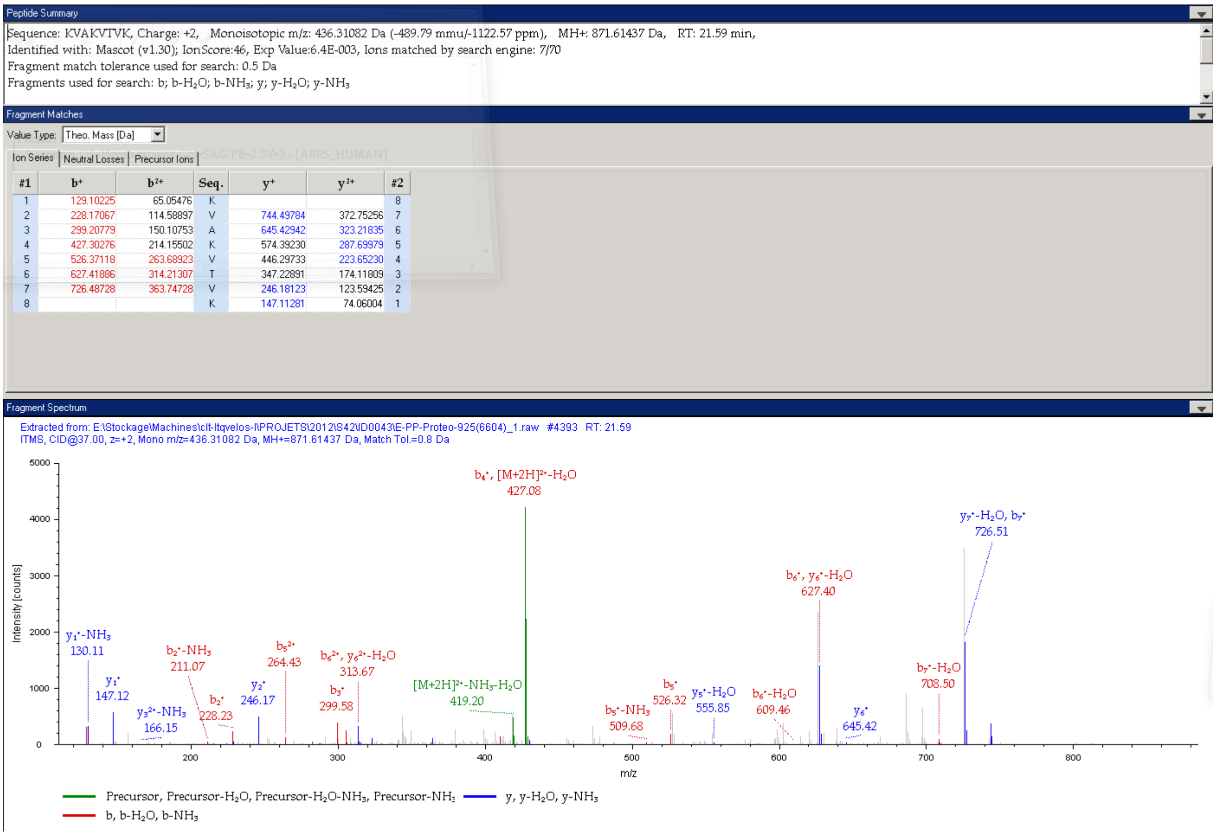
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	219.11282	110.06005	F	1328.54891	664.77809	12
3	290.14994	145.57861	A	1181.48049	591.24388	11
4	391.19762	196.10245	T	1110.44337	555.72532	10
5	506.22457	253.61592	D	1009.39569	505.20148	9
6	593.25660	297.13194	S	894.36874	447.68801	8
7	694.30428	347.65578	T	807.33671	404.17199	7
8	809.33123	405.16925	D	706.28903	353.64815	6
9	880.36835	440.68781	A	591.26208	296.13468	5
10	1009.41095	505.20911	E	520.22496	260.61612	4
11	1138.45355	569.73041	E	391.18236	196.09482	3
12	1253.48050	627.24389	D	262.13976	131.57352	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #7478 RT: 30.28
ITMS, CID@37.00, z=+2, Mono m/z=700.27999 Da, MH+=1399.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- DNA repair protein complementing XP-C cells OS=Homo sapiens GN=XPC PE=1 SV=4 - [XPC_HUMAN]



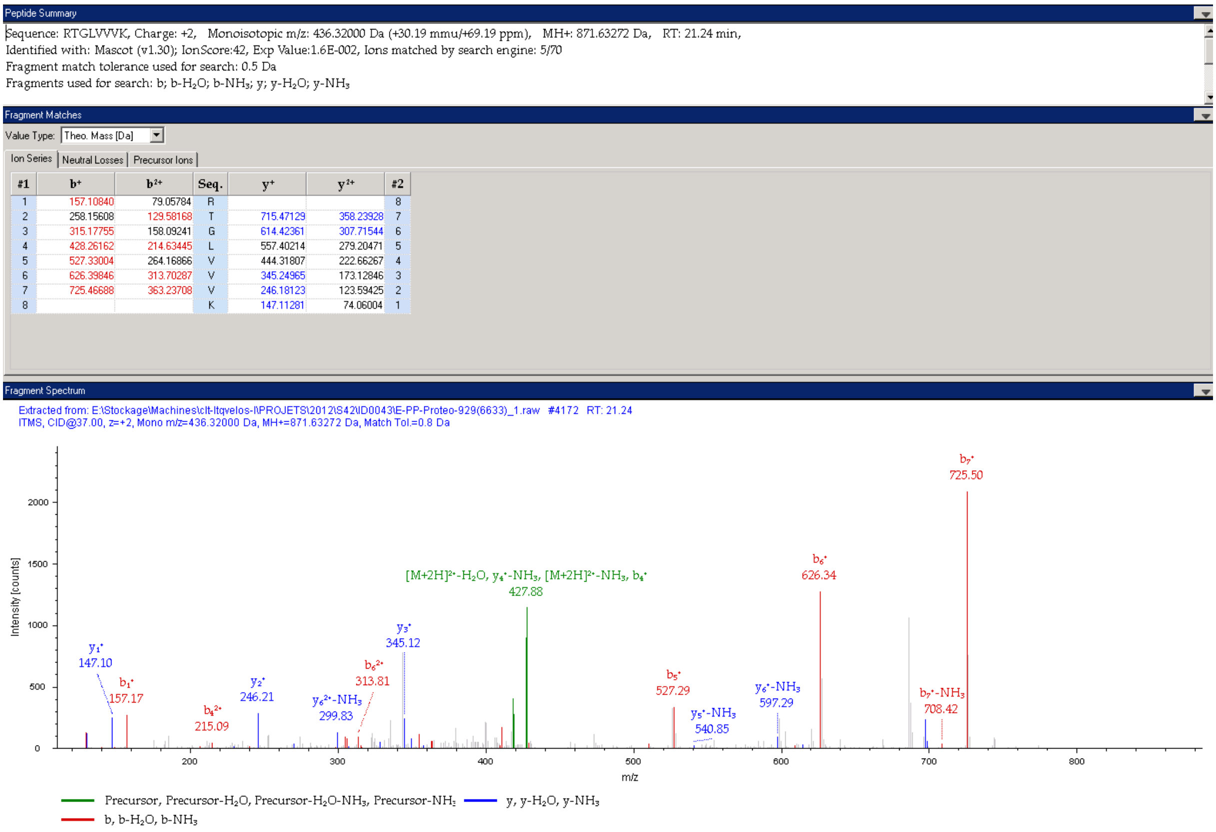
Sequence: KVAKVTVK, Charge: +2, Monoisotopic m/z: 436.31082 Da (-489.79 mmu/-1122.57 ppm), MH+: 871.61437 Da, RT: 21.59 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:6.4E-003, Ions matched by search engine: 7/70
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.10225	65.05476	K			8
2	228.17067	114.58897	V	744.49784	372.75256	7
3	299.20779	150.10753	A	645.42942	323.21835	6
4	427.30276	214.15502	K	574.39230	287.69979	5
5	526.37118	263.68923	V	446.29733	223.65230	4
6	627.41886	314.21307	T	347.22891	174.11809	3
7	726.48728	363.74728	V	246.18123	123.59425	2
8			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #4393 RT: 21.59
ITMS, CID@37.00, z=+2, Mono m/z=436.31082 Da, MH+=871.61437 Da, Match Tol.=0.8 Da

Protein references (1):
- Cytidine and dCMP deaminase domain-containing protein 1 OS=Homo sapiens GN=CDADC1 PE=2 SV=1 - [CDAC1_HUMAN]



Peptide Summary

Sequence: RTGLVVVK, Charge: +2, Monoisotopic m/z: 436.32000 Da (+30.19 mmu/+69.19 ppm), MH+: 871.63272 Da, RT: 21.24 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.6E-002, Ions matched by search engine: 5/70
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

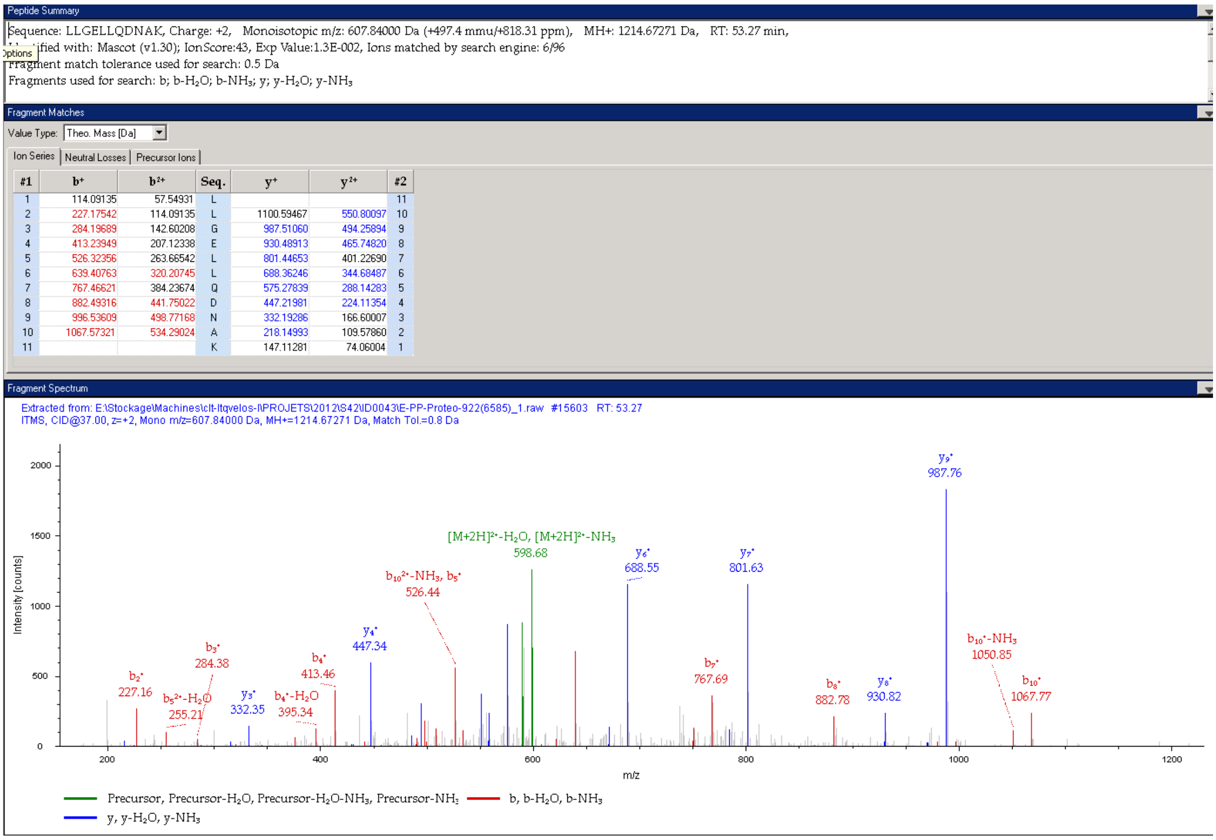
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	157.10840	79.05784	R			8
2	258.15608	129.58168	T	715.47129	358.23928	7
3	315.17755	158.09241	G	614.42361	307.71544	6
4	428.26162	214.63445	L	557.40214	279.20471	5
5	527.33004	264.16866	V	444.31807	222.66267	4
6	626.39846	313.70287	V	345.24965	173.12846	3
7	725.46688	363.23708	V	246.18123	123.59425	2
8			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_1.raw #4172 RT: 21.24
ITMS, CID@37.00, z=+2, Mono m/z=436.32000 Da, MH+=871.63272 Da, Match Tol.=0.8 Da

Protein references (1):
- Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]



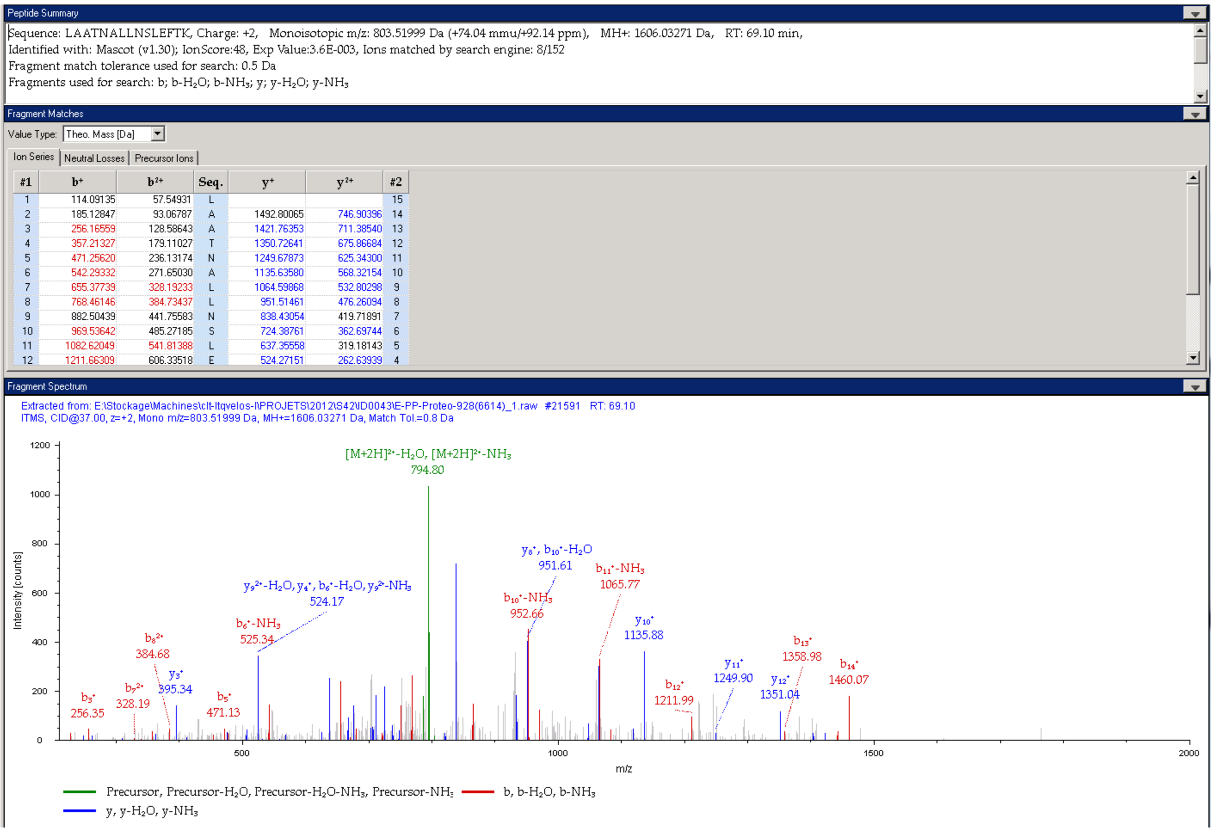
Sequence: LLGELLQDNAK, Charge: +2, Monoisotopic m/z: 607.84000 Da (+497.4 mmu/+818.31 ppm), MH+: 1214.67271 Da, RT: 53.27 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.3E-002, Ions matched by search engine: 6/96
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			11
2	227.17542	114.09135	L	1100.59467	550.80097	10
3	284.19689	142.60208	G	987.51060	494.25894	9
4	413.23949	207.12338	E	930.48913	465.74820	8
5	526.32356	263.66542	L	801.44653	401.22690	7
6	639.40763	320.20745	L	688.36246	344.68487	6
7	767.46621	384.23674	Q	575.27839	288.14283	5
8	882.49316	441.75022	D	447.21981	224.11354	4
9	996.53609	498.77168	N	332.19286	166.60007	3
10	1067.57321	534.29024	A	218.14993	109.57860	2
11			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_1.raw #15603 RT: 53.27
ITMS, CID@37.00, z=+2, Mono m/z=607.84000 Da, MH+=1214.67271 Da, Match Tol.=0.8 Da

Protein references (1):
- Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]



Peptide Summary

Sequence: LAATNALLNSLEFTK, Charge: +2, Monoisotopic m/z: 803.51999 Da (+74.04 mmu/+92.14 ppm), MH+: 1606.03271 Da, RT: 69.10 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:3.6E-003, Ions matched by search engine: 8/152
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

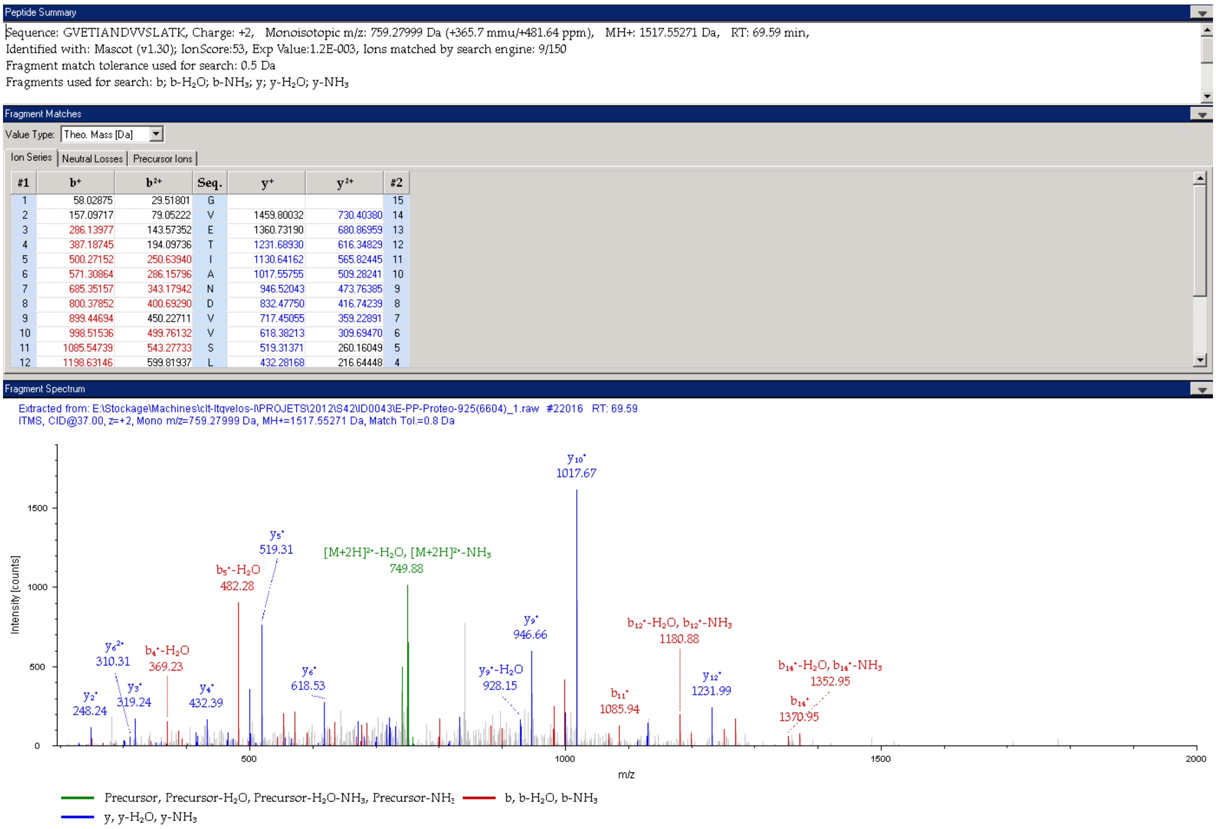
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			15
2	185.12847	93.06787	A	1492.80065	746.90396	14
3	256.16559	128.58643	A	1421.76353	711.38540	13
4	357.21327	179.11027	T	1350.72641	675.86684	12
5	471.25620	236.13174	N	1249.67873	625.34300	11
6	542.29332	271.65030	A	1135.63580	568.32154	10
7	655.37739	328.19233	L	1064.59868	532.80298	9
8	768.46146	384.73437	L	951.51461	476.26094	8
9	882.50439	441.75583	N	838.43054	419.71891	7
10	969.53642	485.27185	S	724.38761	362.69744	6
11	1082.62049	541.81388	L	637.35558	319.18143	5
12	1211.66309	606.33518	E	524.27151	262.63939	4

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_1.raw #21591 RT: 69.10
ITMS, CID@37.00, z=+2, Mono m/z=803.51999 Da, MH+=1606.03271 Da, Match Tol.=0.8 Da

Protein references (1):

- Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3 - [ODP2_HUMAN]



Sequence: GVETIANDVVSLATK, Charge: +2, Monoisotopic m/z: 759.27999 Da (+365.7 mmu/+481.64 ppm), MH+: 1517.55271 Da, RT: 69.59 min,
Identified with: Mascot (v1.30); IonScore:53, Exp Value:1.2E-003, Ions matched by search engine: 9/150
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

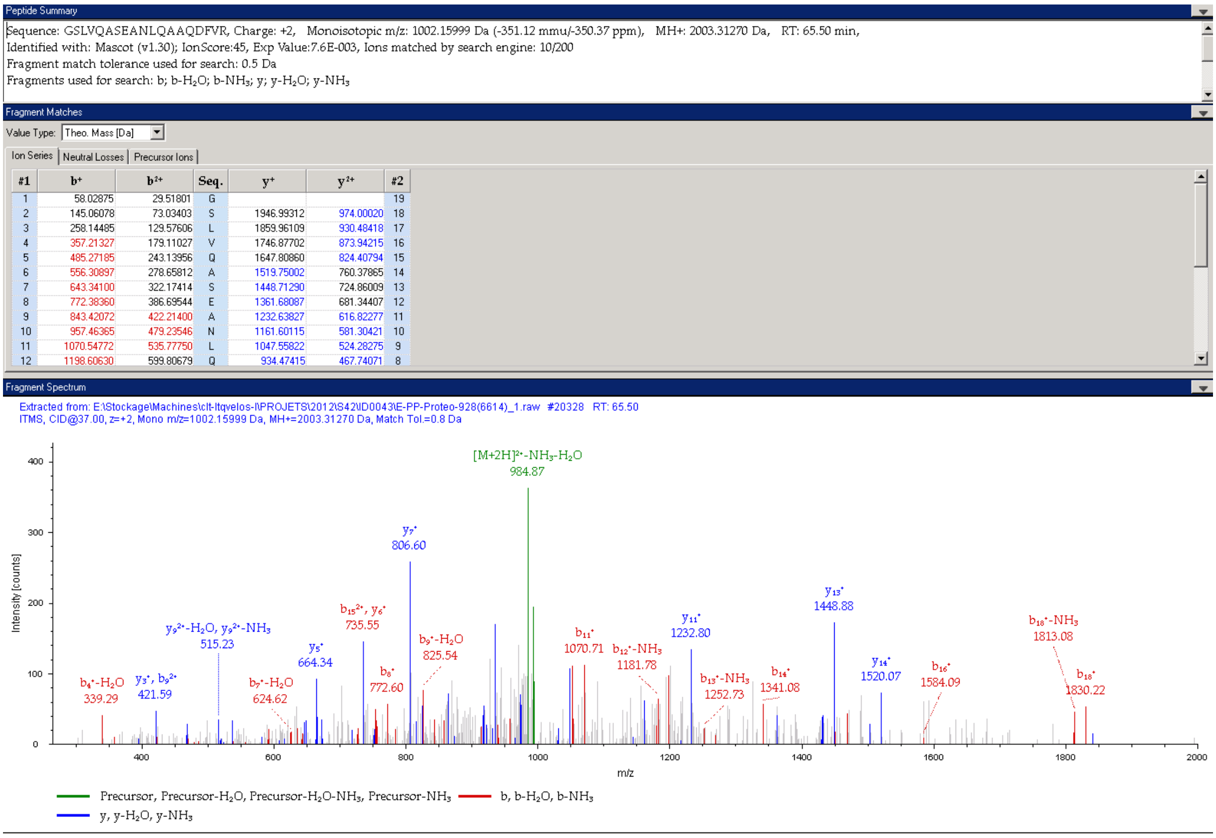
#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	58.02875	29.51801	G			15
2	157.09717	79.05222	V	1459.80032	730.40380	14
3	286.13977	143.57352	E	1360.73190	680.86959	13
4	387.18745	194.09736	T	1231.68930	616.34829	12
5	500.27152	250.63940	I	1130.64162	565.82445	11
6	571.30864	286.15796	A	1017.55755	509.28241	10
7	685.35157	343.17942	N	946.52043	473.76385	9
8	800.37852	400.69290	D	832.47750	416.74239	8
9	899.44694	450.22711	V	717.45055	359.22891	7
10	998.51536	499.76132	V	618.38213	309.69470	6
11	1085.54739	543.27733	S	519.31371	260.16049	5
12	1198.63146	599.81937	L	432.28168	216.64448	4

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #22016 RT: 69.59
ITMS, CID@37.00, z=+2, Mono m/z=759.27999 Da, MH+=1517.55271 Da, Match Tol.=0.8 Da

🟩 Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
🟥 b, b-H_2O, b-NH_3
🟦 y, y-H_2O, y-NH_3

Protein references (1):

- Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]



Peptide Summary

Sequence: GSLVQASEANLQAAQDFVR, Charge: +2, Monoisotopic m/z: 1002.15999 Da (-351.12 mmu/-350.37 ppm), MH+: 2003.31270 Da, RT: 65.50 min,
Identified with: Mascot (v1.30); IonScore:45, Exp Value:7.6E-003, Ions matched by search engine: 10/200
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

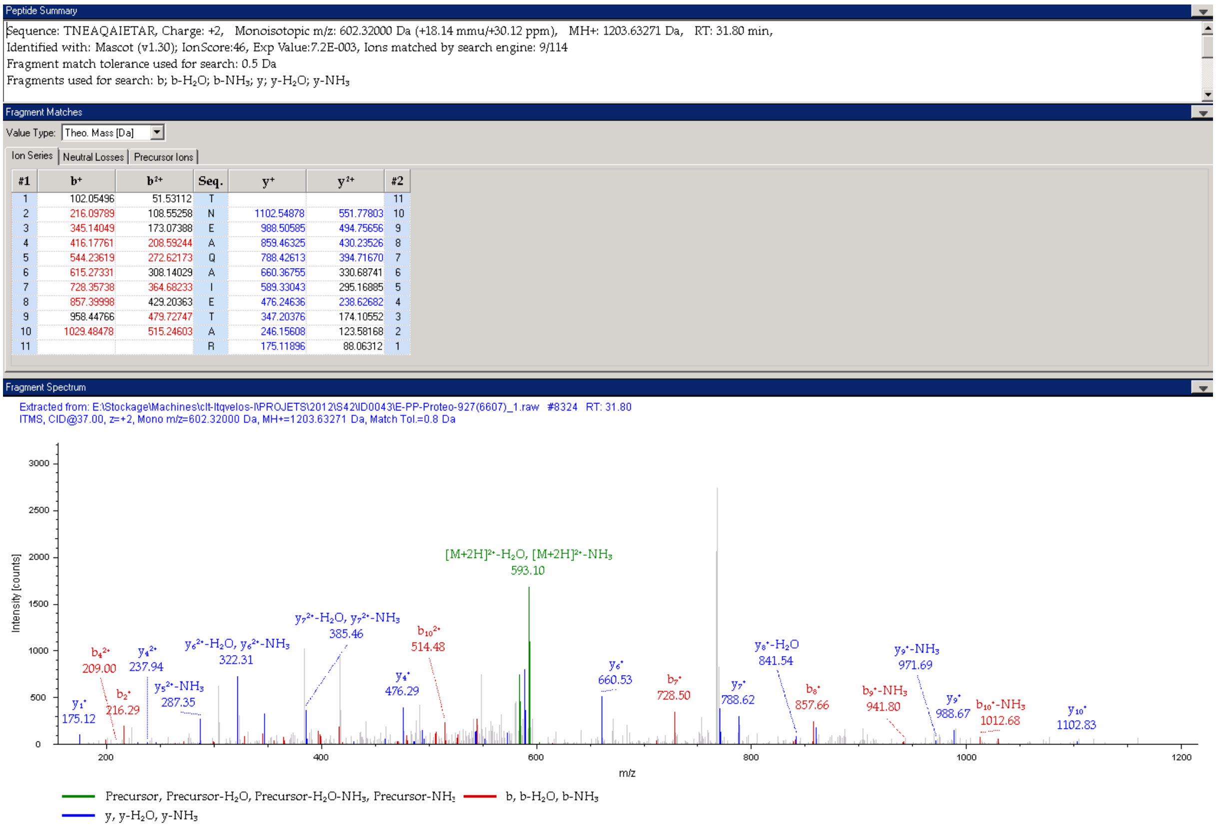
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			19
2	145.06078	73.03403	S	1946.99312	974.00020	18
3	258.14485	129.57606	L	1859.96109	930.48418	17
4	357.21327	179.11027	V	1746.87702	873.94215	16
5	485.27185	243.13956	Q	1647.80860	824.40794	15
6	556.30897	278.65812	A	1519.75002	760.37865	14
7	643.34100	322.17414	S	1448.71290	724.86009	13
8	772.38360	386.69544	E	1361.68087	681.34407	12
9	843.42072	422.21400	A	1232.63827	616.82277	11
10	957.46365	479.23546	N	1161.60115	581.30421	10
11	1070.54772	535.77750	L	1047.55822	524.28275	9
12	1198.60630	599.80679	Q	934.47415	467.74071	8

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_1.raw #20328 RT: 65.50
ITMS, CID@37.00, z=+2, Mono m/z=1002.15999 Da, MH+=2003.31270 Da, Match Tol.=0.8 Da

Protein references (2):
- Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1 - [UBE2N_HUMAN]



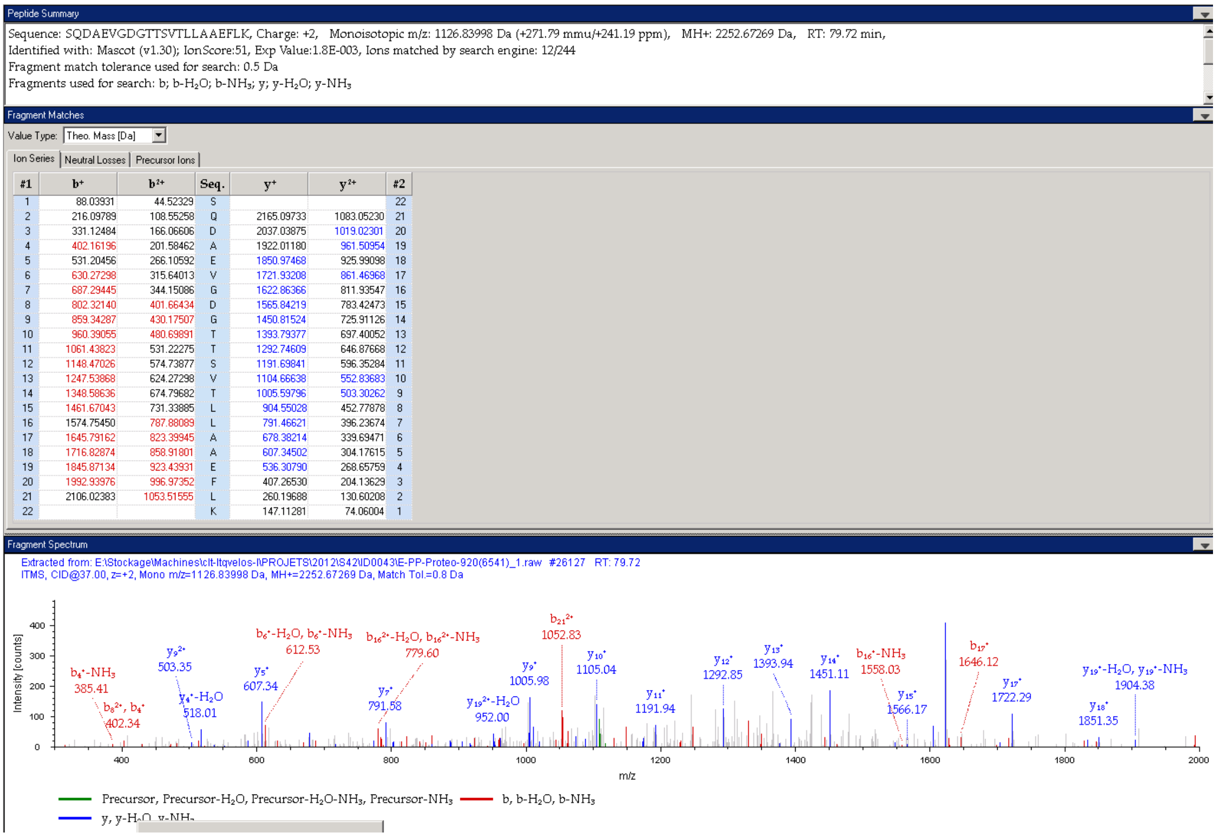
Sequence: TNEAQAIETAR, Charge: +2, Monoisotopic m/z: 602.32000 Da (+18.14 mmu/+30.12 ppm), MH+: 1203.63271 Da, RT: 31.80 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:7.2E-003, Ions matched by search engine: 9/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			11
2	216.09789	108.55258	N	1102.54878	551.77803	10
3	345.14049	173.07388	E	988.50585	494.75656	9
4	416.17761	208.59244	A	859.46325	430.23526	8
5	544.23619	272.62173	Q	788.42613	394.71670	7
6	615.27331	308.14029	A	660.36755	330.68741	6
7	728.35738	364.68233	I	589.33043	295.16885	5
8	857.39998	429.20363	E	476.24636	238.62682	4
9	958.44766	479.72747	T	347.20376	174.10552	3
10	1029.48478	515.24603	A	246.15608	123.58168	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #8324 RT: 31.80
ITMS, CID@37.00, z=+2, Mono m/z=602.32000 Da, MH+=1203.63271 Da, Match Tol.=0.8 Da

Protein references (1):

- T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]



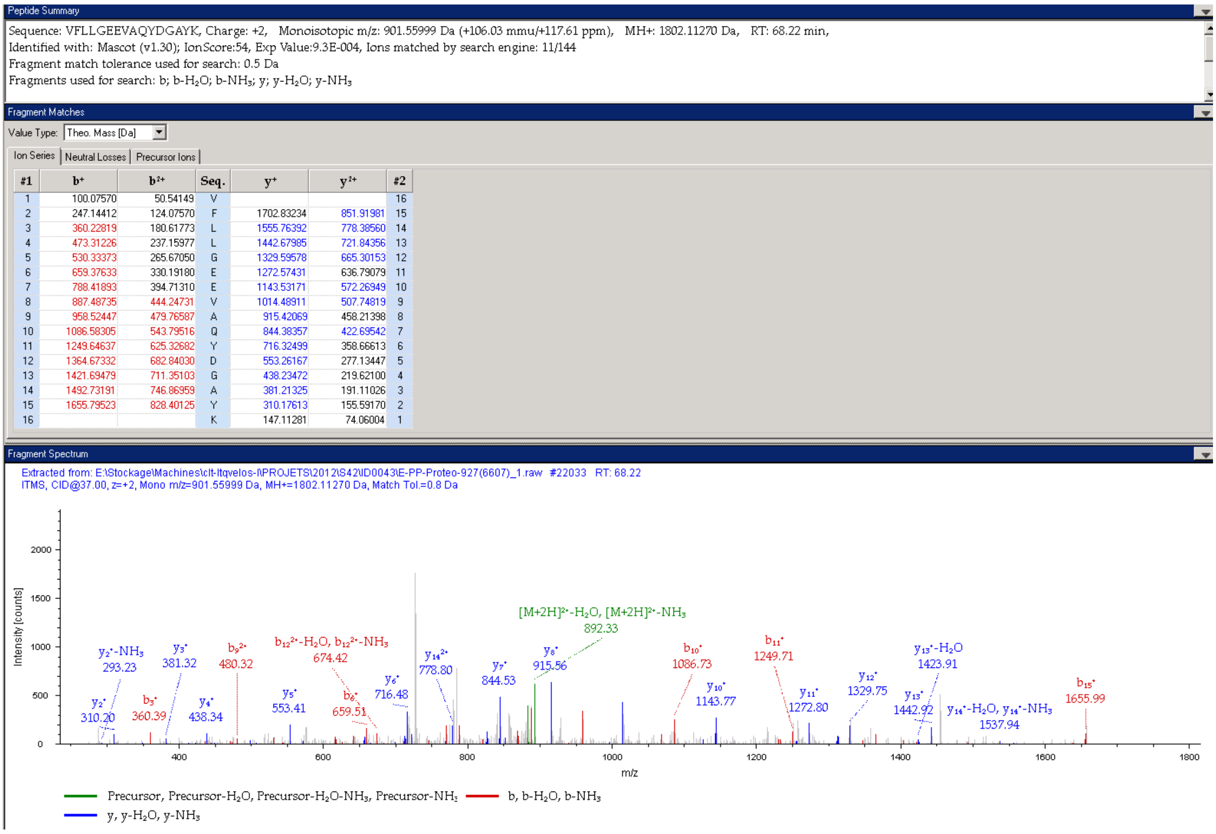
Sequence: SQDAEVGDGTTSVTLLAAEFLK, Charge: +2, Monoisotopic m/z: 1126.83998 Da (+271.79 mmu/+241.19 ppm), MH+: 2252.67269 Da, RT: 79.72 min,
Identified with: Mascot (v1.30); IonScore:51, Exp Value:1.8E-003, Ions matched by search engine: 12/244
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			22
2	216.09789	108.55258	Q	2165.09733	1083.05230	21
3	331.12484	166.06606	D	2037.03875	1019.02301	20
4	402.16196	201.58462	A	1922.01180	961.50954	19
5	531.20456	266.10592	E	1850.97468	925.99098	18
6	630.27298	315.64013	V	1721.93208	861.46968	17
7	687.29445	344.15086	G	1622.86366	811.93547	16
8	802.32140	401.66434	D	1565.84219	783.42473	15
9	859.34287	430.17507	G	1450.81524	725.91126	14
10	960.39055	480.69891	T	1393.79377	697.40052	13
11	1061.43823	531.22275	T	1292.74609	646.87668	12
12	1148.47026	574.73877	S	1191.69841	596.35284	11
13	1247.53868	624.27298	V	1104.66638	552.83683	10
14	1348.58636	674.79682	T	1005.59796	503.30262	9
15	1461.67043	731.33885	L	904.55028	452.77878	8
16	1574.75450	787.88089	L	791.46621	396.23674	7
17	1645.79162	823.39945	A	678.38214	339.69471	6
18	1716.82874	858.91801	A	607.34502	304.17615	5
19	1845.87134	923.43931	E	536.30790	268.65759	4
20	1992.93976	996.97352	F	407.26530	204.13629	3
21	2106.02383	1053.51555	L	260.19688	130.60208	2
22			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_1.raw #26127 RT: 79.72
ITMS, CID@37.00, z=+2, Mono m/z=1126.83998 Da, MH+=2252.67269 Da, Match Tol.=0.8 Da

Protein references (1):
- Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3 - [ODPB_HUMAN]



Sequence: VFLLGEEVAQYDGAYK, Charge: +2, Monoisotopic m/z: 901.55999 Da (+106.03 mmu/+117.61 ppm), MH+: 1802.11270 Da, RT: 68.22 min,
Identified with: Mascot (v1.30); IonScore:54, Exp Value:9.3E-004, Ions matched by search engine: 11/144
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

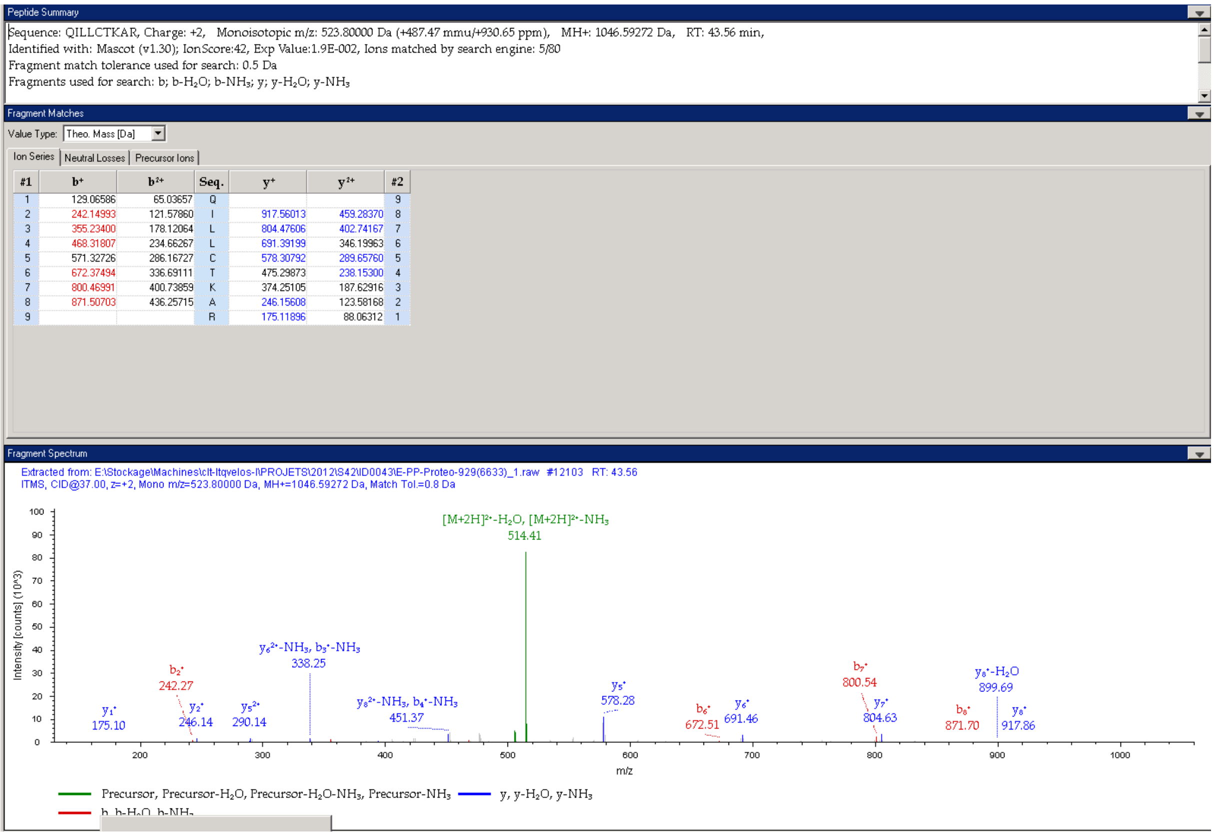
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			16
2	247.14412	124.07570	F	1702.83234	851.91981	15
3	360.22819	180.61773	L	1555.76392	778.38560	14
4	473.31226	237.15977	L	1442.67985	721.84356	13
5	530.33373	265.67050	G	1329.59578	665.30153	12
6	659.37633	330.19180	E	1272.57431	636.79079	11
7	788.41893	394.71310	E	1143.53171	572.26949	10
8	887.48735	444.24731	V	1014.48911	507.74819	9
9	958.52447	479.76587	A	915.42069	458.21398	8
10	1086.58305	543.79516	Q	844.38357	422.69542	7
11	1249.64637	625.32682	Y	716.32499	358.66613	6
12	1364.67332	682.84030	D	553.26167	277.13447	5
13	1421.69479	711.35103	G	438.23472	219.62100	4
14	1492.73191	746.86959	A	381.21325	191.11026	3
15	1655.79523	828.40125	Y	310.17613	155.59170	2
16			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #22033 RT: 68.22
ITMS, CID@37.00, z=+2, Mono m/z=901.55999 Da, MH+=1802.11270 Da, Match Tol.=0.8 Da

Protein references (1):

- Growth arrest-specific protein 8 OS=Homo sapiens GN=GAS8 PE=1 SV=1 - [GAS8_HUMAN]



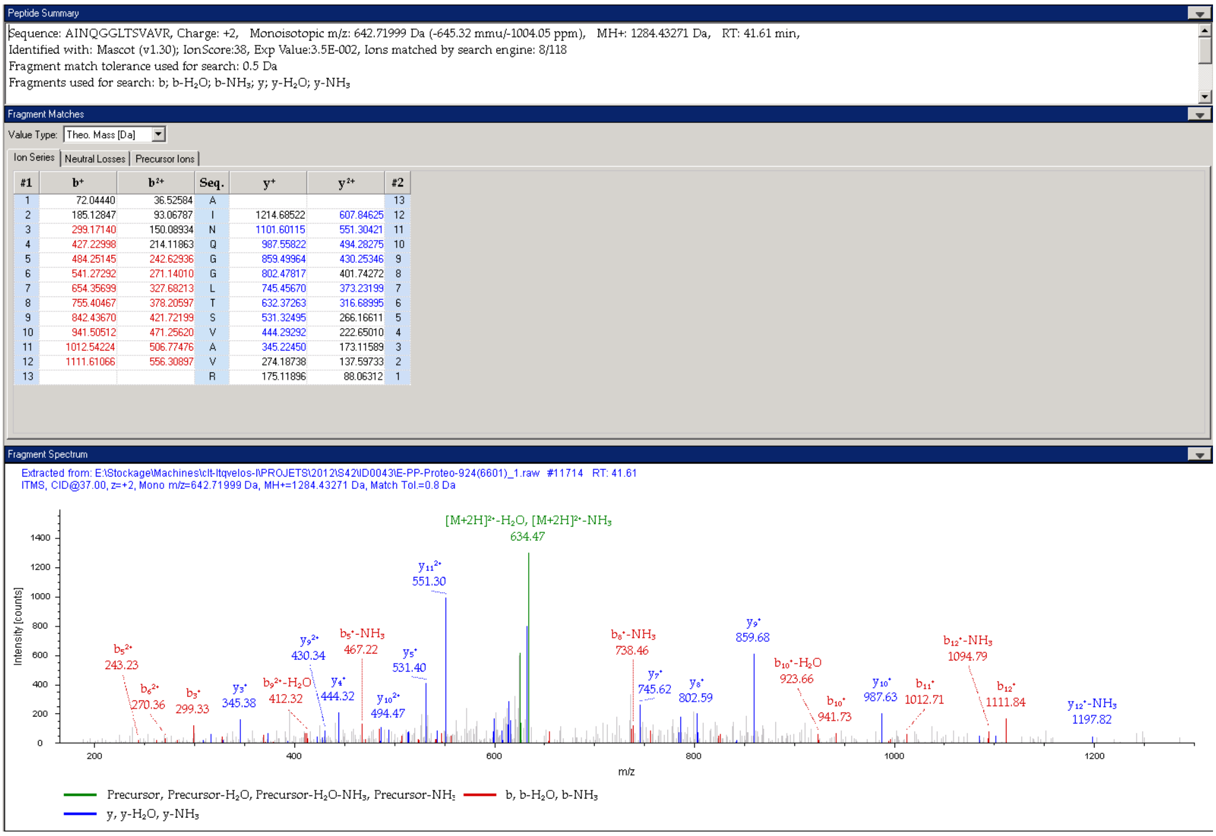
Sequence: QILLCTKAR, Charge: +2, Monoisotopic m/z: 523.80000 Da (+487.47 mmu/+930.65 ppm), MH+: 1046.59272 Da, RT: 43.56 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.9E-002, Ions matched by search engine: 5/80
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			9
2	242.14993	121.57860	I	917.56013	459.28370	8
3	355.23400	178.12064	L	804.47606	402.74167	7
4	468.31807	234.66267	L	691.39199	346.19963	6
5	571.32726	286.16727	C	578.30792	289.65760	5
6	672.37494	336.69111	T	475.29873	238.15300	4
7	800.46991	400.73859	K	374.25105	187.62916	3
8	871.50703	436.25715	A	246.15608	123.58168	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_1.raw #12103 RT: 43.56
ITMS, CID@37.00, z=+2, Mono m/z=523.80000 Da, MH+=1046.59272 Da, Match Tol.=0.8 Da

Protein references (1):
- Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]



Sequence: AINQGGLTSVAVR, Charge: +2, Monoisotopic m/z: 642.71999 Da (-645.32 mmu/-1004.05 ppm), MH+: 1284.43271 Da, RT: 41.61 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.5E-002, Ions matched by search engine: 8/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

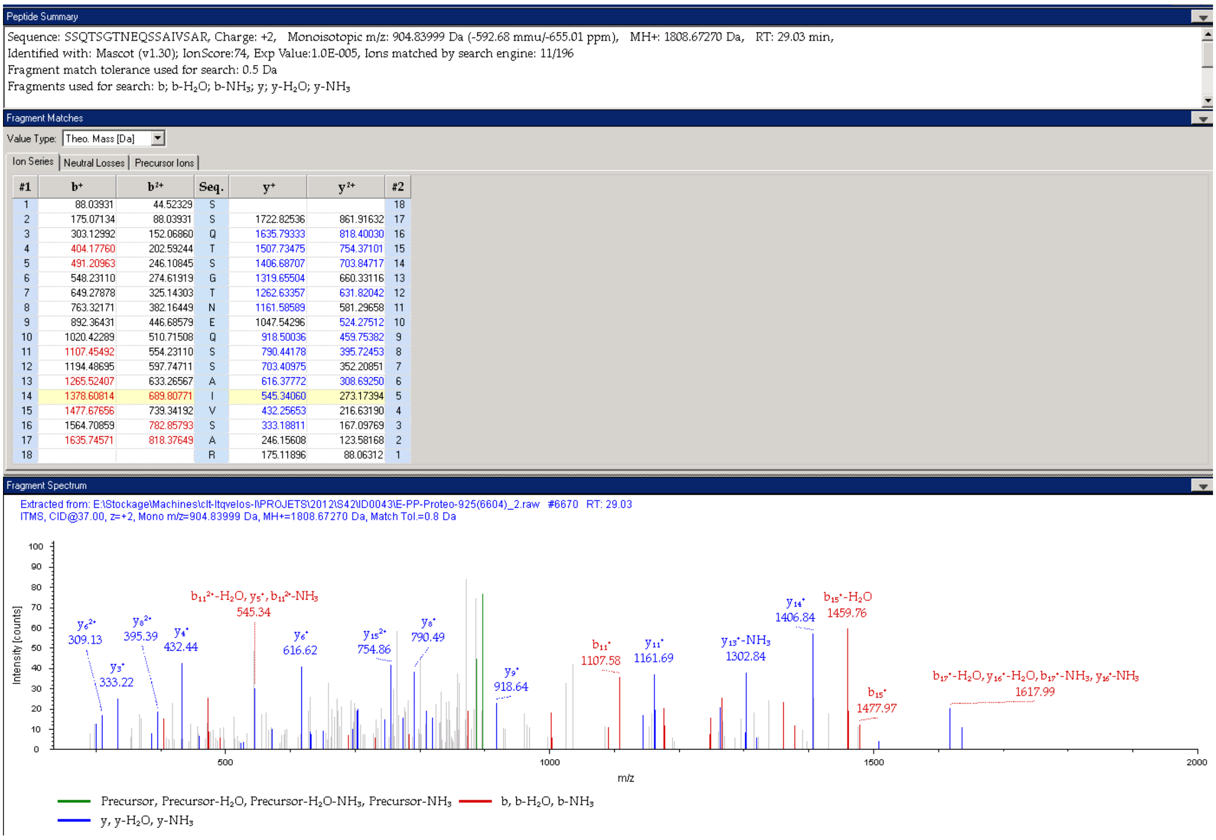
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	185.12847	93.06787	I	1214.68522	607.84625	12
3	299.17140	150.08934	N	1101.60115	551.30421	11
4	427.22998	214.11863	Q	987.55822	494.28275	10
5	484.25145	242.62936	G	859.49964	430.25346	9
6	541.27292	271.14010	G	802.47817	401.74272	8
7	654.35699	327.68213	L	745.45670	373.23199	7
8	755.40467	378.20597	T	632.37263	316.68995	6
9	842.43670	421.72199	S	531.32495	266.16611	5
10	941.50512	471.25620	V	444.29292	222.65010	4
11	1012.54224	506.77476	A	345.22450	173.11589	3
12	1111.61066	556.30897	V	274.18738	137.59733	2
13			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_1.raw #11714 RT: 41.61
ITMS, CID@37.00, z=+2, Mono m/z=642.71999 Da, MH+=1284.43271 Da, Match Tol.=0.8 Da

Protein references (1):

- General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 - [USO1_HUMAN]



Sequence: SSQTSGTNEQSSAIVSAR, Charge: +2, Monoisotopic m/z: 904.83999 Da (-592.68 mmu/-655.01 ppm), MH+: 1808.67270 Da, RT: 29.03 min,
Identified with: Mascot (v1.30); IonScore:74, Exp Value:1.0E-005, Ions matched by search engine: 11/196
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

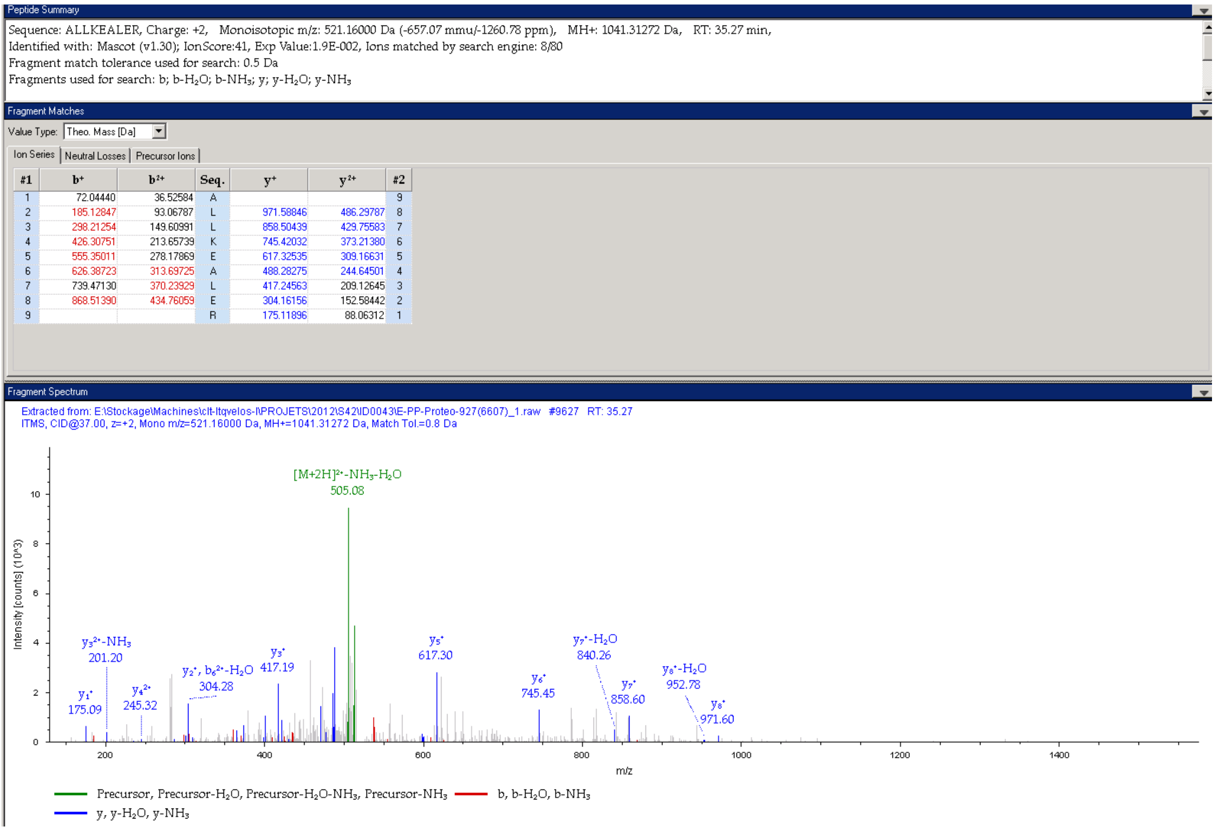
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			18
2	175.07134	88.03931	S	1722.82536	861.91632	17
3	303.12992	152.06860	Q	1635.79333	818.40030	16
4	404.17760	202.59244	T	1507.73475	754.37101	15
5	491.20963	246.10845	S	1406.68707	703.84717	14
6	548.23110	274.61919	G	1319.65504	660.33116	13
7	649.27878	325.14303	T	1262.63357	631.82042	12
8	763.32171	382.16449	N	1161.58589	581.29658	11
9	892.36431	446.68579	E	1047.54296	524.27512	10
10	1020.42289	510.71508	Q	918.50036	459.75382	9
11	1107.45492	554.23110	S	790.44178	395.72453	8
12	1194.48695	597.74711	S	703.40975	352.20851	7
13	1265.52407	633.26567	A	616.37772	308.69250	6
14	1378.60814	689.80771	I	545.34060	273.17394	5
15	1477.67656	739.34192	V	432.25653	216.63190	4
16	1564.70859	782.85793	S	333.18811	167.09769	3
17	1635.74571	818.37649	A	246.15608	123.58168	2
18			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #6670 RT: 29.03
ITMS, CID@37.00, z=+2, Mono m/z=904.83999 Da, MH+=1808.67270 Da, Match Tol.=0.8 Da

Protein references (1):

- Forkhead-associated domain-containing protein 1 OS=Homo sapiens GN=FHAD1 PE=2 SV=2 - [FHAD1_HUMAN]

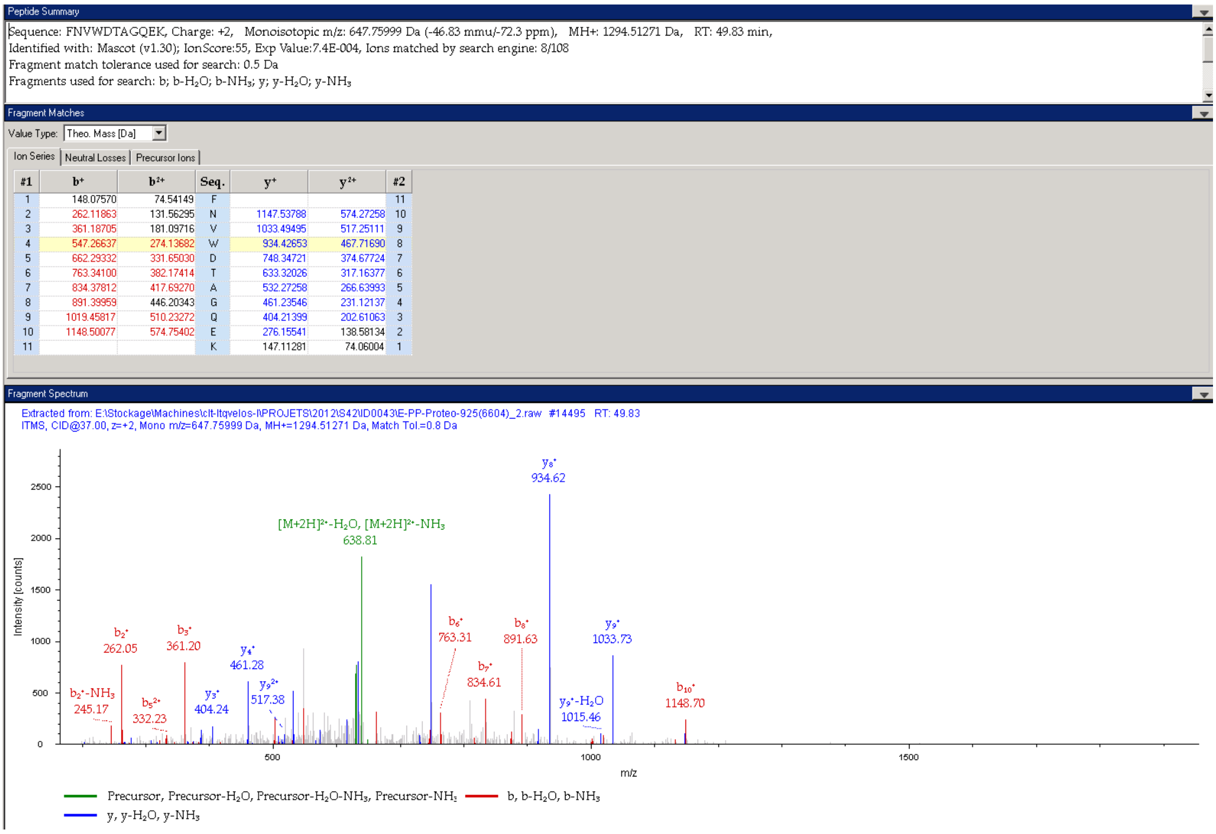


Sequence: ALLKEALER, Charge: +2, Monoisotopic m/z: 521.16000 Da (-657.07 mmu/-1260.78 ppm), MH+: 1041.31272 Da, RT: 35.27 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.9E-002, Ions matched by search engine: 8/80
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			9
2	185.12847	93.06787	L	971.58846	486.29787	8
3	298.21254	149.60991	L	858.50439	429.75583	7
4	426.30751	213.65739	K	745.42032	373.21380	6
5	555.35011	278.17869	E	617.32535	309.16631	5
6	626.38723	313.69725	A	488.28275	244.64501	4
7	739.47130	370.23929	L	417.24563	209.12645	3
8	868.51390	434.76059	E	304.16156	152.58442	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #9627 RT: 35.27
ITMS, CID@37.00, z=+2, Mono m/z=521.16000 Da, MH+=1041.31272 Da, Match Tol.=0.8 Da

Protein references (1):
- GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]



Peptide Summary

Sequence: FNVWDTAGQEK, Charge: +2, Monoisotopic m/z: 647.75999 Da (-46.83 mmu/-72.3 ppm), MH+: 1294.51271 Da, RT: 49.83 min,
Identified with: Mascot (v1.30); IonScore:55, Exp Value:7.4E-004, Ions matched by search engine: 8/108
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

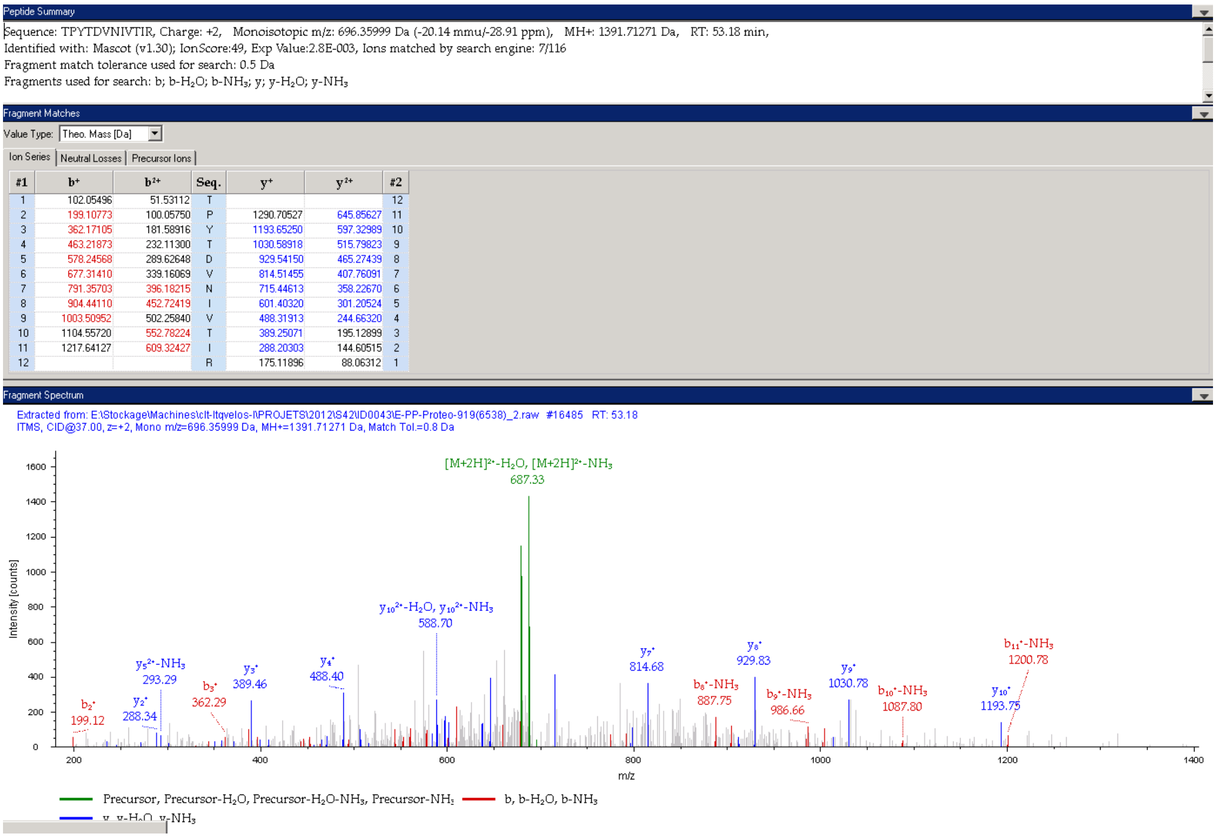
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			11
2	262.11863	131.56295	N	1147.53788	574.27258	10
3	361.18705	181.09716	V	1033.49495	517.25111	9
4	547.26637	274.13682	W	934.42653	467.71690	8
5	662.29332	331.65030	D	748.34721	374.67724	7
6	763.34100	382.17414	T	633.32026	317.16377	6
7	834.37812	417.69270	A	532.27258	266.63993	5
8	891.39959	446.20343	G	461.23546	231.12137	4
9	1019.45817	510.23272	Q	404.21399	202.61063	3
10	1148.50077	574.75402	E	276.15541	138.58134	2
11			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #14495 RT: 49.83
ITMS, CID@37.00, z=+2, Mono m/z=647.75999 Da, MH+=1294.51271 Da, Match Tol.=0.8 Da

Protein references (1):
- Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 - [IDH3A_HUMAN]



Sequence: TPYTDVNIVTIR, Charge: +2, Monoisotopic m/z: 696.35999 Da (-20.14 mmu/-28.91 ppm), MH+: 1391.71271 Da, RT: 53.18 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:2.8E-003, Ions matched by search engine: 7/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

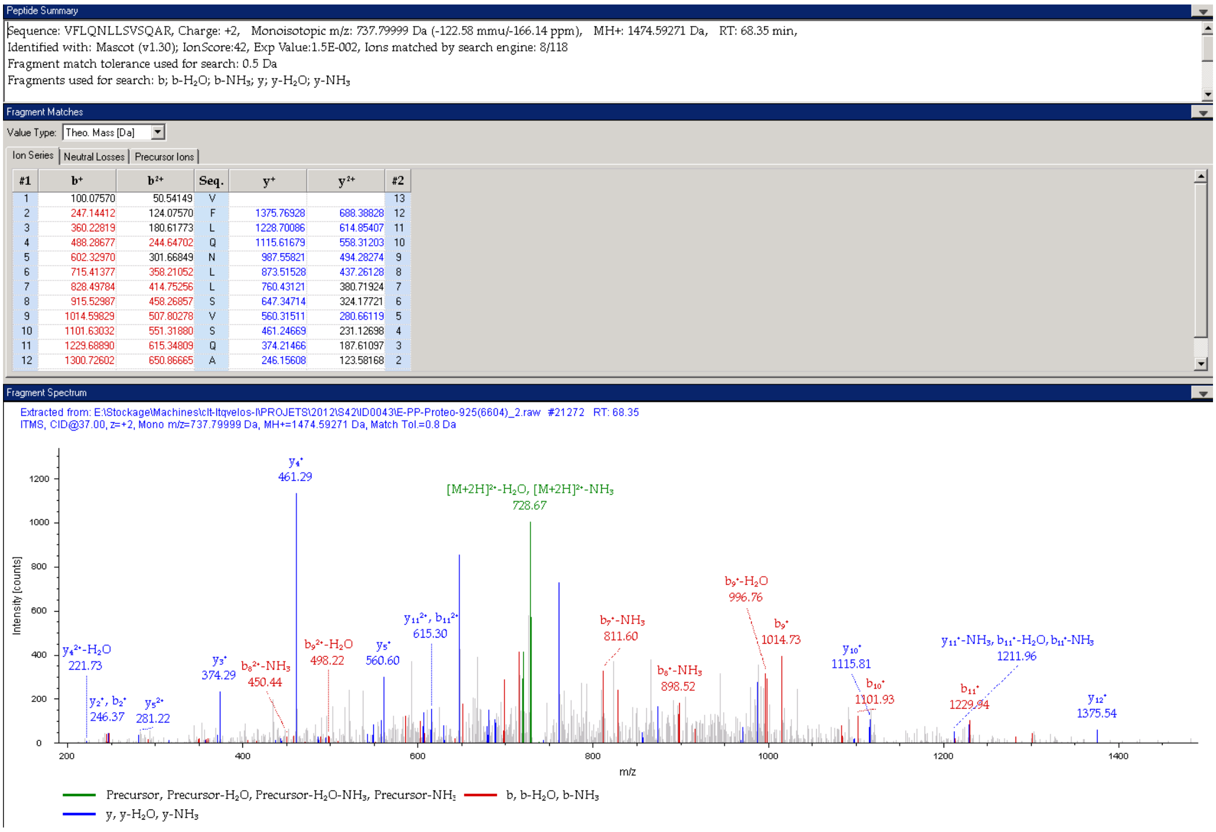
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			12
2	199.10773	100.05750	P	1290.70527	645.85627	11
3	362.17105	181.58916	Y	1193.65250	597.32989	10
4	463.21873	232.11300	T	1030.58918	515.79823	9
5	578.24568	289.62648	D	929.54150	465.27439	8
6	677.31410	339.16069	V	814.51455	407.76091	7
7	791.35703	396.18215	N	715.44613	358.22670	6
8	904.44110	452.72419	I	601.40320	301.20524	5
9	1003.50952	502.25840	V	488.31913	244.66320	4
10	1104.55720	552.78224	T	389.25071	195.12899	3
11	1217.64127	609.32427	I	288.20303	144.60515	2
12			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #16485 RT: 53.18
ITMS, CID@37.00, z=+2, Mono m/z=696.35999 Da, MH+=1391.71271 Da, Match Tol.=0.8 Da

Protein references (1):

- Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]



Peptide Summary

Sequence: VFLQNLLSVSQAR, Charge: +2, Monoisotopic m/z: 737.79999 Da (-122.58 mmu/-166.14 ppm), MH+: 1474.59271 Da, RT: 68.35 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.5E-002, Ions matched by search engine: 8/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

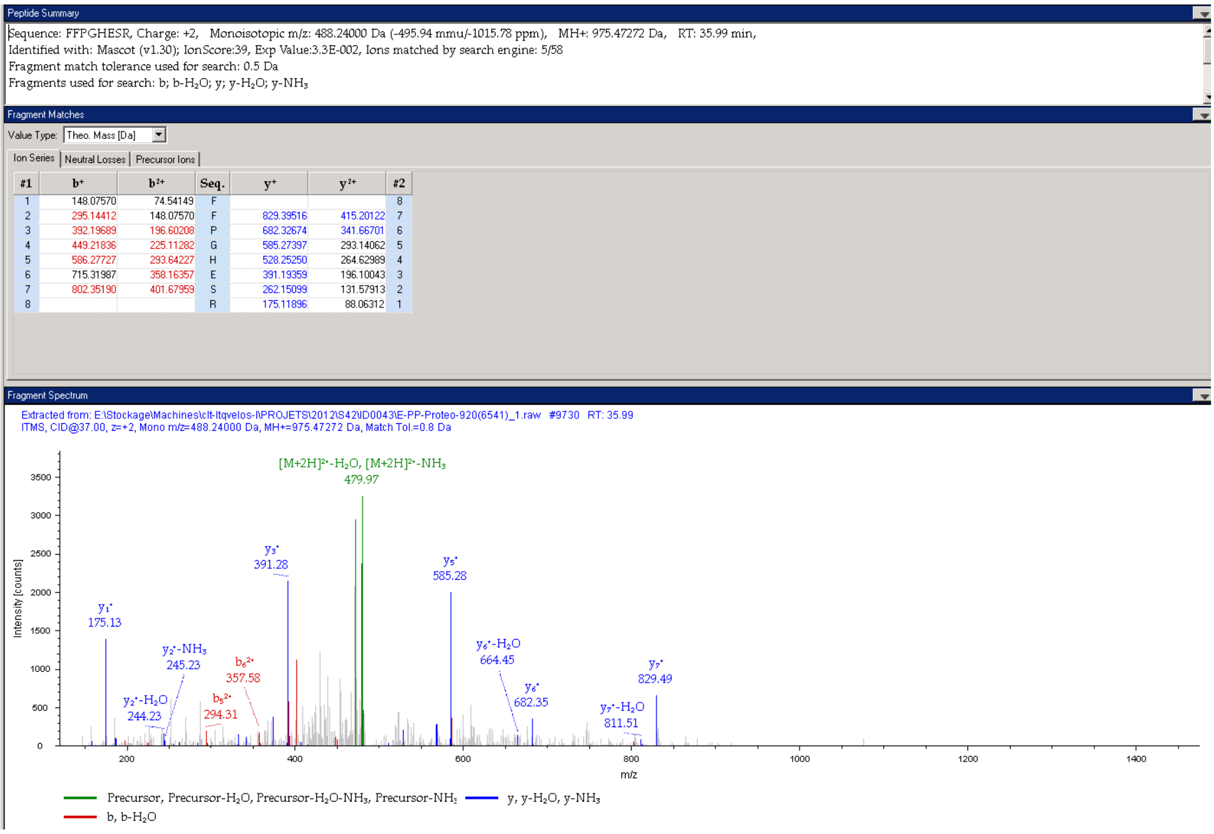
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			13
2	247.14412	124.07570	F	1375.76928	688.38828	12
3	360.22819	180.61773	L	1228.70086	614.85407	11
4	488.28677	244.64702	Q	1115.61679	558.31203	10
5	602.32970	301.66849	N	987.55821	494.28274	9
6	715.41377	358.21052	L	873.51528	437.26128	8
7	828.49784	414.75256	L	760.43121	380.71924	7
8	915.52987	458.26857	S	647.34714	324.17721	6
9	1014.59829	507.80278	V	560.31511	280.66119	5
10	1101.63032	551.31880	S	461.24669	231.12698	4
11	1229.68890	615.34809	Q	374.21466	187.61097	3
12	1300.72602	650.86665	A	246.15608	123.58168	2

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #21272 RT: 68.35
ITMS, CID@37.00, z=+2, Mono m/z=737.79999 Da, MH+=1474.59271 Da, Match Tol.=0.8 Da

Protein references (1):

- Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1 - [CIR1A_HUMAN]



Peptide Summary

Sequence: FFPGHESR, Charge: +2, Monoisotopic m/z: 488.24000 Da (-495.94 mmu/-1015.78 ppm), MH+: 975.47272 Da, RT: 35.99 min,
Identified with: Mascot (v1.30); IonScore:39, Exp Value:3.3E-002, Ions matched by search engine: 5/58
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

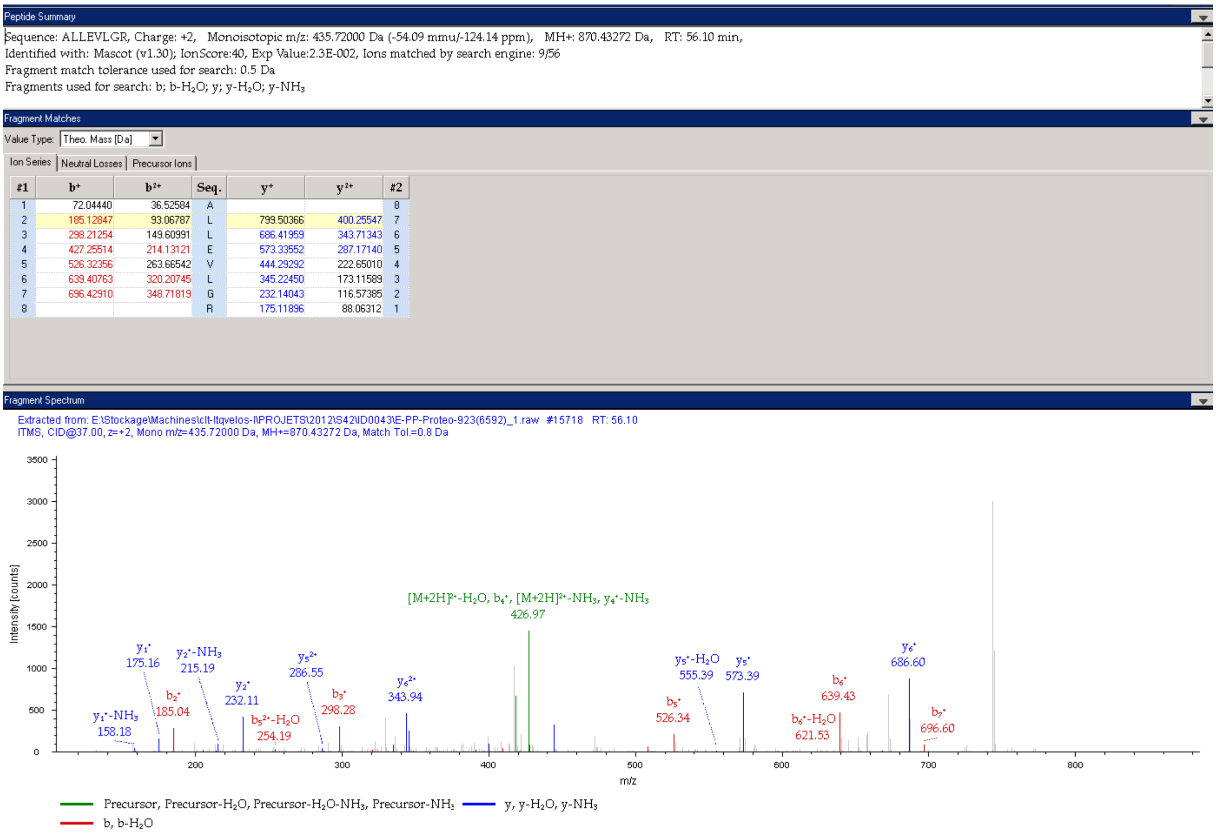
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			8
2	295.14412	148.07570	F	829.39516	415.20122	7
3	392.19689	196.60208	P	682.32674	341.66701	6
4	449.21836	225.11282	G	585.27397	293.14062	5
5	586.27727	293.64227	H	528.25250	264.62989	4
6	715.31987	358.16357	E	391.19359	196.10043	3
7	802.35190	401.67959	S	262.15099	131.57913	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_1.raw #9730 RT: 35.99
ITMS, CID@37.00, z=+2, Mono m/z=488.24000 Da, MH+=975.47272 Da, Match Tol.=0.8 Da

Protein references (1):
- Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]



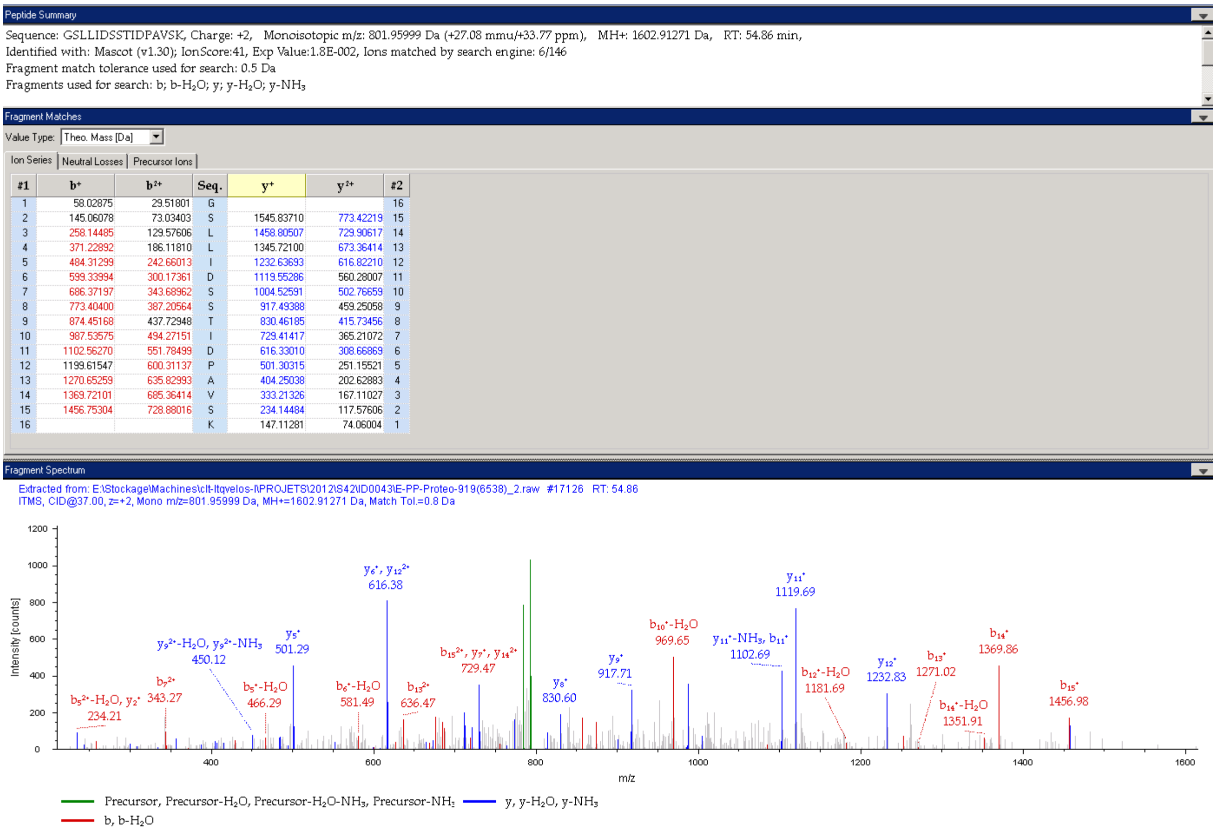
Sequence: ALLEVLGR, Charge: +2, Monoisotopic m/z: 435.72000 Da (-54.09 mmu/-124.14 ppm), MH+: 870.43272 Da, RT: 56.10 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.3E-002, Ions matched by search engine: 9/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			8
2	185.12847	93.06787	L	799.50366	400.25547	7
3	298.21254	149.60991	L	686.41959	343.71343	6
4	427.25514	214.13121	E	573.33552	287.17140	5
5	526.32356	263.66542	V	444.29292	222.65010	4
6	639.40763	320.20745	L	345.22450	173.11589	3
7	696.42910	348.71819	G	232.14043	116.57385	2
8			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw #15718 RT: 56.10
ITMS, CID@37.00, z=+2, Mono m/z=435.72000 Da, MH+=870.43272 Da, Match Tol.=0.8 Da

Protein references (1):

- 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]



Peptide Summary

Sequence: GSLLIDSSTIDPAVSK, Charge: +2, Monoisotopic m/z: 801.95999 Da (+27.08 mmu/+33.77 ppm), MH+: 1602.91271 Da, RT: 54.86 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.8E-002, Ions matched by search engine: 6/146
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

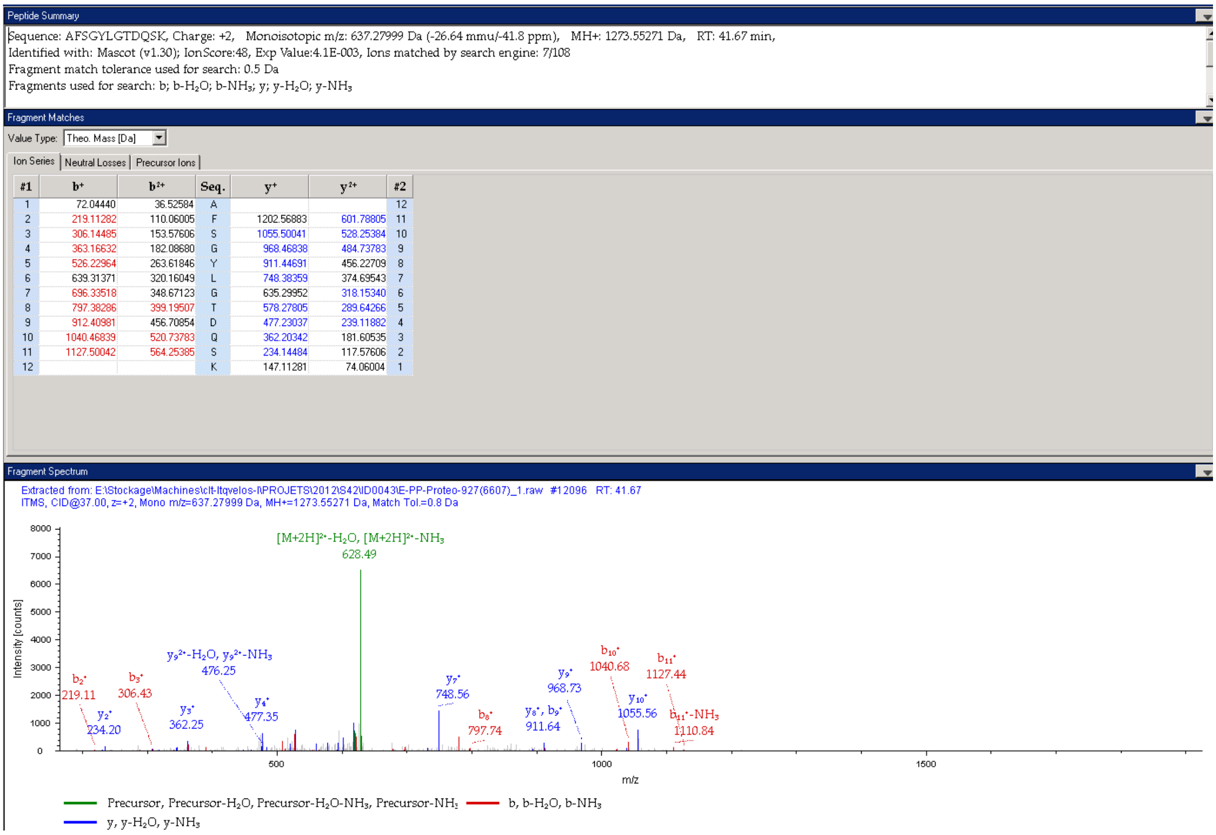
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			16
2	145.06078	73.03403	S	1545.83710	773.42219	15
3	258.14485	129.57606	L	1458.80507	729.90617	14
4	371.22892	186.11810	L	1345.72100	673.36414	13
5	484.31299	242.66013	I	1232.63693	616.82210	12
6	599.33994	300.17361	D	1119.55286	560.28007	11
7	686.37197	343.68962	S	1004.52591	502.76659	10
8	773.40400	387.20564	S	917.49388	459.25058	9
9	874.45168	437.72948	T	830.46185	415.73456	8
10	987.53575	494.27151	I	729.41417	365.21072	7
11	1102.56270	551.78499	D	616.33010	308.66869	6
12	1199.61547	600.31137	P	501.30315	251.15521	5
13	1270.65259	635.82993	A	404.25038	202.62883	4
14	1369.72101	685.36414	V	333.21326	167.11027	3
15	1456.75304	728.88016	S	234.14484	117.57606	2
16			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #17126 RT: 54.86
ITMS, CID@37.00, z=+2, Mono m/z=801.95999 Da, MH+=1602.91271 Da, Match Tol.=0.8 Da

Protein references (1):
- S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]



Peptide Summary

Sequence: AFSGYLGTDQSK, Charge: +2, Monoisotopic m/z: 637.27999 Da (-26.64 mmu/-41.8 ppm), MH+: 1273.55271 Da, RT: 41.67 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:4.1E-003, Ions matched by search engine: 7/108
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

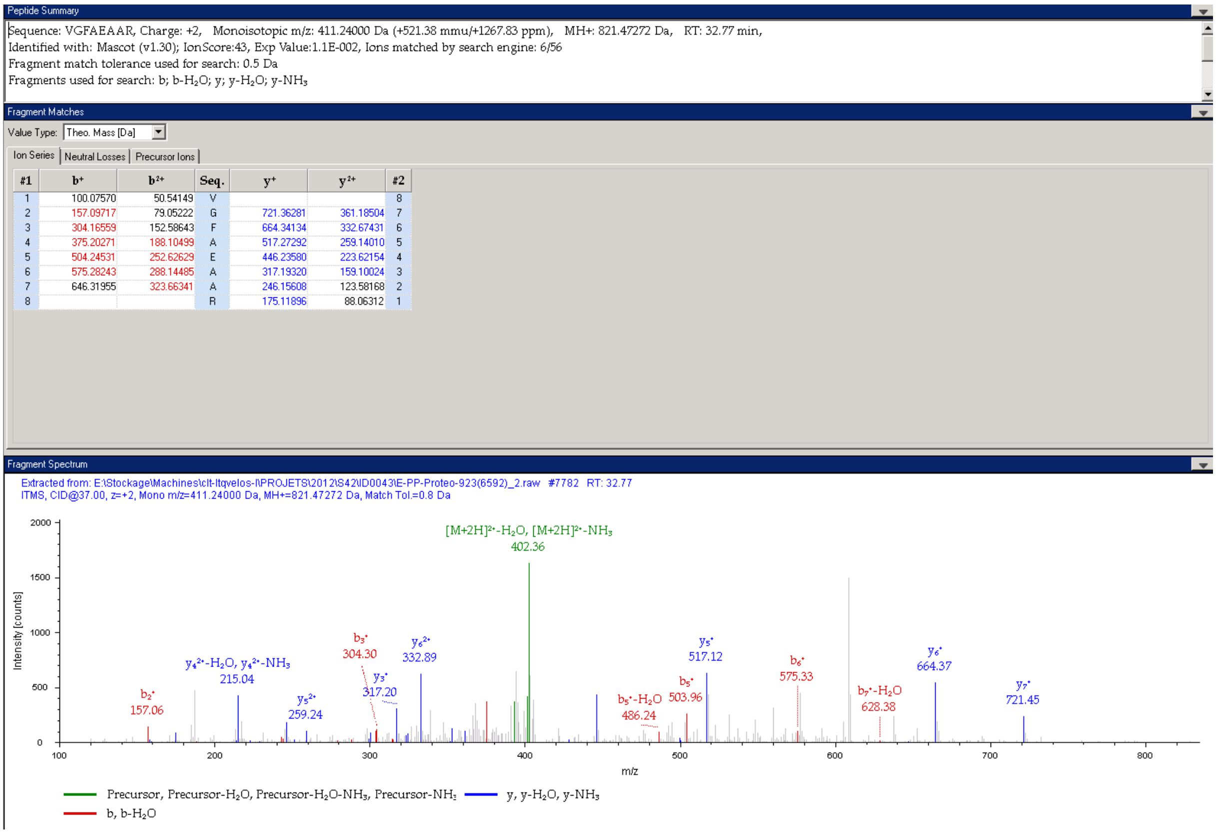
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			12
2	219.11282	110.06005	F	1202.56883	601.78805	11
3	306.14485	153.57606	S	1055.50041	528.25384	10
4	363.16632	182.08680	G	968.46838	484.73783	9
5	526.22964	263.61846	Y	911.44691	456.22709	8
6	639.31371	320.16049	L	748.38359	374.69543	7
7	696.33518	348.67123	G	635.29952	318.15340	6
8	797.38286	399.19507	T	578.27805	289.64266	5
9	912.40981	456.70854	D	477.23037	239.11882	4
10	1040.46839	520.73783	Q	362.20342	181.60535	3
11	1127.50042	564.25385	S	234.14484	117.57606	2
12			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #12096 RT: 41.67
ITMS, CID@37.00, z=+2, Mono m/z=637.27999 Da, MH+=1273.55271 Da, Match Tol.=0.8 Da

Protein references (1):
- Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]



Peptide Summary

Sequence: VGFAEAAR, Charge: +2, Monoisotopic m/z: 411.24000 Da (+521.38 mmu/+1267.83 ppm), MH+: 821.47272 Da, RT: 32.77 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.1E-002, Ions matched by search engine: 6/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

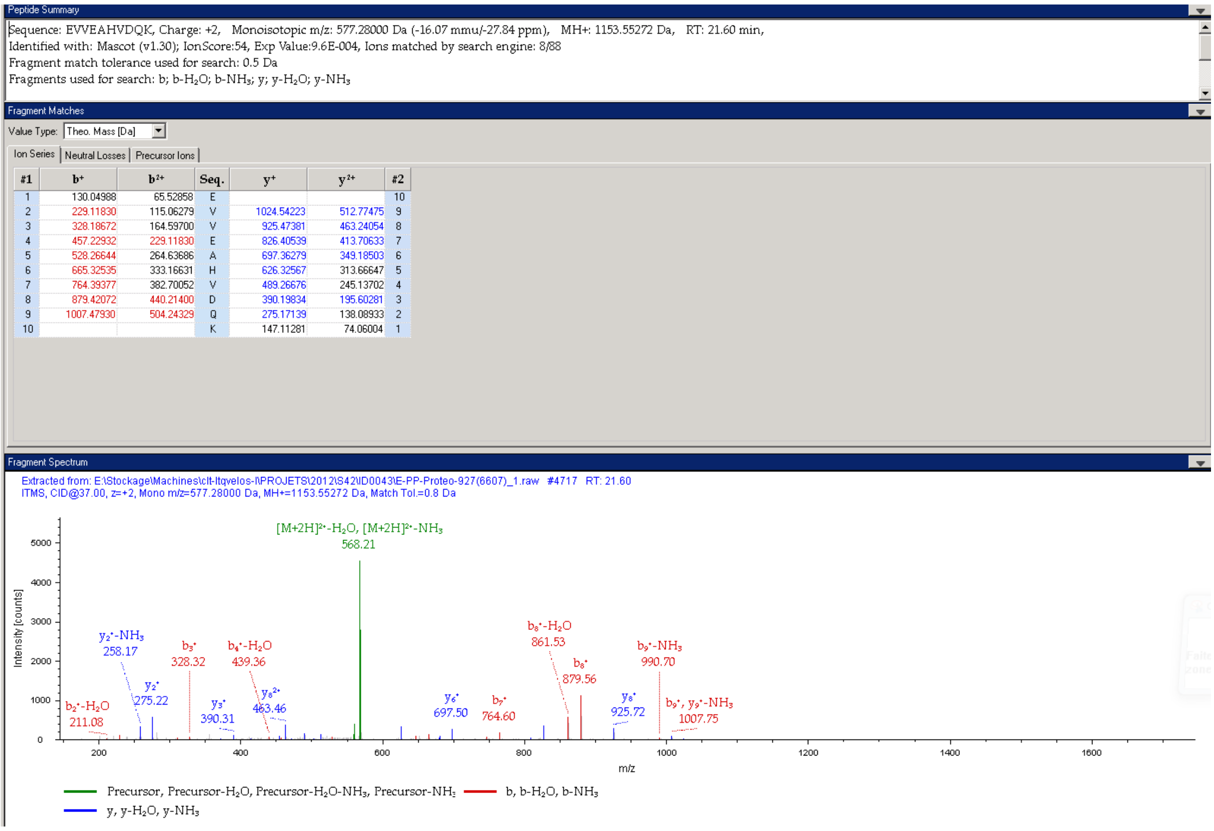
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			8
2	157.09717	79.05222	G	721.36281	361.18504	7
3	304.16559	152.58643	F	664.34134	332.67431	6
4	375.20271	188.10499	A	517.27292	259.14010	5
5	504.24531	252.62629	E	446.23580	223.62154	4
6	575.28243	288.14485	A	317.19320	159.10024	3
7	646.31955	323.66341	A	246.15608	123.58168	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_2.raw #7782 RT: 32.77
ITMS, CID@37.00, z=+2, Mono m/z=411.24000 Da, MH+=821.47272 Da, Match Tol.=0.8 Da

Protein references (1):
- ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN]



Peptide Summary

Sequence: EVVEAHVDQK, Charge: +2, Monoisotopic m/z: 577.28000 Da (-16.07 mmu/-27.84 ppm), MH+: 1153.55272 Da, RT: 21.60 min,
Identified with: Mascot (v1.30); IonScore:54, Exp Value:9.6E-004, Ions matched by search engine: 8/88
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

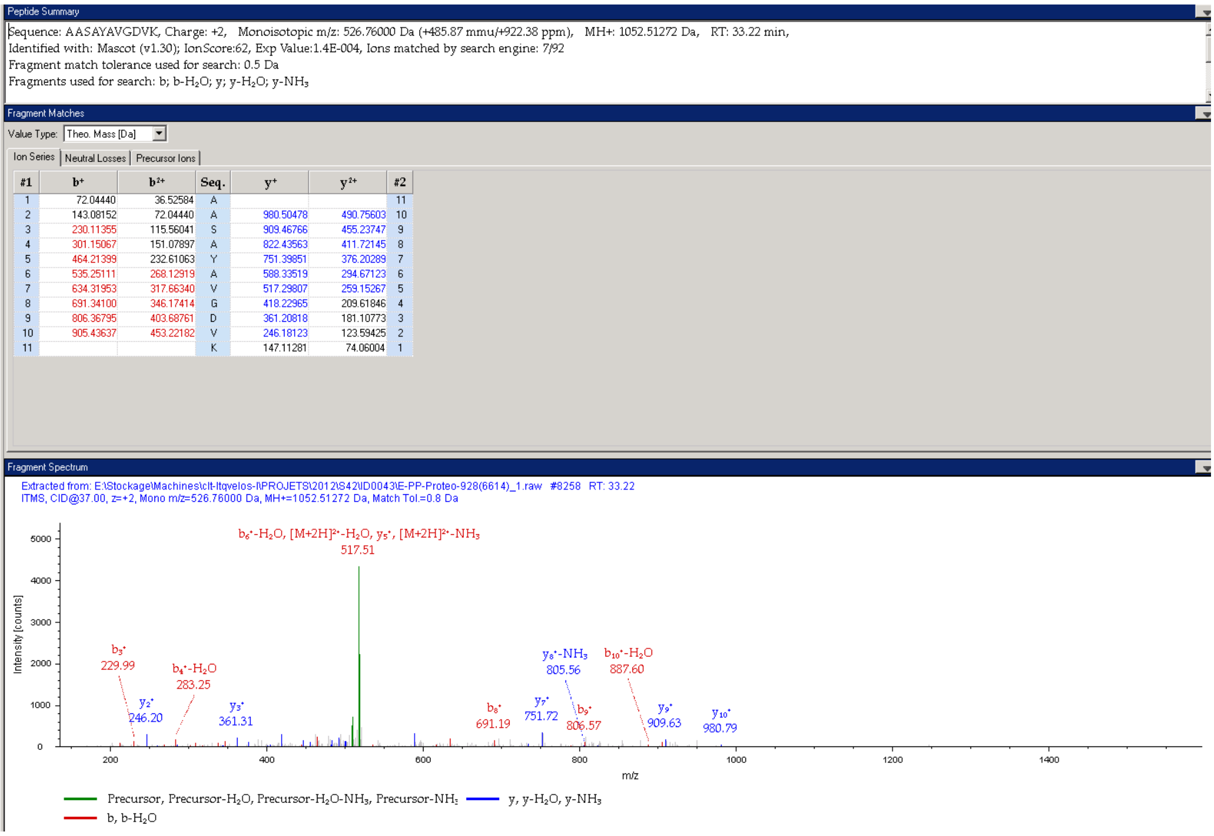
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			10
2	229.11830	115.06279	V	1024.54223	512.77475	9
3	328.18672	164.59700	V	925.47381	463.24054	8
4	457.22932	229.11830	E	826.40539	413.70633	7
5	528.26644	264.63686	A	697.36279	349.18503	6
6	665.32535	333.16631	H	626.32567	313.66647	5
7	764.39377	382.70052	V	489.26676	245.13702	4
8	879.42072	440.21400	D	390.19834	195.60281	3
9	1007.47930	504.24329	Q	275.17139	138.08933	2
10			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #4717 RT: 21.60
ITMS, CID@37.00, z=+2, Mono m/z=577.28000 Da, MH+=1153.55272 Da, Match Tol.=0.8 Da

Protein references (1):

- cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 - [KAP2_HUMAN]



Sequence: AASAYAVGDVK, Charge: +2, Monoisotopic m/z: 526.76000 Da (+485.87 mmu/+922.38 ppm), MH+: 1052.51272 Da, RT: 33.22 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.4E-004, Ions matched by search engine: 7/92
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

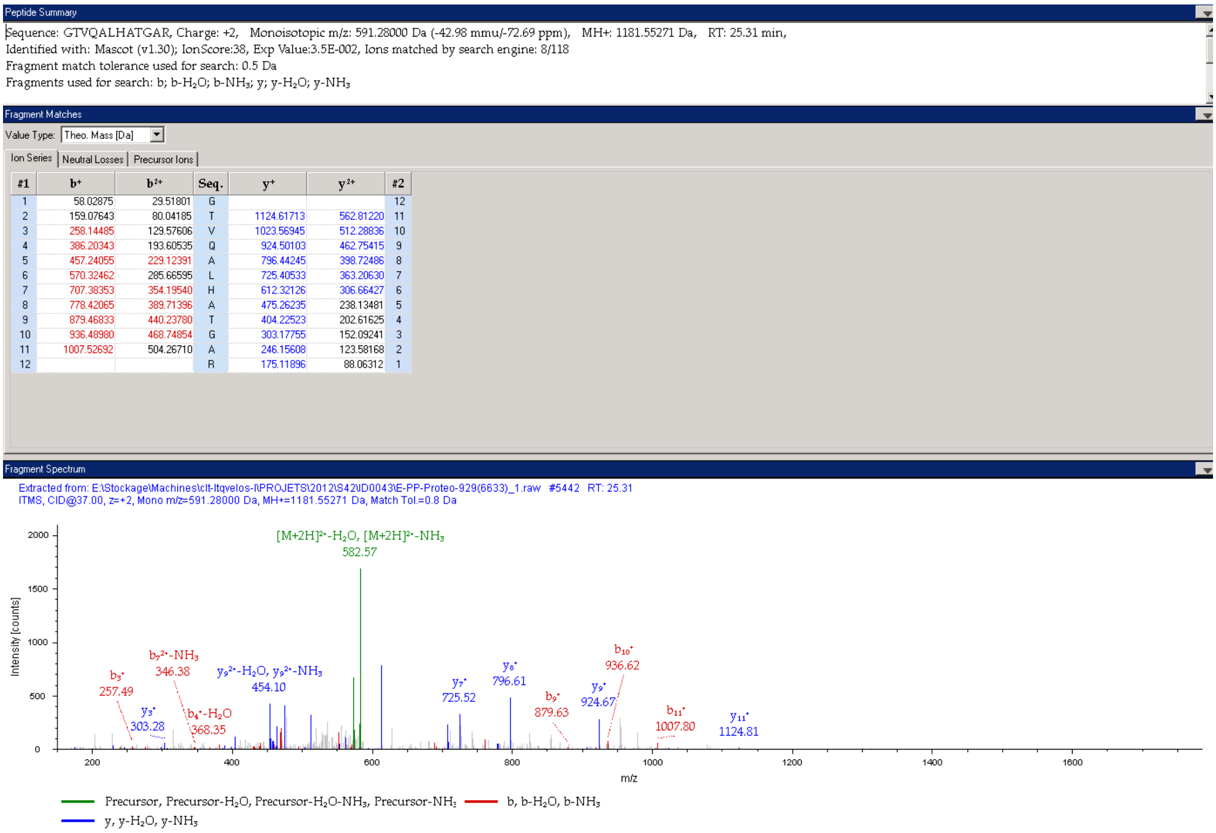
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			11
2	143.08152	72.04440	A	980.50478	490.75603	10
3	230.11355	115.56041	S	909.46766	455.23747	9
4	301.15067	151.07897	A	822.43563	411.72145	8
5	464.21399	232.61063	Y	751.39851	376.20289	7
6	535.25111	268.12919	A	588.33519	294.67123	6
7	634.31953	317.66340	V	517.29807	259.15267	5
8	691.34100	346.17414	G	418.22965	209.61846	4
9	806.36795	403.68761	D	361.20818	181.10773	3
10	905.43637	453.22182	V	246.18123	123.59425	2
11			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_1.raw #8258 RT: 33.22
ITMS, CID@37.00, z=+2, Mono m/z=526.76000 Da, MH+=1052.51272 Da, Match Tol.=0.8 Da

Protein references (1):

- L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]



Sequence: GTVQALHATGAR, Charge: +2, Monoisotopic m/z: 591.28000 Da (-42.98 mmu/-72.69 ppm), MH+: 1181.55271 Da, RT: 25.31 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.5E-002, Ions matched by search engine: 8/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

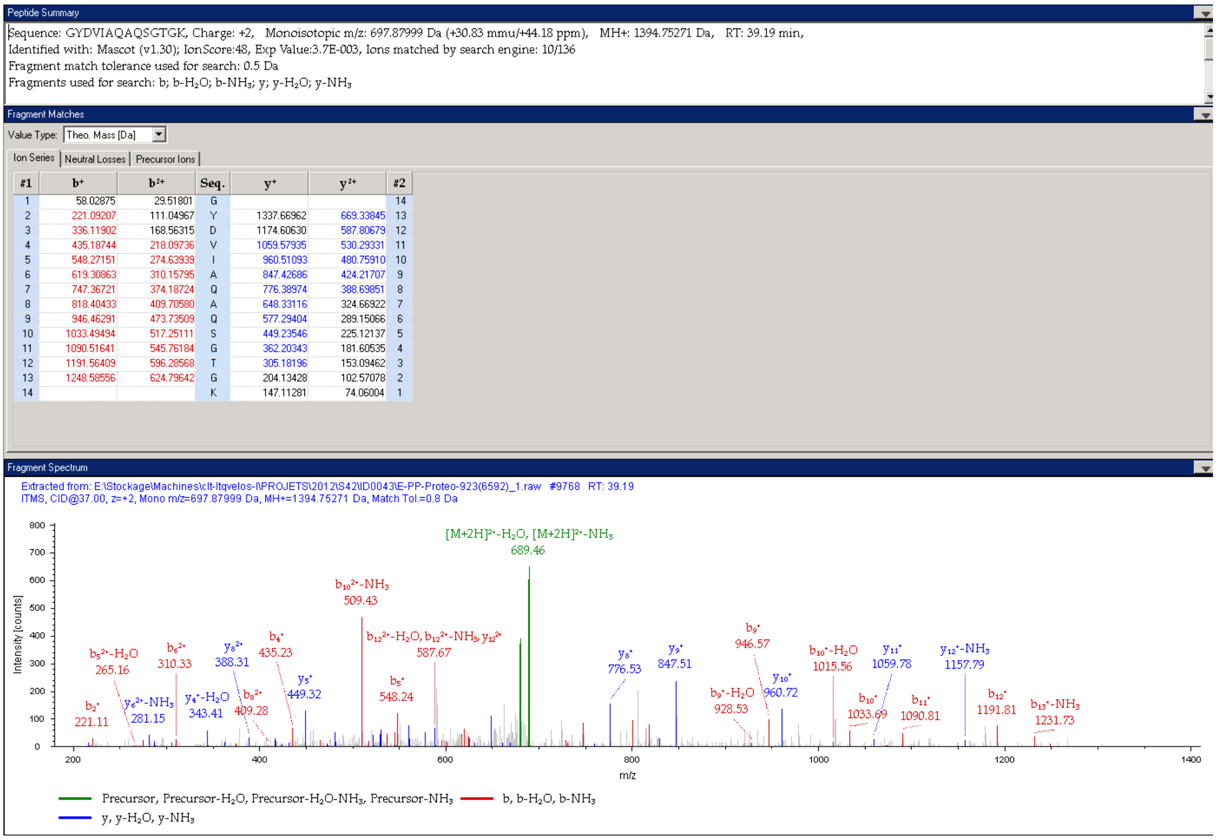
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			12
2	159.07643	80.04185	T	1124.61713	562.81220	11
3	258.14485	129.57606	V	1023.56945	512.28836	10
4	386.20343	193.60535	Q	924.50103	462.75415	9
5	457.24055	229.12391	A	796.44245	398.72486	8
6	570.32462	285.66595	L	725.40533	363.20630	7
7	707.38353	354.19540	H	612.32126	306.66427	6
8	778.42065	389.71396	A	475.26235	238.13481	5
9	879.46833	440.23780	T	404.22523	202.61625	4
10	936.48980	468.74854	G	303.17755	152.09241	3
11	1007.52692	504.26710	A	246.15608	123.58168	2
12			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_1.raw #5442 RT: 25.31
ITMS, CID@37.00, z=+2, Mono m/z=591.28000 Da, MH+=1181.55271 Da, Match Tol.=0.8 Da

Protein references (2):

- Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]



Peptide Summary

Sequence: GYDVIAQAQSGTGK, Charge: +2, Monoisotopic m/z: 697.87999 Da (+30.83 mmu/+44.18 ppm), MH+: 1394.75271 Da, RT: 39.19 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:3.7E-003, Ions matched by search engine: 10/136
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			14
2	221.09207	111.04967	Y	1337.66962	669.33845	13
3	336.11902	168.56315	D	1174.60630	587.80679	12
4	435.18744	218.09736	V	1059.57935	530.29331	11
5	548.27151	274.63939	I	960.51093	480.75910	10
6	619.30863	310.15795	A	847.42686	424.21707	9
7	747.36721	374.18724	Q	776.38974	388.69851	8
8	818.40433	409.70580	A	648.33116	324.66922	7
9	946.46291	473.73509	Q	577.29404	289.15066	6
10	1033.49494	517.25111	S	449.23546	225.12137	5
11	1090.51641	545.76184	G	362.20343	181.60535	4
12	1191.56409	596.28568	T	305.18196	153.09462	3
13	1248.58556	624.79642	G	204.13428	102.57078	2
14			K	147.11281	74.06004	1

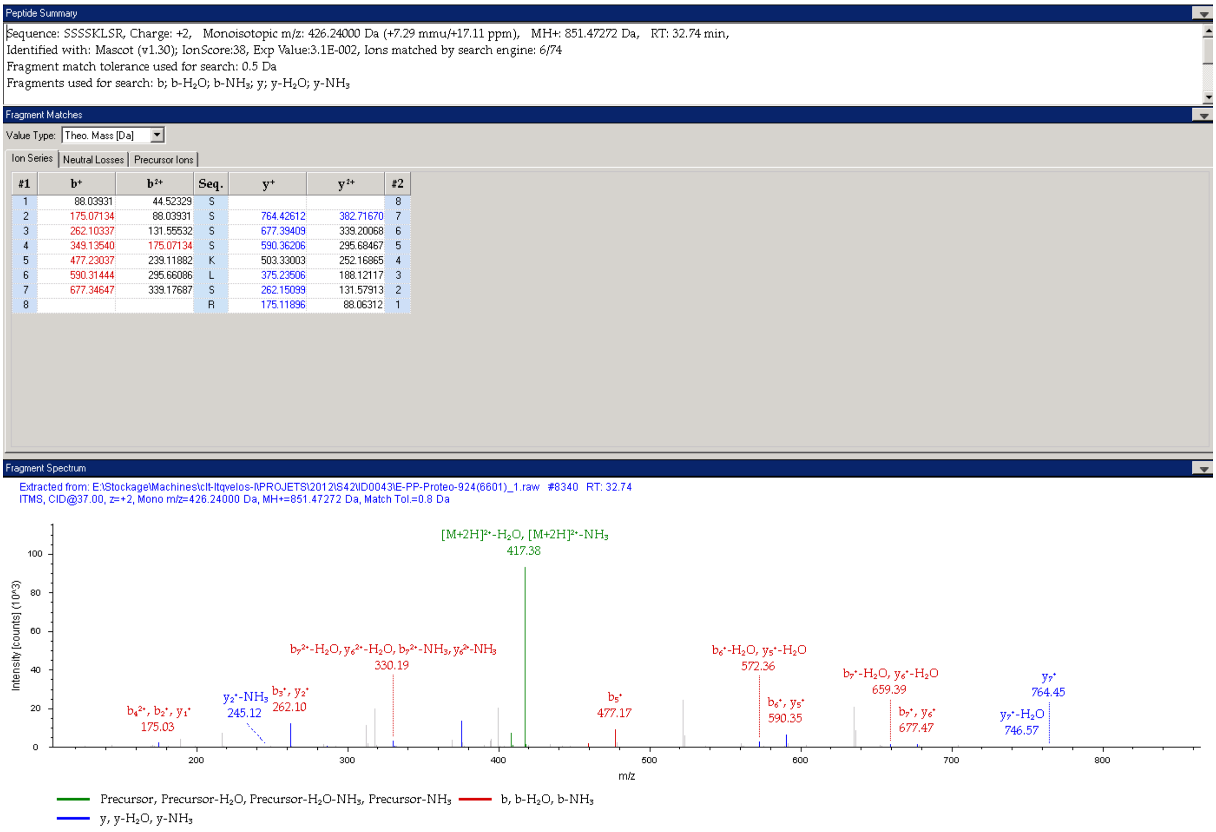
Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw #9768 RT: 39.19
ITMS, CID@37.00, z=+2, Mono m/z=697.87999 Da, MH+=1394.75271 Da, Match Tol.=0.8 Da

Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
b, b-H_2O, b-NH_3
y, y-H_2O, y-NH_3

Protein references (1):

- Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2 - [E41L3_HUMAN]



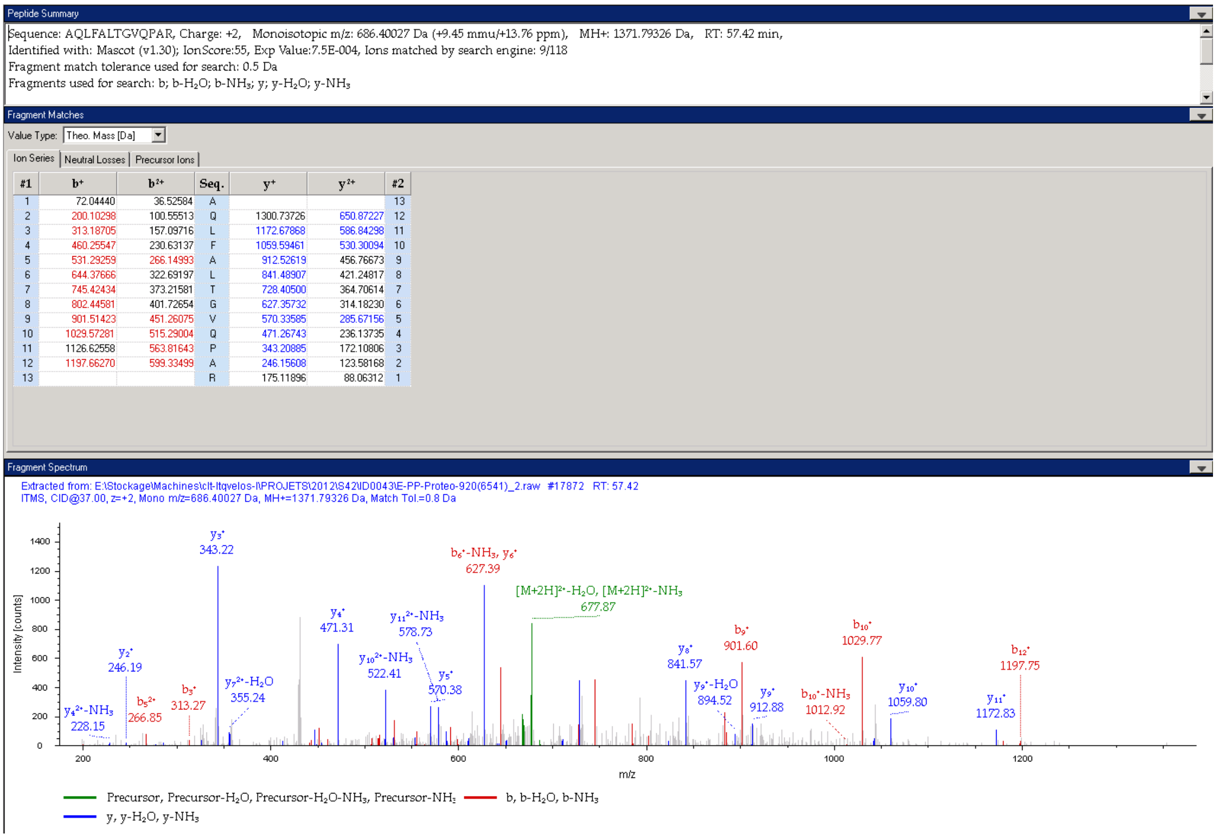
Sequence: *SSSSKLSR*, Charge: +2, Monoisotopic m/z: 426.24000 Da (+7.29 mmu/+17.11 ppm), MH+: 851.47272 Da, RT: 32.74 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.1E-002, Ions matched by search engine: 6/74
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			8
2	175.07134	88.03931	S	764.42612	382.71670	7
3	262.10337	131.55532	S	677.39409	339.20068	6
4	349.13540	175.07134	S	590.36206	295.68467	5
5	477.23037	239.11882	K	503.33003	252.16865	4
6	590.31444	295.66086	L	375.23506	188.12117	3
7	677.34647	339.17687	S	262.15099	131.57913	2
8			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_1.raw #8340 RT: 32.74
ITMS, CID@37.00, z=+2, Mono m/z=426.24000 Da, MH+=851.47272 Da, Match Tol.=0.8 Da

Protein references (1):
- Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3 - [UBP14_HUMAN]



Peptide Summary

Sequence: AQLFALTGVQPAR, Charge: +2, Monoisotopic m/z: 686.40027 Da (+9.45 mmu/+13.76 ppm), MH+: 1371.79326 Da, RT: 57.42 min,
Identified with: Mascot (v1.30); IonScore:55, Exp Value:7.5E-004, Ions matched by search engine: 9/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

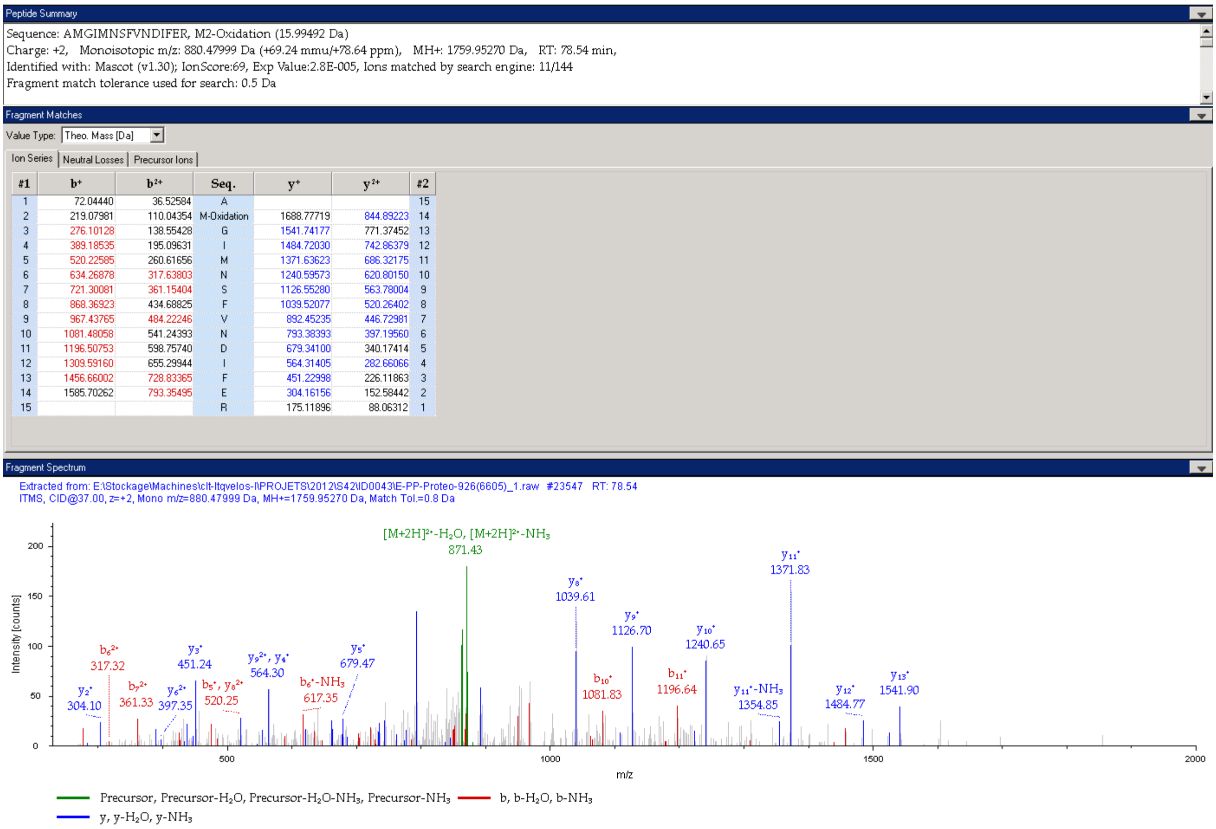
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	200.10298	100.55513	Q	1300.73726	650.87227	12
3	313.18705	157.09716	L	1172.67868	586.84298	11
4	460.25547	230.63137	F	1059.59461	530.30094	10
5	531.29259	266.14993	A	912.52619	456.76673	9
6	644.37666	322.69197	L	841.48907	421.24817	8
7	745.42434	373.21581	T	728.40500	364.70614	7
8	802.44581	401.72654	G	627.35732	314.18230	6
9	901.51423	451.26075	V	570.33585	285.67156	5
10	1029.57281	515.29004	Q	471.26743	236.13735	4
11	1126.62558	563.81643	P	343.20885	172.10806	3
12	1197.66270	599.33499	A	246.15608	123.58168	2
13			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #17872 RT: 57.42
ITMS, CID@37.00, z=+2, Mono m/z=686.40027 Da, MH+=1371.79326 Da, Match Tol.=0.8 Da

Protein references (14):
- Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]
- Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]



Sequence: AMGIMNSFVNDIFER, M2-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 880.47999 Da (+69.24 mmu/+78.64 ppm), MH+: 1759.95270 Da, RT: 78.54 min,
Identified with: Mascot (v1.30); IonScore:69, Exp Value:2.8E-005, Ions matched by search engine: 11/144
Fragment match tolerance used for search: 0.5 Da

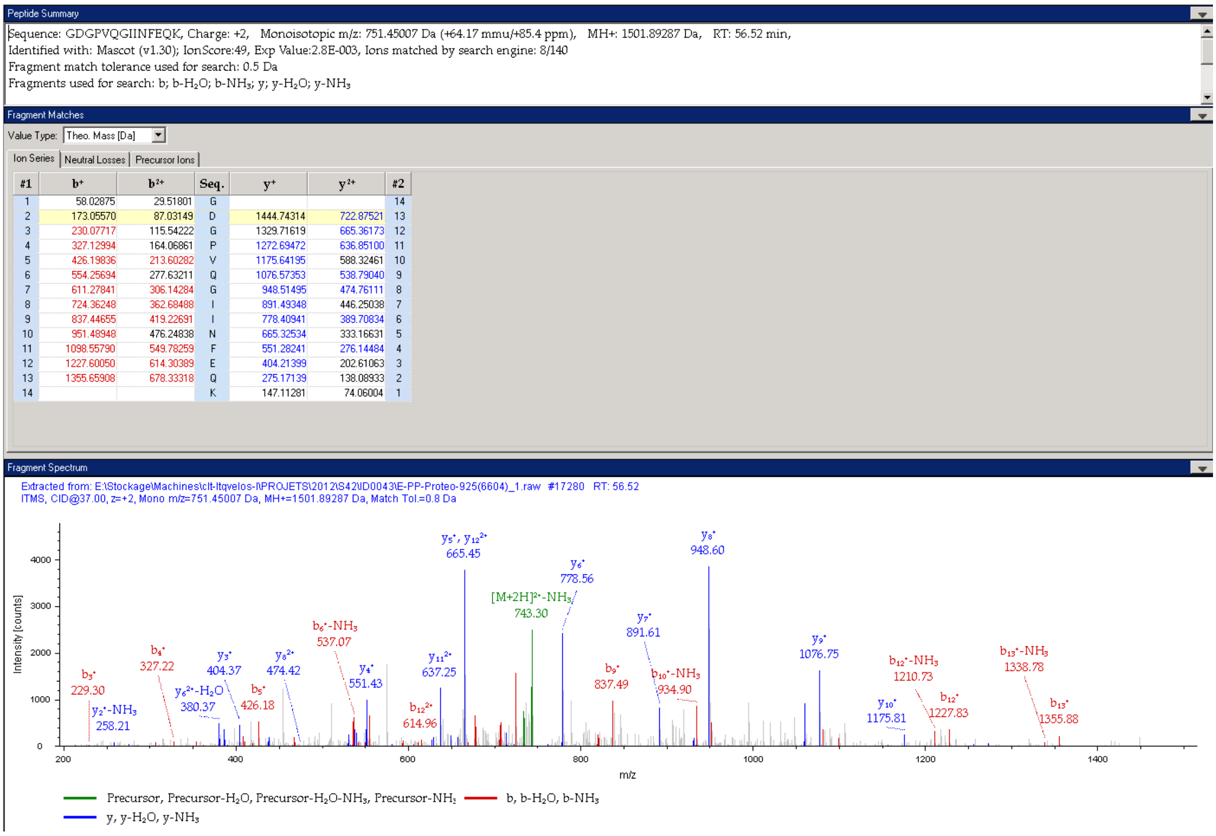
Value Type: Theo. Mass [Da]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	72.04440	36.52584	A			15
2	219.07981	110.04354	M-Oxidation	1688.77719	844.89223	14
3	276.10128	138.55428	G	1541.74177	771.37452	13
4	389.18535	195.09631	I	1484.72030	742.86379	12
5	520.22585	260.61656	M	1371.63623	686.32175	11
6	634.26878	317.63803	N	1240.59573	620.80150	10
7	721.30081	361.15404	S	1126.55280	563.78004	9
8	868.36923	434.68825	F	1039.52077	520.26402	8
9	967.43765	484.22246	V	892.45235	446.72981	7
10	1081.48058	541.24393	N	793.38393	397.19560	6
11	1196.50753	598.75740	D	679.34100	340.17414	5
12	1309.59160	655.29944	I	564.31405	282.66066	4
13	1456.66002	728.83365	F	451.22998	226.11863	3
14	1585.70262	793.35495	E	304.16156	152.58442	2
15			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #23547 RT: 78.54
ITMS, CID@37.00, z=+2, Mono m/z=880.47999 Da, MH+=1759.95270 Da, Match Tol.=0.8 Da

Protein references (1):

- Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]



Peptide Summary

Sequence: GDGPVQGIINFEQK, Charge: +2, Monoisotopic m/z: 751.45007 Da (+64.17 mmu/+85.4 ppm), MH+: 1501.89287 Da, RT: 56.52 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:2.8E-003, Ions matched by search engine: 8/140
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

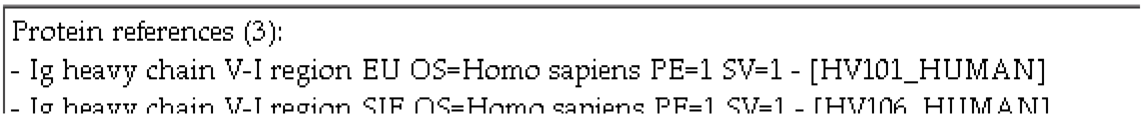
Fragment Matches

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			14
2	173.05570	87.03149	D	1444.74314	722.87521	13
3	230.07717	115.54222	G	1329.71619	665.36173	12
4	327.12994	164.06861	P	1272.69472	636.85100	11
5	426.19836	213.60282	V	1175.64195	588.32461	10
6	554.25694	277.63211	Q	1076.57353	538.79040	9
7	611.27841	306.14284	G	948.51495	474.76111	8
8	724.36248	362.68488	I	891.49348	446.25038	7
9	837.44655	419.22691	I	778.40941	389.70834	6
10	951.48948	476.24838	N	665.32534	333.16631	5
11	1098.55790	549.78259	F	551.28241	276.14484	4
12	1227.60050	614.30389	E	404.21399	202.61063	3
13	1355.65908	678.33318	Q	275.17139	138.08933	2
14			K	147.11281	74.06004	1

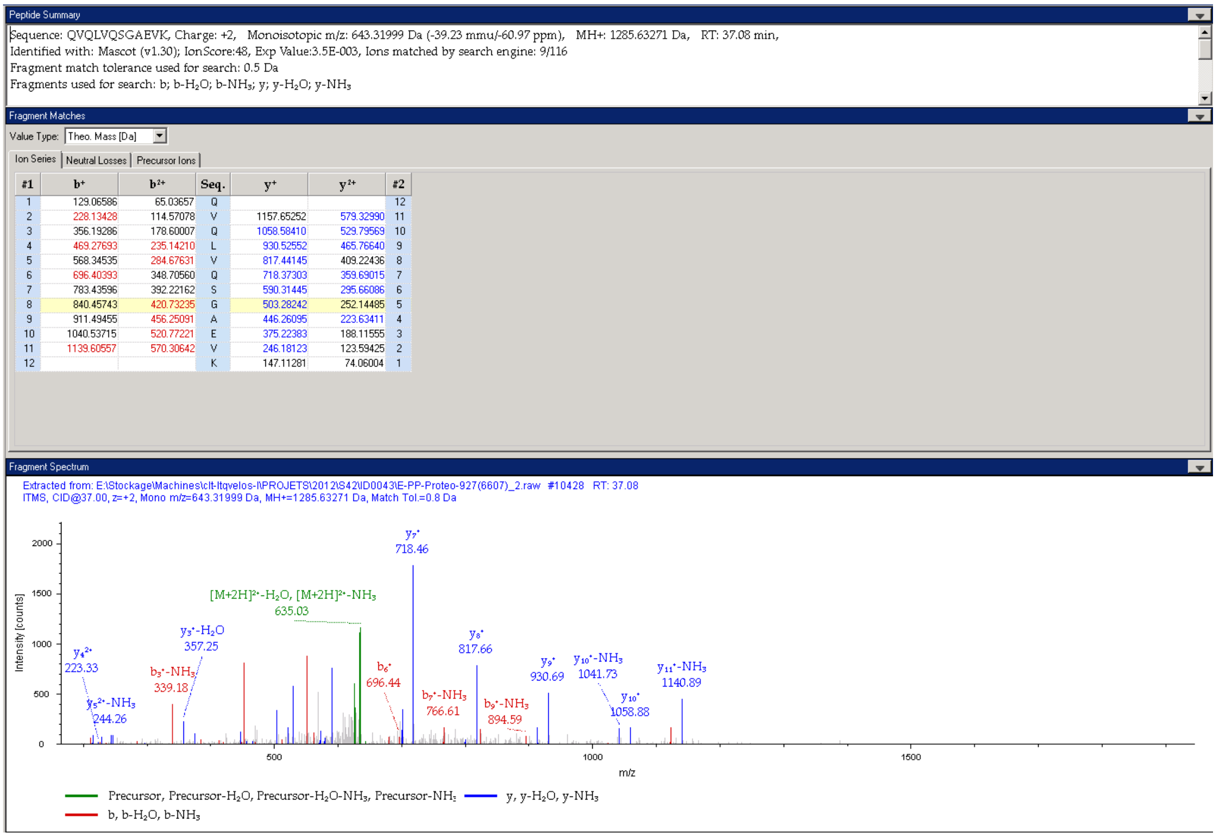
Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #17280 RT: 56.52
ITMS, CID@37.00, z=+2, Mono m/z=751.45007 Da, MH+=1501.89287 Da, Match Tol.=0.8 Da



Protein references (3):

- Ig heavy chain V-I region EU OS=Homo sapiens PE=1 SV=1 - [HV101_HUMAN]
- Ig heavy chain V-I region SIE OS=Homo sapiens PE=1 SV=1 - [HV106_HUMAN]



Peptide Summary

Sequence: QVQLVQSGAEVK, Charge: +2, Monoisotopic m/z: 643.31999 Da (-39.23 mmu/-60.97 ppm), MH+: 1285.63271 Da, RT: 37.08 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:3.5E-003, Ions matched by search engine: 9/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

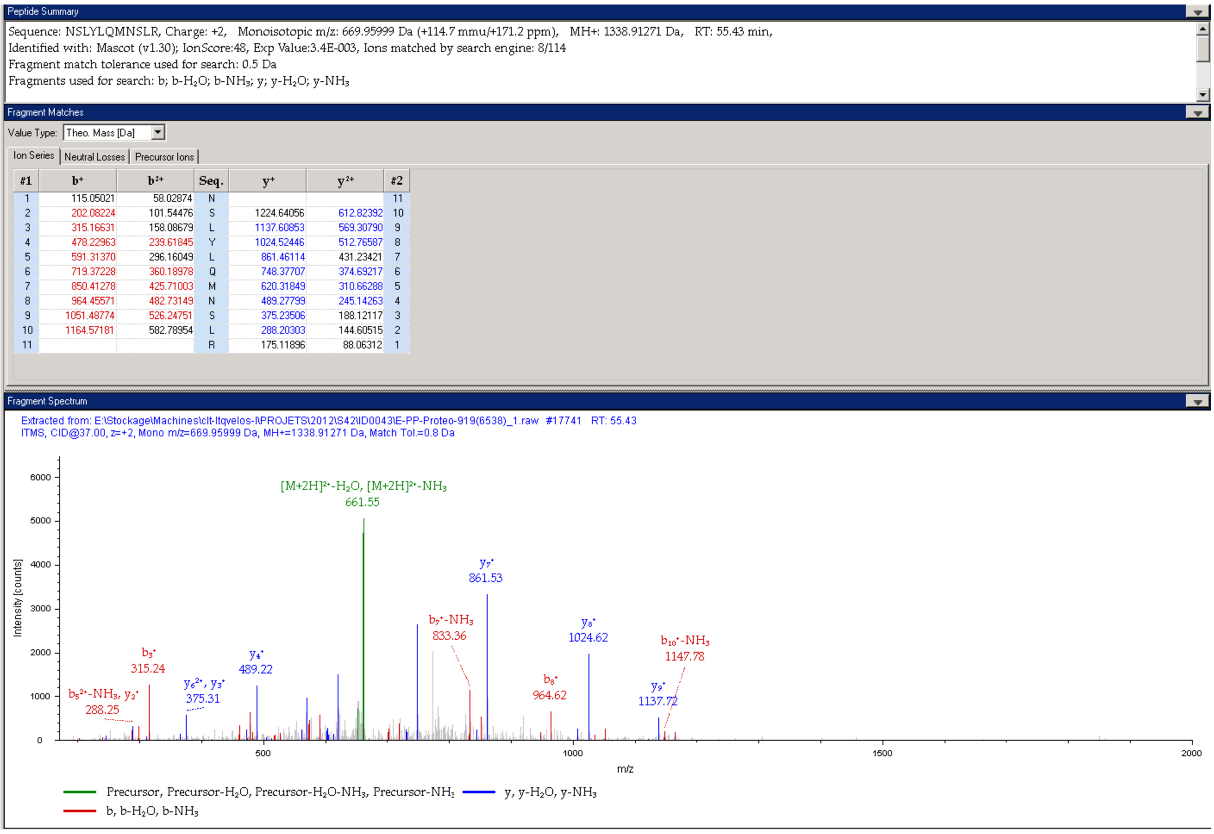
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			12
2	228.13428	114.57078	V	1157.65252	579.32990	11
3	356.19286	178.60007	Q	1058.58410	529.79569	10
4	469.27693	235.14210	L	930.52552	465.76640	9
5	568.34535	284.67631	V	817.44145	409.22436	8
6	696.40393	348.70560	Q	718.37303	359.69015	7
7	783.43596	392.22162	S	590.31445	295.66086	6
8	840.45743	420.73235	G	503.28242	252.14485	5
9	911.49455	456.25091	A	446.26095	223.63411	4
10	1040.53715	520.77221	E	375.22383	188.11555	3
11	1139.60557	570.30642	V	246.18123	123.59425	2
12			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #10428 RT: 37.08
ITMS, CID@37.00, z=+2, Mono m/z=643.31999 Da, MH+=1285.63271 Da, Match Tol.=0.8 Da

Protein references (1):

- Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1 - [HV320_HUMAN]



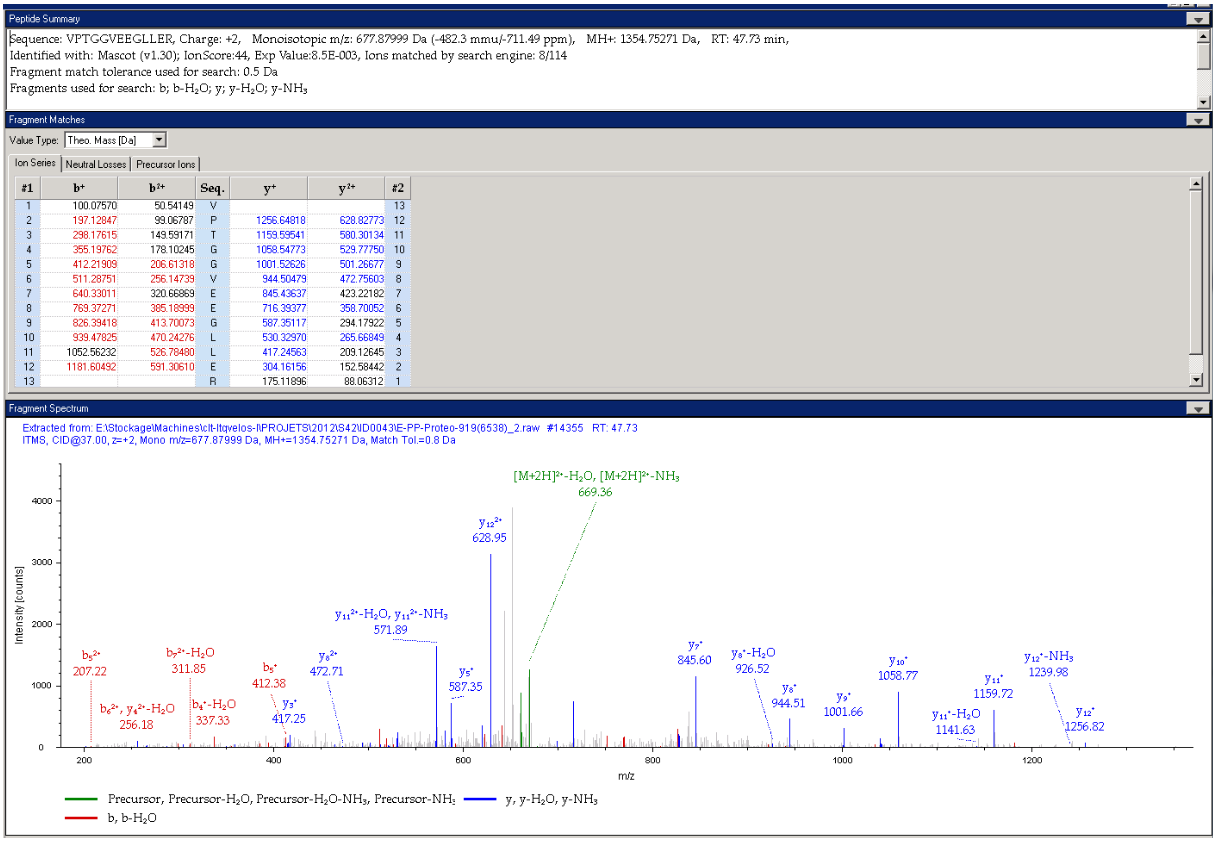
Sequence: NSLYLQMNSLR, Charge: +2, Monoisotopic m/z: 669.95999 Da (+114.7 mmu/+171.2 ppm), MH+: 1338.91271 Da, RT: 55.43 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:3.4E-003, Ions matched by search engine: 8/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			11
2	202.08224	101.54476	S	1224.64056	612.82392	10
3	315.16631	158.08679	L	1137.60853	569.30790	9
4	478.22963	239.61845	Y	1024.52446	512.76587	8
5	591.31370	296.16049	L	861.46114	431.23421	7
6	719.37228	360.18978	Q	748.37707	374.69217	6
7	850.41278	425.71003	M	620.31849	310.66288	5
8	964.45571	482.73149	N	489.27799	245.14263	4
9	1051.48774	526.24751	S	375.23506	188.12117	3
10	1164.57181	582.78954	L	288.20303	144.60515	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_1.raw #17741 RT: 55.43
ITMS, CID@37.00, z=+2, Mono m/z=669.95999 Da, MH+=1338.91271 Da, Match Tol.=0.8 Da

Protein references (1):
- Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2 - [IGHD_HUMAN]



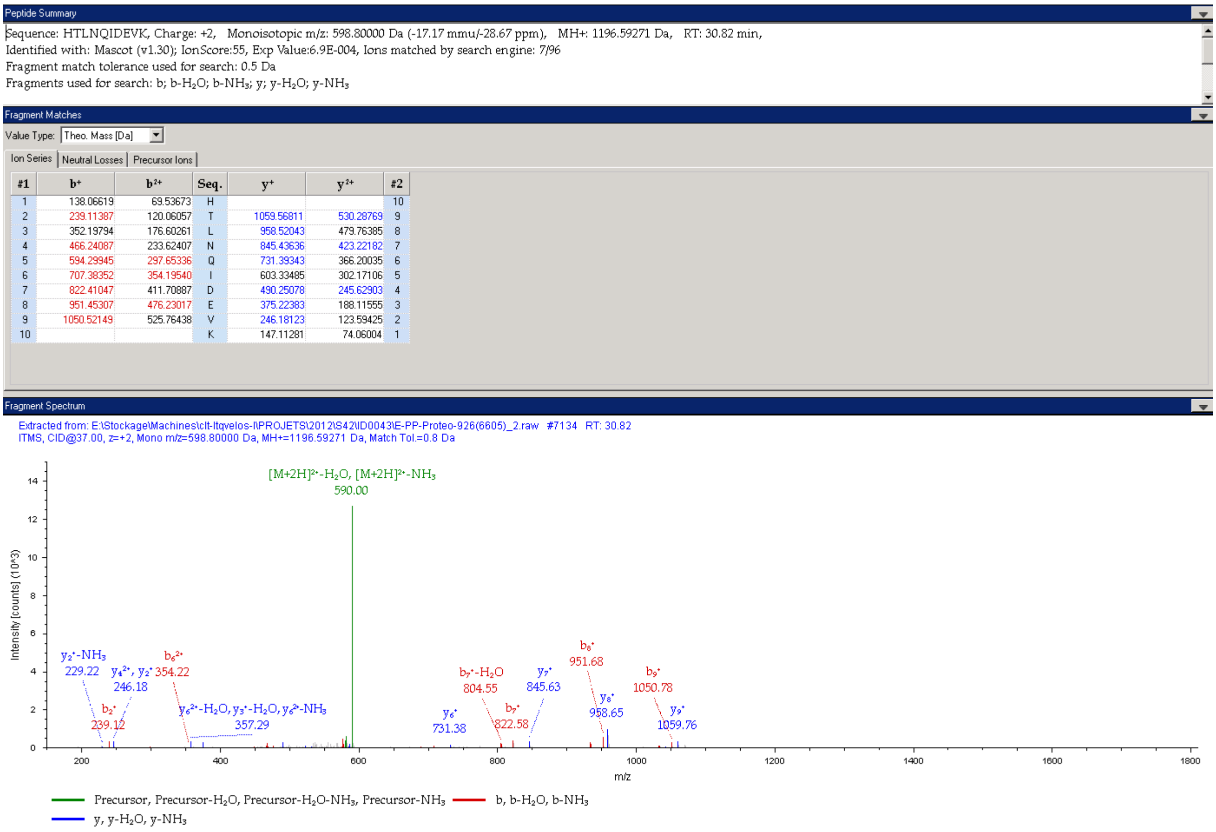
Sequence: VPTGGVEEGLLER, Charge: +2, Monoisotopic m/z: 677.87999 Da (-482.3 mmu/-711.49 ppm), MH+: 1354.75271 Da, RT: 47.73 min,
Identified with: Mascot (v1.30); IonScore:44, Exp Value:8.5E-003, Ions matched by search engine: 8/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			13
2	197.12847	99.06787	P	1256.64818	628.82773	12
3	298.17615	149.59171	T	1159.59541	580.30134	11
4	355.19762	178.10245	G	1058.54773	529.77750	10
5	412.21909	206.61318	G	1001.52626	501.26677	9
6	511.28751	256.14739	V	944.50479	472.75603	8
7	640.33011	320.66869	E	845.43637	423.22182	7
8	769.37271	385.18999	E	716.39377	358.70052	6
9	826.39418	413.70073	G	587.35117	294.17922	5
10	939.47825	470.24276	L	530.32970	265.66849	4
11	1052.56232	526.78480	L	417.24563	209.12645	3
12	1181.60492	591.30610	E	304.16156	152.58442	2
13			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #14355 RT: 47.73
ITMS, CID@37.00, z=+2, Mono m/z=677.87999 Da, MH+=1354.75271 Da, Match Tol.=0.8 Da

Protein references (1):
- Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]

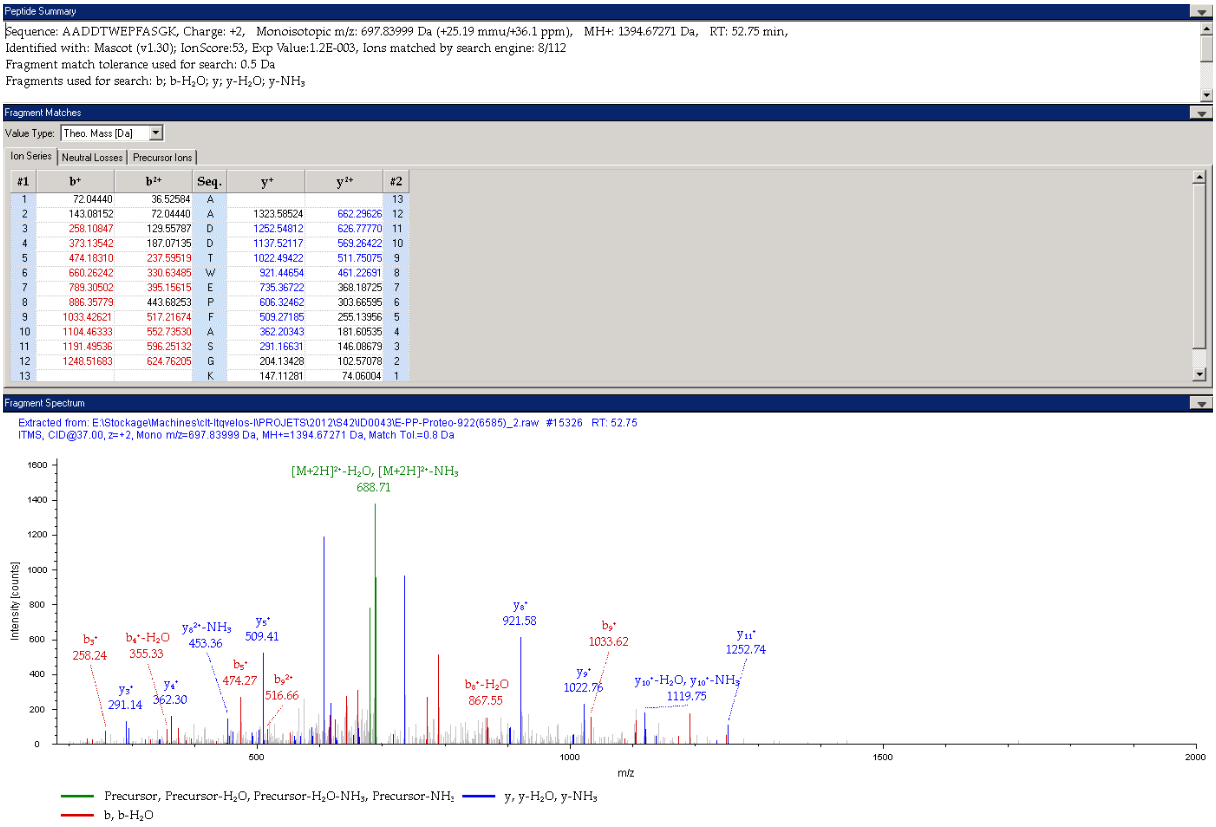


Sequence: HTLNQIDEVK, Charge: +2, Monoisotopic m/z: 598.80000 Da (-17.17 mmu/-28.67 ppm), MH+: 1196.59271 Da, RT: 30.82 min,
Identified with: Mascot (v1.30); IonScore:55, Exp Value:6.9E-004, Ions matched by search engine: 7/96
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	138.06619	69.53673	H			10
2	239.11387	120.06057	T	1059.56811	530.28769	9
3	352.19794	176.60261	L	958.52043	479.76385	8
4	466.24087	233.62407	N	845.43636	423.22182	7
5	594.29945	297.65336	Q	731.39343	366.20035	6
6	707.38352	354.19540	I	603.33485	302.17106	5
7	822.41047	411.70887	D	490.25078	245.62903	4
8	951.45307	476.23017	E	375.22383	188.11555	3
9	1050.52149	525.76438	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_2.raw #7134 RT: 30.82
ITMS, CID@37.00, z=+2, Mono m/z=598.80000 Da, MH+=1196.59271 Da, Match Tol.=0.8 Da

Protein references (1):
- Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1 - [TTHY_HUMAN]



Peptide Summary

Sequence: AADDTWEPFASGK, Charge: +2, Monoisotopic m/z: 697.83999 Da (+25.19 mmu/+36.1 ppm), MH+: 1394.67271 Da, RT: 52.75 min,
Identified with: Mascot (v1.30); IonScore:53, Exp Value:1.2E-003, Ions matched by search engine: 8/112
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

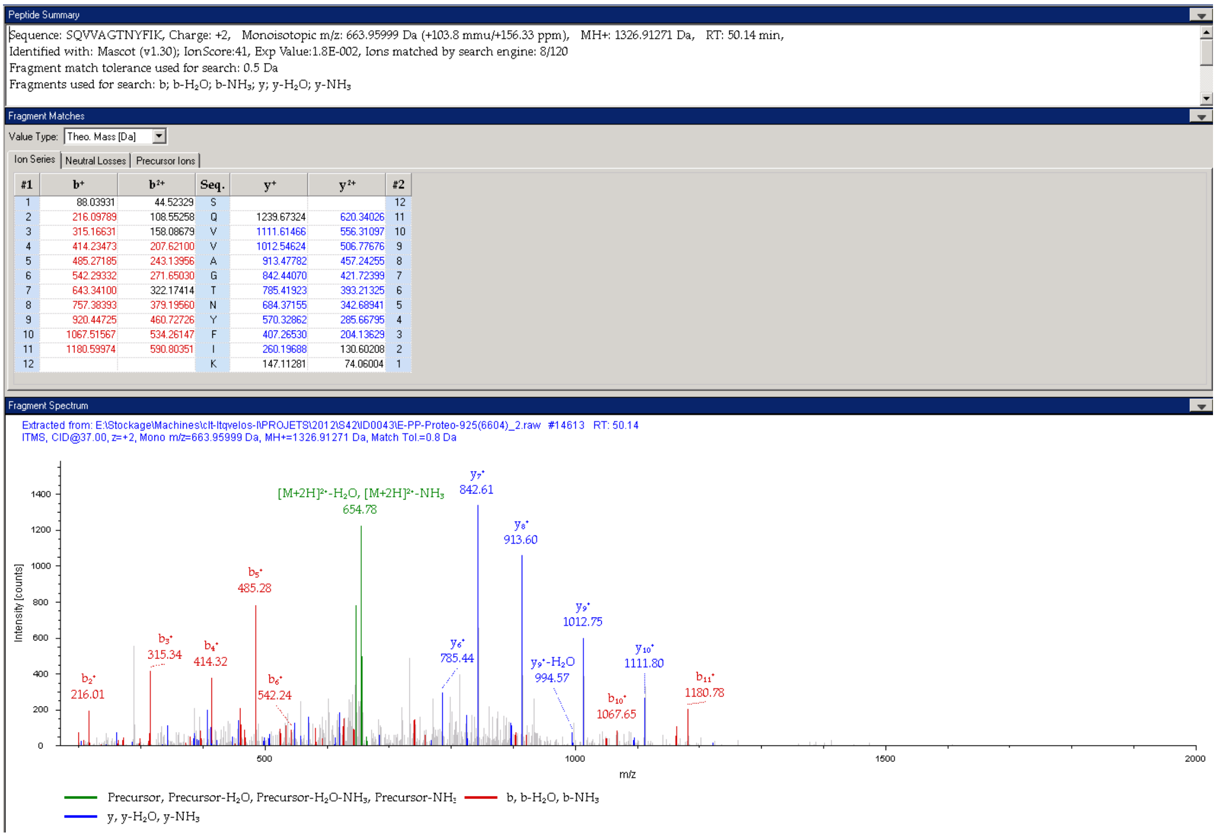
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	143.08152	72.04440	A	1323.58524	662.29626	12
3	258.10847	129.55787	D	1252.54812	626.77770	11
4	373.13542	187.07135	D	1137.52117	569.26422	10
5	474.18310	237.59519	T	1022.49422	511.75075	9
6	660.26242	330.63485	W	921.44654	461.22691	8
7	789.30502	395.15615	E	735.36722	368.18725	7
8	886.35779	443.68253	P	606.32462	303.66595	6
9	1033.42621	517.21674	F	509.27185	255.13956	5
10	1104.46333	552.73530	A	362.20343	181.60535	4
11	1191.49536	596.25132	S	291.16631	146.08679	3
12	1248.51683	624.76205	G	204.13428	102.57078	2
13			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_2.raw #15326 RT: 52.75
ITMS, CID@37.00, z=+2, Mono m/z=697.83999 Da, MH+=1394.67271 Da, Match Tol.=0.8 Da

Protein references (1):

- Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]



Peptide Summary

Sequence: SQVVAGTNYFIK, Charge: +2, Monoisotopic m/z: 663.95999 Da (+103.8 mmu/+156.33 ppm), MH+: 1326.91271 Da, RT: 50.14 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.8E-002, Ions matched by search engine: 8/120
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

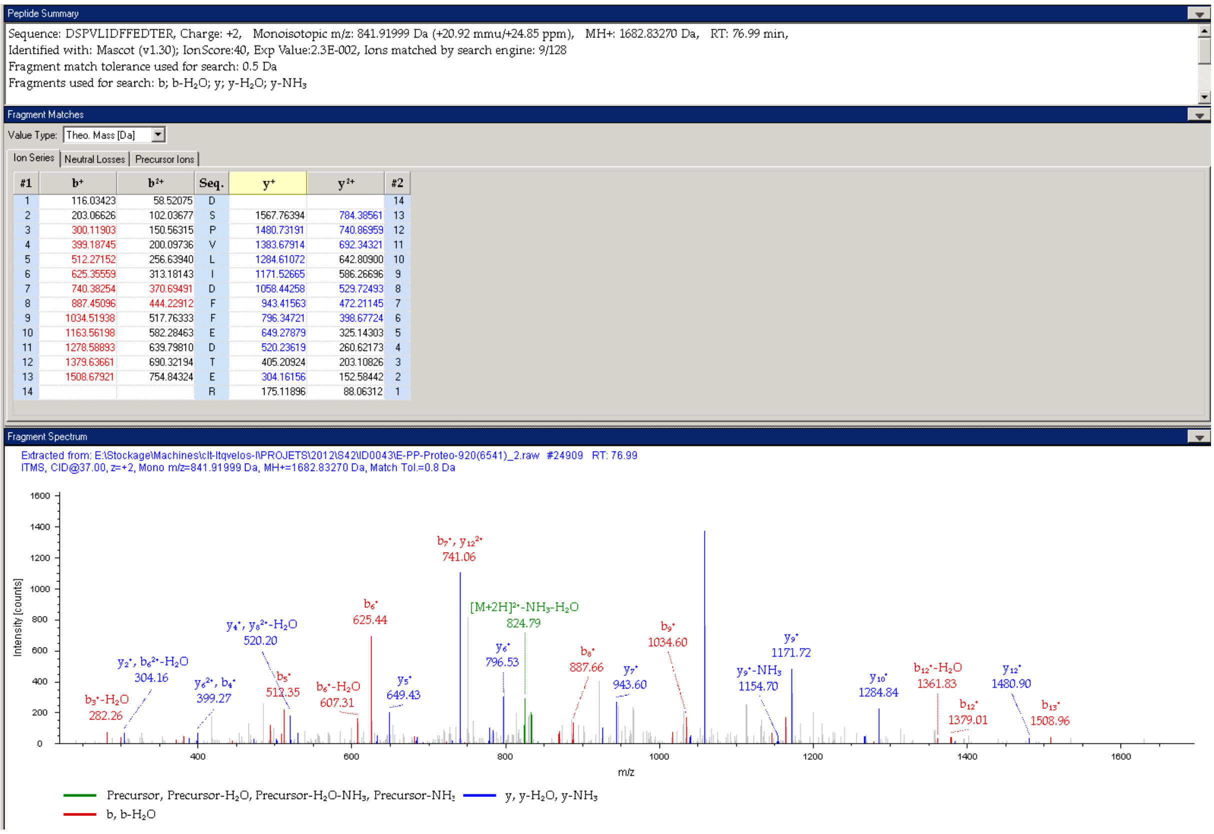
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			12
2	216.09789	108.55258	Q	1239.67324	620.34026	11
3	315.16631	158.08679	V	1111.61466	556.31097	10
4	414.23473	207.62100	V	1012.54624	506.77676	9
5	485.27185	243.13956	A	913.47782	457.24255	8
6	542.29332	271.65030	G	842.44070	421.72399	7
7	643.34100	322.17414	T	785.41923	393.21325	6
8	757.38393	379.19560	N	684.37155	342.68941	5
9	920.44725	460.72726	Y	570.32862	285.66795	4
10	1067.51567	534.26147	F	407.26530	204.13629	3
11	1180.59974	590.80351	I	260.19688	130.60208	2
12			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #14613 RT: 50.14
ITMS, CID@37.00, z=+2, Mono m/z=663.95999 Da, MH+=1326.91271 Da, Match Tol.=0.8 Da

Protein references (1):

- Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1 - [HRG_HUMAN]



Peptide Summary

Sequence: DSPVLIDFFEDTER, Charge: +2, Monoisotopic m/z: 841.91999 Da (+20.92 mmu/+24.85 ppm), MH+: 1682.83270 Da, RT: 76.99 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.3E-002, Ions matched by search engine: 9/128
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			14
2	203.06626	102.03677	S	1567.76394	784.38561	13
3	300.11903	150.56315	P	1480.73191	740.86959	12
4	399.18745	200.09736	V	1383.67914	692.34321	11
5	512.27152	256.63940	L	1284.61072	642.80900	10
6	625.35559	313.18143	I	1171.52665	586.26696	9
7	740.38254	370.69491	D	1058.44258	529.72493	8
8	887.45096	444.22912	F	943.41563	472.21145	7
9	1034.51938	517.76333	F	796.34721	398.67724	6
10	1163.56198	582.28463	E	649.27879	325.14303	5
11	1278.58893	639.79810	D	520.23619	260.62173	4
12	1379.63661	690.32194	T	405.20924	203.10826	3
13	1508.67921	754.84324	E	304.16156	152.58442	2
14			R	175.11896	88.06312	1

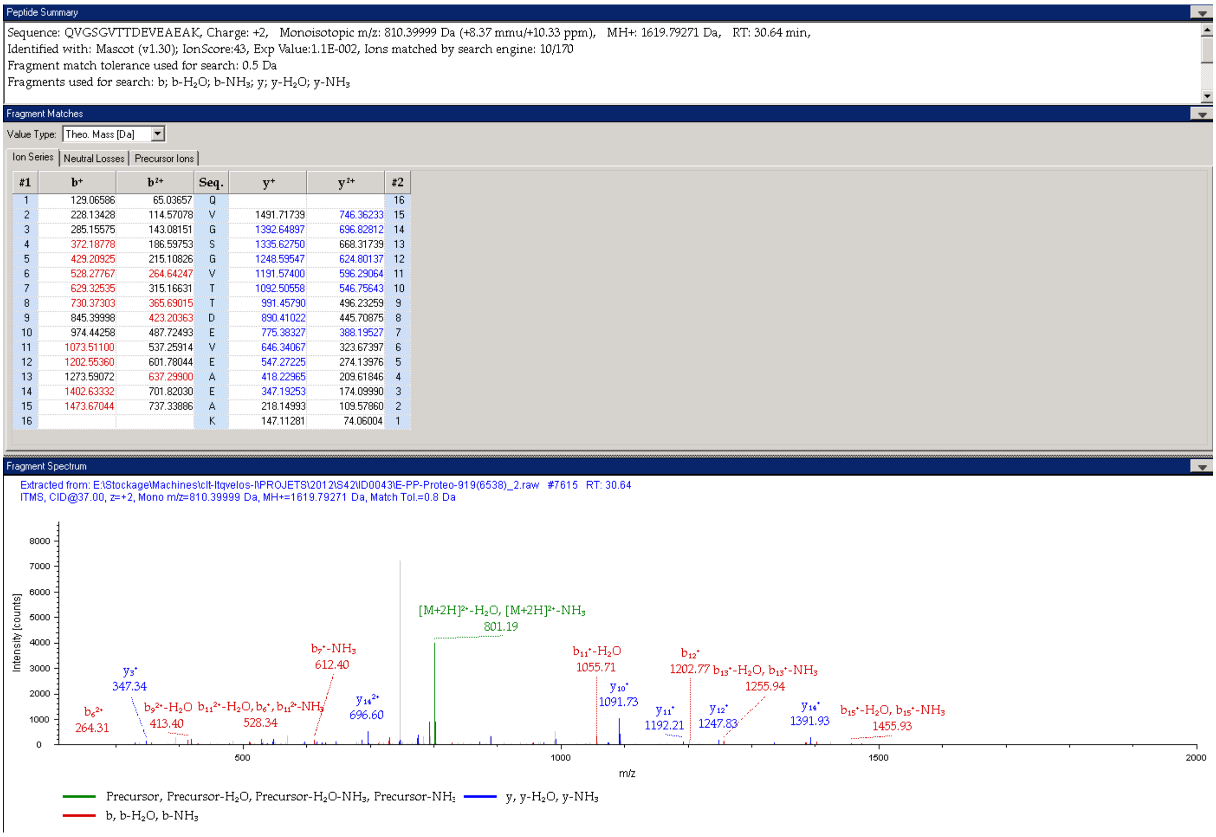
Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #24909 RT: 76.99
ITMS, CID@37.00, z=+2, Mono m/z=841.91999 Da, MH+=1682.83270 Da, Match Tol.=0.8 Da

Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3 — y, y-H_2O, y-NH_3
b, b-H_2O

Protein references (1):

- Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1 - [MUCB_HUMAN]



Sequence: QVGSGVTTDEVEAEAK, Charge: +2, Monoisotopic m/z: 810.39999 Da (+8.37 mmu/+10.33 ppm), MH+: 1619.79271 Da, RT: 30.64 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.1E-002, Ions matched by search engine: 10/170
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

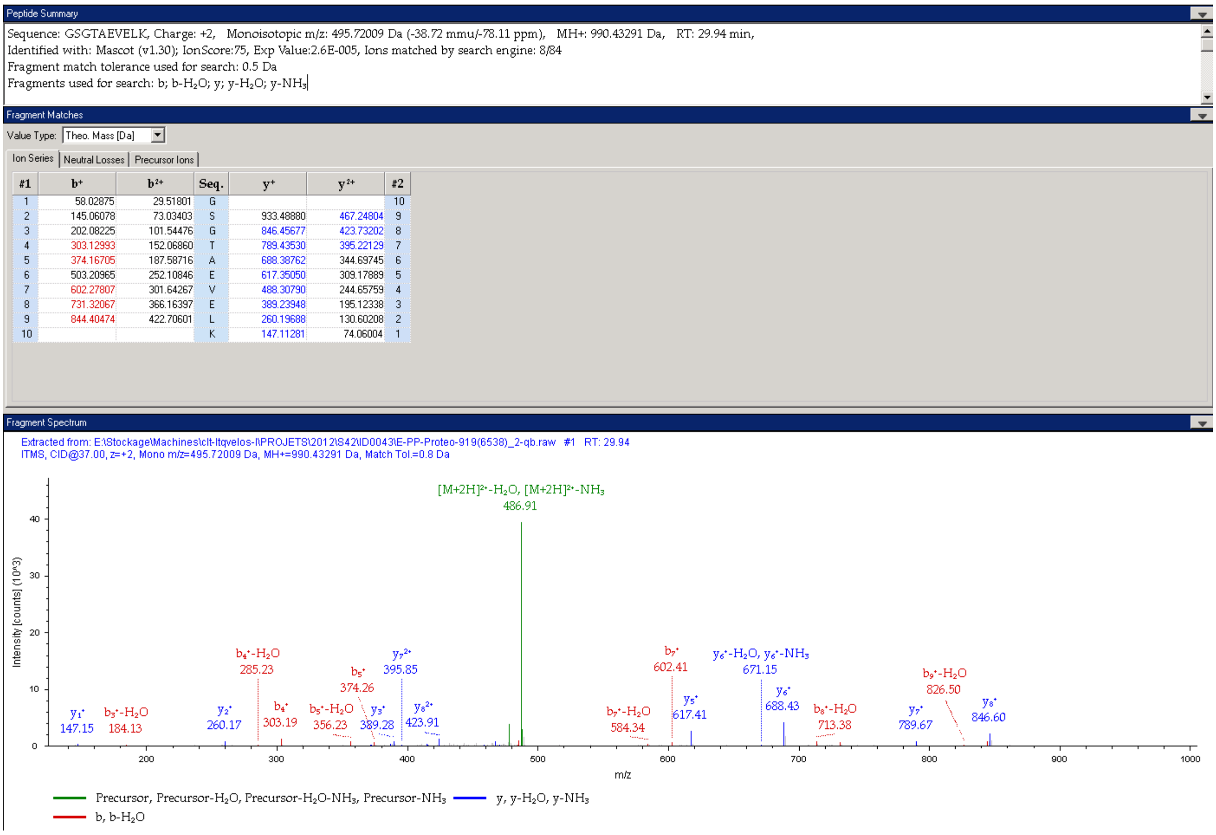
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			16
2	228.13428	114.57078	V	1491.71739	746.36233	15
3	285.15575	143.08151	G	1392.64897	696.82812	14
4	372.18778	186.59753	S	1335.62750	668.31739	13
5	429.20925	215.10826	G	1248.59547	624.80137	12
6	528.27767	264.64247	V	1191.57400	596.29064	11
7	629.32535	315.16631	T	1092.50558	546.75643	10
8	730.37303	365.69015	T	991.45790	496.23259	9
9	845.39998	423.20363	D	890.41022	445.70875	8
10	974.44258	487.72493	E	775.38327	388.19527	7
11	1073.51100	537.25914	V	646.34067	323.67397	6
12	1202.55360	601.78044	E	547.27225	274.13976	5
13	1273.59072	637.29900	A	418.22965	209.61846	4
14	1402.63332	701.82030	E	347.19253	174.09990	3
15	1473.67044	737.33886	A	218.14993	109.57860	2
16			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #7615 RT: 30.64
ITMS, CID@37.00, z=+2, Mono m/z=810.39999 Da, MH+=1619.79271 Da, Match Tol.=0.8 Da

Protein reference :

2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=3



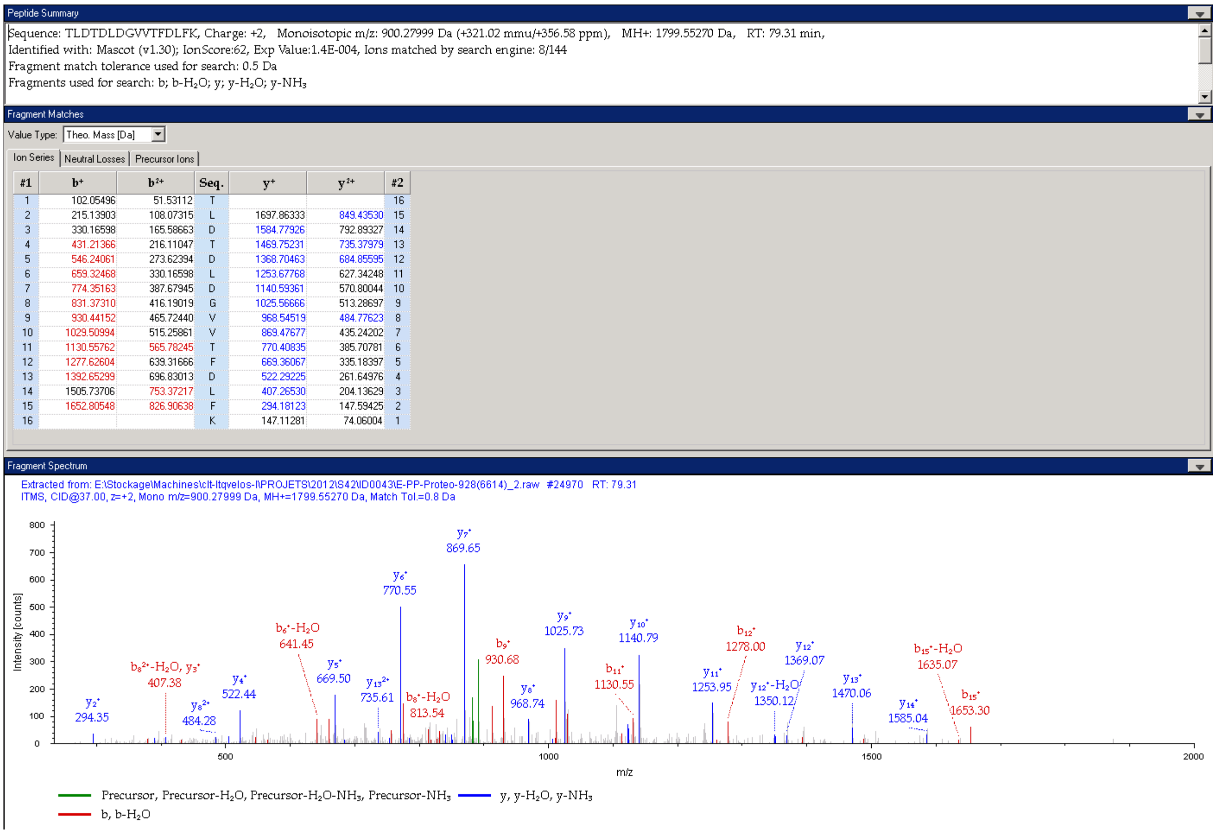
Sequence: GSGTAEVELK, Charge: +2, Monoisotopic m/z: 495.72009 Da (-38.72 mmu/-78.11 ppm), MH+: 990.43291 Da, RT: 29.94 min,
Identified with: Mascot (v1.30); IonScore:75, Exp Value:2.6E-005, Ions matched by search engine: 8/84
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			10
2	145.06078	73.03403	S	933.48880	467.24804	9
3	202.08225	101.54476	G	846.45677	423.73202	8
4	303.12993	152.06860	T	789.43530	395.22129	7
5	374.16705	187.58716	A	688.38762	344.69745	6
6	503.20965	252.10846	E	617.35050	309.17889	5
7	602.27807	301.64267	V	488.30790	244.65759	4
8	731.32067	366.16397	E	389.23948	195.12338	3
9	844.40474	422.70601	L	260.19688	130.60208	2
10			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2-qb.raw #1 RT: 29.94
ITMS, CID@37.00, z=+2, Mono m/z=495.72009 Da, MH+=990.43291 Da, Match Tol.=0.8 Da

Protein references (1):
- Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]



Sequence: TLDTDLDGVVTFDLFK, Charge: +2, Monoisotopic m/z: 900.27999 Da (+321.02 mmu/+356.58 ppm), MH+: 1799.55270 Da, RT: 79.31 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.4E-004, Ions matched by search engine: 8/144
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

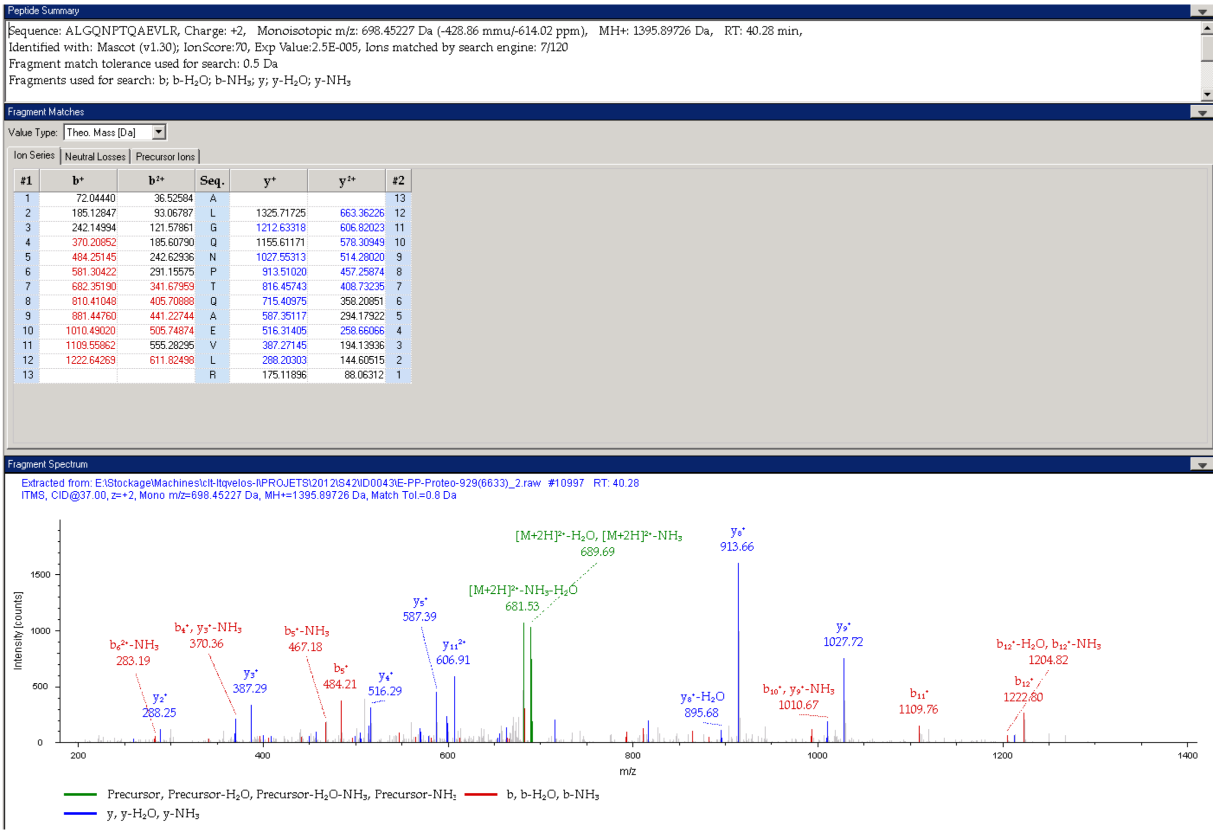
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			16
2	215.13903	108.07315	L	1697.86333	849.43530	15
3	330.16598	165.58663	D	1584.77926	792.89327	14
4	431.21366	216.11047	T	1469.75231	735.37979	13
5	546.24061	273.62394	D	1368.70463	684.85595	12
6	659.32468	330.16598	L	1253.67768	627.34248	11
7	774.35163	387.67945	D	1140.59361	570.80044	10
8	831.37310	416.19019	G	1025.56666	513.28697	9
9	930.44152	465.72440	V	968.54519	484.77623	8
10	1029.50994	515.25861	V	869.47677	435.24202	7
11	1130.55762	565.78245	T	770.40835	385.70781	6
12	1277.62604	639.31666	F	669.36067	335.18397	5
13	1392.65299	696.83013	D	522.29225	261.64976	4
14	1505.73706	753.37217	L	407.26530	204.13629	3
15	1652.80548	826.90638	F	294.18123	147.59425	2
16			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_2.raw #24970 RT: 79.31
ITMS, CID@37.00, z=+2, Mono m/z=900.27999 Da, MH+=1799.55270 Da, Match Tol.=0.8 Da

Protein references (1):

- Myosin light chain 3 OS=Homo sapiens GN=MYL3 PE=1 SV=3 - [MYL3_HUMAN]



Sequence: ALGQNPTQAEVLR, Charge: +2, Monoisotopic m/z: 698.45227 Da (-428.86 mmu/-614.02 ppm), MH+: 1395.89726 Da, RT: 40.28 min,
Identified with: Mascot (v1.30); IonScore:70, Exp Value:2.5E-005, Ions matched by search engine: 7/120
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

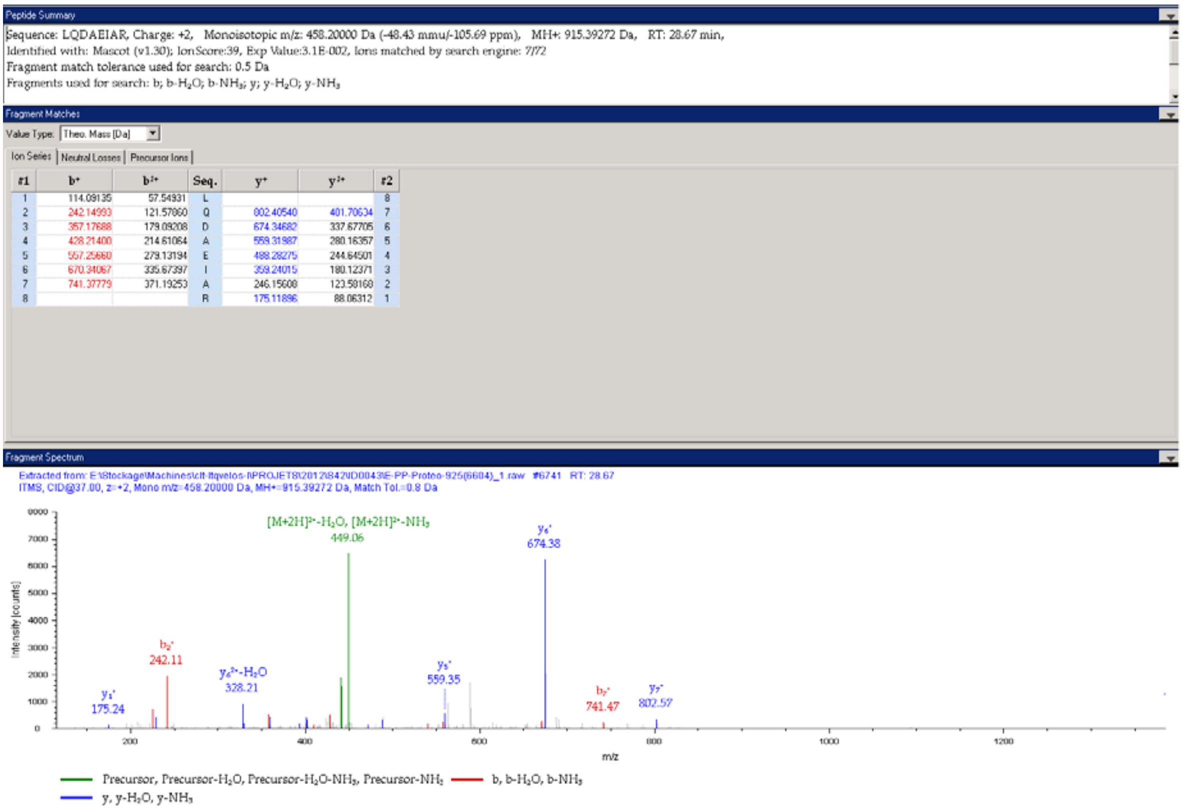
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	185.12847	93.06787	L	1325.71725	663.36226	12
3	242.14994	121.57861	G	1212.63318	606.82023	11
4	370.20852	185.60790	Q	1155.61171	578.30949	10
5	484.25145	242.62936	N	1027.55313	514.28020	9
6	581.30422	291.15575	P	913.51020	457.25874	8
7	682.35190	341.67959	T	816.45743	408.73235	7
8	810.41048	405.70888	Q	715.40975	358.20851	6
9	881.44760	441.22744	A	587.35117	294.17922	5
10	1010.49020	505.74874	E	516.31405	258.66066	4
11	1109.55862	555.28295	V	387.27145	194.13936	3
12	1222.64269	611.82498	L	288.20303	144.60515	2
13			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #10997 RT: 40.28
ITMS, CID@37.00, z=+2, Mono m/z=698.45227 Da, MH+=1395.89726 Da, Match Tol.=0.8 Da

🟩 Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
🟥 b, $b-H_2O$, $b-NH_3$
🟦 y, $y-H_2O$, $y-NH_3$

Protein references (1):
- Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]



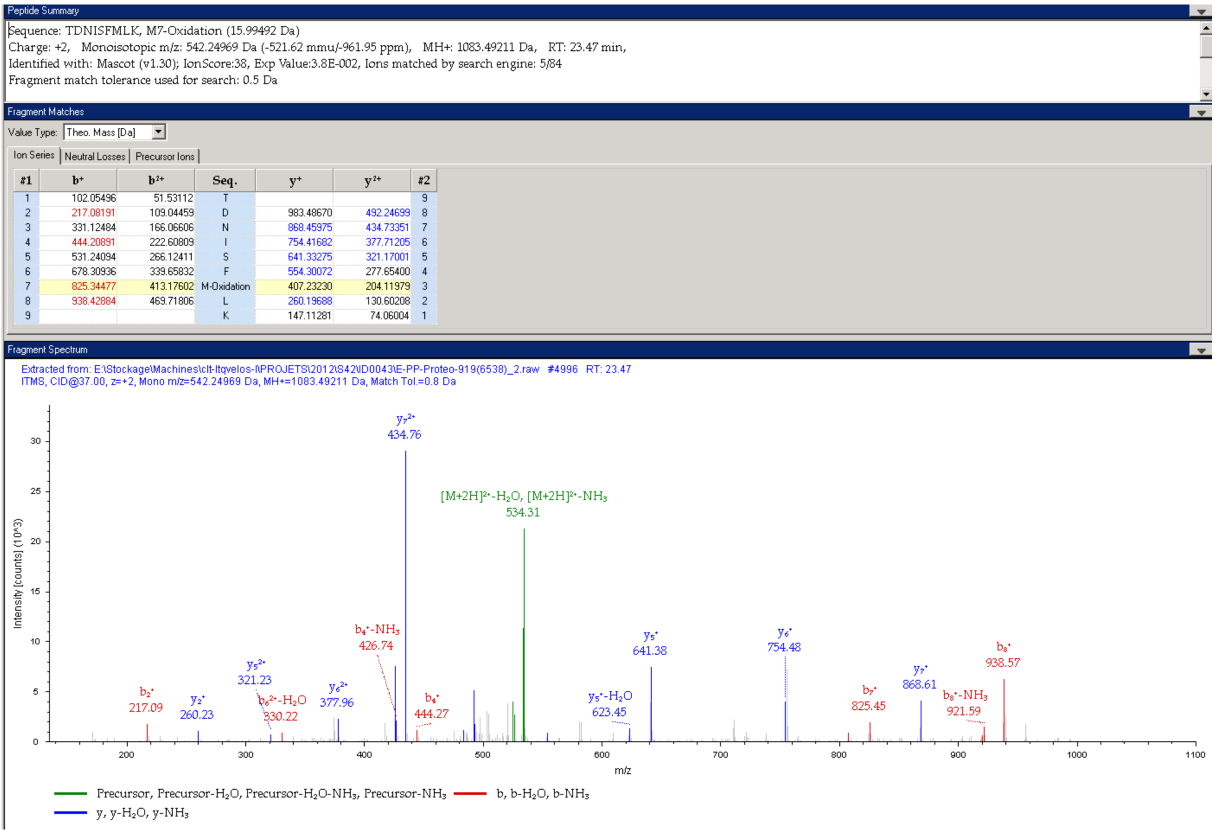
Sequence: LQDAEIAR, Charge: +2, Monoisotopic m/z: 458.20000 Da (-48.43 mmu/-105.69 ppm), MH+: 915.39272 Da, RT: 28.67 min,
Identified with: Mascot (v1.30); IonScore:39, Exp Value:3.1E-002, Ions matched by search engine: 7/72
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			8
2	242.14993	121.57860	Q	802.40540	401.70634	7
3	357.17688	179.09208	D	674.34682	337.67705	6
4	428.21400	214.61064	A	559.31987	280.16357	5
5	557.25660	279.13194	E	488.28275	244.64501	4
6	670.34067	335.67397	I	359.24015	180.12371	3
7	741.37779	371.19253	A	246.15608	123.58168	2
8			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\842\D0043\E-PP-Proteo-925(6604)_1.raw #6741 RT: 28.67
ITMS, CID@37.00, z=+2, Mono m/z=458.20000 Da, MH+=915.39272 Da, Match Tol.=0.8 Da

Protein references (1):
- Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2 - [JAK1_HUMAN]



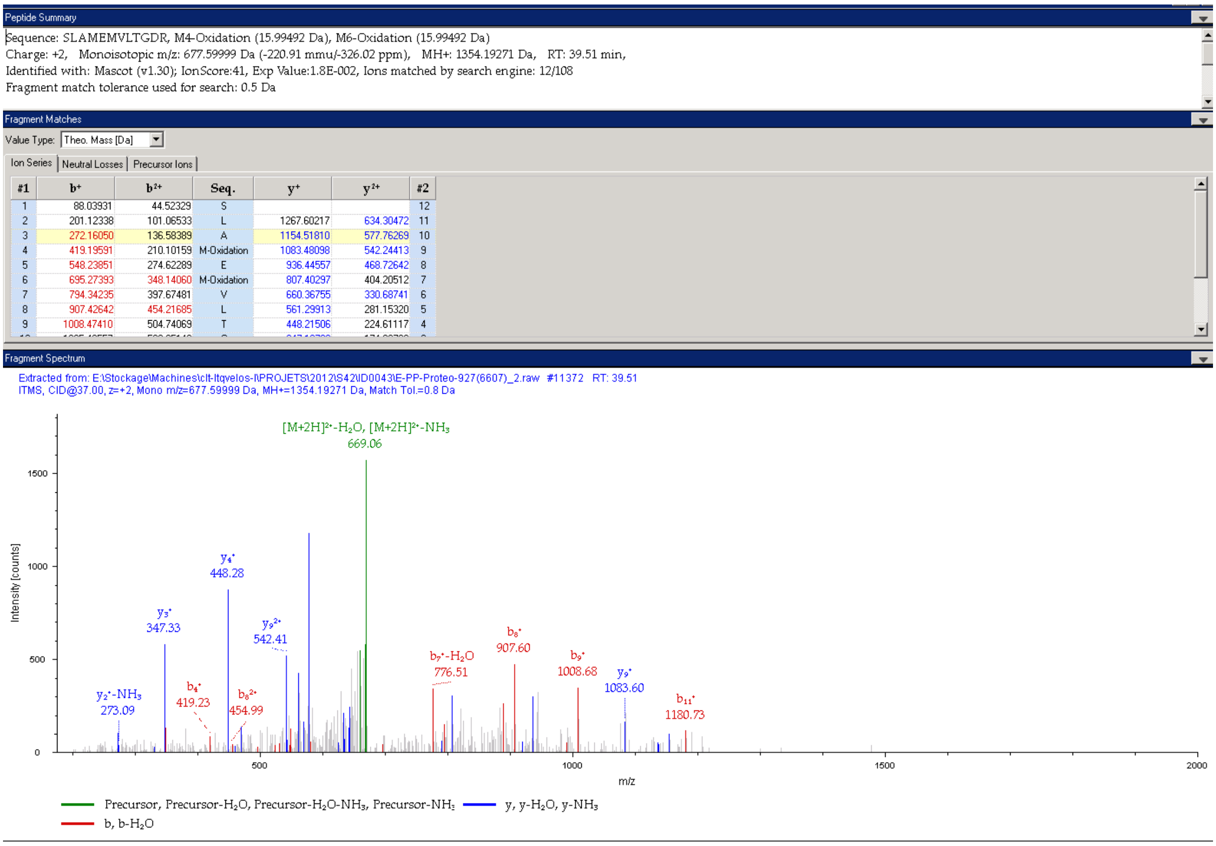
Sequence: TDNISFMLK, M7-Oxidation (15.99492 Da)
Charge: +2,   Monoisotopic m/z: 542.24969 Da (-521.62 mmu/-961.95 ppm),   MH+: 1083.49211 Da,   RT: 23.47 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.8E-002, Ions matched by search engine: 5/84
Fragment match tolerance used for search: 0.5 Da

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			9
2	217.08191	109.04459	D	983.48670	492.24699	8
3	331.12484	166.06606	N	868.45975	434.73351	7
4	444.20891	222.60809	I	754.41682	377.71205	6
5	531.24094	266.12411	S	641.33275	321.17001	5
6	678.30936	339.65832	F	554.30072	277.65400	4
7	825.34477	413.17602	M-Oxidation	407.23230	204.11979	3
8	938.42884	469.71806	L	260.19688	130.60208	2
9			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw   #4996   RT: 23.47
ITMS, CID@37.00, z=+2, Mono m/z=542.24969 Da, MH+=1083.49211 Da, Match Tol.=0.8 Da

Protein references (1):
- Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]



Sequence: SLAMEMVLTGDR, M4-Oxidation (15.99492 Da), M6-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 677.59999 Da (-220.91 mmu/-326.02 ppm), MH+: 1354.19271 Da, RT: 39.51 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.8E-002, Ions matched by search engine: 12/108
Fragment match tolerance used for search: 0.5 Da

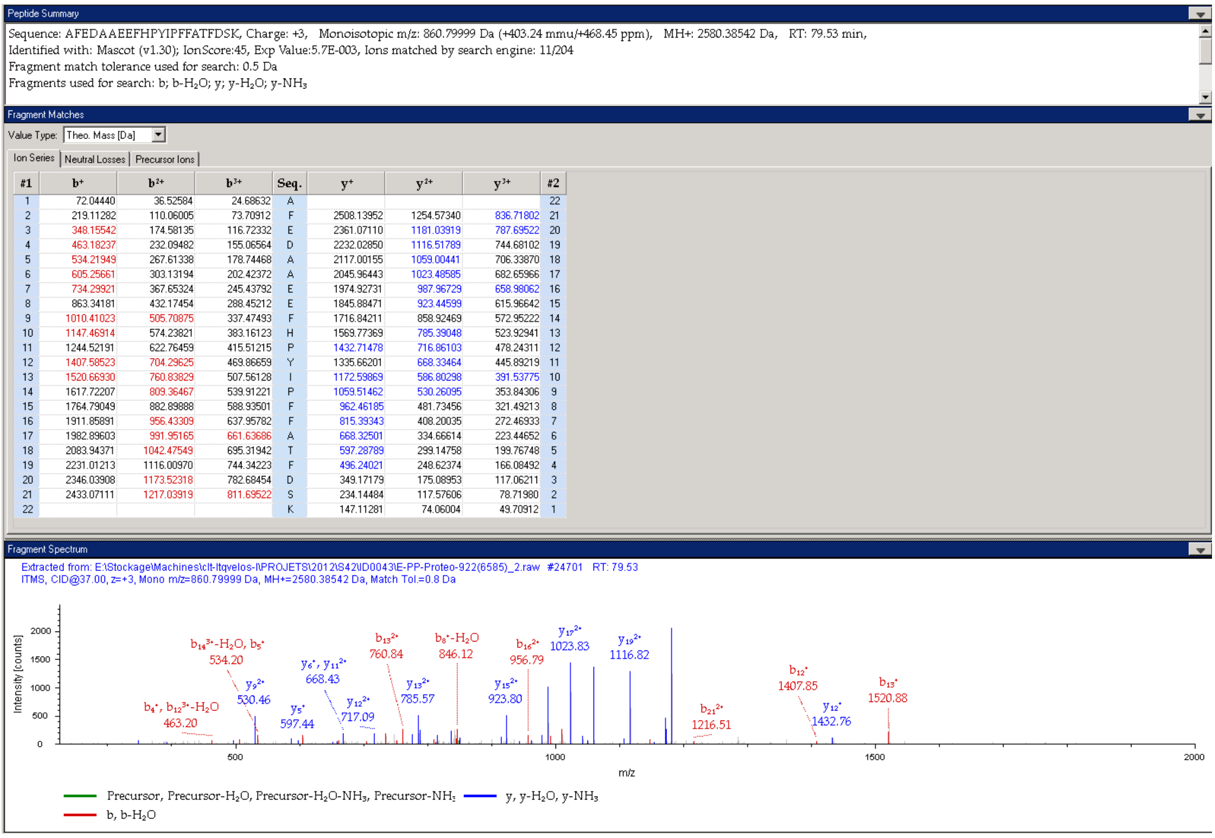
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			12
2	201.12338	101.06533	L	1267.60217	634.30472	11
3	272.16050	136.58389	A	1154.51810	577.76269	10
4	419.19591	210.10159	M-Oxidation	1083.48098	542.24413	9
5	548.23851	274.62289	E	936.44557	468.72642	8
6	695.27393	348.14060	M-Oxidation	807.40297	404.20512	7
7	794.34235	397.67481	V	660.36755	330.68741	6
8	907.42642	454.21685	L	561.29913	281.15320	5
9	1008.47410	504.74069	T	448.21506	224.61117	4

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #11372 RT: 39.51
ITMS, CID@37.00, z=+2, Mono m/z=677.59999 Da, MH+=1354.19271 Da, Match Tol.=0.8 Da

Protein references (1):

- Calsequestrin-1 OS=Homo sapiens GN=CASQ1 PE=1 SV=3 - [CASQ1_HUMAN]



Peptide Summary

Sequence: AFEDAAEEFHPYIPFFATFDSK, Charge: +3, Monoisotopic m/z: 860.79999 Da (+403.24 mmu/+468.45 ppm), MH+: 2580.38542 Da, RT: 79.53 min,
Identified with: Mascot (v1.30); IonScore:45, Exp Value:5.7E-003, Ions matched by search engine: 11/204
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

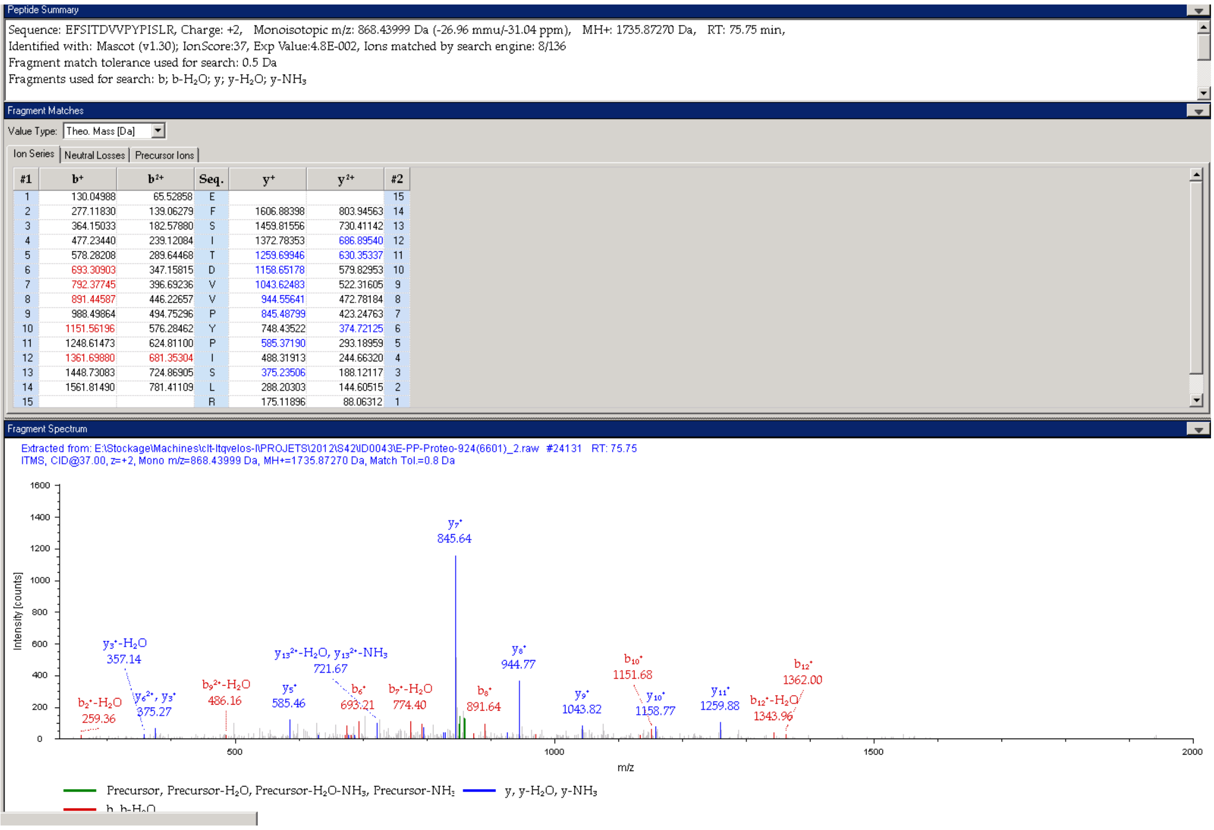
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	72.04440	36.52584	24.68632	A				22
2	219.11282	110.06005	73.70912	F	2508.13952	1254.57340	836.71802	21
3	348.15542	174.58135	116.72332	E	2361.07110	1181.03919	787.69522	20
4	463.18237	232.09482	155.06564	D	2232.02850	1116.51789	744.68102	19
5	534.21949	267.61338	178.74468	A	2117.00155	1059.00441	706.33870	18
6	605.25661	303.13194	202.42372	A	2045.96443	1023.48585	682.65966	17
7	734.29921	367.65324	245.43792	E	1974.92731	987.96729	658.98062	16
8	863.34181	432.17454	288.45212	E	1845.88471	923.44599	615.96642	15
9	1010.41023	505.70875	337.47493	F	1716.84211	858.92469	572.95222	14
10	1147.46914	574.23821	383.16123	H	1569.77369	785.39048	523.92941	13
11	1244.52191	622.76459	415.51215	P	1432.71478	716.86103	478.24311	12
12	1407.58523	704.29625	469.86659	Y	1335.66201	668.33464	445.89219	11
13	1520.66930	760.83829	507.56128	I	1172.59869	586.80298	391.53775	10
14	1617.72207	809.36467	539.91221	P	1059.51462	530.26095	353.84306	9
15	1764.79049	882.89888	588.93501	F	962.46185	481.73456	321.49213	8
16	1911.85891	956.43309	637.95782	F	815.39343	408.20035	272.46933	7
17	1982.89603	991.95165	661.63686	A	668.32501	334.66614	223.44652	6
18	2083.94371	1042.47549	695.31942	T	597.28789	299.14758	199.76748	5
19	2231.01213	1116.00970	744.34223	F	496.24021	248.62374	166.08492	4
20	2346.03908	1173.52318	782.68454	D	349.17179	175.08953	117.06211	3
21	2433.07111	1217.03919	811.69522	S	234.14484	117.57606	78.71980	2
22				K	147.11281	74.06004	49.70912	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_2.raw #24701 RT: 79.53
ITMS, CID@37.00, z=+3, Mono m/z=860.79999 Da, MH+=2580.38542 Da, Match Tol.=0.8 Da

Protein references (1):

- Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]



Peptide Summary

Sequence: EFSITDVVPYPISLR, Charge: +2, Monoisotopic m/z: 868.43999 Da (-26.96 mmu/-31.04 ppm), MH+: 1735.87270 Da, RT: 75.75 min,
Identified with: Mascot (v1.30); IonScore:37, Exp Value:4.8E-002, Ions matched by search engine: 8/136
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

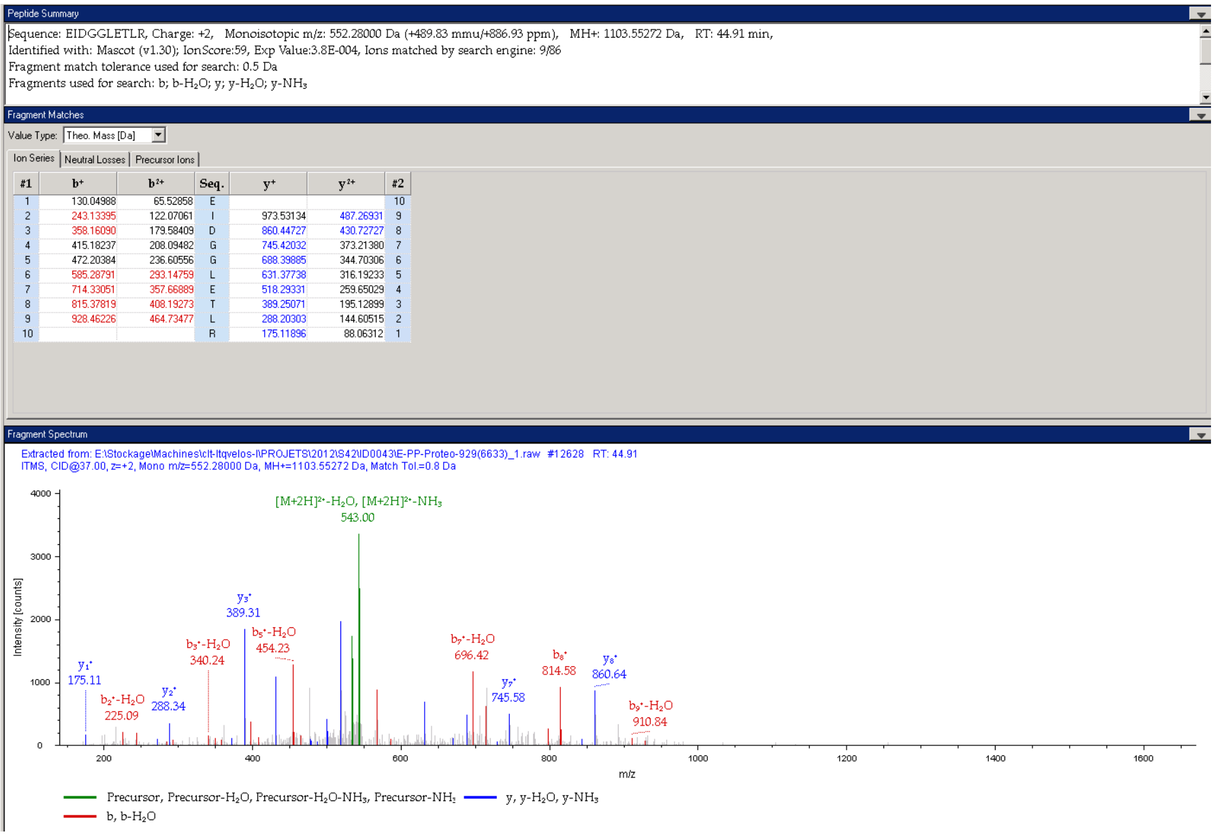
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			15
2	277.11830	139.06279	F	1606.88398	803.94563	14
3	364.15033	182.57880	S	1459.81556	730.41142	13
4	477.23440	239.12084	I	1372.78353	686.89540	12
5	578.28208	289.64468	T	1259.69946	630.35337	11
6	693.30903	347.15815	D	1158.65178	579.82953	10
7	792.37745	396.69236	V	1043.62483	522.31605	9
8	891.44587	446.22657	V	944.55641	472.78184	8
9	988.49864	494.75296	P	845.48799	423.24763	7
10	1151.56196	576.28462	Y	748.43522	374.72125	6
11	1248.61473	624.81100	P	585.37190	293.18959	5
12	1361.69880	681.35304	I	488.31913	244.66320	4
13	1448.73083	724.86905	S	375.23506	188.12117	3
14	1561.81490	781.41109	L	288.20303	144.60515	2
15			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #24131 RT: 75.75
ITMS, CID@37.00, z=+2, Mono m/z=868.43999 Da, MH+=1735.87270 Da, Match Tol.=0.8 Da

Protein references (1):
- Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 - [ETFB_HUMAN]



Peptide Summary

Sequence: EIDGGLETLR, Charge: +2, Monoisotopic m/z: 552.28000 Da (+489.83 mmu/+886.93 ppm), MH+: 1103.55272 Da, RT: 44.91 min,
Identified with: Mascot (v1.30); IonScore:59, Exp Value:3.8E-004, Ions matched by search engine: 9/86
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

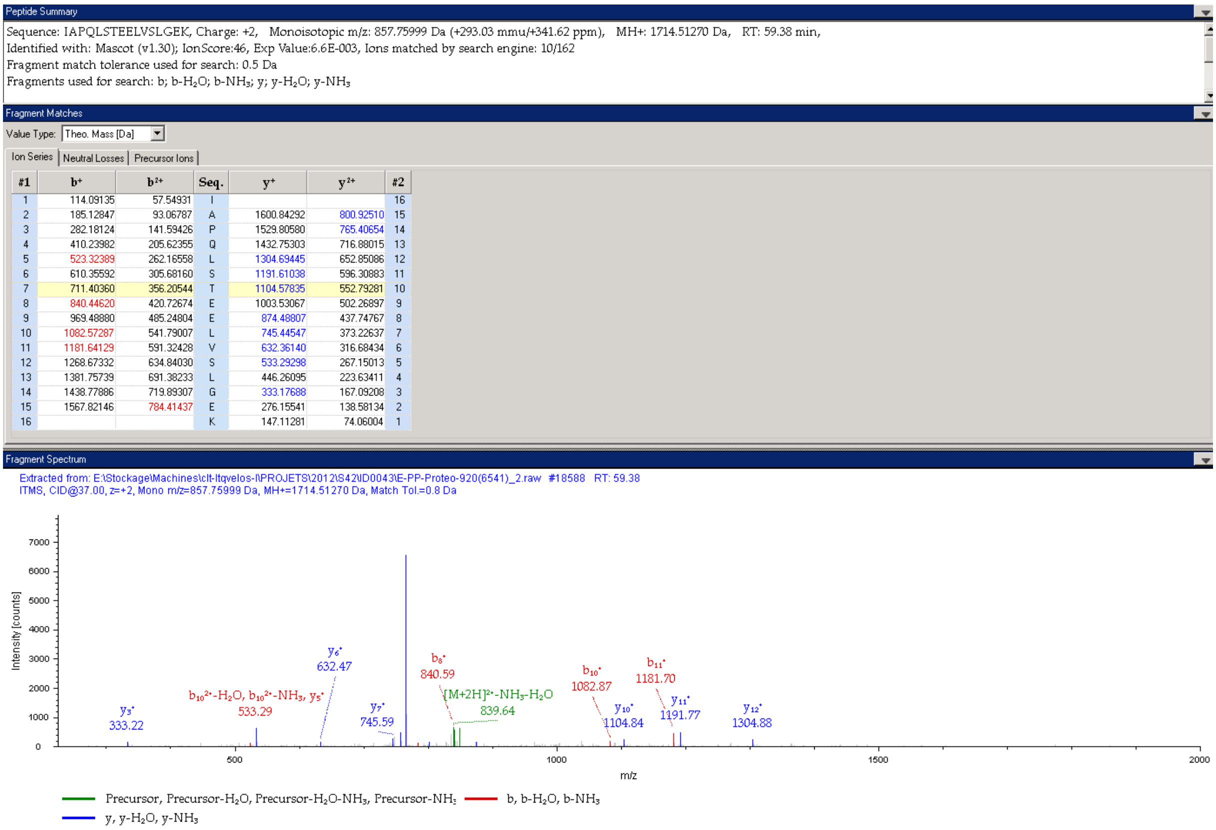
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			10
2	243.13395	122.07061	I	973.53134	487.26931	9
3	358.16090	179.58409	D	860.44727	430.72727	8
4	415.18237	208.09482	G	745.42032	373.21380	7
5	472.20384	236.60556	G	688.39885	344.70306	6
6	585.28791	293.14759	L	631.37738	316.19233	5
7	714.33051	357.66889	E	518.29331	259.65029	4
8	815.37819	408.19273	T	389.25071	195.12899	3
9	928.46226	464.73477	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_1.raw #12628 RT: 44.91
ITMS, CID@37.00, z=+2, Mono m/z=552.28000 Da, MH+=1103.55272 Da, Match Tol.=0.8 Da

Protein references (1):
- Afamin OS=Homo sapiens GN=AFM PE=1 SV=1 - [AFAM_HUMAN]



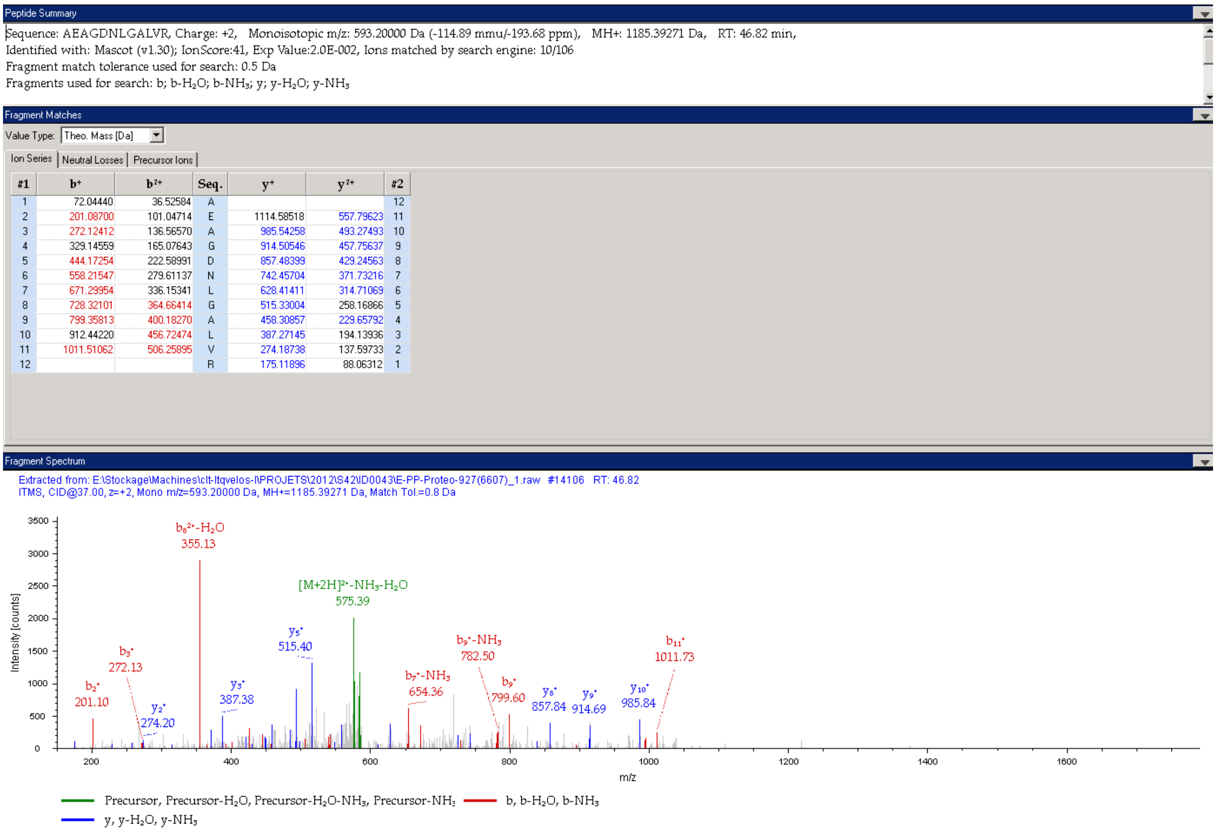
Sequence: IAPQLSTEELVSLGEK, Charge: +2, Monoisotopic m/z: 857.75999 Da (+293.03 mmu/+341.62 ppm), MH+: 1714.51270 Da, RT: 59.38 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:6.6E-003, Ions matched by search engine: 10/162
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			16
2	185.12847	93.06787	A	1600.84292	800.92510	15
3	282.18124	141.59426	P	1529.80580	765.40654	14
4	410.23982	205.62355	Q	1432.75303	716.88015	13
5	523.32389	262.16558	L	1304.69445	652.85086	12
6	610.35592	305.68160	S	1191.61038	596.30883	11
7	711.40360	356.20544	T	1104.57835	552.79281	10
8	840.44620	420.72674	E	1003.53067	502.26897	9
9	969.48880	485.24804	E	874.48807	437.74767	8
10	1082.57287	541.79007	L	745.44547	373.22637	7
11	1181.64129	591.32428	V	632.36140	316.68434	6
12	1268.67332	634.84030	S	533.29298	267.15013	5
13	1381.75739	691.38233	L	446.26095	223.63411	4
14	1438.77886	719.89307	G	333.17688	167.09208	3
15	1567.82146	784.41437	E	276.15541	138.58134	2
16			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #18588 RT: 59.38
ITMS, CID@37.00, z=+2, Mono m/z=857.75999 Da, MH+=1714.51270 Da, Match Tol.=0.8 Da

Protein references (1):

- Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]



Sequence: AEAGDNLGALVR, Charge: +2, Monoisotopic m/z: 593.20000 Da (-114.89 mmu/-193.68 ppm), MH+: 1185.39271 Da, RT: 46.82 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 10/106
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

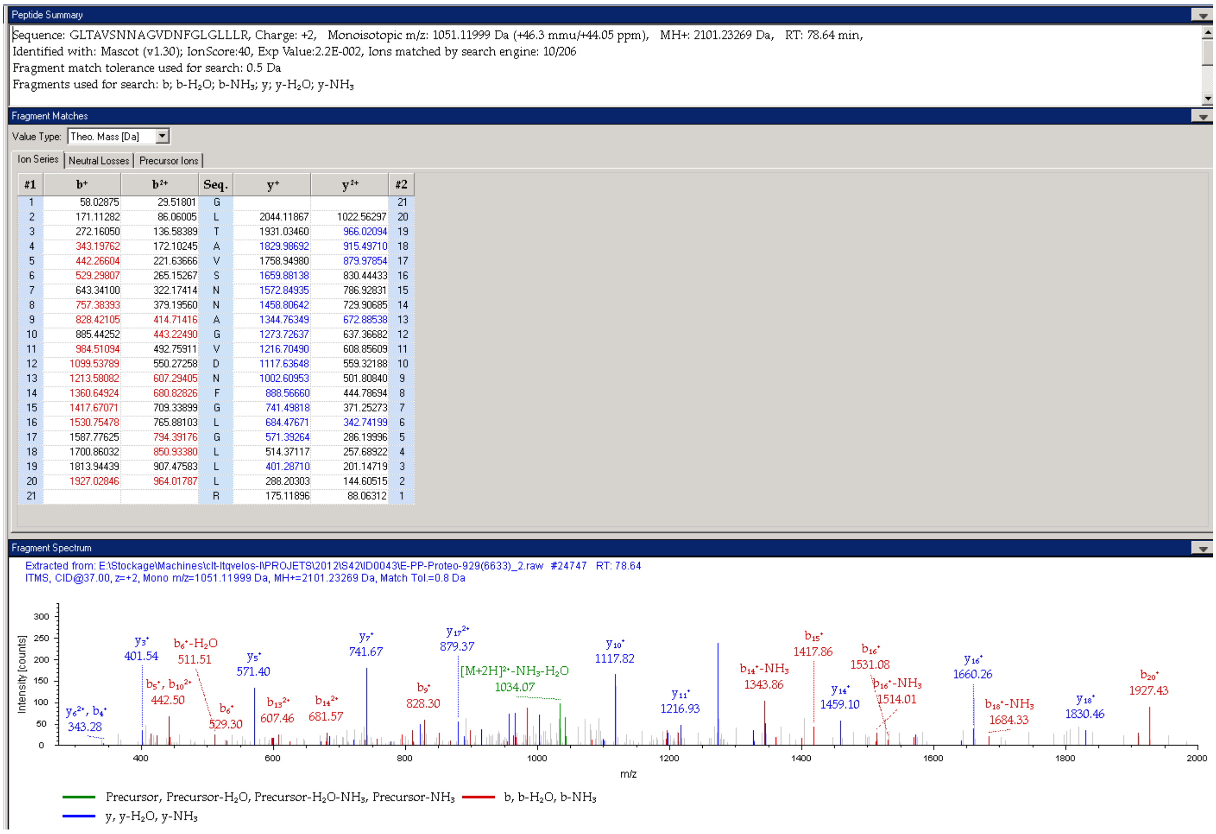
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			12
2	201.08700	101.04714	E	1114.58518	557.79623	11
3	272.12412	136.56570	A	985.54258	493.27493	10
4	329.14559	165.07643	G	914.50546	457.75637	9
5	444.17254	222.58991	D	857.48399	429.24563	8
6	558.21547	279.61137	N	742.45704	371.73216	7
7	671.29954	336.15341	L	628.41411	314.71069	6
8	728.32101	364.66414	G	515.33004	258.16866	5
9	799.35813	400.18270	A	458.30857	229.65792	4
10	912.44220	456.72474	L	387.27145	194.13936	3
11	1011.51062	506.25895	V	274.18738	137.59733	2
12			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #14106 RT: 46.82
ITMS, CID@37.00, z=+2, Mono m/z=593.20000 Da, MH+=1185.39271 Da, Match Tol.=0.8 Da

Protein references (1):

- Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 - [SCOT1_HUMAN]



Peptide Summary

Sequence: GLTAVSNNAGVDNFGLGLLLR, Charge: +2, Monoisotopic m/z: 1051.11999 Da (+46.3 mmu/+44.05 ppm), MH+: 2101.23269 Da, RT: 78.64 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.2E-002, Ions matched by search engine: 10/206
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

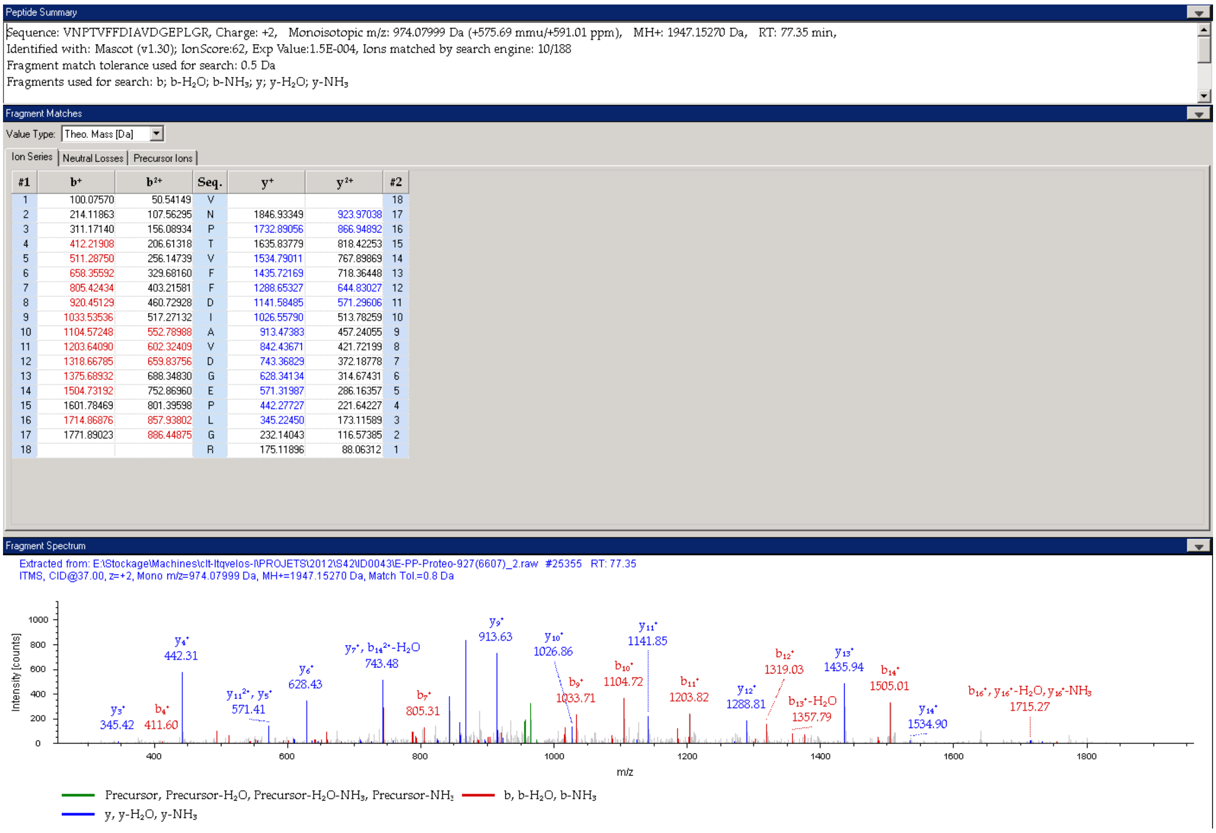
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			21
2	171.11282	86.06005	L	2044.11867	1022.56297	20
3	272.16050	136.58389	T	1931.03460	966.02094	19
4	343.19762	172.10245	A	1829.98692	915.49710	18
5	442.26604	221.63666	V	1758.94980	879.97854	17
6	529.29807	265.15267	S	1659.88138	830.44433	16
7	643.34100	322.17414	N	1572.84935	786.92831	15
8	757.38393	379.19560	N	1458.80642	729.90685	14
9	828.42105	414.71416	A	1344.76349	672.88538	13
10	885.44252	443.22490	G	1273.72637	637.36682	12
11	984.51094	492.75911	V	1216.70490	608.85609	11
12	1099.53789	550.27258	D	1117.63648	559.32188	10
13	1213.58082	607.29405	N	1002.60953	501.80840	9
14	1360.64924	680.82826	F	888.56660	444.78694	8
15	1417.67071	709.33899	G	741.49818	371.25273	7
16	1530.75478	765.88103	L	684.47671	342.74199	6
17	1587.77625	794.39176	G	571.39264	286.19996	5
18	1700.86032	850.93380	L	514.37117	257.68922	4
19	1813.94439	907.47583	L	401.28710	201.14719	3
20	1927.02846	964.01787	L	288.20303	144.60515	2
21			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #24747 RT: 78.64
ITMS, CID@37.00, z=+2, Mono m/z=1051.11999 Da, MH+=2101.23269 Da, Match Tol.=0.8 Da

Protein references (1):

- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]



Sequence: VNPTVFFDIAVDGEPLGR, Charge: +2, Monoisotopic m/z: 974.07999 Da (+575.69 mmu/+591.01 ppm), MH+: 1947.15270 Da, RT: 77.35 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.5E-004, Ions matched by search engine: 10/188
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

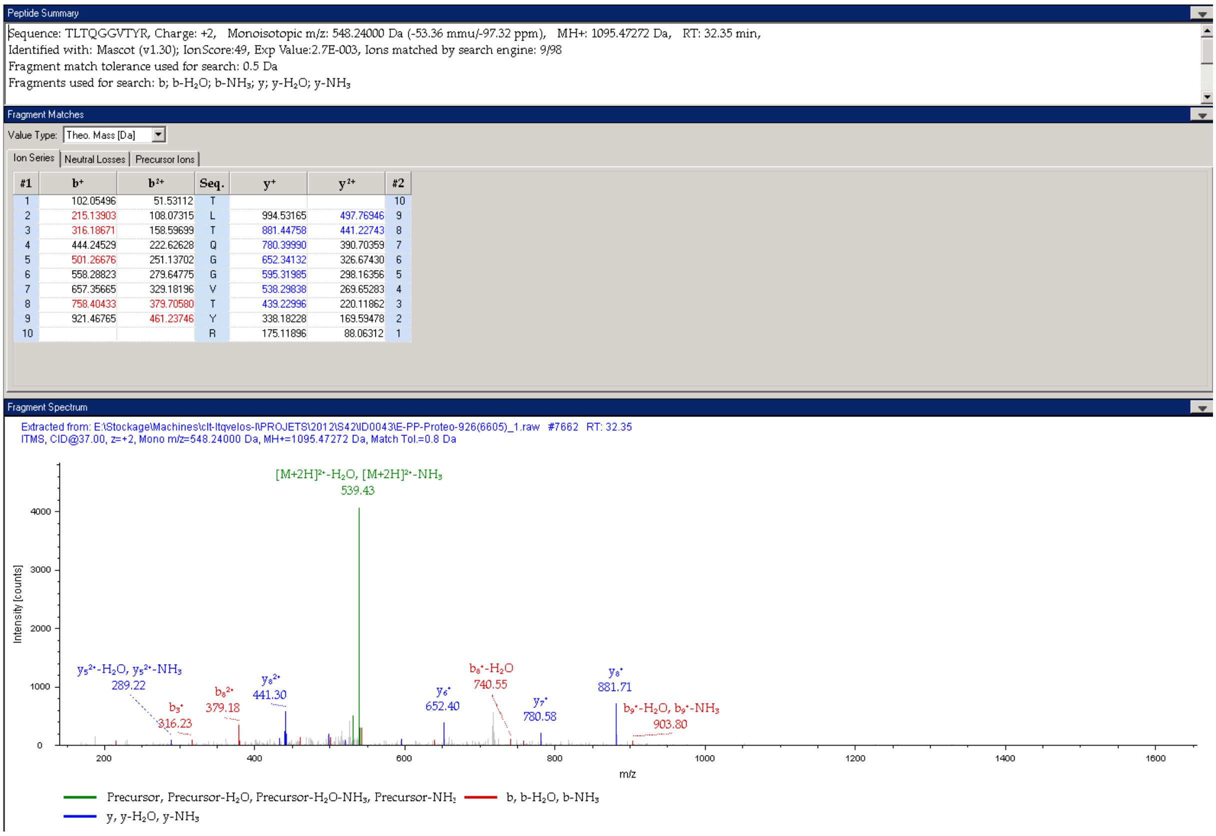
Value Type: Theo. Mass [Da]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	100.07570	50.54149	V			18
2	214.11863	107.56295	N	1846.93349	923.97038	17
3	311.17140	156.08934	P	1732.89056	866.94892	16
4	412.21908	206.61318	T	1635.83779	818.42253	15
5	511.28750	256.14739	V	1534.79011	767.89869	14
6	658.35592	329.68160	F	1435.72169	718.36448	13
7	805.42434	403.21581	F	1288.65327	644.83027	12
8	920.45129	460.72928	D	1141.58485	571.29606	11
9	1033.53536	517.27132	I	1026.55790	513.78259	10
10	1104.57248	552.78988	A	913.47383	457.24055	9
11	1203.64090	602.32409	V	842.43671	421.72199	8
12	1318.66785	659.83756	D	743.36829	372.18778	7
13	1375.68932	688.34830	G	628.34134	314.67431	6
14	1504.73192	752.86960	E	571.31987	286.16357	5
15	1601.78469	801.39598	P	442.27727	221.64227	4
16	1714.86876	857.93802	L	345.22450	173.11589	3
17	1771.89023	886.44875	G	232.14043	116.57385	2
18			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #25355 RT: 77.35
ITMS, CID@37.00, z=+2, Mono m/z=974.07999 Da, MH+=1947.15270 Da, Match Tol.=0.8 Da

Protein references (1):

- Four and a half LIM domains protein 3 OS=Homo sapiens GN=FHL3 PE=1 SV=4 - [FHL3_HUMAN]



Sequence: TLTQGGVTYR, Charge: +2, Monoisotopic m/z: 548.24000 Da (-53.36 mmu/-97.32 ppm), MH+: 1095.47272 Da, RT: 32.35 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:2.7E-003, Ions matched by search engine: 9/98
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

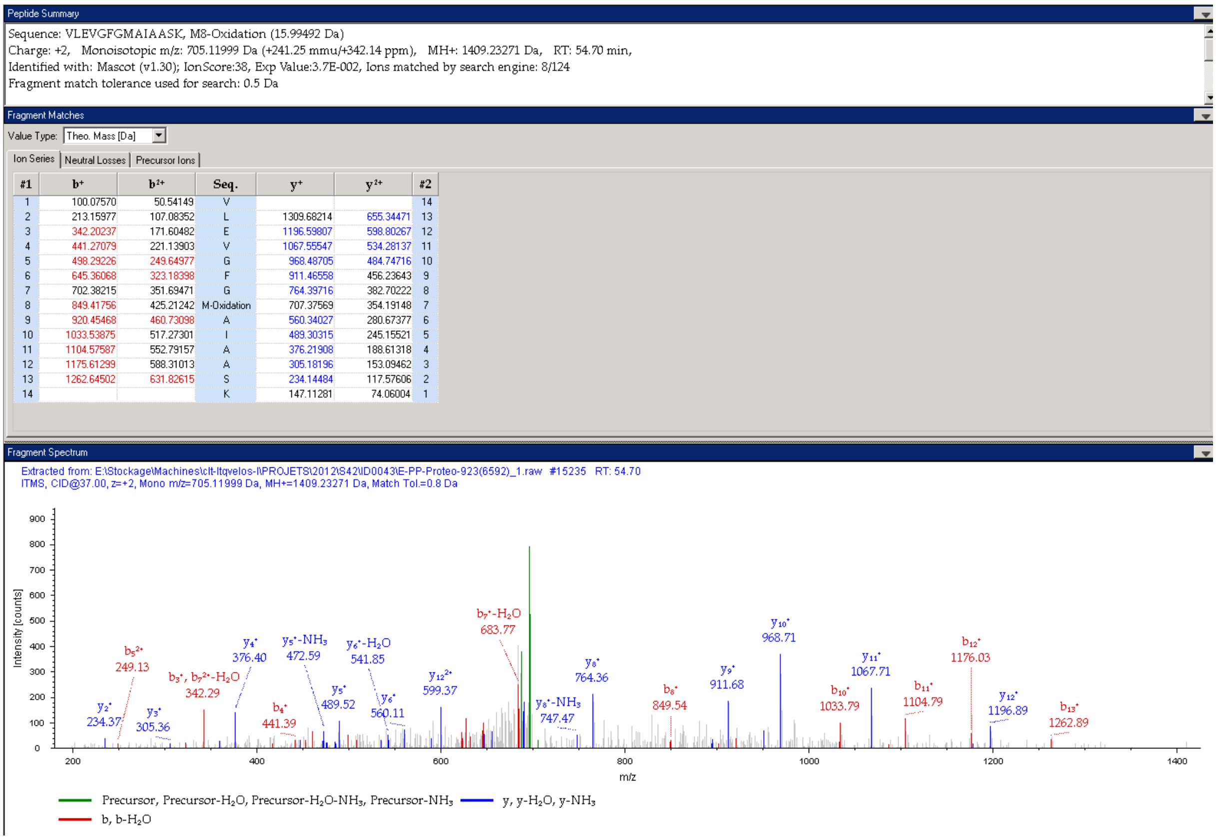
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			10
2	215.13903	108.07315	L	994.53165	497.76946	9
3	316.18671	158.59699	T	881.44758	441.22743	8
4	444.24529	222.62628	Q	780.39990	390.70359	7
5	501.26676	251.13702	G	652.34132	326.67430	6
6	558.28823	279.64775	G	595.31985	298.16356	5
7	657.35665	329.18196	V	538.29838	269.65283	4
8	758.40433	379.70580	T	439.22996	220.11862	3
9	921.46765	461.23746	Y	338.18228	169.59478	2
10			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #7662 RT: 32.35
ITMS, CID@37.00, z=+2, Mono m/z=548.24000 Da, MH+=1095.47272 Da, Match Tol.=0.8 Da

Protein references (1):

- Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 - [GAMT_HUMAN]



Peptide Summary

Sequence: VLEVGFGMAIAASK, M8-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 705.11999 Da (+241.25 mmu/+342.14 ppm), MH+: 1409.23271 Da, RT: 54.70 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.7E-002, Ions matched by search engine: 8/124
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

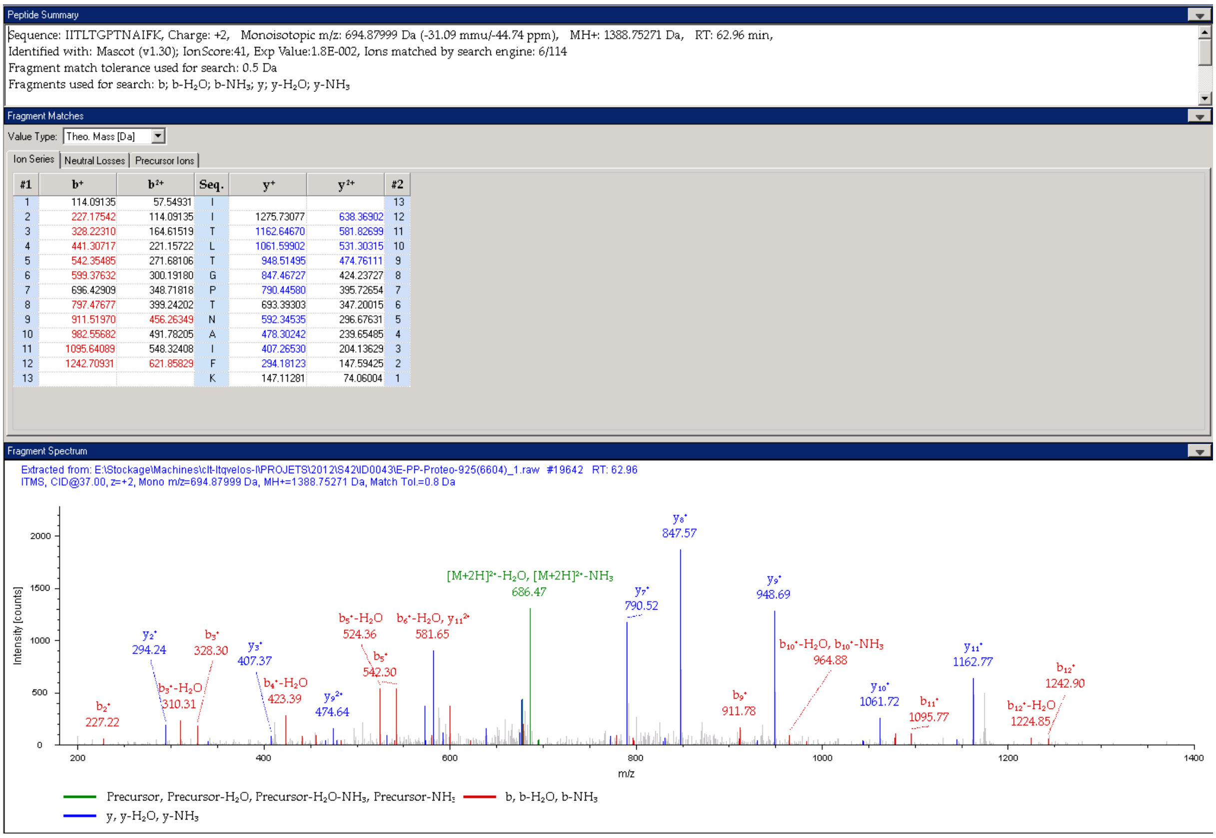
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			14
2	213.15977	107.08352	L	1309.68214	655.34471	13
3	342.20237	171.60482	E	1196.59807	598.80267	12
4	441.27079	221.13903	V	1067.55547	534.28137	11
5	498.29226	249.64977	G	968.48705	484.74716	10
6	645.36068	323.18398	F	911.46558	456.23643	9
7	702.38215	351.69471	G	764.39716	382.70222	8
8	849.41756	425.21242	M-Oxidation	707.37569	354.19148	7
9	920.45468	460.73098	A	560.34027	280.67377	6
10	1033.53875	517.27301	I	489.30315	245.15521	5
11	1104.57587	552.79157	A	376.21908	188.61318	4
12	1175.61299	588.31013	A	305.18196	153.09462	3
13	1262.64502	631.82615	S	234.14484	117.57606	2
14			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw #15235 RT: 54.70
ITMS, CID@37.00, z=+2, Mono m/z=705.11999 Da, MH+=1409.23271 Da, Match Tol.=0.8 Da

Protein references (1):
- Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]



Sequence: IITLTGPTNAIFK, Charge: +2, Monoisotopic m/z: 694.87999 Da (-31.09 mmu/-44.74 ppm), MH+: 1388.75271 Da, RT: 62.96 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.8E-002, Ions matched by search engine: 6/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

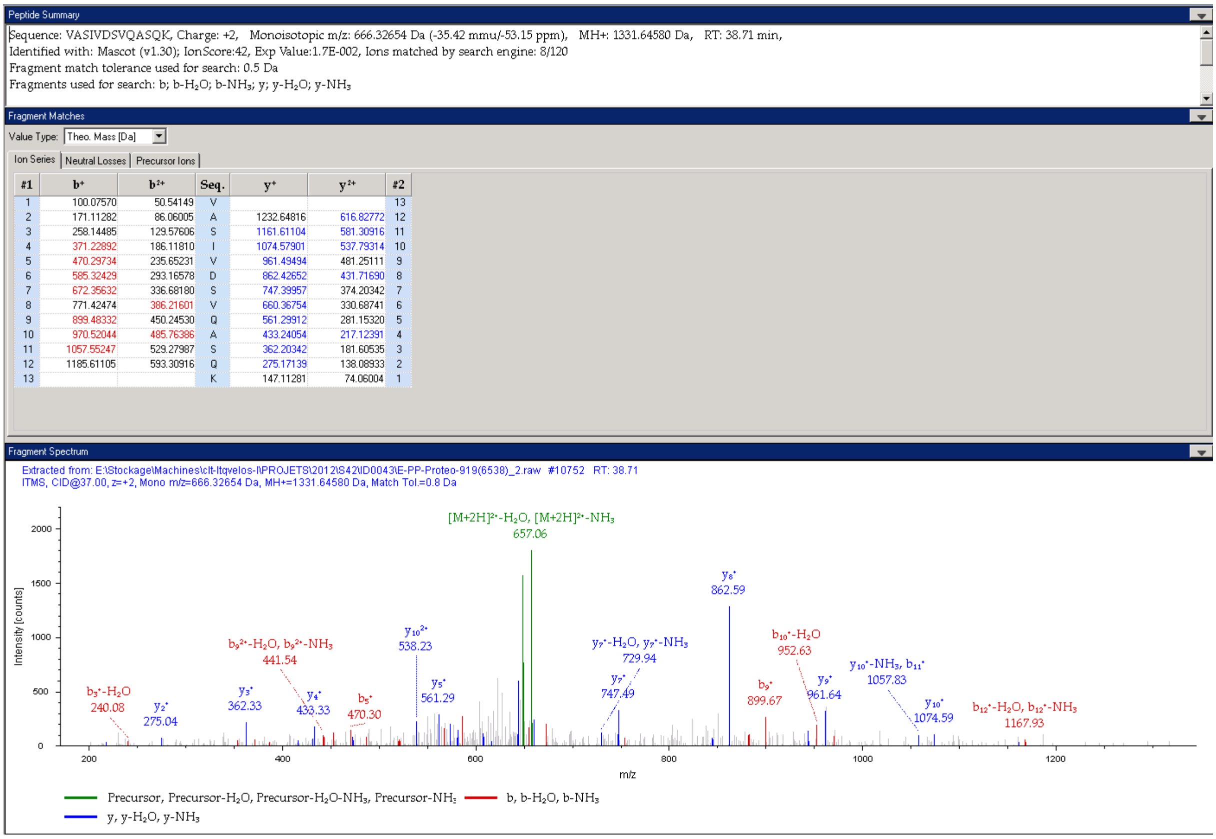
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			13
2	227.17542	114.09135	I	1275.73077	638.36902	12
3	328.22310	164.61519	T	1162.64670	581.82699	11
4	441.30717	221.15722	L	1061.59902	531.30315	10
5	542.35485	271.68106	T	948.51495	474.76111	9
6	599.37632	300.19180	G	847.46727	424.23727	8
7	696.42909	348.71818	P	790.44580	395.72654	7
8	797.47677	399.24202	T	693.39303	347.20015	6
9	911.51970	456.26349	N	592.34535	296.67631	5
10	982.55682	491.78205	A	478.30242	239.65485	4
11	1095.64089	548.32408	I	407.26530	204.13629	3
12	1242.70931	621.85829	F	294.18123	147.59425	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #19642 RT: 62.96
ITMS, CID@37.00, z=+2, Mono m/z=694.87999 Da, MH+=1388.75271 Da, Match Tol.=0.8 Da

Protein references (1):

- Muscle-related coiled-coil protein OS=Homo sapiens GN=MURC PE=1 SV=2 - [MURC_HUMAN]



Sequence: VASIVDSVQASQK, Charge: +2, Monoisotopic m/z: 666.32654 Da (-35.42 mmu/-53.15 ppm), MH+: 1331.64580 Da, RT: 38.71 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.7E-002, Ions matched by search engine: 8/120
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

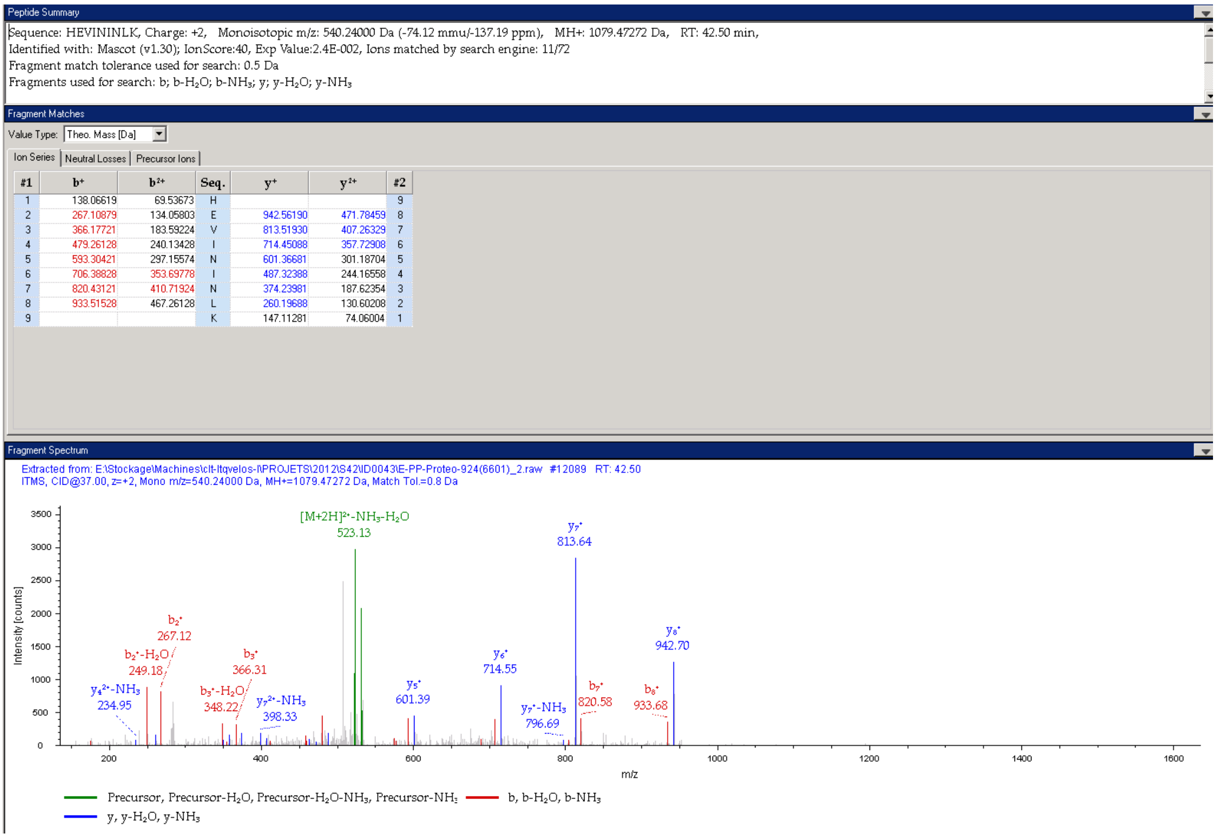
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			13
2	171.11282	86.06005	A	1232.64816	616.82772	12
3	258.14485	129.57606	S	1161.61104	581.30916	11
4	371.22892	186.11810	I	1074.57901	537.79314	10
5	470.29734	235.65231	V	961.49494	481.25111	9
6	585.32429	293.16578	D	862.42652	431.71690	8
7	672.35632	336.68180	S	747.39957	374.20342	7
8	771.42474	386.21601	V	660.36754	330.68741	6
9	899.48332	450.24530	Q	561.29912	281.15320	5
10	970.52044	485.76386	A	433.24054	217.12391	4
11	1057.55247	529.27987	S	362.20342	181.60535	3
12	1185.61105	593.30916	Q	275.17139	138.08933	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #10752 RT: 38.71
ITMS, CID@37.00, z=+2, Mono m/z=666.32654 Da, MH+=1331.64580 Da, Match Tol.=0.8 Da

Protein references (1):

- Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]



Sequence: HEVININLK, Charge: +2, Monoisotopic m/z: 540.24000 Da (-74.12 mmu/-137.19 ppm), MH+: 1079.47272 Da, RT: 42.50 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.4E-002, Ions matched by search engine: 11/72
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

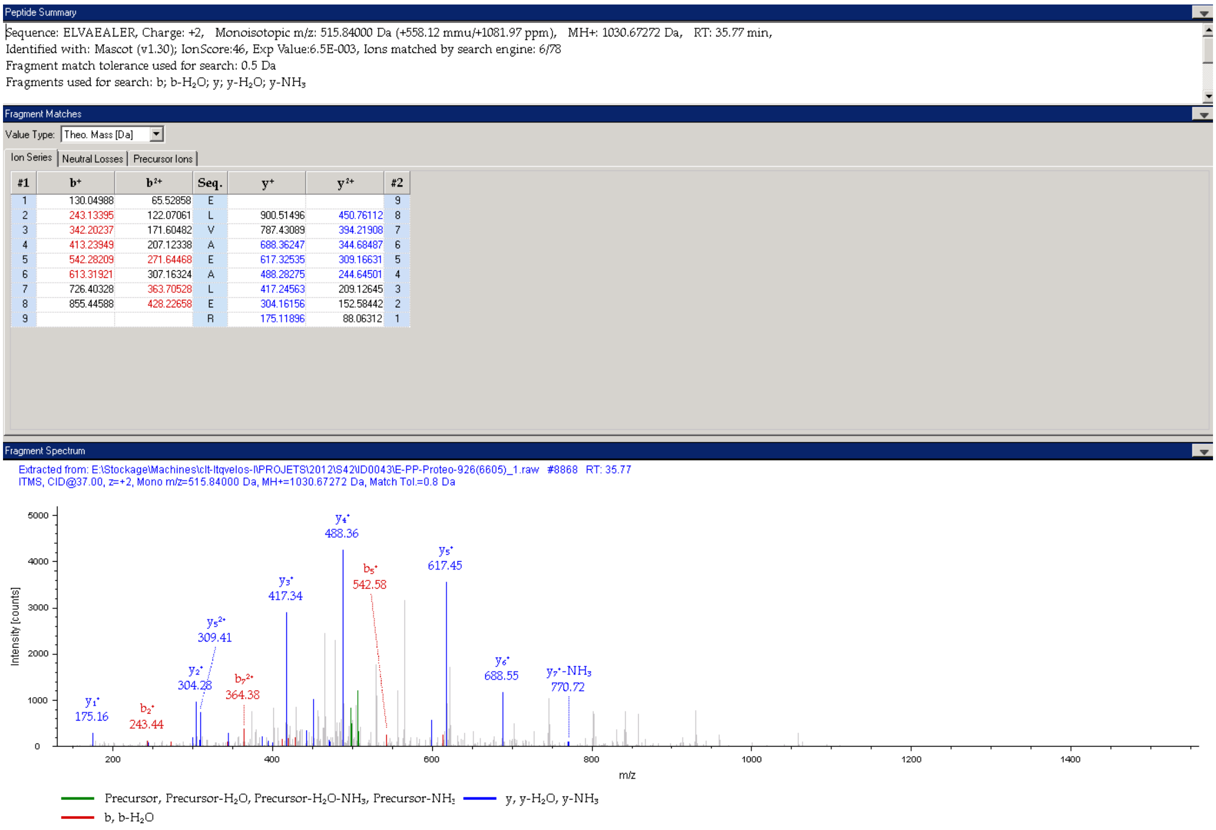
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	138.06619	69.53673	H			9
2	267.10879	134.05803	E	942.56190	471.78459	8
3	366.17721	183.59224	V	813.51930	407.26329	7
4	479.26128	240.13428	I	714.45088	357.72908	6
5	593.30421	297.15574	N	601.36681	301.18704	5
6	706.38828	353.69778	I	487.32388	244.16558	4
7	820.43121	410.71924	N	374.23981	187.62354	3
8	933.51528	467.26128	L	260.19688	130.60208	2
9			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #12089 RT: 42.50
ITMS, CID@37.00, z=+2, Mono m/z=540.24000 Da, MH+=1079.47272 Da, Match Tol.=0.8 Da

Protein references (1):

- Ras-interacting protein 1 OS=Homo sapiens GN=RASIP1 PE=1 SV=1 - [RAIN_HUMAN]



Sequence: ELVAEALER, Charge: +2, Monoisotopic m/z: 515.84000 Da (+558.12 mmu/+1081.97 ppm), MH+: 1030.67272 Da, RT: 35.77 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:6.5E-003, Ions matched by search engine: 6/78
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

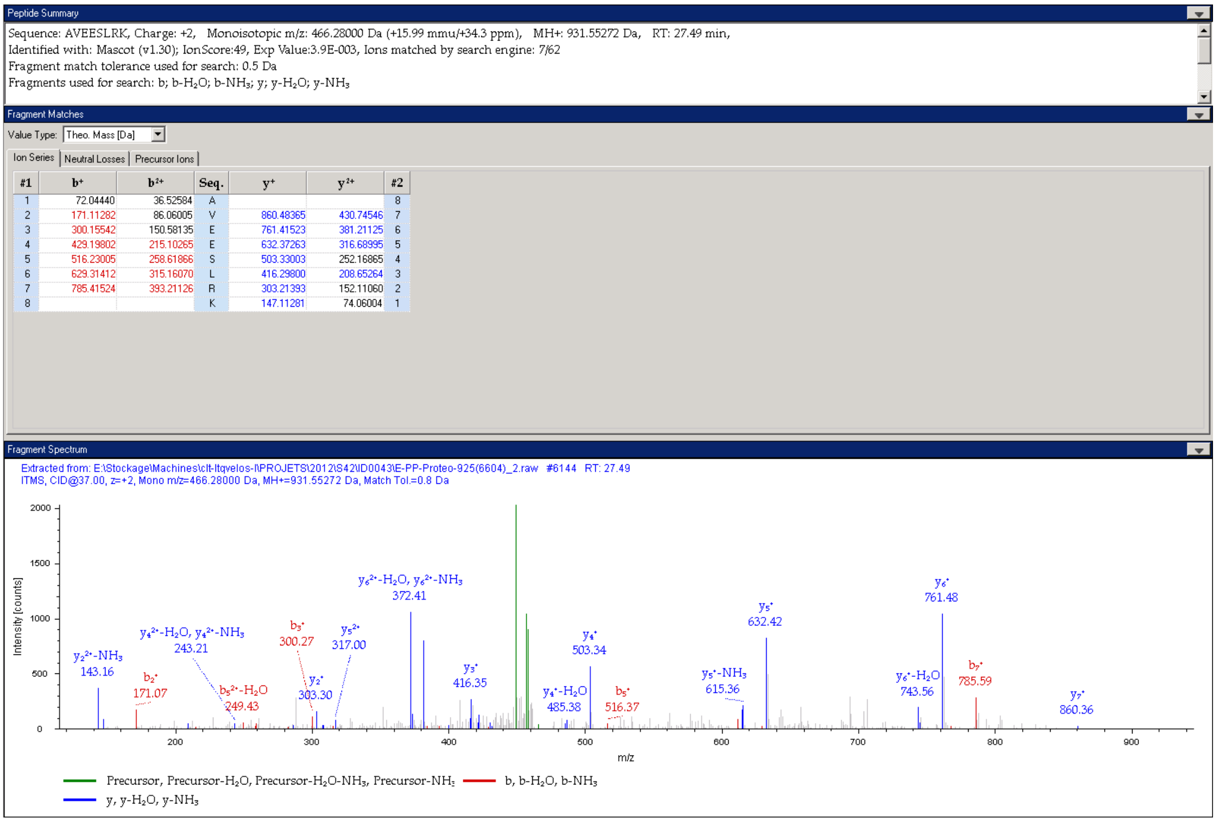
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			9
2	243.13395	122.07061	L	900.51496	450.76112	8
3	342.20237	171.60482	V	787.43089	394.21908	7
4	413.23949	207.12338	A	688.36247	344.68487	6
5	542.28209	271.64468	E	617.32535	309.16631	5
6	613.31921	307.16324	A	488.28275	244.64501	4
7	726.40328	363.70528	L	417.24563	209.12645	3
8	855.44588	428.22658	E	304.16156	152.58442	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #8868 RT: 35.77
ITMS, CID@37.00, z=+2, Mono m/z=515.84000 Da, MH+=1030.67272 Da, Match Tol.=0.8 Da

Protein references (1):

- Fatty-acid amide hydrolase 2 OS=Homo sapiens GN=FAAH2 PE=2 SV=1 - [FAAH2_HUMAN]



Peptide Summary

Sequence: AVEESLRK, Charge: +2, Monoisotopic m/z: 466.28000 Da (+15.99 mmu/+34.3 ppm), MH+: 931.55272 Da, RT: 27.49 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:3.9E-003, Ions matched by search engine: 7/62
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

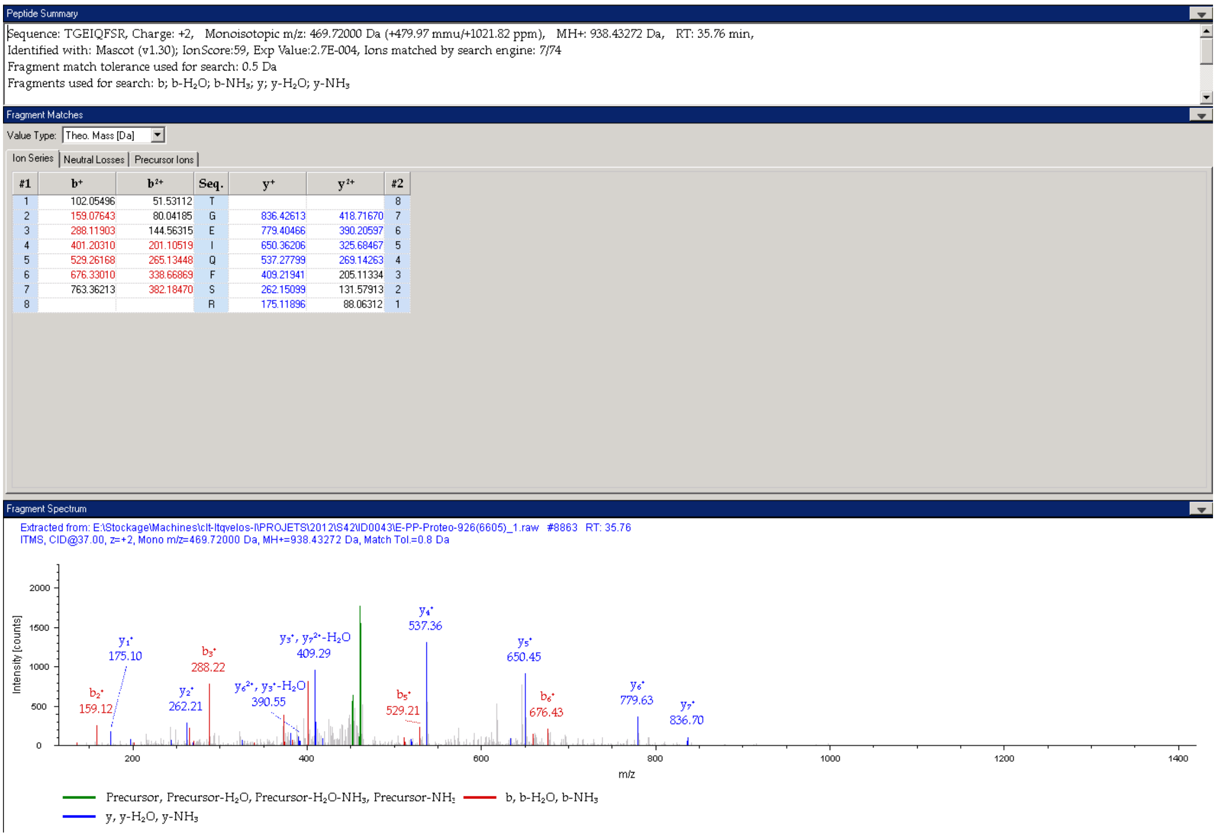
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			8
2	171.11282	86.06005	V	860.48365	430.74546	7
3	300.15542	150.58135	E	761.41523	381.21125	6
4	429.19802	215.10265	E	632.37263	316.68995	5
5	516.23005	258.61866	S	503.33003	252.16865	4
6	629.31412	315.16070	L	416.29800	208.65264	3
7	785.41524	393.21126	R	303.21393	152.11060	2
8			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_2.raw #6144 RT: 27.49
ITMS, CID@37.00, z=+2, Mono m/z=466.28000 Da, MH+=931.55272 Da, Match Tol.=0.8 Da

Protein references (1):

- Desmoglein-4 OS=Homo sapiens GN=DSG4 PE=1 SV=1 - [DSG4_HUMAN]



Peptide Summary

Sequence: TGEIQFSR, Charge: +2, Monoisotopic m/z: 469.72000 Da (+479.97 mmu/+1021.82 ppm), MH+: 938.43272 Da, RT: 35.76 min,
Identified with: Mascot (v1.30); IonScore:59, Exp Value:2.7E-004, Ions matched by search engine: 7/74
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

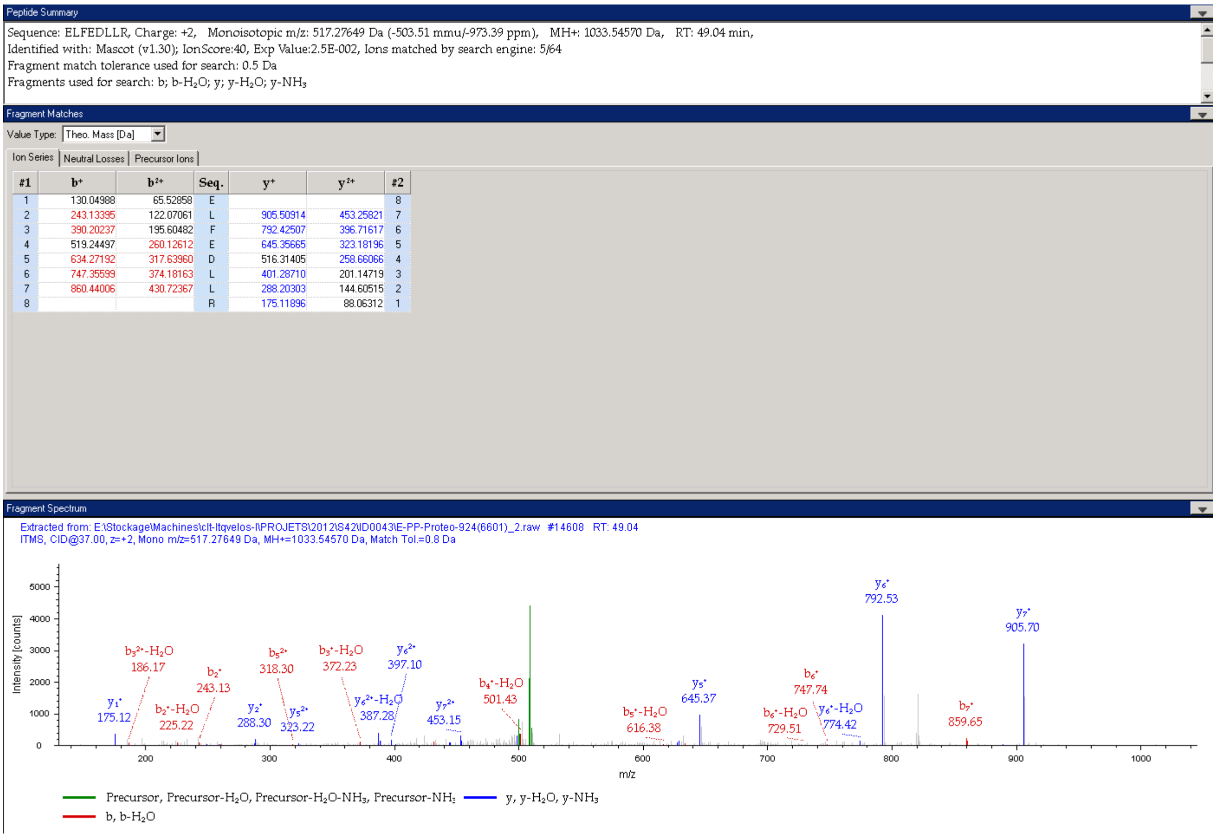
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			8
2	159.07643	80.04185	G	836.42613	418.71670	7
3	288.11903	144.56315	E	779.40466	390.20597	6
4	401.20310	201.10519	I	650.36206	325.68467	5
5	529.26168	265.13448	Q	537.27799	269.14263	4
6	676.33010	338.66869	F	409.21941	205.11334	3
7	763.36213	382.18470	S	262.15099	131.57913	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #8863 RT: 35.76
ITMS, CID@37.00, z=+2, Mono m/z=469.72000 Da, MH+=938.43272 Da, Match Tol.=0.8 Da

Protein references (1):
- Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1 - [SPG20_HUMAN]



Sequence: ELFEDLLR, Charge: +2, Monoisotopic m/z: 517.27649 Da (-503.51 mmu/-973.39 ppm), MH+: 1033.54570 Da, RT: 49.04 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.5E-002, Ions matched by search engine: 5/64
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

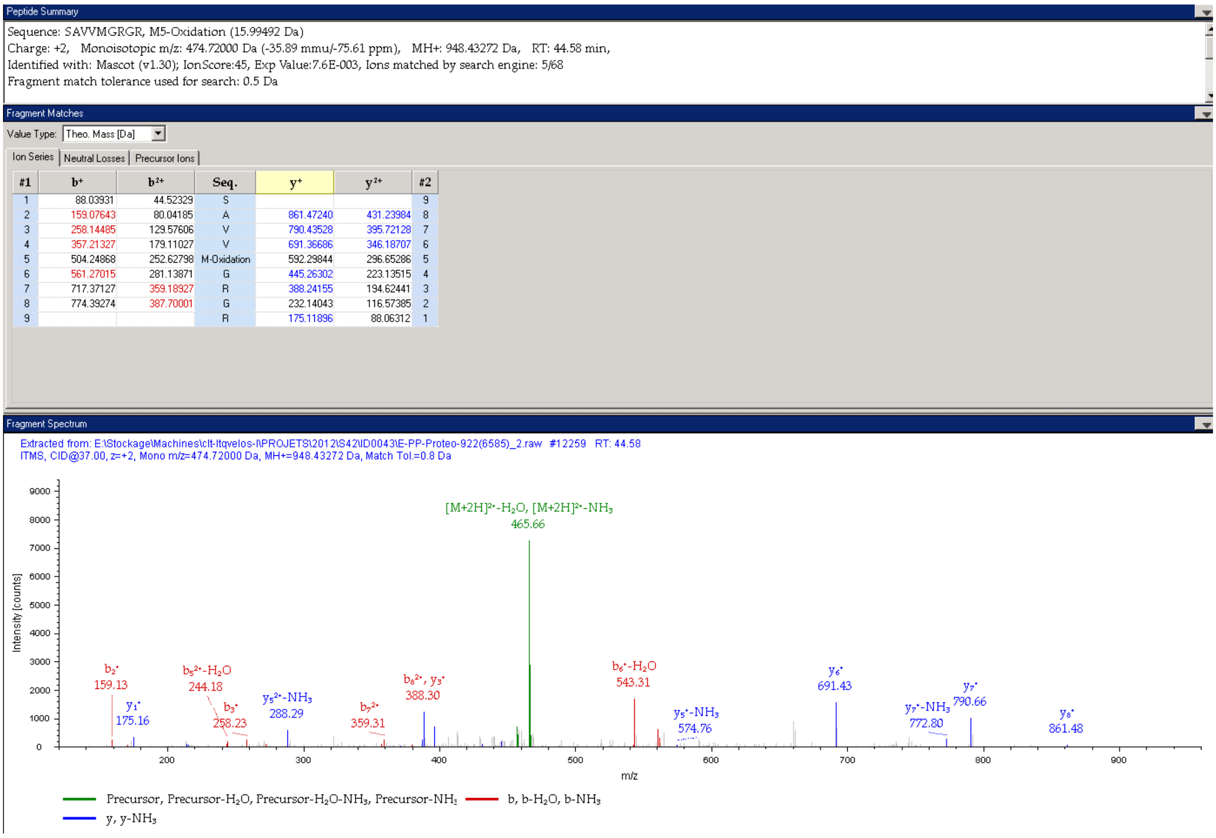
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			8
2	243.13395	122.07061	L	905.50914	453.25821	7
3	390.20237	195.60482	F	792.42507	396.71617	6
4	519.24497	260.12612	E	645.35665	323.18196	5
5	634.27192	317.63960	D	516.31405	258.66066	4
6	747.35599	374.18163	L	401.28710	201.14719	3
7	860.44006	430.72367	L	288.20303	144.60515	2
8			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #14608 RT: 49.04
ITMS, CID@37.00, z=+2, Mono m/z=517.27649 Da, MH+=1033.54570 Da, Match Tol.=0.8 Da

Protein references (1):

- Protein SMG8 OS=Homo sapiens GN=SMG8 PE=1 SV=1 - [SMG8_HUMAN]



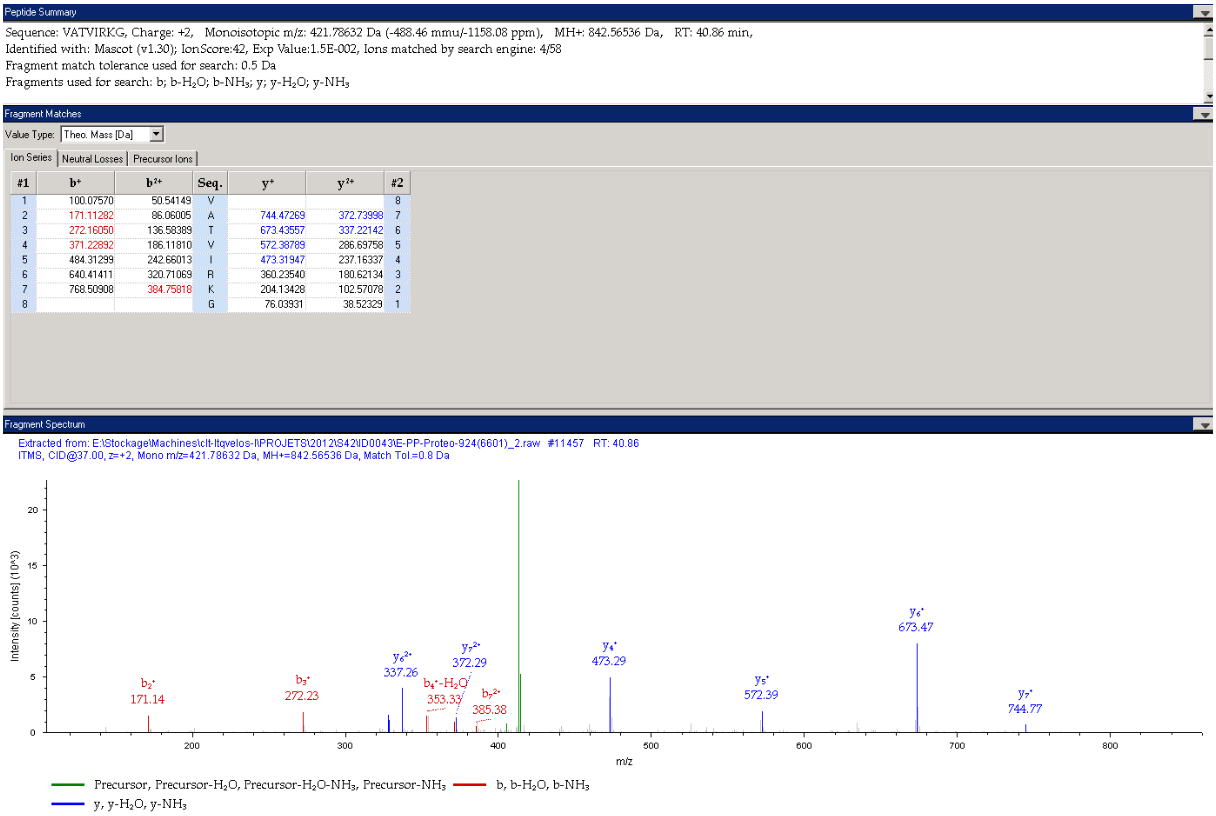
Sequence: SAVVMGRGR, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 474.72000 Da (-35.89 mmu/-75.61 ppm), MH+: 948.43272 Da, RT: 44.58 min,
Identified with: Mascot (v1.30); IonScore:45, Exp Value:7.6E-003, Ions matched by search engine: 5/68
Fragment match tolerance used for search: 0.5 Da

Value Type: Theo. Mass [Da]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	88.03931	44.52329	S			9
2	159.07643	80.04185	A	861.47240	431.23984	8
3	258.14485	129.57606	V	790.43528	395.72128	7
4	357.21327	179.11027	V	691.36686	346.18707	6
5	504.24868	252.62798	M-Oxidation	592.29844	296.65286	5
6	561.27015	281.13871	G	445.26302	223.13515	4
7	717.37127	359.18927	R	388.24155	194.62441	3
8	774.39274	387.70001	G	232.14043	116.57385	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_2.raw #12259 RT: 44.58
ITMS, CID@37.00, z=+2, Mono m/z=474.72000 Da, MH+=948.43272 Da, Match Tol.=0.8 Da

Protein references (2):
- Olfactory receptor 2T2 OS=Homo sapiens GN=OR2T2 PE=2 SV=1 - [OR2T2_HUMAN]
- Olfactory receptor 2T35 OS=Homo sapiens GN=OR2T35 PE=2 SV=1 - [O2T35_HUMAN]



Peptide Summary

Sequence: VATVIRKG, Charge: +2, Monoisotopic m/z: 421.78632 Da (-488.46 mmu/-1158.08 ppm), MH+: 842.56536 Da, RT: 40.86 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.5E-002, Ions matched by search engine: 4/58
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

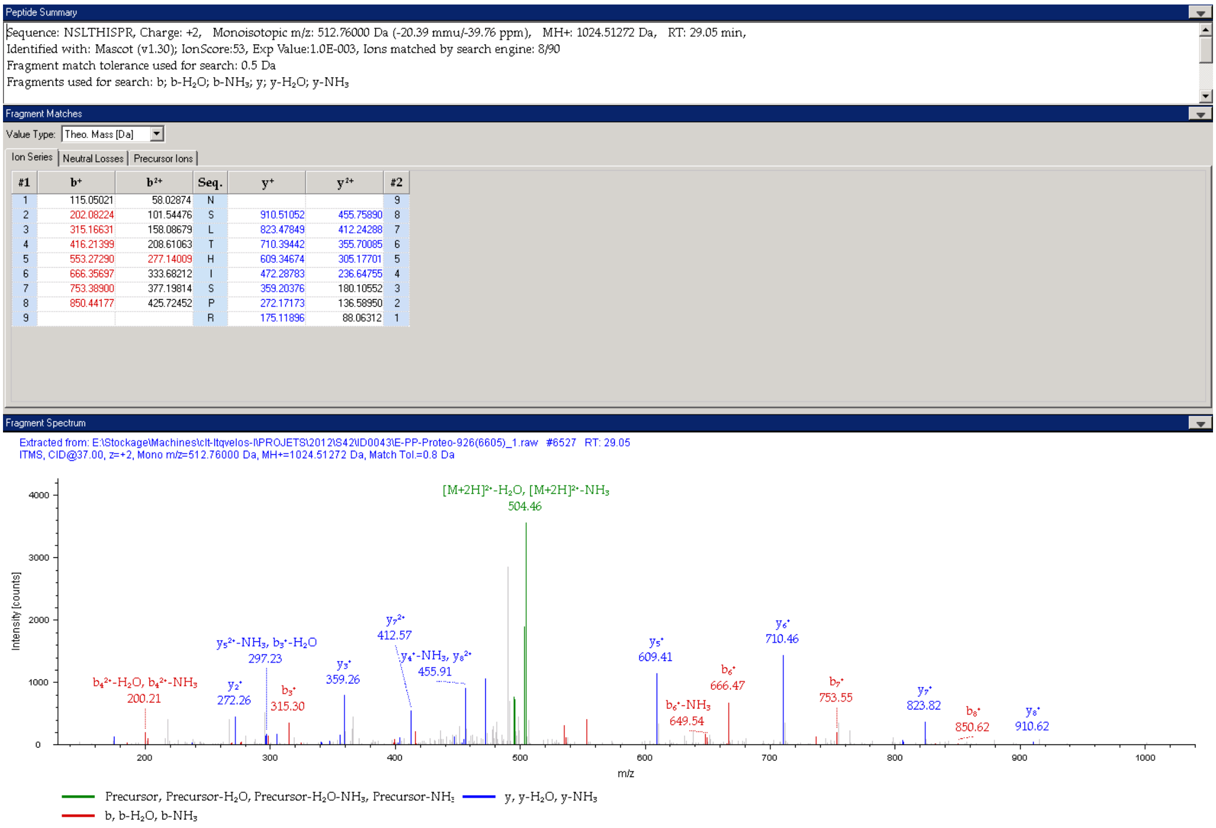
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			8
2	171.11282	86.06005	A	744.47269	372.73998	7
3	272.16050	136.58389	T	673.43557	337.22142	6
4	371.22892	186.11810	V	572.38789	286.69758	5
5	484.31299	242.66013	I	473.31947	237.16337	4
6	640.41411	320.71069	R	360.23540	180.62134	3
7	768.50908	384.75818	K	204.13428	102.57078	2
8			G	76.03931	38.52329	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #11457 RT: 40.86
ITMS, CID@37.00, z=+2, Mono m/z=421.78632 Da, MH+=842.56536 Da, Match Tol.=0.8 Da

Protein references (1):

- Leucine-rich repeat-containing protein 15 OS=Homo sapiens GN=LRRC15 PE=1 SV=2 - [LRC15_HUMAN]



Sequence: NSLTHISPR, Charge: +2, Monoisotopic m/z: 512.76000 Da (-20.39 mmu/-39.76 ppm), MH+: 1024.51272 Da, RT: 29.05 min,
Identified with: Mascot (v1.30); IonScore:53, Exp Value:1.0E-003, Ions matched by search engine: 8/90
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

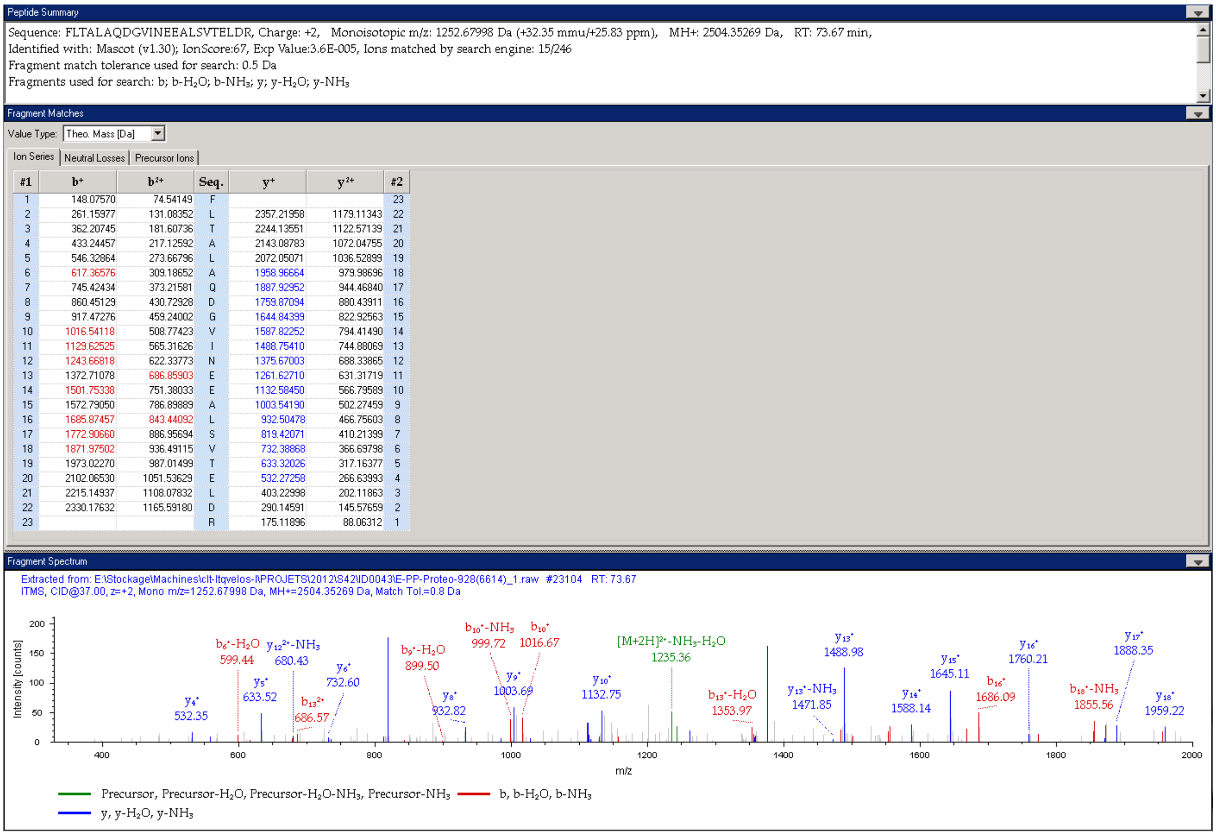
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			9
2	202.08224	101.54476	S	910.51052	455.75890	8
3	315.16631	158.08679	L	823.47849	412.24288	7
4	416.21399	208.61063	T	710.39442	355.70085	6
5	553.27290	277.14009	H	609.34674	305.17701	5
6	666.35697	333.68212	I	472.28783	236.64755	4
7	753.38900	377.19814	S	359.20376	180.10552	3
8	850.44177	425.72452	P	272.17173	136.58950	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #6527 RT: 29.05
ITMS, CID@37.00, z=+2, Mono m/z=512.76000 Da, MH+=1024.51272 Da, Match Tol.=0.8 Da

Protein references (1):

- Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]



Peptide Summary

Sequence: FLTALAQDGVINEEALSVTELDR, Charge: +2, Monoisotopic m/z: 1252.67998 Da (+32.35 mmu/+25.83 ppm), MH+: 2504.35269 Da, RT: 73.67 min,
Identified with: Mascot (v1.30); IonScore:67, Exp Value:3.6E-005, Ions matched by search engine: 15/246
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

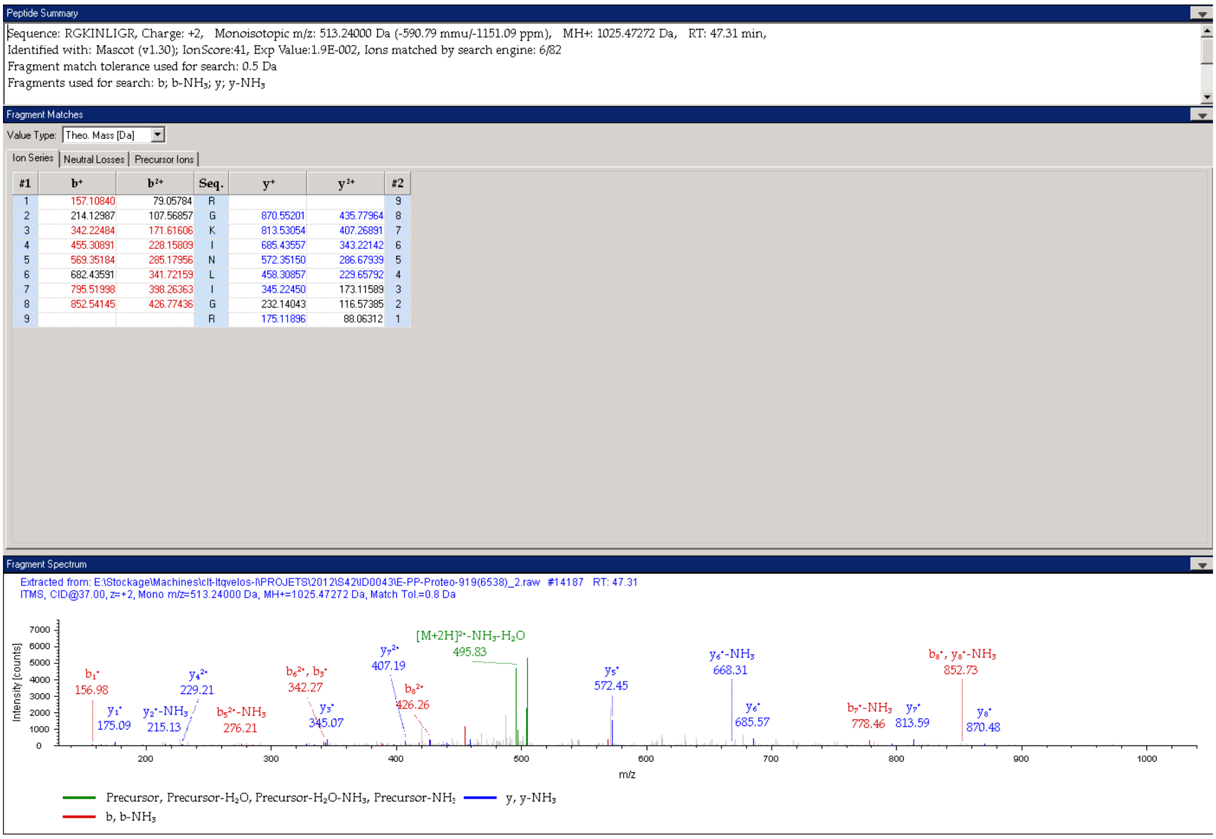
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			23
2	261.15977	131.08352	L	2357.21958	1179.11343	22
3	362.20745	181.60736	T	2244.13551	1122.57139	21
4	433.24457	217.12592	A	2143.08783	1072.04755	20
5	546.32864	273.66796	L	2072.05071	1036.52899	19
6	617.36576	309.18652	A	1958.96664	979.98696	18
7	745.42434	373.21581	Q	1887.92952	944.46840	17
8	860.45129	430.72928	D	1759.87094	880.43911	16
9	917.47276	459.24002	G	1644.84399	822.92563	15
10	1016.54118	508.77423	V	1587.82252	794.41490	14
11	1129.62525	565.31626	I	1488.75410	744.88069	13
12	1243.66818	622.33773	N	1375.67003	688.33865	12
13	1372.71078	686.85903	E	1261.62710	631.31719	11
14	1501.75338	751.38033	E	1132.58450	566.79589	10
15	1572.79050	786.89889	A	1003.54190	502.27459	9
16	1685.87457	843.44092	L	932.50478	466.75603	8
17	1772.90660	886.95694	S	819.42071	410.21399	7
18	1871.97502	936.49115	V	732.38868	366.69798	6
19	1973.02270	987.01499	T	633.32026	317.16377	5
20	2102.06530	1051.53629	E	532.27258	266.63993	4
21	2215.14937	1108.07832	L	403.22998	202.11863	3
22	2330.17632	1165.59180	D	290.14591	145.57659	2
23			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_1.raw #23104 RT: 73.67
ITMS, CID@37.00, z=+2, Mono m/z=1252.67998 Da, MH+=2504.35269 Da, Match Tol.=0.8 Da

Protein references (1):

- Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4 - [CUL5_HUMAN]



Peptide Summary

Sequence: RGKINLIGR, Charge: +2,   Monoisotopic m/z: 513.24000 Da (-590.79 mmu/-1151.09 ppm),   MH+: 1025.47272 Da,   RT: 47.31 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.9E-002, Ions matched by search engine: 6/82
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-NH_3; y; y-NH_3

Fragment Matches

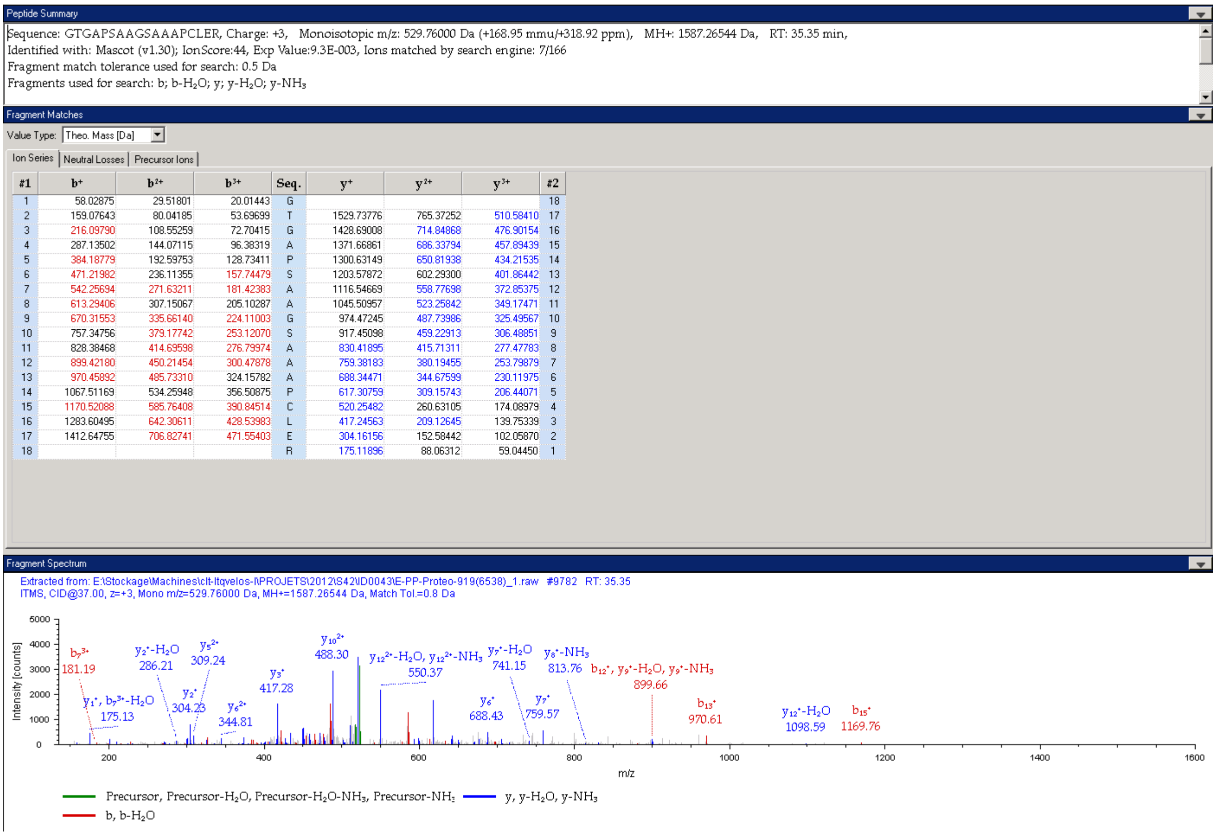
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	157.10840	79.05784	R			9
2	214.12987	107.56857	G	870.55201	435.77964	8
3	342.22484	171.61606	K	813.53054	407.26891	7
4	455.30891	228.15809	I	685.43557	343.22142	6
5	569.35184	285.17956	N	572.35150	286.67939	5
6	682.43591	341.72159	L	458.30857	229.65792	4
7	795.51998	398.26363	I	345.22450	173.11589	3
8	852.54145	426.77436	G	232.14043	116.57385	2
9			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #14187   RT: 47.31
ITMS, CID@37.00, z=+2, Mono m/z=513.24000 Da, MH+=1025.47272 Da, Match Tol.=0.8 Da

Protein references (1):
- Class E basic helix-loop-helix protein 41 OS=Homo sapiens GN=BHLHE41 PE=2 SV=1 - [BHE41_HUMAN]



Peptide Summary

Sequence: GTGAPSAAGSAAAPCLER, Charge: +3, Monoisotopic m/z: 529.76000 Da (+168.95 mmu/+318.92 ppm), MH+: 1587.26544 Da, RT: 35.35 min,
Identified with: Mascot (v1.30); IonScore:44, Exp Value:9.3E-003, Ions matched by search engine: 7/166
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

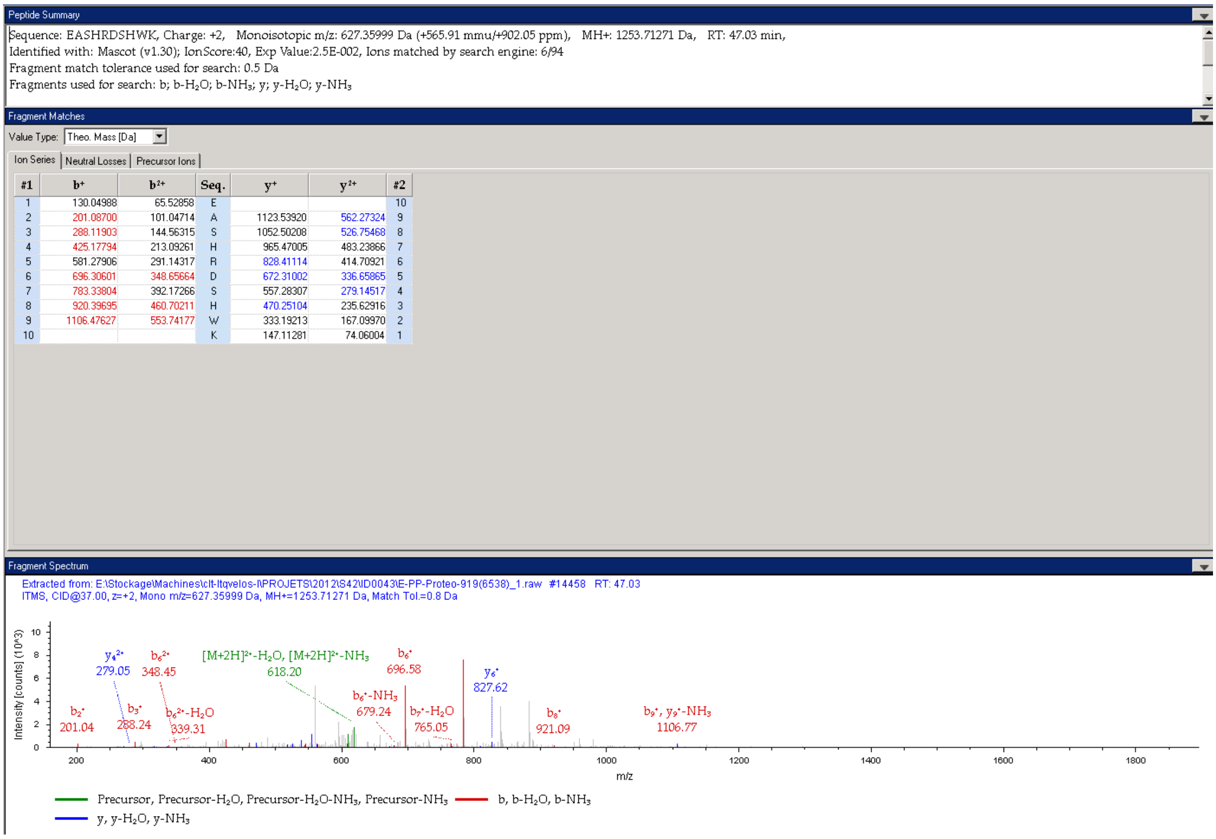
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	58.02875	29.51801	20.01443	G				18
2	159.07643	80.04185	53.69699	T	1529.73776	765.37252	510.58410	17
3	216.09790	108.55259	72.70415	G	1428.69008	714.84868	476.90154	16
4	287.13502	144.07115	96.38319	A	1371.66861	686.33794	457.89439	15
5	384.18779	192.59753	128.73411	P	1300.63149	650.81938	434.21535	14
6	471.21982	236.11355	157.74479	S	1203.57872	602.29300	401.86442	13
7	542.25694	271.63211	181.42383	A	1116.54669	558.77698	372.85375	12
8	613.29406	307.15067	205.10287	A	1045.50957	523.25842	349.17471	11
9	670.31553	335.66140	224.11003	G	974.47245	487.73986	325.49567	10
10	757.34756	379.17742	253.12070	S	917.45098	459.22913	306.48851	9
11	828.38468	414.69598	276.79974	A	830.41895	415.71311	277.47783	8
12	899.42180	450.21454	300.47878	A	759.38183	380.19455	253.79879	7
13	970.45892	485.73310	324.15782	A	688.34471	344.67599	230.11975	6
14	1067.51169	534.25948	356.50875	P	617.30759	309.15743	206.44071	5
15	1170.52088	585.76408	390.84514	C	520.25482	260.63105	174.08979	4
16	1283.60495	642.30611	428.53983	L	417.24563	209.12645	139.75339	3
17	1412.64755	706.82741	471.55403	E	304.16156	152.58442	102.05870	2
18				R	175.11896	88.06312	59.04450	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_1.raw #9782 RT: 35.35
ITMS, CID@37.00, z=+3, Mono m/z=529.76000 Da, MH+=1587.26544 Da, Match Tol.=0.8 Da

🟩 Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3 🟦 y, y-H_2O, y-NH_3
🟥 b, b-H_2O

Protein references (1):
- Nuclear speckle splicing regulatory protein 1 OS=Homo sapiens GN=NSRP1 PE=1 SV=1 - [NSRP1_HUMAN]



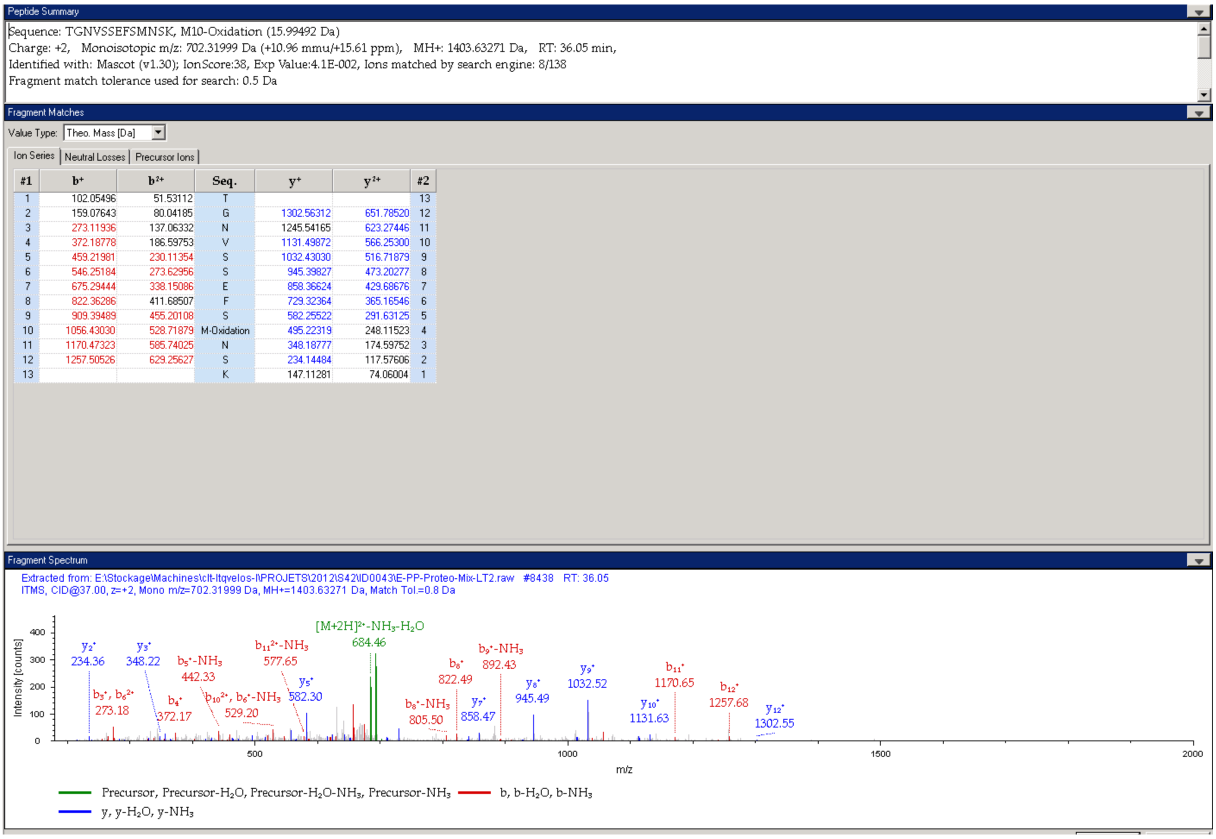
Sequence: EASHRDSHWK, Charge: +2, Monoisotopic m/z: 627.35999 Da (+565.91 mmu/+902.05 ppm), MH+: 1253.71271 Da, RT: 47.03 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.5E-002, Ions matched by search engine: 6/94
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			10
2	201.08700	101.04714	A	1123.53920	562.27324	9
3	288.11903	144.56315	S	1052.50208	526.75468	8
4	425.17794	213.09261	H	965.47005	483.23866	7
5	581.27906	291.14317	R	828.41114	414.70921	6
6	696.30601	348.65664	D	672.31002	336.65865	5
7	783.33804	392.17266	S	557.28307	279.14517	4
8	920.39695	460.70211	H	470.25104	235.62916	3
9	1106.47627	553.74177	W	333.19213	167.09970	2
10			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_1.raw #14458 RT: 47.03
ITMS, CID@37.00, z=+2, Mono m/z=627.35999 Da, MH+=1253.71271 Da, Match Tol.=0.8 Da

Protein references (1):
- Myosin light chain kinase 2, skeletal/cardiac muscle OS=Homo sapiens GN=MYLK2 PE=1 SV=3 - [MYLK2_HUMAN]

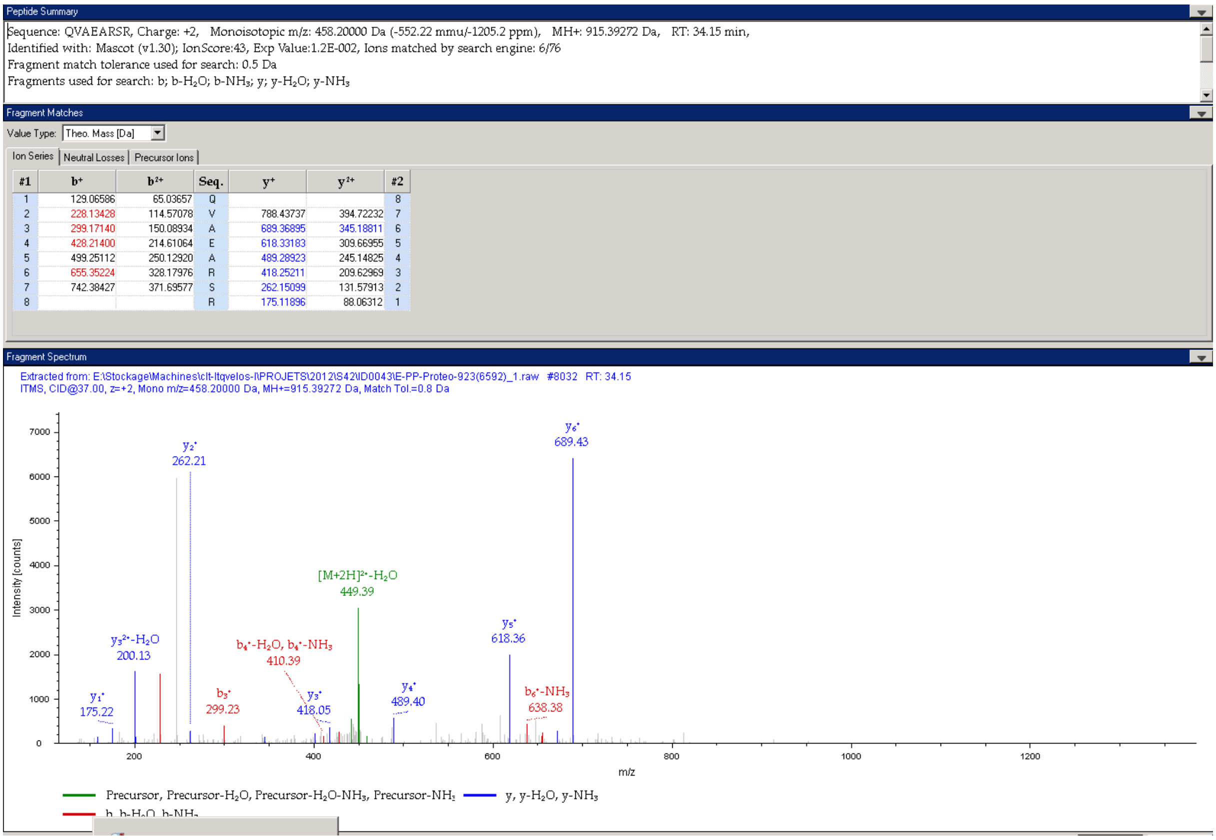


Sequence: TGNVSSEFSMNSK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 702.31999 Da (+10.96 mmu/+15.61 ppm), MH+: 1403.63271 Da, RT: 36.05 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:4.1E-002, Ions matched by search engine: 8/138
Fragment match tolerance used for search: 0.5 Da

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	102.05496	51.53112	T			13
2	159.07643	80.04185	G	1302.56312	651.78520	12
3	273.11936	137.06332	N	1245.54165	623.27446	11
4	372.18778	186.59753	V	1131.49872	566.25300	10
5	459.21981	230.11354	S	1032.43030	516.71879	9
6	546.25184	273.62956	S	945.39827	473.20277	8
7	675.29444	338.15086	E	858.36624	429.68676	7
8	822.36286	411.68507	F	729.32364	365.16546	6
9	909.39489	455.20108	S	582.25522	291.63125	5
10	1056.43030	528.71879	M-Oxidation	495.22319	248.11523	4
11	1170.47323	585.74025	N	348.18777	174.59752	3
12	1257.50526	629.25627	S	234.14484	117.57606	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-Mix-LT2.raw #8438 RT: 36.05
ITMS, CID@37.00, z=+2, Mono m/z=702.31999 Da, MH+=1403.63271 Da, Match Tol.=0.8 Da

Protein references (1):
- Armadillo repeat-containing protein 7 OS=Homo sapiens GN=ARMC7 PE=1 SV=1 - [ARMC7_HUMAN]



Peptide Summary

Sequence: QVAEARSR, Charge: +2,   Monoisotopic m/z: 458.20000 Da (-552.22 mmu/-1205.2 ppm),   MH+: 915.39272 Da,   RT: 34.15 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.2E-002, Ions matched by search engine: 6/76
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

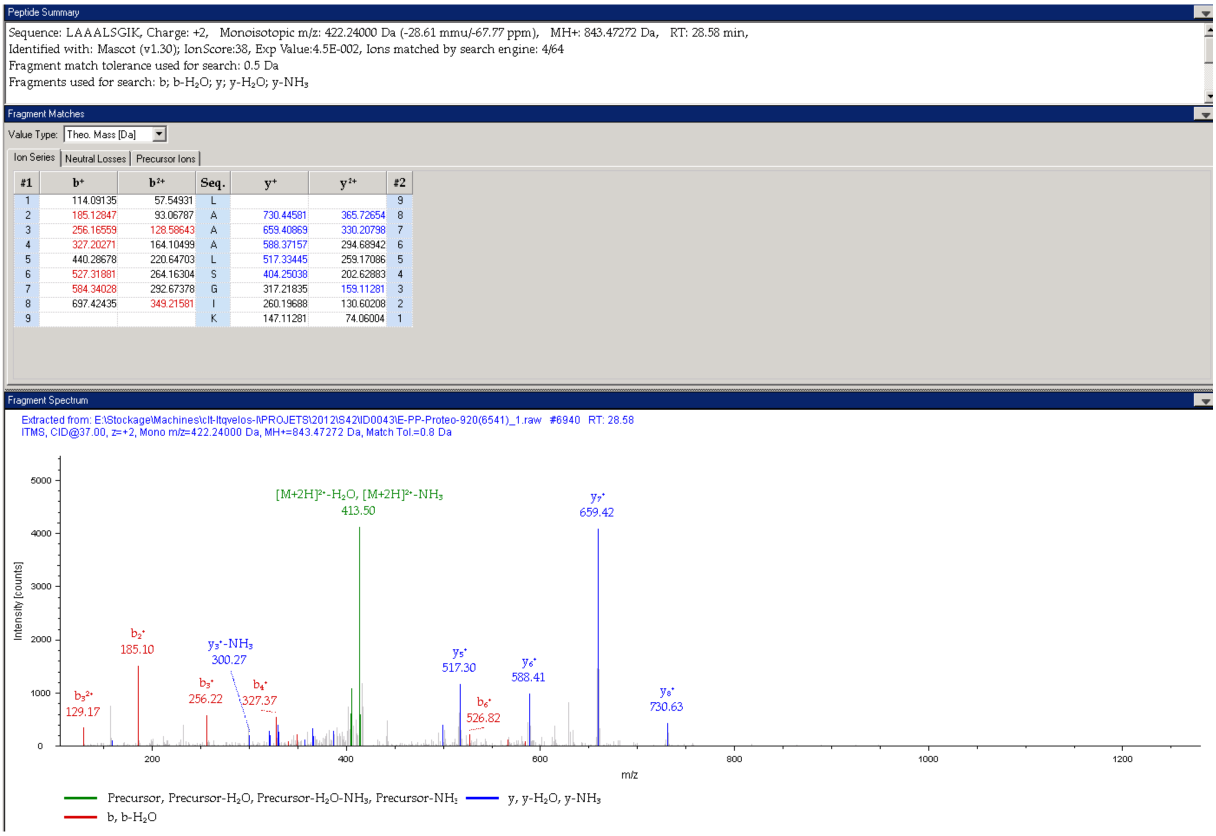
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			8
2	228.13428	114.57078	V	788.43737	394.72232	7
3	299.17140	150.08934	A	689.36895	345.18811	6
4	428.21400	214.61064	E	618.33183	309.66955	5
5	499.25112	250.12920	A	489.28923	245.14825	4
6	655.35224	328.17976	R	418.25211	209.62969	3
7	742.38427	371.69577	S	262.15099	131.57913	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_1.raw   #8032   RT: 34.15
ITMS, CID@37.00, z=+2, Mono m/z=458.20000 Da, MH+=915.39272 Da, Match Tol.=0.8 Da

Protein references (1):

- HERV-K_16p3.3 provirus ancestral Env polyprotein OS=Homo sapiens PE=2 SV=2 - [ENK14_HUMAN]



Sequence: LAAALSGIK, Charge: +2, Monoisotopic m/z: 422.24000 Da (-28.61 mmu/-67.77 ppm), MH+: 843.47272 Da, RT: 28.58 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:4.5E-002, Ions matched by search engine: 4/64
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

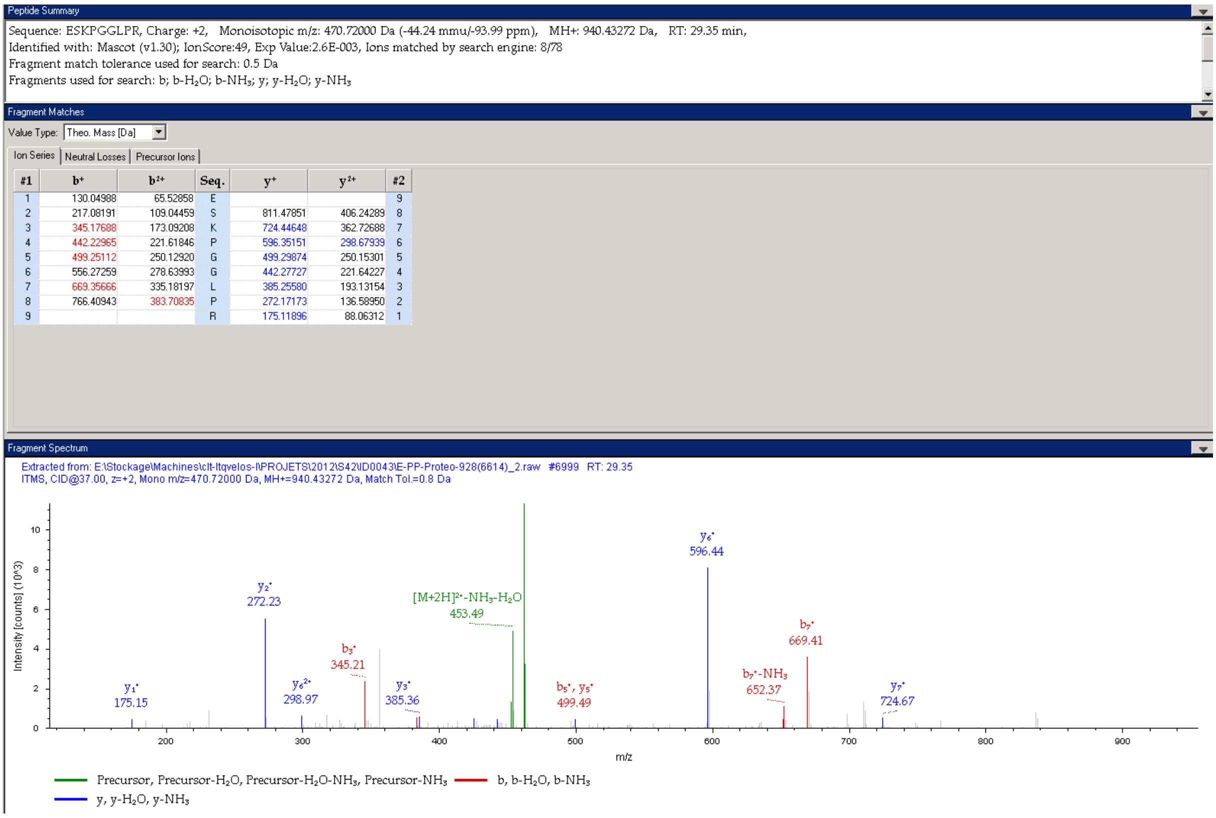
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			9
2	185.12847	93.06787	A	730.44581	365.72654	8
3	256.16559	128.58643	A	659.40869	330.20798	7
4	327.20271	164.10499	A	588.37157	294.68942	6
5	440.28678	220.64703	L	517.33445	259.17086	5
6	527.31881	264.16304	S	404.25038	202.62883	4
7	584.34028	292.67378	G	317.21835	159.11281	3
8	697.42435	349.21581	I	260.19688	130.60208	2
9			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_1.raw #6940 RT: 28.58
ITMS, CID@37.00, z=+2, Mono m/z=422.24000 Da, MH+=843.47272 Da, Match Tol.=0.8 Da

Protein references (1):

- Inactive phospholipase C-like protein 2 OS=Homo sapiens GN=PLCL2 PE=1 SV=2 - [PLCL2_HUMAN]



Peptide Summary

Sequence: ESKPGGLPR, Charge: +2, Monoisotopic m/z: 470.72000 Da (-44.24 mmu/-93.99 ppm), MH+: 940.43272 Da, RT: 29.35 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:2.6E-003, Ions matched by search engine: 8/78
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			9
2	217.08191	109.04459	S	811.47851	406.24289	8
3	345.17688	173.09208	K	724.44648	362.72688	7
4	442.22965	221.61846	P	596.35151	298.67939	6
5	499.25112	250.12920	G	499.29874	250.15301	5
6	556.27259	278.63993	G	442.27727	221.64227	4
7	669.35666	335.18197	L	385.25580	193.13154	3
8	766.40943	383.70835	P	272.17173	136.58950	2
9			R	175.11896	88.06312	1

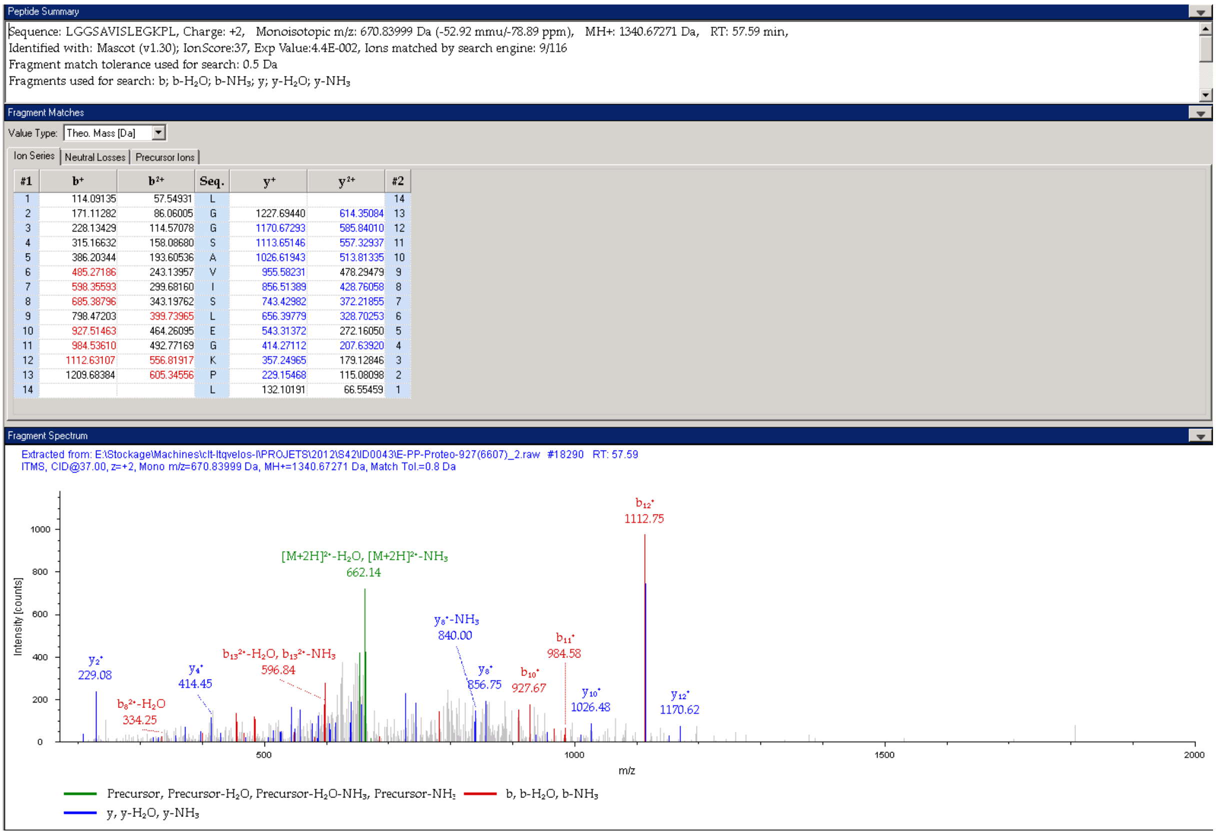
Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_2.raw #6999 RT: 29.35
ITMS, CID@37.00, z=+2, Mono m/z=470.72000 Da, MH+=940.43272 Da, Match Tol.=0.8 Da

🟩 Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3 🟥 b, b-H_2O, b-NH_3
🟦 y, y-H_2O, y-NH_3

Protein references (1):

- Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]



Sequence: LGGSAVISLEGKPL, Charge: +2, Monoisotopic m/z: 670.83999 Da (-52.92 mmu/-78.89 ppm), MH+: 1340.67271 Da, RT: 57.59 min,
Identified with: Mascot (v1.30); IonScore:37, Exp Value:4.4E-002, Ions matched by search engine: 9/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

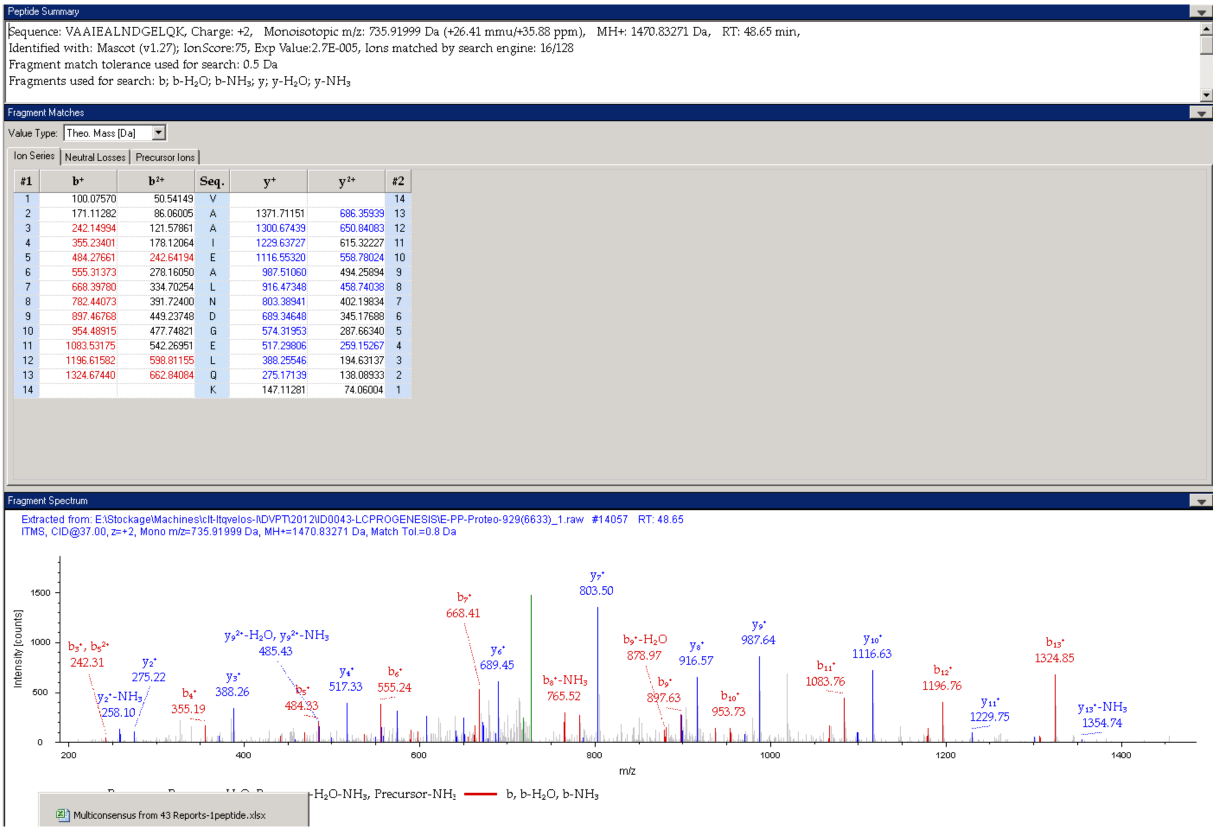
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			14
2	171.11282	86.06005	G	1227.69440	614.35084	13
3	228.13429	114.57078	G	1170.67293	585.84010	12
4	315.16632	158.08680	S	1113.65146	557.32937	11
5	386.20344	193.60536	A	1026.61943	513.81335	10
6	485.27186	243.13957	V	955.58231	478.29479	9
7	598.35593	299.68160	I	856.51389	428.76058	8
8	685.38796	343.19762	S	743.42982	372.21855	7
9	798.47203	399.73965	L	656.39779	328.70253	6
10	927.51463	464.26095	E	543.31372	272.16050	5
11	984.53610	492.77169	G	414.27112	207.63920	4
12	1112.63107	556.81917	K	357.24965	179.12846	3
13	1209.68384	605.34556	P	229.15468	115.08098	2
14			L	132.10191	66.55459	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #18290 RT: 57.59
ITMS, CID@37.00, z=+2, Mono m/z=670.83999 Da, MH+=1340.67271 Da, Match Tol.=0.8 Da

Protein references (4):

- Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]



Peptide Summary

Sequence: VAAIEALNDGELQK, Charge: +2, Monoisotopic m/z: 735.91999 Da (+26.41 mmu/+35.88 ppm), MH+: 1470.83271 Da, RT: 48.65 min,
Identified with: Mascot (v1.27); IonScore:75, Exp Value:2.7E-005, Ions matched by search engine: 16/128
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

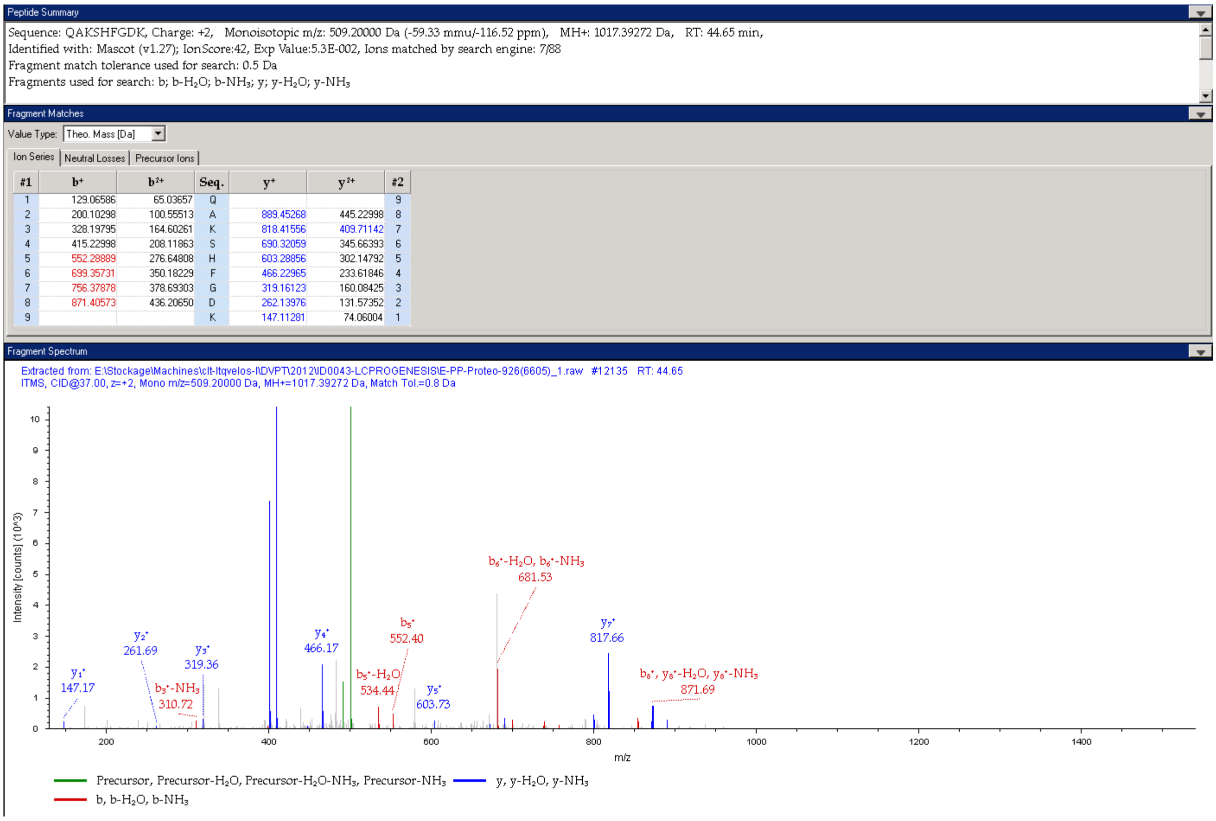
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			14
2	171.11282	86.06005	A	1371.71151	686.35939	13
3	242.14994	121.57861	A	1300.67439	650.84083	12
4	355.23401	178.12064	I	1229.63727	615.32227	11
5	484.27661	242.64194	E	1116.55320	558.78024	10
6	555.31373	278.16050	A	987.51060	494.25894	9
7	668.39780	334.70254	L	916.47348	458.74038	8
8	782.44073	391.72400	N	803.38941	402.19834	7
9	897.46768	449.23748	D	689.34648	345.17688	6
10	954.48915	477.74821	G	574.31953	287.66340	5
11	1083.53175	542.26951	E	517.29806	259.15267	4
12	1196.61582	598.81155	L	388.25546	194.63137	3
13	1324.67440	662.84084	Q	275.17139	138.08933	2
14			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-929(6633)_1.raw #14057 RT: 48.65
ITMS, CID@37.00, z=+2, Mono m/z=735.91999 Da, MH+=1470.83271 Da, Match Tol.=0.8 Da

Protein references (2):
- BUD13 homolog OS=Homo sapiens GN=BUD13 PE=1 SV=1 - [BUD13_HUMAN]



Sequence: QAKSHFGDK, Charge: +2, Monoisotopic m/z: 509.20000 Da (-59.33 mmu/-116.52 ppm), MH+: 1017.39272 Da, RT: 44.65 min,
Identified with: Mascot (v1.27); IonScore:42, Exp Value:5.3E-002, Ions matched by search engine: 7/88
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

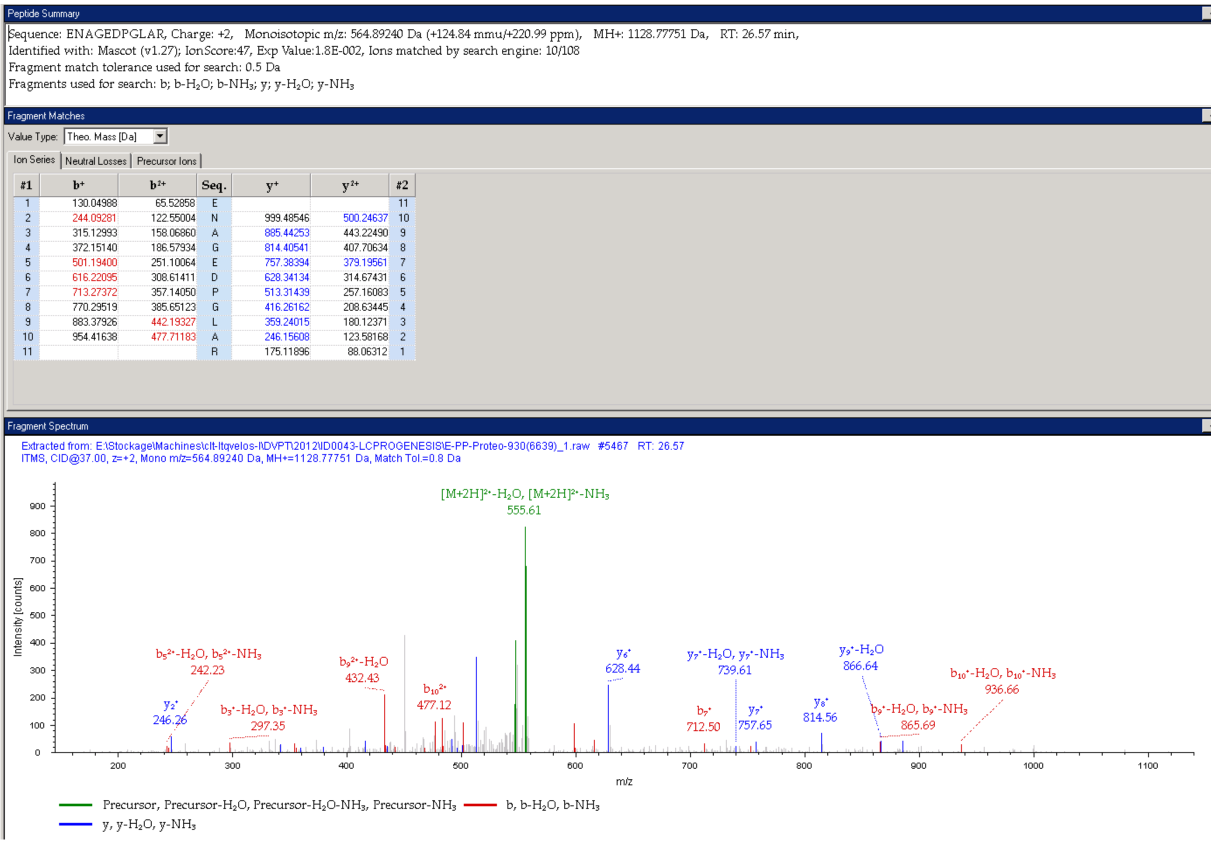
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			9
2	200.10298	100.55513	A	889.45268	445.22998	8
3	328.19795	164.60261	K	818.41556	409.71142	7
4	415.22998	208.11863	S	690.32059	345.66393	6
5	552.28889	276.64808	H	603.28856	302.14792	5
6	699.35731	350.18229	F	466.22965	233.61846	4
7	756.37878	378.69303	G	319.16123	160.08425	3
8	871.40573	436.20650	D	262.13976	131.57352	2
9			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-926(6605)_1.raw #12135 RT: 44.65
ITMS, CID@37.00, z=+2, Mono m/z=509.20000 Da, MH+=1017.39272 Da, Match Tol.=0.8 Da

Protein references (2):

- Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]



Peptide Summary

Sequence: ENAGEDPGLAR, Charge: +2, Monoisotopic m/z: 564.89240 Da (+124.84 mmu/+220.99 ppm), MH+: 1128.77751 Da, RT: 26.57 min,
Identified with: Mascot (v1.27); IonScore:47, Exp Value:1.8E-002, Ions matched by search engine: 10/108
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

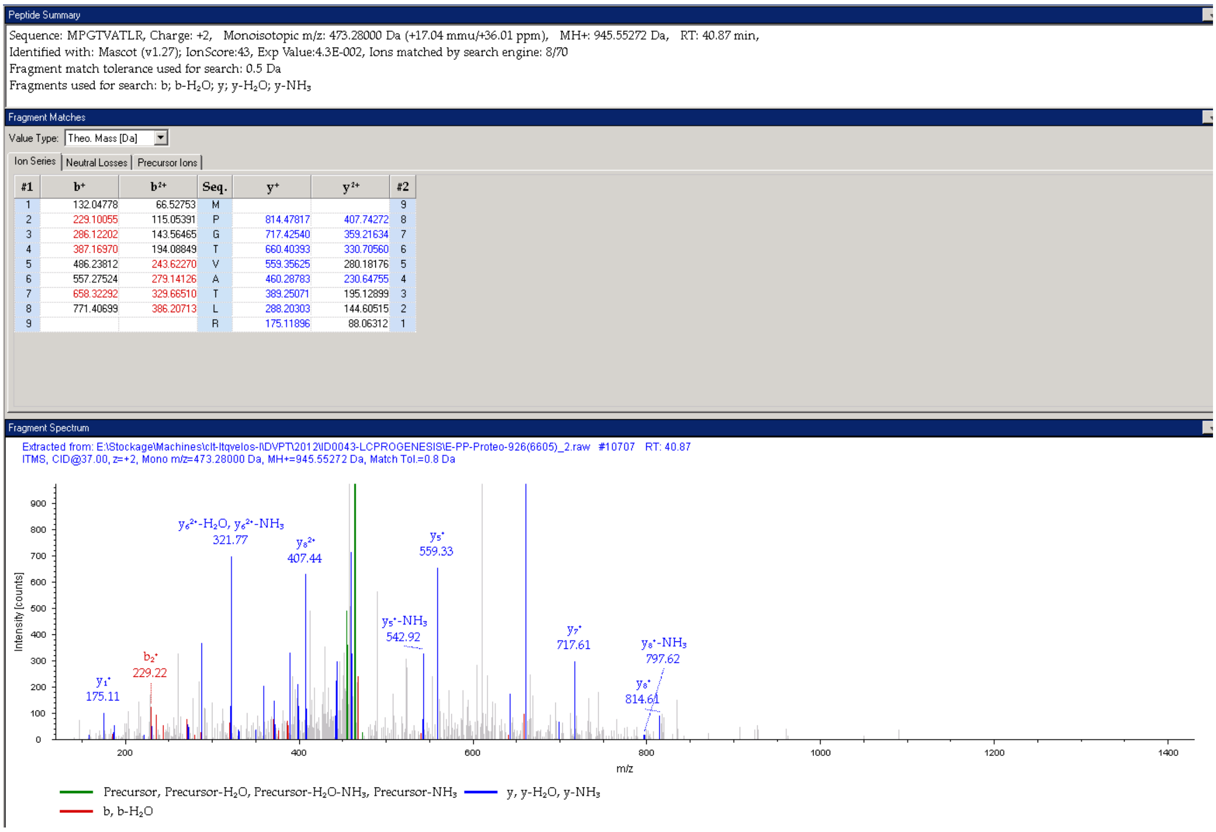
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			11
2	244.09281	122.55004	N	999.48546	500.24637	10
3	315.12993	158.06860	A	885.44253	443.22490	9
4	372.15140	186.57934	G	814.40541	407.70634	8
5	501.19400	251.10064	E	757.38394	379.19561	7
6	616.22095	308.61411	D	628.34134	314.67431	6
7	713.27372	357.14050	P	513.31439	257.16083	5
8	770.29519	385.65123	G	416.26162	208.63445	4
9	883.37926	442.19327	L	359.24015	180.12371	3
10	954.41638	477.71183	A	246.15608	123.58168	2
11			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_1.raw #5467 RT: 26.57
ITMS, CID@37.00, z=+2, Mono m/z=564.89240 Da, MH+=1128.77751 Da, Match Tol.=0.8 Da

Protein references (2):
- Transmembrane protein 198 OS=Homo sapiens GN=TMEM198 PE=2 SV=1 - [TM198_HUMAN]



Sequence: MPGTVATLR, Charge: +2, Monoisotopic m/z: 473.28000 Da (+17.04 mmu/+36.01 ppm), MH+: 945.55272 Da, RT: 40.87 min,
Identified with: Mascot (v1.27); IonScore:43, Exp Value:4.3E-002, Ions matched by search engine: 8/70
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

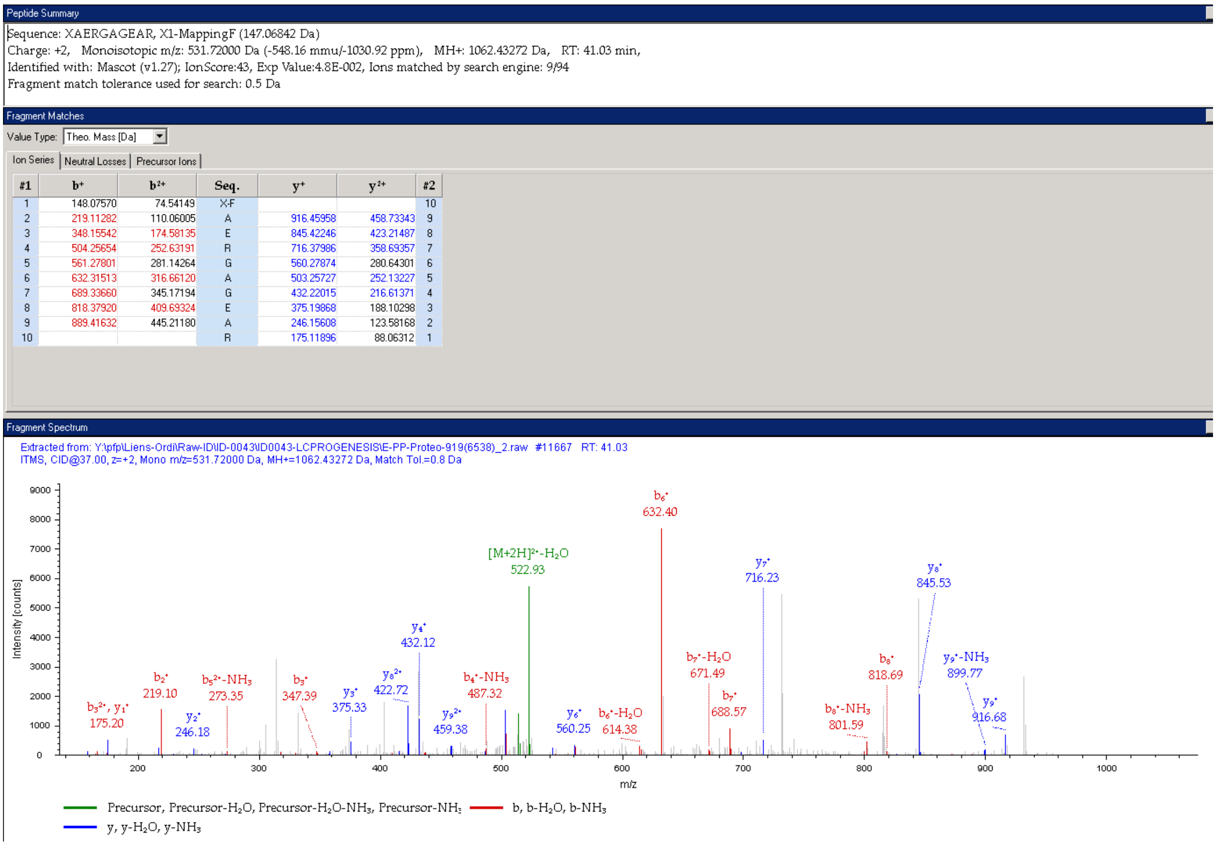
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	132.04778	66.52753	M			9
2	229.10055	115.05391	P	814.47817	407.74272	8
3	286.12202	143.56465	G	717.42540	359.21634	7
4	387.16970	194.08849	T	660.40393	330.70560	6
5	486.23812	243.62270	V	559.35625	280.18176	5
6	557.27524	279.14126	A	460.28783	230.64755	4
7	658.32292	329.66510	T	389.25071	195.12899	3
8	771.40699	386.20713	L	288.20303	144.60515	2
9			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-926(6605)_2.raw #10707 RT: 40.87
ITMS, CID@37.00, z=+2, Mono m/z=473.28000 Da, MH+=945.55272 Da, Match Tol.=0.8 Da

Protein references (1):

- Telomeric repeat-binding factor 2 (Fragment) OS=Homo sapiens GN=TERF2 PE=4 SV=2 - [H3BR37_HUMAN]



Peptide Summary

Sequence: XAERGAGEAR, X1-MappingF (147.06842 Da)
Charge: +2,   Monoisotopic m/z: 531.72000 Da (-548.16 mmu/-1030.92 ppm),   MH+: 1062.43272 Da,   RT: 41.03 min,
Identified with: Mascot (v1.27); IonScore:43, Exp Value:4.8E-002, Ions matched by search engine: 9/94
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

Value Type: Theo. Mass [Da]

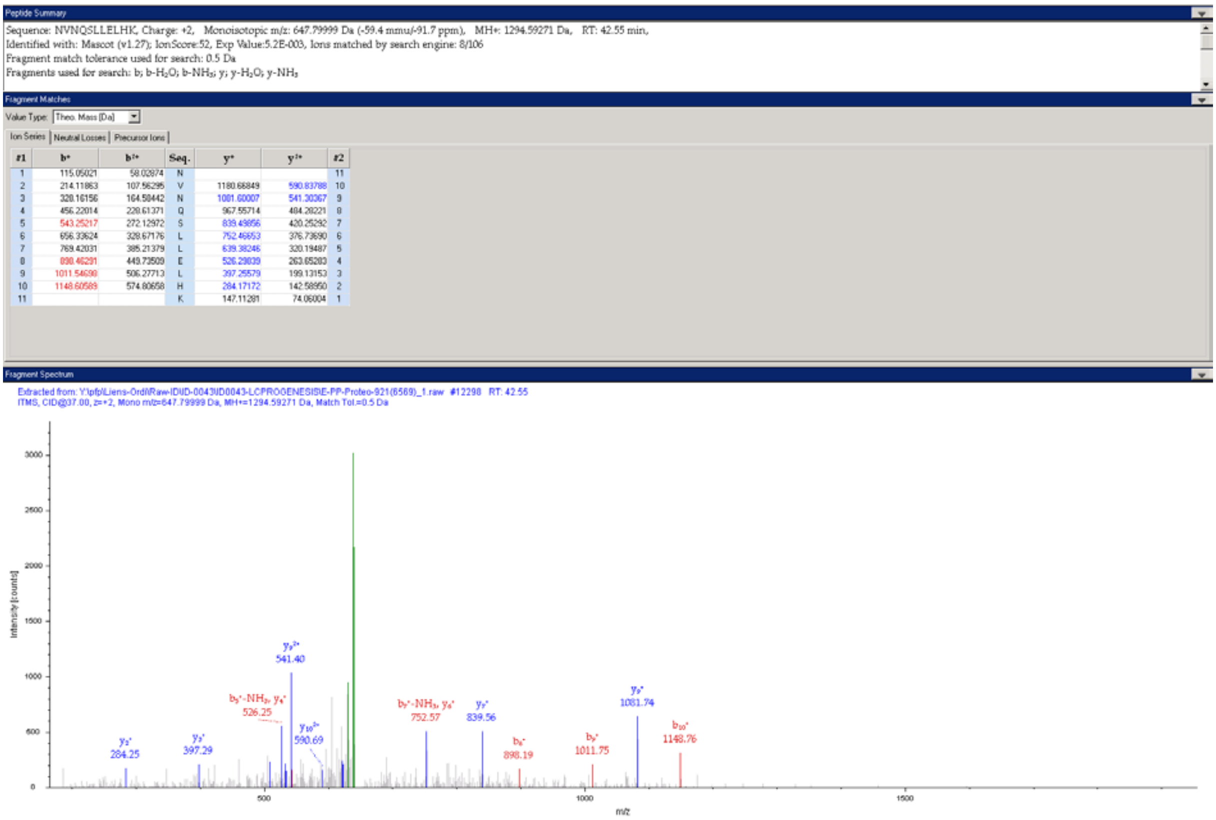
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	X-F			10
2	219.11282	110.06005	A	916.45958	458.73343	9
3	348.15542	174.58135	E	845.42246	423.21487	8
4	504.25654	252.63191	R	716.37986	358.69357	7
5	561.27801	281.14264	G	560.27874	280.64301	6
6	632.31513	316.66120	A	503.25727	252.13227	5
7	689.33660	345.17194	G	432.22015	216.61371	4
8	818.37920	409.69324	E	375.19868	188.10298	3
9	889.41632	445.21180	A	246.15608	123.58168	2
10			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: Y:\pfp\Liens-Ordi\Raw-ID\ID-0043\ID0043-LCPROGENESIS\E-PP-Proteo-919(6538)_2.raw   #11667   RT: 41.03
ITMS, CID@37.00, z=+2, Mono m/z=531.72000 Da, MH+=1062.43272 Da, Match Tol.=0.8 Da

Protein references (4):
- Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN]



Peptide Summary

Sequence: NVNQSLLELHK, Charge: +2, Monoisotopic m/z: 647.79999 Da (-59.4 mmu/-91.7 ppm), MH+: 1294.59271 Da, RT: 42.55 min,
Identified with: Mascot (v1.27); IonScore:52, Exp Value:5.2E-003, Ions matched by search engine: 8/106
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

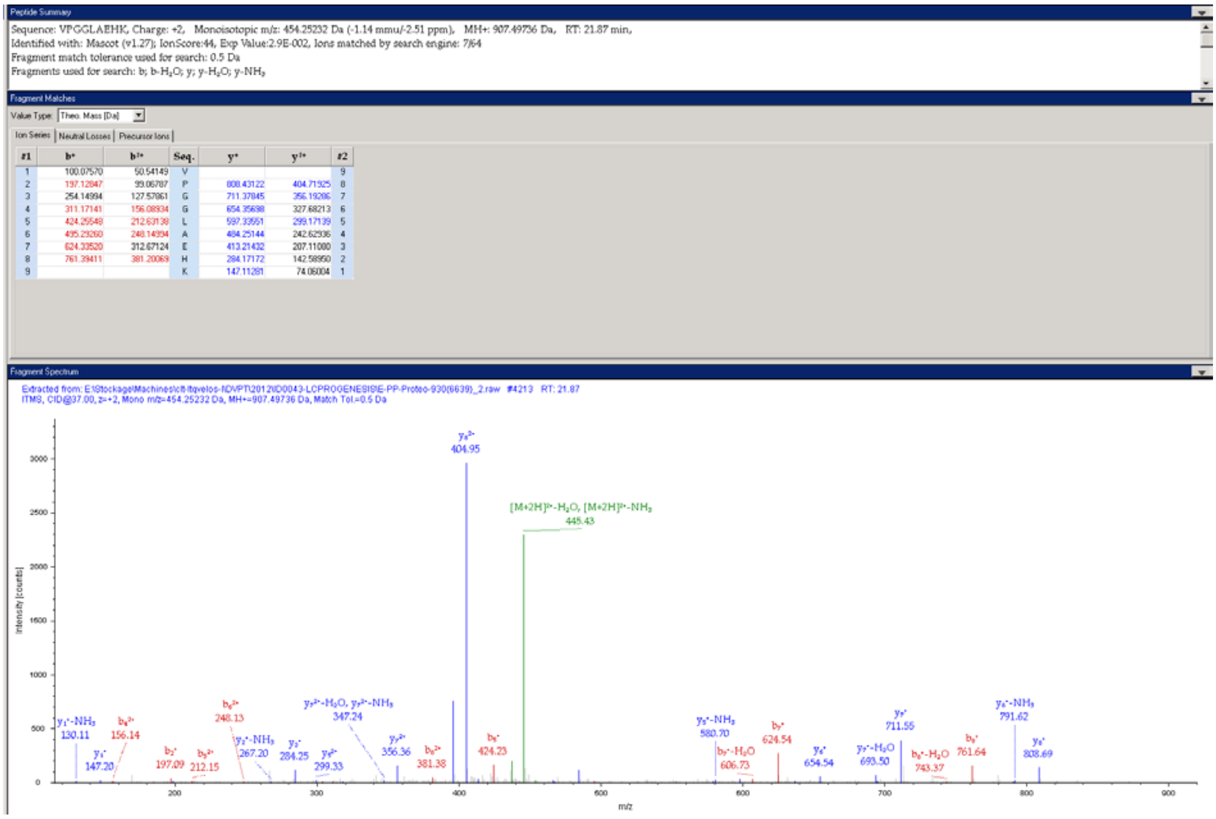
Value Type: Theo. Mass [Da]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	115.05021	58.02874	N			11
2	214.11863	107.56295	V	1180.66849	590.83788	10
3	328.16156	164.58442	N	1081.60007	541.30367	9
4	456.22014	228.61371	Q	967.55714	484.28221	8
5	543.25217	272.12972	S	839.49856	420.25292	7
6	656.33624	328.67176	L	752.46653	376.73690	6
7	769.42031	385.21379	L	639.38246	320.19487	5
8	898.46291	449.73509	E	526.29839	263.65283	4
9	1011.54698	506.27713	L	397.25579	199.13153	3
10	1148.60589	574.80658	H	284.17172	142.58950	2
11			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: Y:\pfp\Liens-Ord\Raw-ID\ID-0043\ID0043-LCPROGENESIS\E-PP-Proteo-921(6569)_1.raw #12298 RT: 42.55
ITMS, CID@37.00, z=+2, Mono m/z=647.79999 Da, MH+=1294.59271 Da, Match Tol.=0.5 Da

Protein references (5):
- Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]



Peptide Summary

Sequence: VPGGLAEHK, Charge: +2, Monoisotopic m/z: 454.25232 Da (-1.14 mmu/-2.51 ppm), MH+: 907.49736 Da, RT: 21.87 min,
Identified with: Mascot (v1.27); IonScore:44, Exp Value:2.9E-002, Ions matched by search engine: 7/64
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

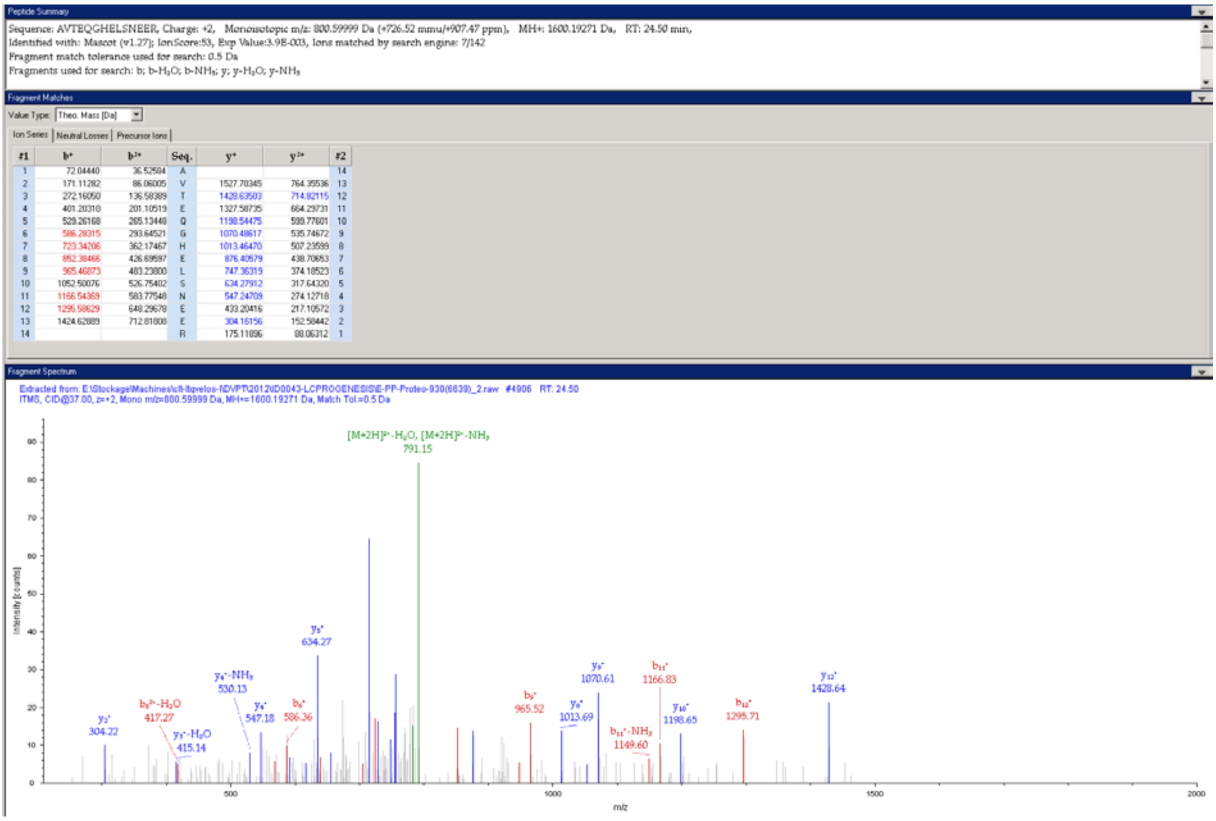
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			9
2	197.12847	99.06787	P	808.43122	404.71925	8
3	254.14994	127.57861	G	711.37845	356.19286	7
4	311.17141	156.08934	G	654.35698	327.68213	6
5	424.25548	212.63138	L	597.33551	299.17139	5
6	495.29260	248.14994	A	484.25144	242.62936	4
7	624.33520	312.67124	E	413.21432	207.11080	3
8	761.39411	381.20069	H	284.17172	142.58950	2
9			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\cft-ltqvelos-f\DVPT\2012\D0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #4213 RT: 21.87
ITMS, CID@37.00, z=+2, Mono m/z=454.25232 Da, MH+=907.49736 Da, Match Tol.=0.5 Da

Protein references (4):

- 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]

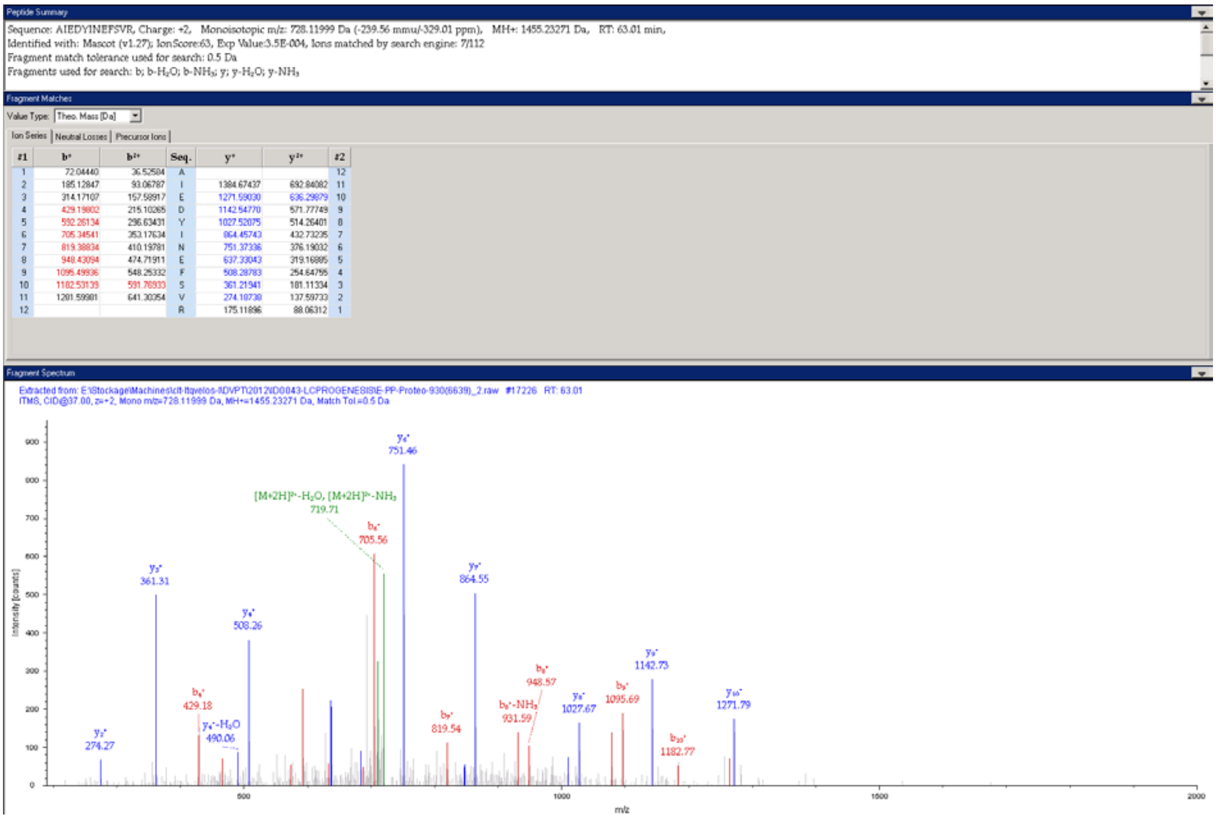


Sequence: AVTEQGHELSNEER, Charge: +2, Monoisotopic m/z: 800.59999 Da (+726.52 mmu/+907.47 ppm), MH+: 1600.19271 Da, RT: 24.50 min,
Identified with: Mascot (v1.27); IonScore:53, Exp Value:3.9E-003, Ions matched by search engine: 7/142
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	72.04440	36.52584	A			14
2	171.11282	86.06005	V	1527.70345	764.35536	13
3	272.16050	136.58389	T	1428.63503	714.82115	12
4	401.20310	201.10519	E	1327.58735	664.29731	11
5	529.26168	265.13440	Q	1198.54475	599.77601	10
6	586.28315	293.64521	G	1070.48617	535.74672	9
7	723.34206	362.17467	H	1013.46470	507.23599	8
8	852.38466	426.69597	E	876.40579	438.70653	7
9	965.46873	483.23800	L	747.36319	374.18523	6
10	1052.50076	526.75402	S	634.27912	317.64320	5
11	1166.54369	583.77548	N	547.24709	274.12718	4
12	1295.58629	648.29678	E	433.20416	217.10572	3
13	1424.62889	712.81808	E	304.16156	152.58442	2
14			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-NDVPT\2012\ND0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #4906 RT: 24.50
ITMS, CID@37.00, z=+2, Mono m/z=800.59999 Da, MH+=1600.19271 Da, Match Tol.=0.5 Da

Protein references (1):
- Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2 - [CO9_HUMAN]



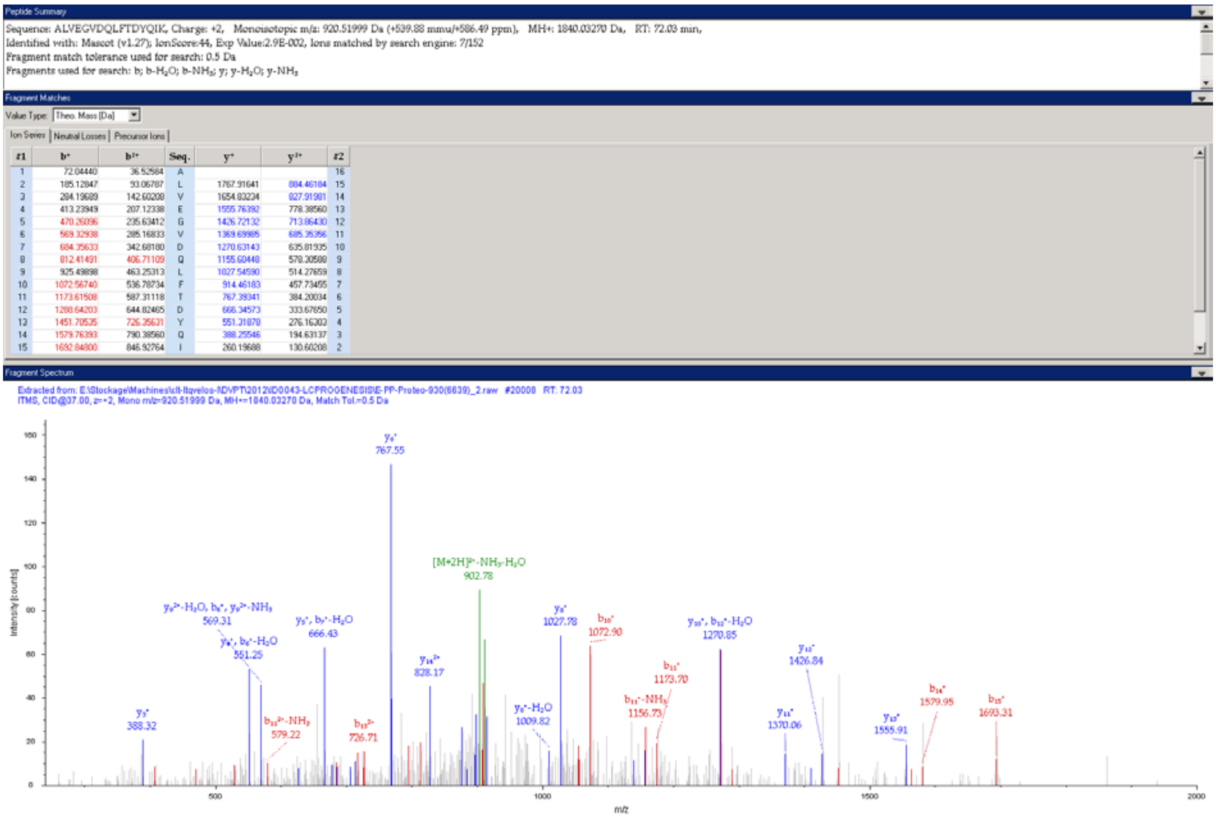
Sequence: AIEDYINEFSVR, Charge: +2, Monoisotopic m/z: 728.11999 Da (-239.56 mmu/-329.01 ppm), MH+: 1455.23271 Da, RT: 63.01 min,
Identified with: Mascot (v1.27); IonScore:63, Exp Value:3.5E-004, Ions matched by search engine: 7/112
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			12
2	185.12847	93.06787	I	1384.67437	692.84082	11
3	314.17107	157.58917	E	1271.59030	636.29879	10
4	429.19802	215.10265	D	1142.54770	571.77749	9
5	592.26134	296.63431	Y	1027.52075	514.26401	8
6	705.34541	353.17634	I	864.45743	432.73235	7
7	819.38834	410.19781	N	751.37336	376.19032	6
8	948.43094	474.71911	E	637.33043	319.16885	5
9	1095.49936	548.25332	F	508.28783	254.64755	4
10	1182.53139	591.76933	S	361.21941	181.11334	3
11	1281.59981	641.30354	V	274.18738	137.59733	2
12			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-ID\VPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #17226 RT: 63.01
ITMS, CID@37.00, z=+2, Mono m/z=728.11999 Da, MH+=1455.23271 Da, Match Tol.=0.5 Da

Protein references (1):
- Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4 - [CO5_HUMAN]



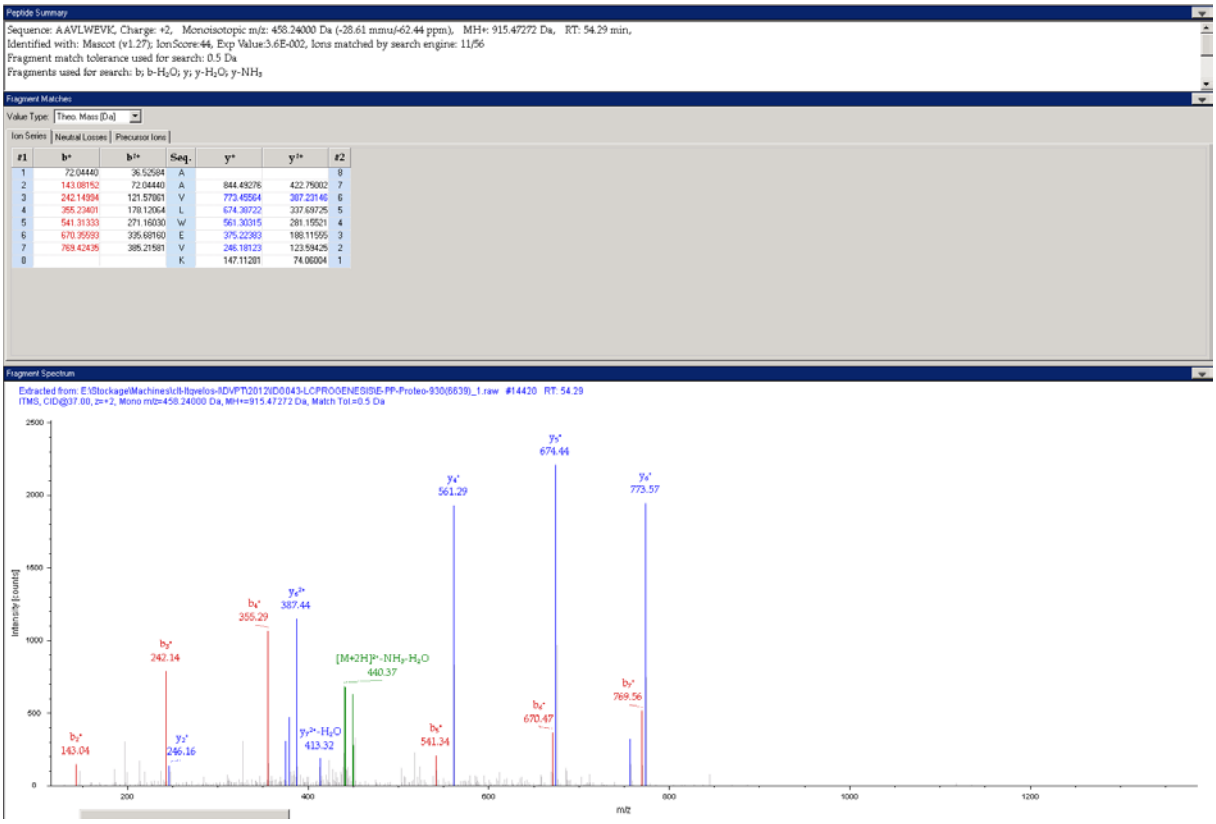
Sequence: ALVEGVDQLFTDYQIK, Charge: +2, Monoisotopic m/z: 920.51999 Da (+539.88 mmu/+586.49 ppm), MH+: 1840.03270 Da, RT: 72.03 min,
Identified with: Mascot (v1.27); IonScore:44, Exp Value:2.9E-002, Ions matched by search engine: 7/152
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			16
2	185.12847	93.06787	L	1767.91641	884.46184	15
3	284.19689	142.60208	V	1654.83234	827.91981	14
4	413.23949	207.12338	E	1555.76392	778.38560	13
5	470.26096	235.63412	G	1426.72132	713.86430	12
6	569.32938	285.16833	V	1369.69985	685.35356	11
7	684.35633	342.68180	D	1270.63143	635.81935	10
8	812.41491	406.71109	Q	1155.60448	578.30588	9
9	925.49898	463.25313	L	1027.54590	514.27659	8
10	1072.56740	536.78734	F	914.46183	457.73455	7
11	1173.61508	587.31118	T	767.39341	384.20034	6
12	1288.64203	644.82465	D	666.34573	333.67650	5
13	1451.70535	726.35631	Y	551.31878	276.16303	4
14	1579.76393	790.38560	Q	388.25546	194.63137	3
15	1692.84800	846.92764	I	260.19688	130.60208	2

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #20000 RT: 72.03
ITMS, CID@37.00, z=+2, Mono m/z=920.51999 Da, MH+=1840.03270 Da, Match Tol.=0.5 Da

Protein references (1):

- Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]



Sequence: AAVLWEVK, Charge: +2, Monoisotopic m/z: 458.24000 Da (-28.61 mmu/-62.44 ppm), MH+: 915.47272 Da, RT: 54.29 min,
Identified with: Mascot (v1.27); IonScore:44, Exp Value:3.6E-002, Ions matched by search engine: 11/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

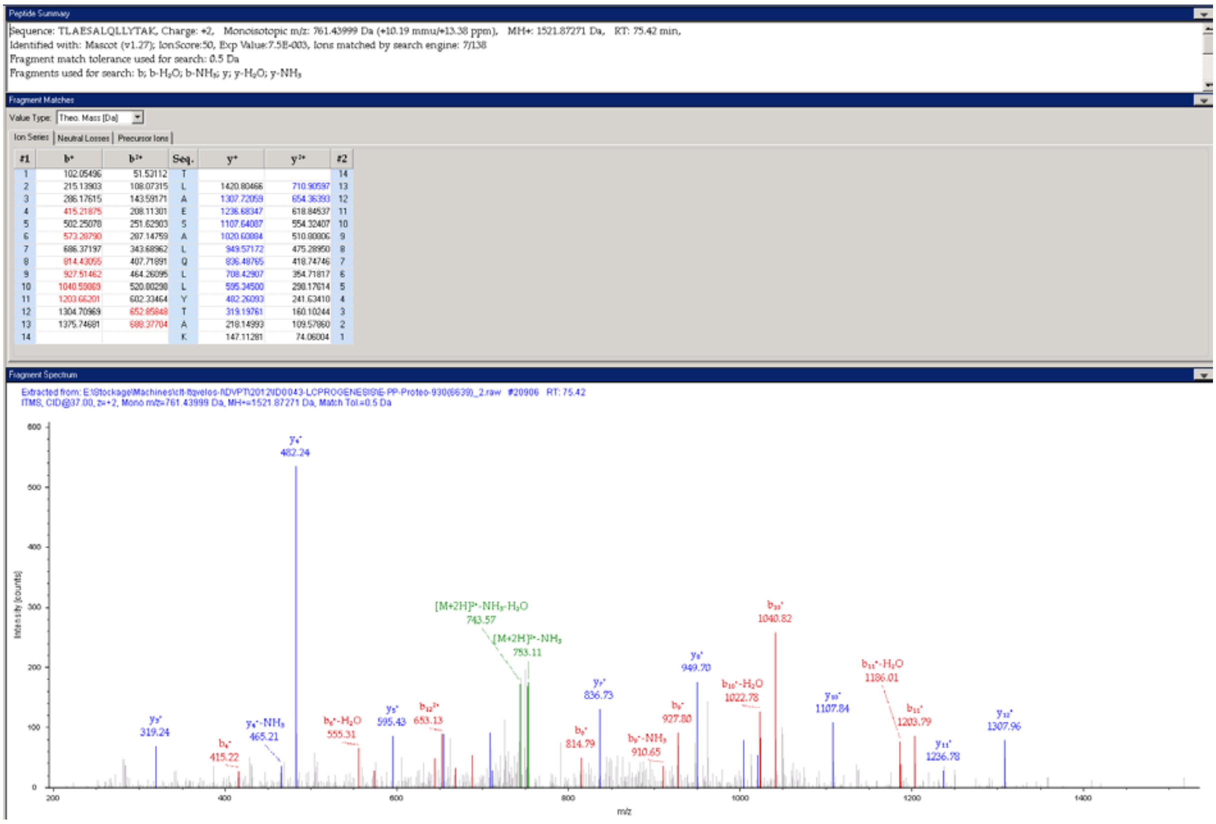
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			8
2	143.08152	72.04440	A	844.49276	422.75002	7
3	242.14994	121.57861	V	773.45564	387.23146	6
4	355.23401	178.12064	L	674.38722	337.69725	5
5	541.31333	271.16030	W	561.30315	281.15521	4
6	670.35593	335.68160	E	375.22383	188.11555	3
7	769.42435	385.21581	V	246.18123	123.59425	2
8			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\cll-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_1.raw #14420 RT: 54.29
ITMS, CID@37.00, z=+2, Mono m/z=458.24000 Da, MH+=915.47272 Da, Match Tol.=0.5 Da

Protein references (2):

- Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]



Peptide Summary

Sequence: TLAESALQLLYTAK, Charge: +2, Monoisotopic m/z: 761.43999 Da (+10.19 mmu/+13.38 ppm), MH+: 1521.87271 Da, RT: 75.42 min,
Identified with: Mascot (v1.27); IonScore:50, Exp Value:7.5E-003, Ions matched by search engine: 7/138
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

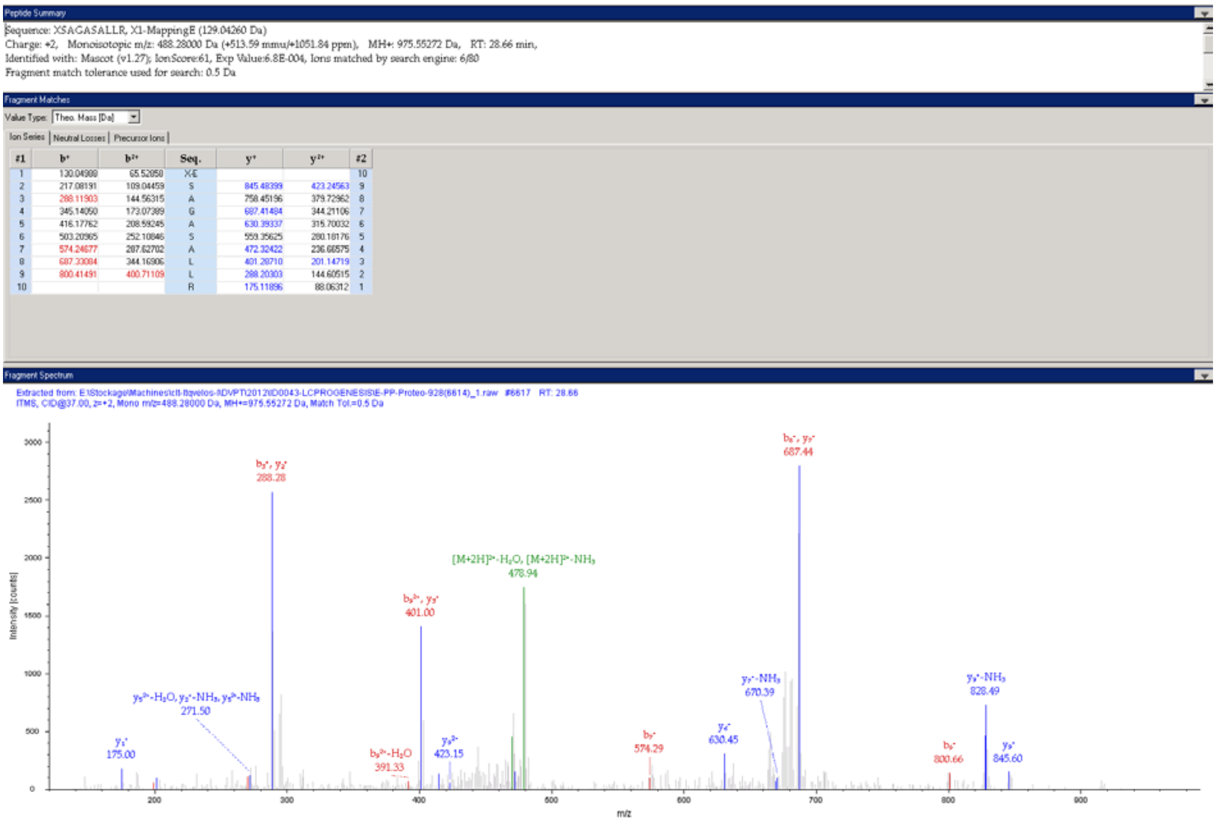
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			14
2	215.13903	108.07315	L	1420.80466	710.90597	13
3	286.17615	143.59171	A	1307.72059	654.36393	12
4	415.21875	208.11301	E	1236.68347	618.84537	11
5	502.25078	251.62903	S	1107.64087	554.32407	10
6	573.28790	287.14759	A	1020.60884	510.80806	9
7	686.37197	343.68962	L	949.57172	475.28950	8
8	814.43055	407.71891	Q	836.48765	418.74746	7
9	927.51462	464.26095	L	708.42907	354.71817	6
10	1040.59869	520.80298	L	595.34500	298.17614	5
11	1203.66201	602.33464	Y	482.26093	241.63410	4
12	1304.70969	652.85848	T	319.19761	160.10244	3
13	1375.74681	688.37704	A	218.14993	109.57860	2
14			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\cit-ltqvelos-IDVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #20906 RT: 75.42
ITMS, CID@37.00, z=+2, Mono m/z=761.43999 Da, MH+=1521.87271 Da, Match Tol.=0.5 Da

Protein references (1):

- Thyroglobulin (Fragment) OS=Homo sapiens GN=TG PE=4 SV=1 - [H0YB42_HUMAN]



Peptide Summary

Sequence: XSAGASALLR, X1-MappingE (129.04260 Da)
Charge: +2, Monoisotopic m/z: 488.28000 Da (+513.59 mmu/+1051.84 ppm), MH+: 975.55272 Da, RT: 28.66 min,
Identified with: Mascot (v1.27); IonScore:61, Exp Value:6.8E-004, Ions matched by search engine: 6/80
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

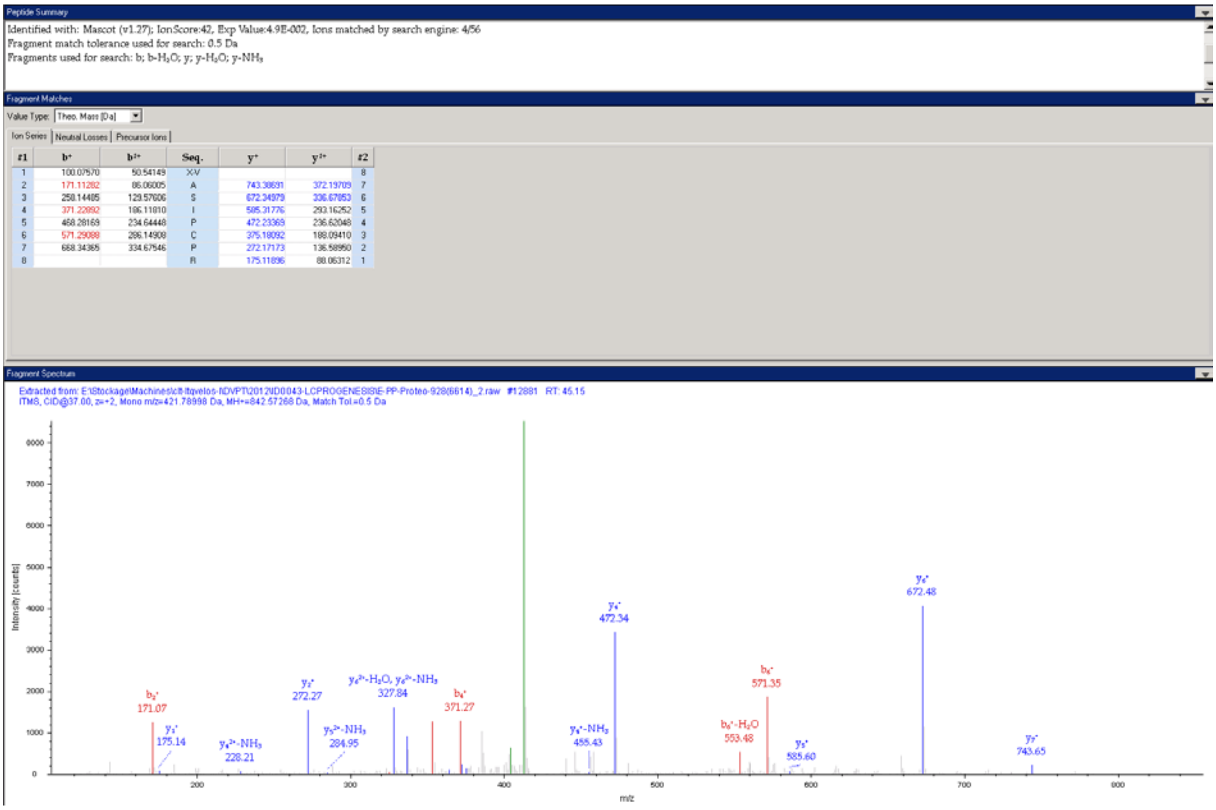
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04908	65.52050	X-E			10
2	217.08191	109.04459	S	845.48399	423.24563	9
3	288.11903	144.56315	A	758.45196	379.72962	8
4	345.14050	173.07389	G	687.41484	344.21106	7
5	416.17762	208.59245	A	630.39337	315.70032	6
6	503.20965	252.10846	S	559.35625	280.18176	5
7	574.24677	287.62702	A	472.32422	236.66575	4
8	687.33084	344.16906	L	401.28710	201.14719	3
9	800.41491	400.71109	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-928(6614)_1.raw #6617 RT: 28.66
ITMS, CID@37.00, z=+2, Mono m/z=488.28000 Da, MH+=975.55272 Da, Match Tol.=0.5 Da

Protein references (1):
- N-glycosylase/DNA lyase (Fragment) OS=Homo sapiens GN=OGG1 PE=4 SV=1 - [H7C0A1_HUMAN]



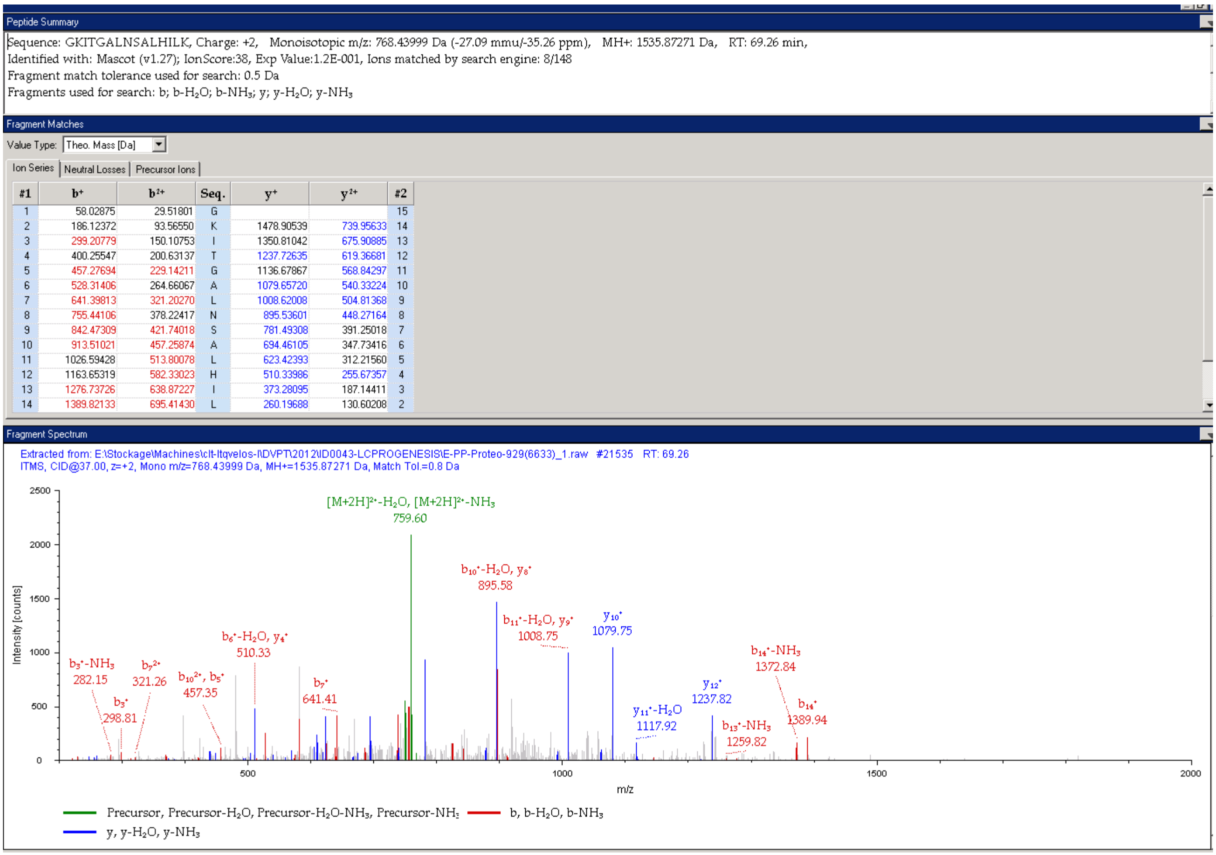
Identified with: Mascot (v1.27); IonScore:42, Exp Value:4.9E-002, Ions matched by search engine: 4/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	X-V			8
2	171.11282	86.06005	A	743.38691	372.19709	7
3	258.14485	129.57606	S	672.34979	336.67853	6
4	371.22892	186.11810	I	585.31776	293.16252	5
5	468.28169	234.64448	P	472.23369	236.62048	4
6	571.29088	286.14908	C	375.18092	188.09410	3
7	668.34365	334.67546	P	272.17173	136.58950	2
8			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\cit-ltqvelos-NDVPT\2012\ND0043-LCPROGENESIS\E-PP-Proteo-928(6614)_2.raw #12881 RT: 45.15
ITMS, CID@37.00, z=+2, Mono m/z=421.78998 Da, MH+=842.57268 Da, Match Tol.=0.5 Da

Protein references (1):
- Isoform 2 of Tudor domain-containing protein 10 OS=Homo sapiens GN=TDRD10 - [TDR10_HUMAN]



Peptide Summary

Sequence: GKITGALNSALHILK, Charge: +2, Monoisotopic m/z: 768.43999 Da (-27.09 mmu/-35.26 ppm), MH+: 1535.87271 Da, RT: 69.26 min,
Identified with: Mascot (v1.27); IonScore:38, Exp Value:1.2E-001, Ions matched by search engine: 8/148
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

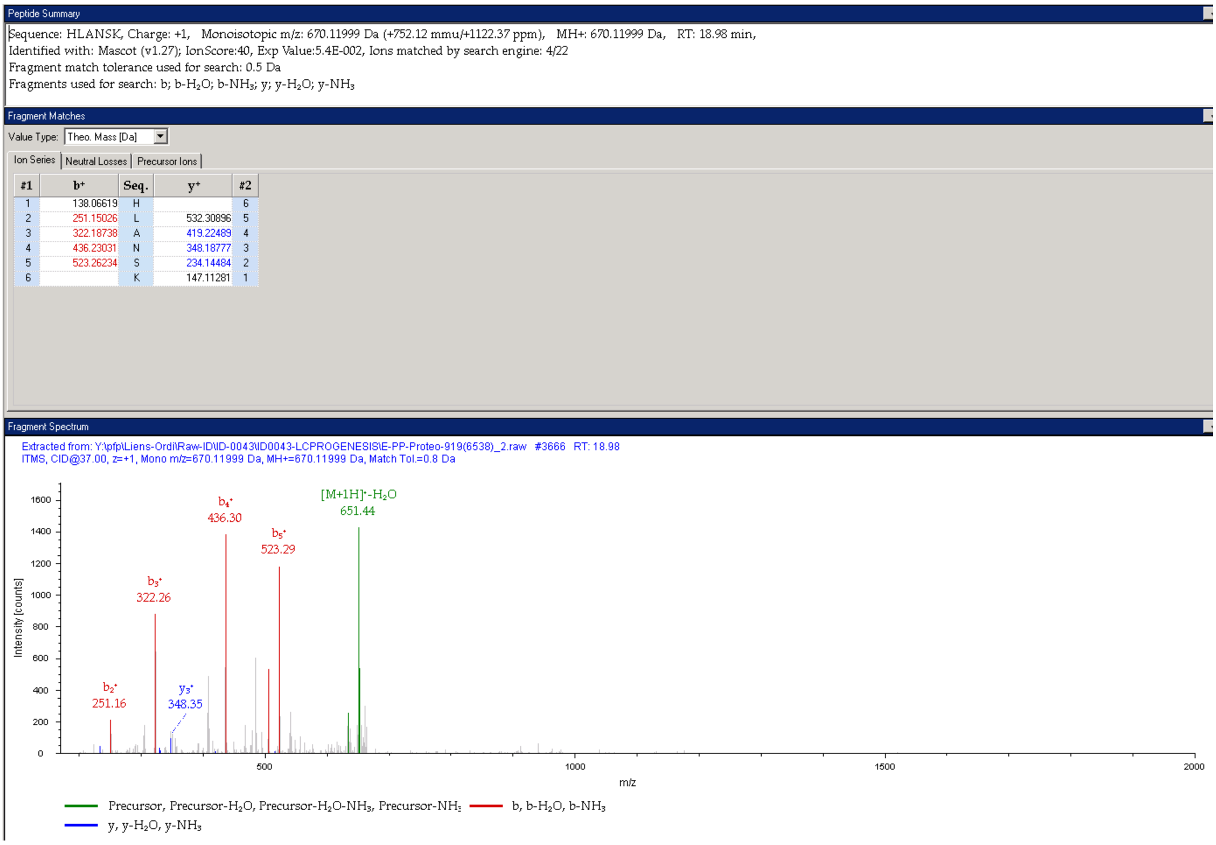
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			15
2	186.12372	93.56550	K	1478.90539	739.95633	14
3	299.20779	150.10753	I	1350.81042	675.90885	13
4	400.25547	200.63137	T	1237.72635	619.36681	12
5	457.27694	229.14211	G	1136.67867	568.84297	11
6	528.31406	264.66067	A	1079.65720	540.33224	10
7	641.39813	321.20270	L	1008.62008	504.81368	9
8	755.44106	378.22417	N	895.53601	448.27164	8
9	842.47309	421.74018	S	781.49308	391.25018	7
10	913.51021	457.25874	A	694.46105	347.73416	6
11	1026.59428	513.80078	L	623.42393	312.21560	5
12	1163.65319	582.33023	H	510.33986	255.67357	4
13	1276.73726	638.87227	I	373.28095	187.14411	3
14	1389.82133	695.41430	L	260.19688	130.60208	2

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-929(6633)_1.raw #21535 RT: 69.26
ITMS, CID@37.00, z=+2, Mono m/z=768.43999 Da, MH+=1535.87271 Da, Match Tol.=0.8 Da

Protein references (1):

- Lysine-specific demethylase 4D OS=Homo sapiens GN=KDM4D PE=1 SV=3 - [KDM4D_HUMAN]



Sequence: HLANSK, Charge: +1, Monoisotopic m/z: 670.11999 Da (+752.12 mmu/+1122.37 ppm), MH+: 670.11999 Da, RT: 18.98 min,
Identified with: Mascot (v1.27); IonScore:40, Exp Value:5.4E-002, Ions matched by search engine: 4/22
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

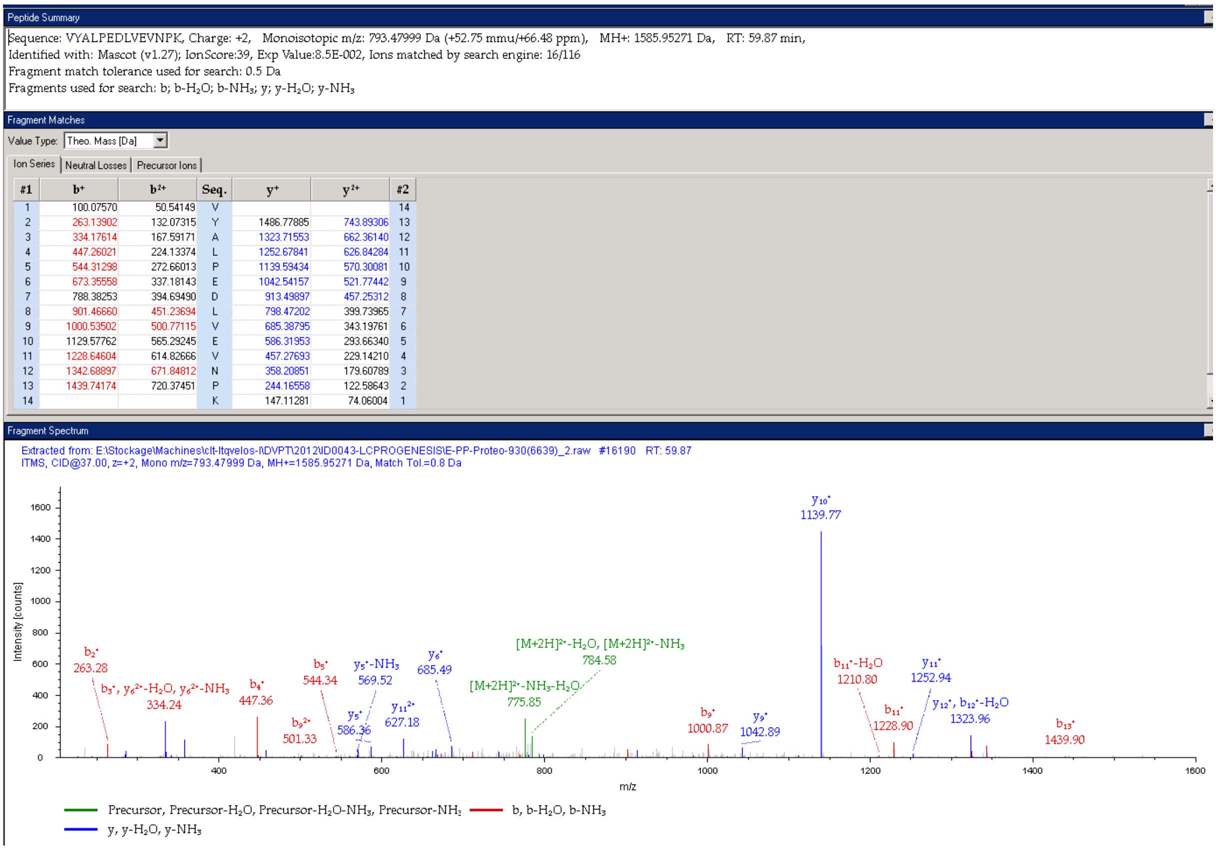
Value Type: Theo. Mass [Da]

#1	b^+	Seq.	y^+	#2
1	138.06619	H		6
2	251.15026	L	532.30896	5
3	322.18738	A	419.22489	4
4	436.23031	N	348.18777	3
5	523.26234	S	234.14484	2
6		K	147.11281	1

Extracted from: Y:\pfp\Liens-Ordi\Raw-ID\ID-0043\ID0043-LCPROGENESIS\E-PP-Proteo-919(6538)_2.raw #3666 RT: 18.98
ITMS, CID@37.00, z=+1, Mono m/z=670.11999 Da, MH+=670.11999 Da, Match Tol.=0.8 Da

Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3 — b, b-H_2O, b-NH_3
y, y-H_2O, y-NH_3

Protein references (2):
- Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]



Peptide Summary

Sequence: VYALPEDLVEVNPK, Charge: +2, Monoisotopic m/z: 793.47999 Da (+52.75 mmu/+66.48 ppm), MH+: 1585.95271 Da, RT: 59.87 min,
Identified with: Mascot (v1.27); IonScore:39, Exp Value:8.5E-002, Ions matched by search engine: 16/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

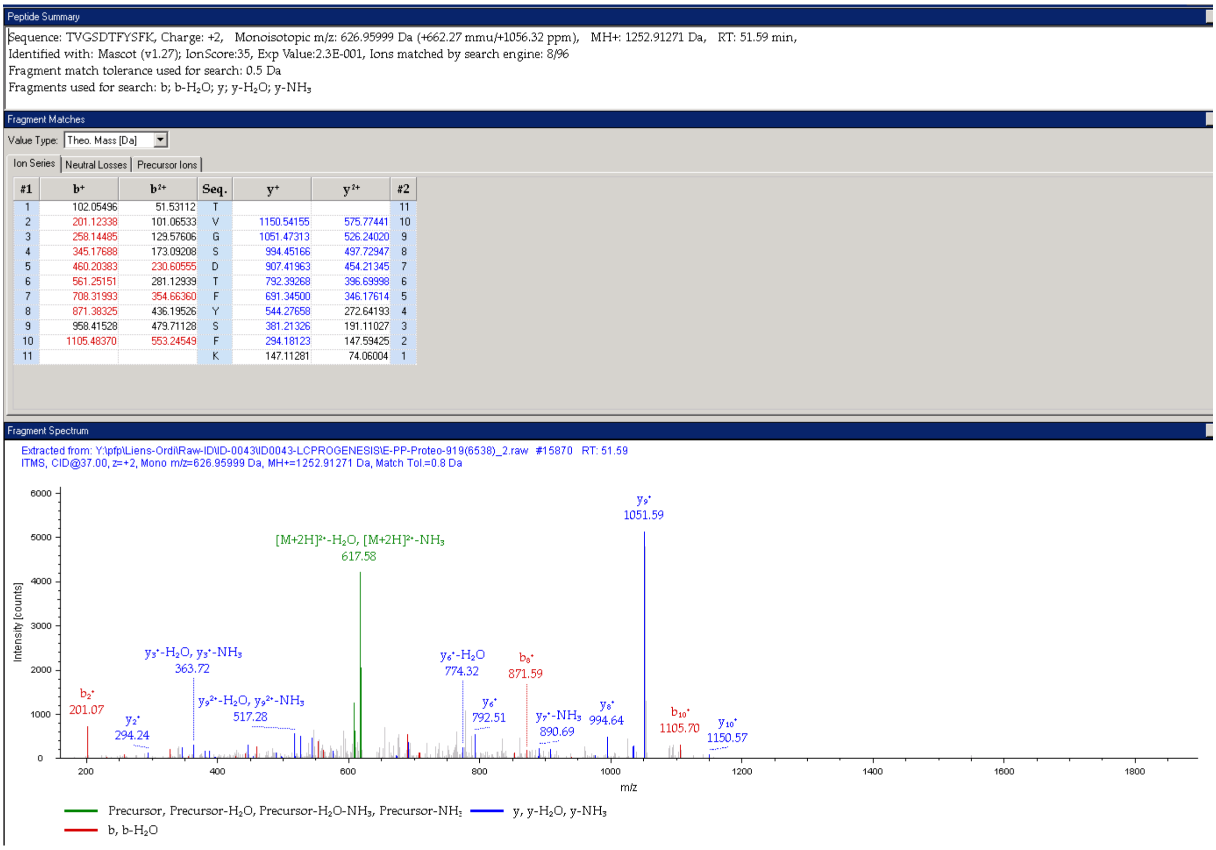
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			14
2	263.13902	132.07315	Y	1486.77885	743.89306	13
3	334.17614	167.59171	A	1323.71553	662.36140	12
4	447.26021	224.13374	L	1252.67841	626.84284	11
5	544.31298	272.66013	P	1139.59434	570.30081	10
6	673.35558	337.18143	E	1042.54157	521.77442	9
7	788.38253	394.69490	D	913.49897	457.25312	8
8	901.46660	451.23694	L	798.47202	399.73965	7
9	1000.53502	500.77115	V	685.38795	343.19761	6
10	1129.57762	565.29245	E	586.31953	293.66340	5
11	1228.64604	614.82666	V	457.27693	229.14210	4
12	1342.68897	671.84812	N	358.20851	179.60789	3
13	1439.74174	720.37451	P	244.16558	122.58643	2
14			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #16190 RT: 59.87
ITMS, CID@37.00, z=+2, Mono m/z=793.47999 Da, MH+=1585.95271 Da, Match Tol.=0.8 Da

Protein references (3):

- Lysyl-bradykinin OS=Homo sapiens GN=KNG1 PE=4 SV=1 - [C9JEX1_HUMAN]



Peptide Summary

Sequence: TVGSDTFYSFK, Charge: +2, Monoisotopic m/z: 626.95999 Da (+662.27 mmu/+1056.32 ppm), MH+: 1252.91271 Da, RT: 51.59 min,
Identified with: Mascot (v1.27); IonScore:35, Exp Value:2.3E-001, Ions matched by search engine: 8/96
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

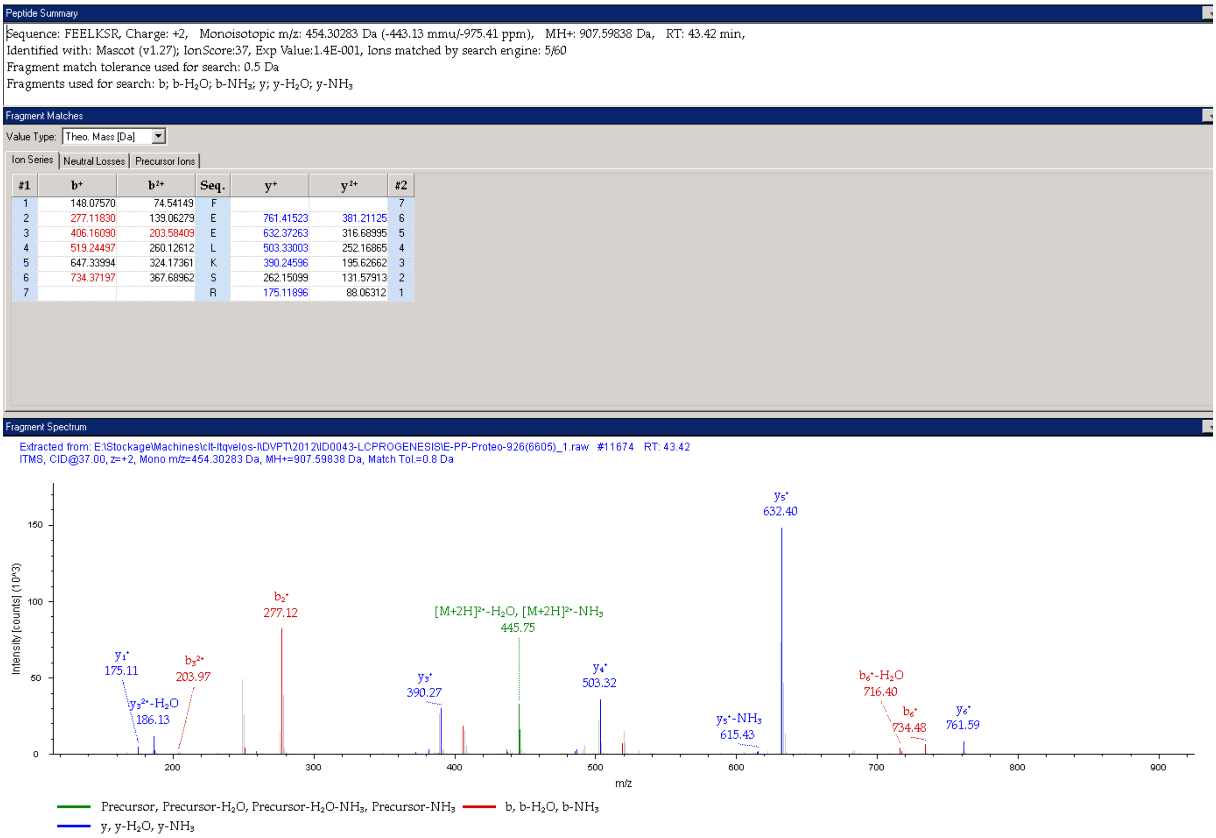
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			11
2	201.12338	101.06533	V	1150.54155	575.77441	10
3	258.14485	129.57606	G	1051.47313	526.24020	9
4	345.17688	173.09208	S	994.45166	497.72947	8
5	460.20383	230.60555	D	907.41963	454.21345	7
6	561.25151	281.12939	T	792.39268	396.69998	6
7	708.31993	354.66360	F	691.34500	346.17614	5
8	871.38325	436.19526	Y	544.27658	272.64193	4
9	958.41528	479.71128	S	381.21326	191.11027	3
10	1105.48370	553.24549	F	294.18123	147.59425	2
11			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: Y:\pfp\Liens-Ordi\Raw-ID\ID-0043\ID0043-LCPROGENESIS\E-PP-Proteo-919(6538)_2.raw #15870 RT: 51.59
ITMS, CID@37.00, z=+2, Mono m/z=626.95999 Da, MH+=1252.91271 Da, Match Tol.=0.8 Da

Protein references (1):
- Tetranectin OS=Homo sapiens GN=CLEC3B PE=4 SV=1 - [E9PHK0_HUMAN]



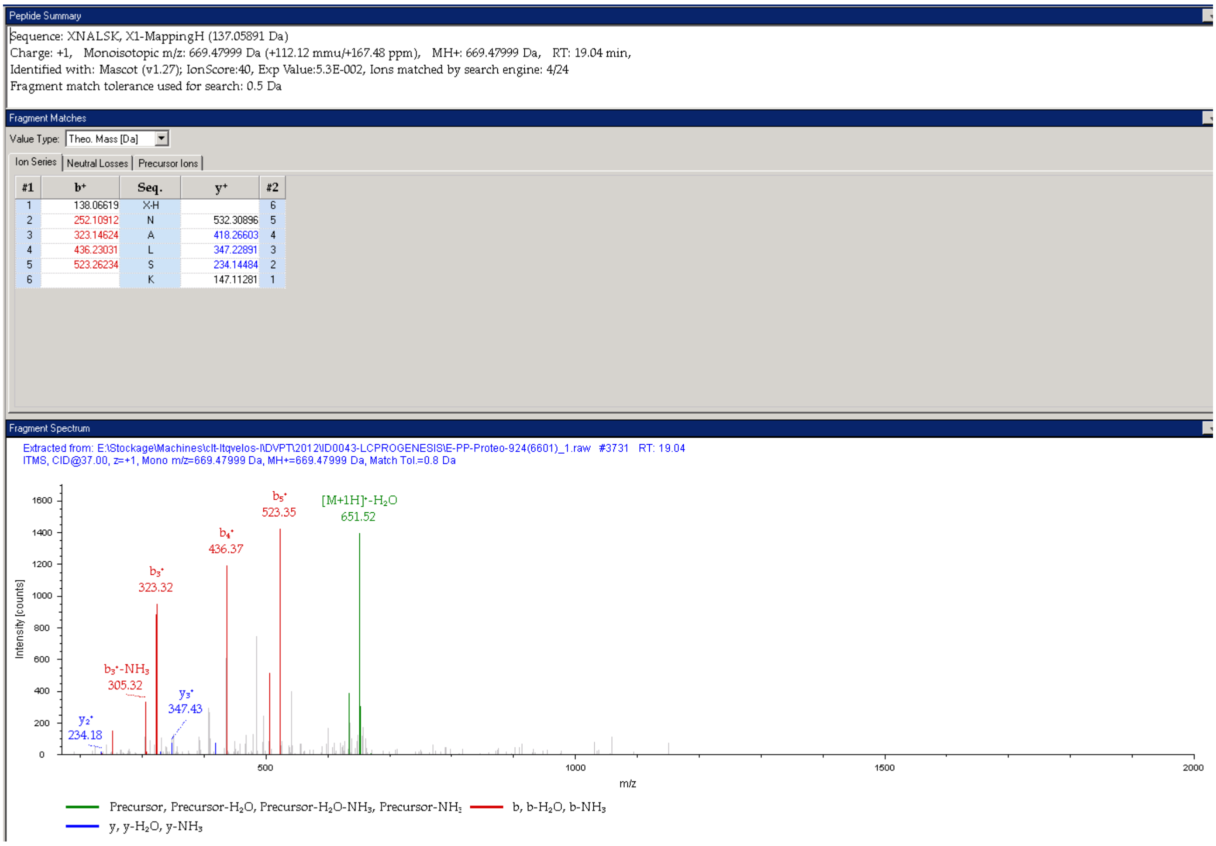
Sequence: FEELKSR, Charge: +2, Monoisotopic m/z: 454.30283 Da (-443.13 mmu/-975.41 ppm), MH+: 907.59838 Da, RT: 43.42 min,
Identified with: Mascot (v1.27); IonScore:37, Exp Value:1.4E-001, Ions matched by search engine: 5/60
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			7
2	277.11830	139.06279	E	761.41523	381.21125	6
3	406.16090	203.58409	E	632.37263	316.68995	5
4	519.24497	260.12612	L	503.33003	252.16865	4
5	647.33994	324.17361	K	390.24596	195.62662	3
6	734.37197	367.68962	S	262.15099	131.57913	2
7			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-926(6605)_1.raw #11674 RT: 43.42
ITMS, CID@37.00, z=+2, Mono m/z=454.30283 Da, MH+=907.59838 Da, Match Tol.=0.8 Da

Protein references (1):
- Centrosomal protein of 192 kDa (Fragment) OS=Homo sapiens GN=CEP192 PE=4 SV=1 - [H0Y9P3_HUMAN]



Sequence: XNALSK, X1-MappingH (137.05891 Da)
Charge: +1, Monoisotopic m/z: 669.47999 Da (+112.12 mmu/+167.48 ppm), MH+: 669.47999 Da, RT: 19.04 min,
Identified with: Mascot (v1.27); IonScore:40, Exp Value:5.3E-002, Ions matched by search engine: 4/24
Fragment match tolerance used for search: 0.5 Da

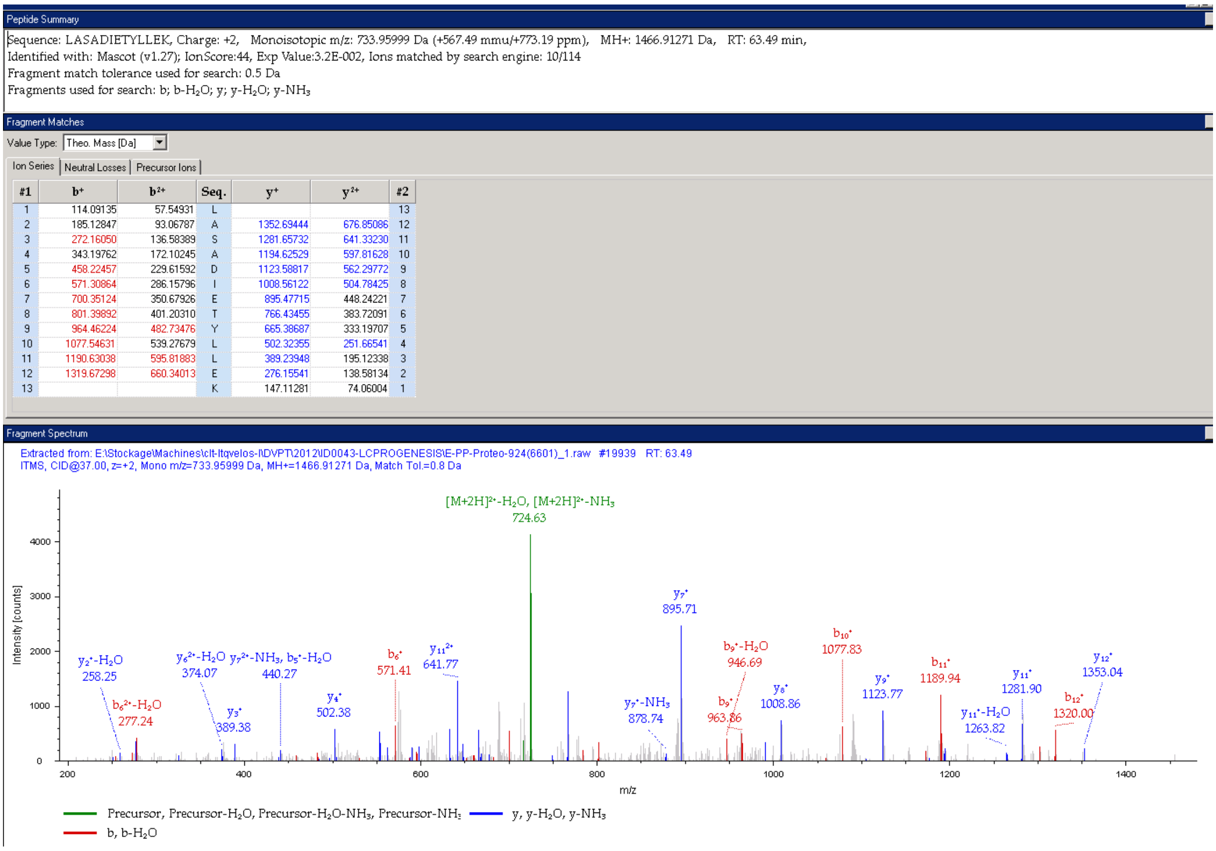
Value Type: Theo. Mass [Da]

#1	b^+	Seq.	y^+	#2
1	138.06619	X-H		6
2	252.10912	N	532.30896	5
3	323.14624	A	418.26603	4
4	436.23031	L	347.22891	3
5	523.26234	S	234.14484	2
6		K	147.11281	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-924(6601)_1.raw #3731 RT: 19.04
ITMS, CID@37.00, z=+1, Mono m/z=669.47999 Da, MH+=669.47999 Da, Match Tol.=0.8 Da

Protein references (9):

- Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3 - [MYH1_HUMAN]



Peptide Summary

Sequence: LASADIETYLLEK, Charge: +2, Monoisotopic m/z: 733.95999 Da (+567.49 mmu/+773.19 ppm), MH+: 1466.91271 Da, RT: 63.49 min,
Identified with: Mascot (v1.27); IonScore:44, Exp Value:3.2E-002, Ions matched by search engine: 10/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

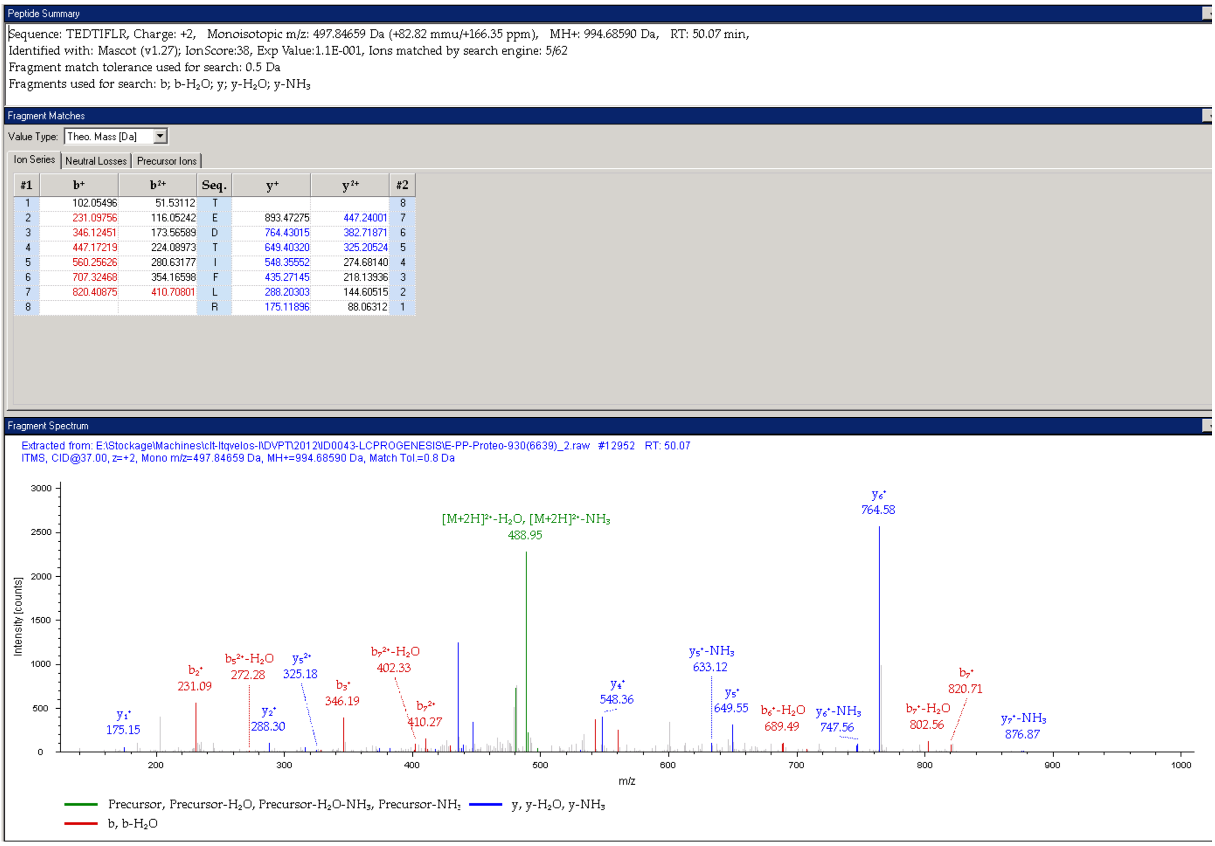
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			13
2	185.12847	93.06787	A	1352.69444	676.85086	12
3	272.16050	136.58389	S	1281.65732	641.33230	11
4	343.19762	172.10245	A	1194.62529	597.81628	10
5	458.22457	229.61592	D	1123.58817	562.29772	9
6	571.30864	286.15796	I	1008.56122	504.78425	8
7	700.35124	350.67926	E	895.47715	448.24221	7
8	801.39892	401.20310	T	766.43455	383.72091	6
9	964.46224	482.73476	Y	665.38687	333.19707	5
10	1077.54631	539.27679	L	502.32355	251.66541	4
11	1190.63038	595.81883	L	389.23948	195.12338	3
12	1319.67298	660.34013	E	276.15541	138.58134	2
13			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-924(6601)_1.raw #19939 RT: 63.49
ITMS, CID@37.00, z=+2, Mono m/z=733.95999 Da, MH+=1466.91271 Da, Match Tol.=0.8 Da

Protein references (2):
- Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1 - [A1AG1_HUMAN]



Peptide Summary

Sequence: TEDTIFLR, Charge: +2, Monoisotopic m/z: 497.84659 Da (+82.82 mmu/+166.35 ppm), MH+: 994.68590 Da, RT: 50.07 min,
Identified with: Mascot (v1.27); IonScore:38, Exp Value:1.1E-001, Ions matched by search engine: 5/62
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

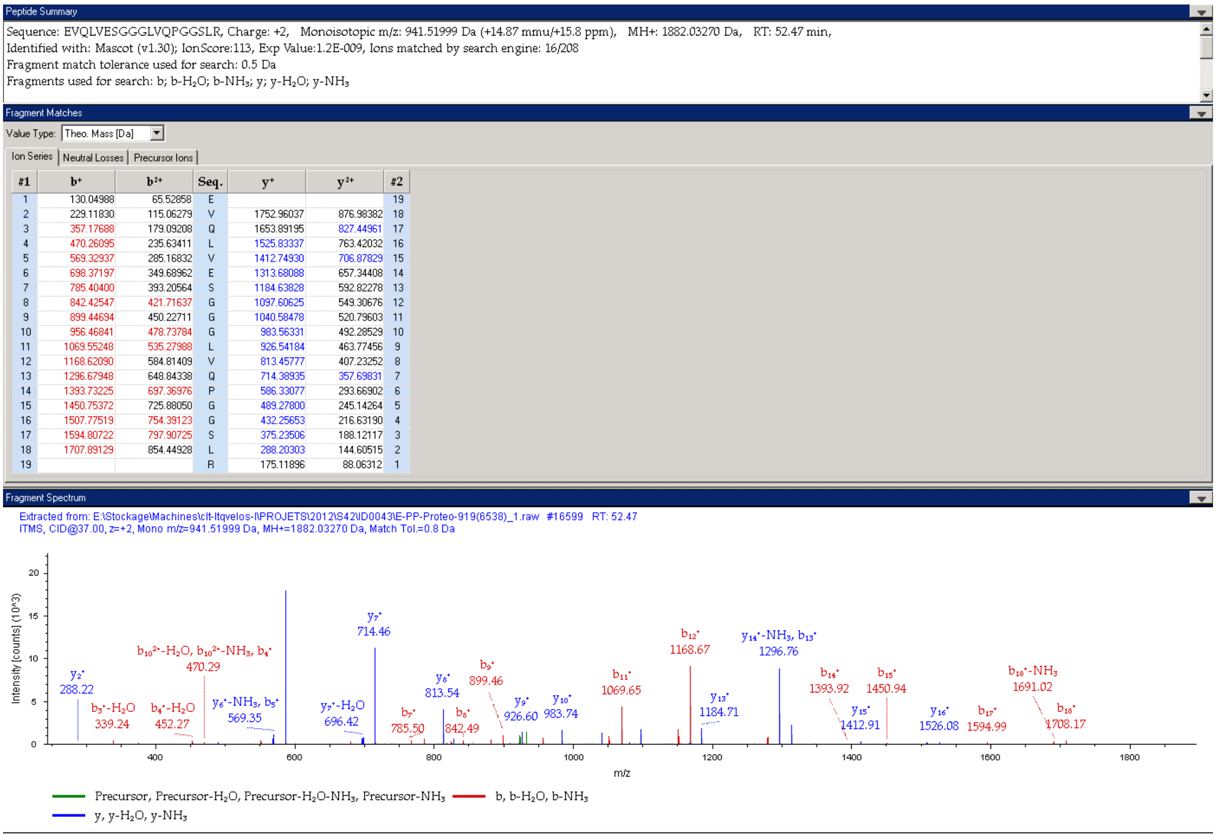
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			8
2	231.09756	116.05242	E	893.47275	447.24001	7
3	346.12451	173.56589	D	764.43015	382.71871	6
4	447.17219	224.08973	T	649.40320	325.20524	5
5	560.25626	280.63177	I	548.35552	274.68140	4
6	707.32468	354.16598	F	435.27145	218.13936	3
7	820.40875	410.70801	L	288.20303	144.60515	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #12952 RT: 50.07
ITMS, CID@37.00, z=+2, Mono m/z=497.84659 Da, MH+=994.68590 Da, Match Tol.=0.8 Da

Protein references (2):

- Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1 - [HV305_HUMAN]



Peptide Summary

Sequence: EVQLVESGGGLVQPGGSLR, Charge: +2, Monoisotopic m/z: 941.51999 Da (+14.87 mmu/+15.8 ppm), MH+: 1882.03270 Da, RT: 52.47 min,
Identified with: Mascot (v1.30); IonScore:113, Exp Value:1.2E-009, Ions matched by search engine: 16/208
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

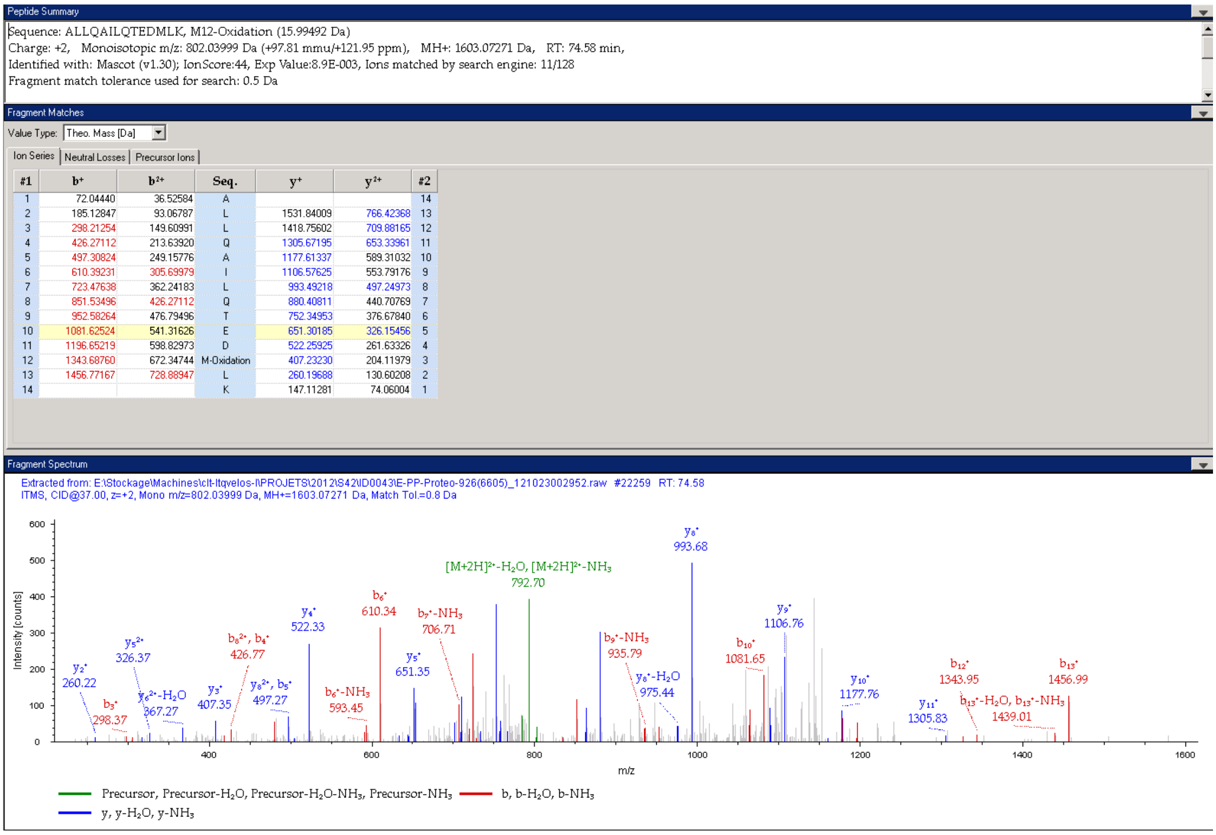
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			19
2	229.11830	115.06279	V	1752.96037	876.98382	18
3	357.17688	179.09208	Q	1653.89195	827.44961	17
4	470.26095	235.63411	L	1525.83337	763.42032	16
5	569.32937	285.16832	V	1412.74930	706.87829	15
6	698.37197	349.68962	E	1313.68088	657.34408	14
7	785.40400	393.20564	S	1184.63828	592.82278	13
8	842.42547	421.71637	G	1097.60625	549.30676	12
9	899.44694	450.22711	G	1040.58478	520.79603	11
10	956.46841	478.73784	G	983.56331	492.28529	10
11	1069.55248	535.27988	L	926.54184	463.77456	9
12	1168.62090	584.81409	V	813.45777	407.23252	8
13	1296.67948	648.84338	Q	714.38935	357.69831	7
14	1393.73225	697.36976	P	586.33077	293.66902	6
15	1450.75372	725.88050	G	489.27800	245.14264	5
16	1507.77519	754.39123	G	432.25653	216.63190	4
17	1594.80722	797.90725	S	375.23506	188.12117	3
18	1707.89129	854.44928	L	288.20303	144.60515	2
19			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_1.raw #16599 RT: 52.47
ITMS, CID@37.00, z=+2, Mono m/z=941.51999 Da, MH+=1882.03270 Da, Match Tol.=0.8 Da

Protein references (1):
- Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]



Sequence: ALLQAILQTEDMLK, M12-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 802.03999 Da (+97.81 mmu/+121.95 ppm), MH+: 1603.07271 Da, RT: 74.58 min,
Identified with: Mascot (v1.30); IonScore:44, Exp Value:8.9E-003, Ions matched by search engine: 11/128
Fragment match tolerance used for search: 0.5 Da

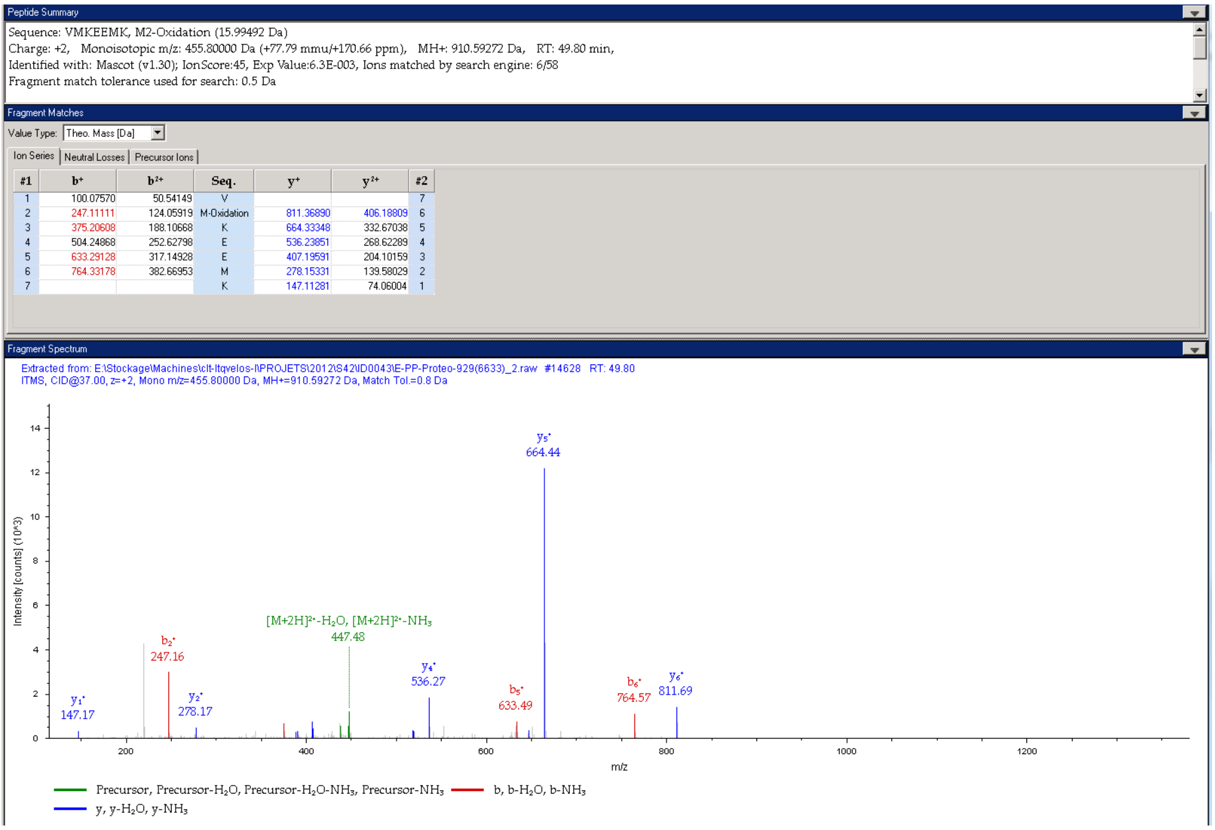
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			14
2	185.12847	93.06787	L	1531.84009	766.42368	13
3	298.21254	149.60991	L	1418.75602	709.88165	12
4	426.27112	213.63920	Q	1305.67195	653.33961	11
5	497.30824	249.15776	A	1177.61337	589.31032	10
6	610.39231	305.69979	I	1106.57625	553.79176	9
7	723.47638	362.24183	L	993.49218	497.24973	8
8	851.53496	426.27112	Q	880.40811	440.70769	7
9	952.58264	476.79496	T	752.34953	376.67840	6
10	1081.62524	541.31626	E	651.30185	326.15456	5
11	1196.65219	598.82973	D	522.25925	261.63326	4
12	1343.68760	672.34744	M-Oxidation	407.23230	204.11979	3
13	1456.77167	728.88947	L	260.19688	130.60208	2
14			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_121023002952.raw #22259 RT: 74.58
ITMS, CID@37.00, z=+2, Mono m/z=802.03999 Da, MH+=1603.07271 Da, Match Tol.=0.8 Da

- Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
- b, b-H_2O, b-NH_3
- y, y-H_2O, y-NH_3

Protein references (1):
- Schlafen family member 14 OS=Homo sapiens GN=SLFN14 PE=2 SV=2 - [SLN14_HUMAN]



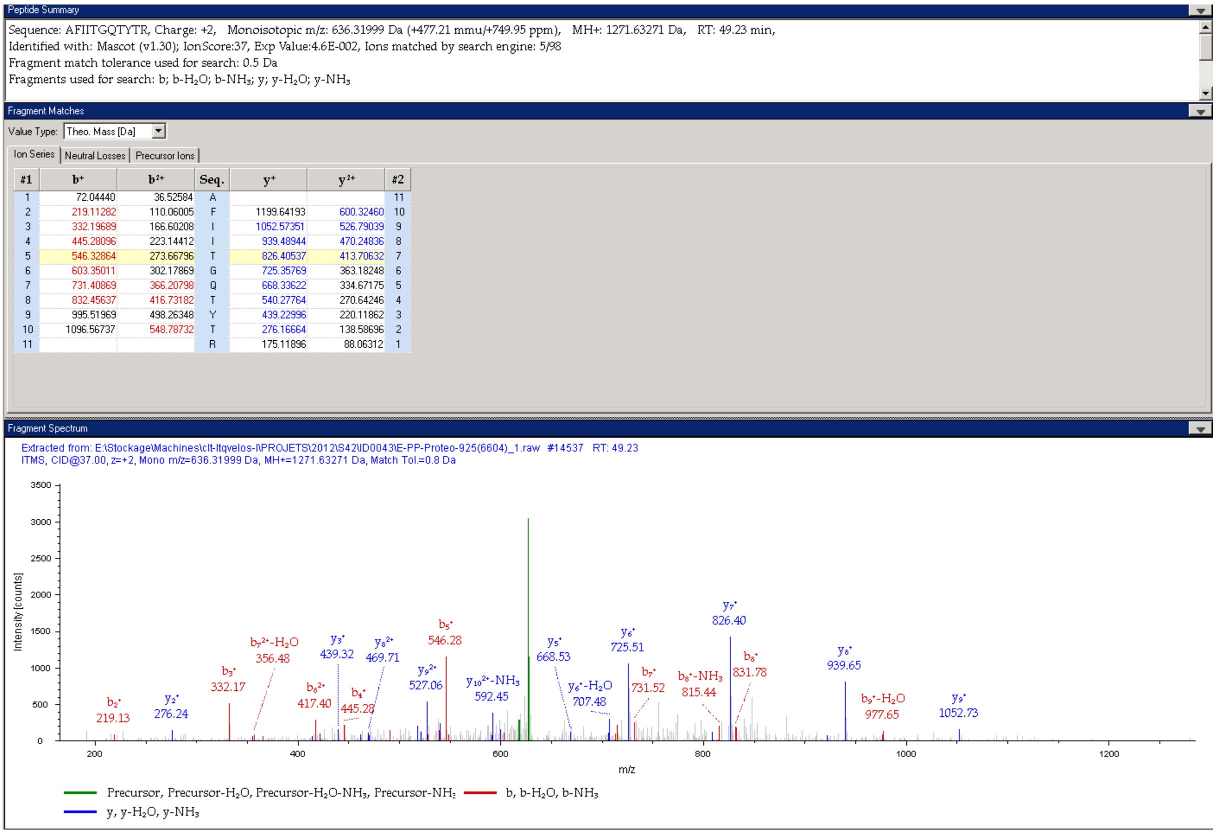
Sequence: VMKEEMK, M2-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 455.80000 Da (+77.79 mmu/+170.66 ppm), MH+: 910.59272 Da, RT: 49.80 min,
Identified with: Mascot (v1.30); IonScore:45, Exp Value:6.3E-003, Ions matched by search engine: 6/58
Fragment match tolerance used for search: 0.5 Da

Value Type: Theo. Mass [Da]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	100.07570	50.54149	V			7
2	247.11111	124.05919	M-Oxidation	811.36890	406.18809	6
3	375.20608	188.10668	K	664.33348	332.67038	5
4	504.24868	252.62798	E	536.23851	268.62289	4
5	633.29128	317.14928	E	407.19591	204.10159	3
6	764.33178	382.66953	M	278.15331	139.58029	2
7			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #14628 RT: 49.80
ITMS, CID@37.00, z=+2, Mono m/z=455.80000 Da, MH+=910.59272 Da, Match Tol.=0.8 Da

Protein references (1):
- Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]



Sequence: AFIITGQTYTR, Charge: +2, Monoisotopic m/z: 636.31999 Da (+477.21 mmu/+749.95 ppm), MH+: 1271.63271 Da, RT: 49.23 min,
Identified with: Mascot (v1.30); IonScore:37, Exp Value:4.6E-002, Ions matched by search engine: 5/98
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

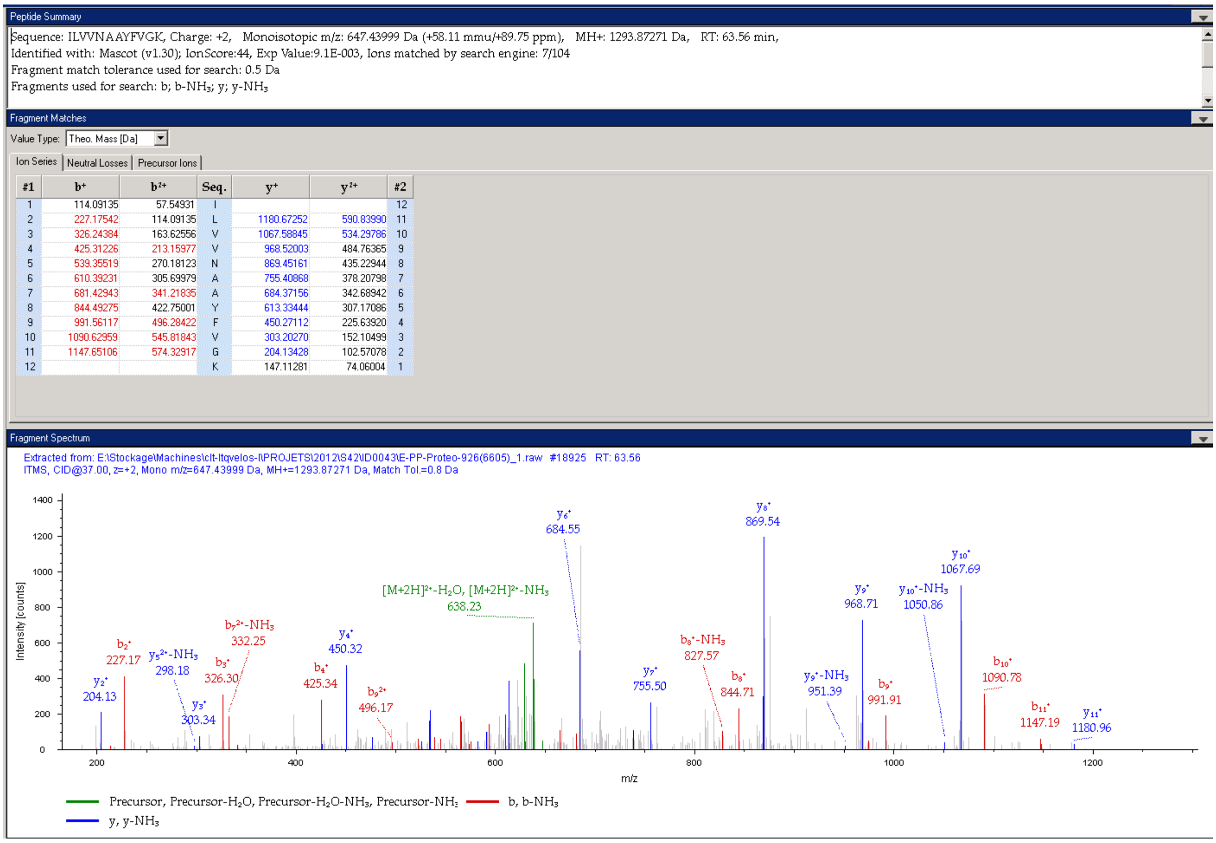
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			11
2	219.11282	110.06005	F	1199.64193	600.32460	10
3	332.19689	166.60208	I	1052.57351	526.79039	9
4	445.28096	223.14412	I	939.48944	470.24836	8
5	546.32864	273.66796	T	826.40537	413.70632	7
6	603.35011	302.17869	G	725.35769	363.18248	6
7	731.40869	366.20798	Q	668.33622	334.67175	5
8	832.45637	416.73182	T	540.27764	270.64246	4
9	995.51969	498.26348	Y	439.22996	220.11862	3
10	1096.56737	548.78732	T	276.16664	138.58696	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-925(6604)_1.raw #14537 RT: 49.23
ITMS, CID@37.00, z=+2, Mono m/z=636.31999 Da, MH+=1271.63271 Da, Match Tol.=0.8 Da

Protein references (1):

- Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2 - [SPB5_HUMAN]



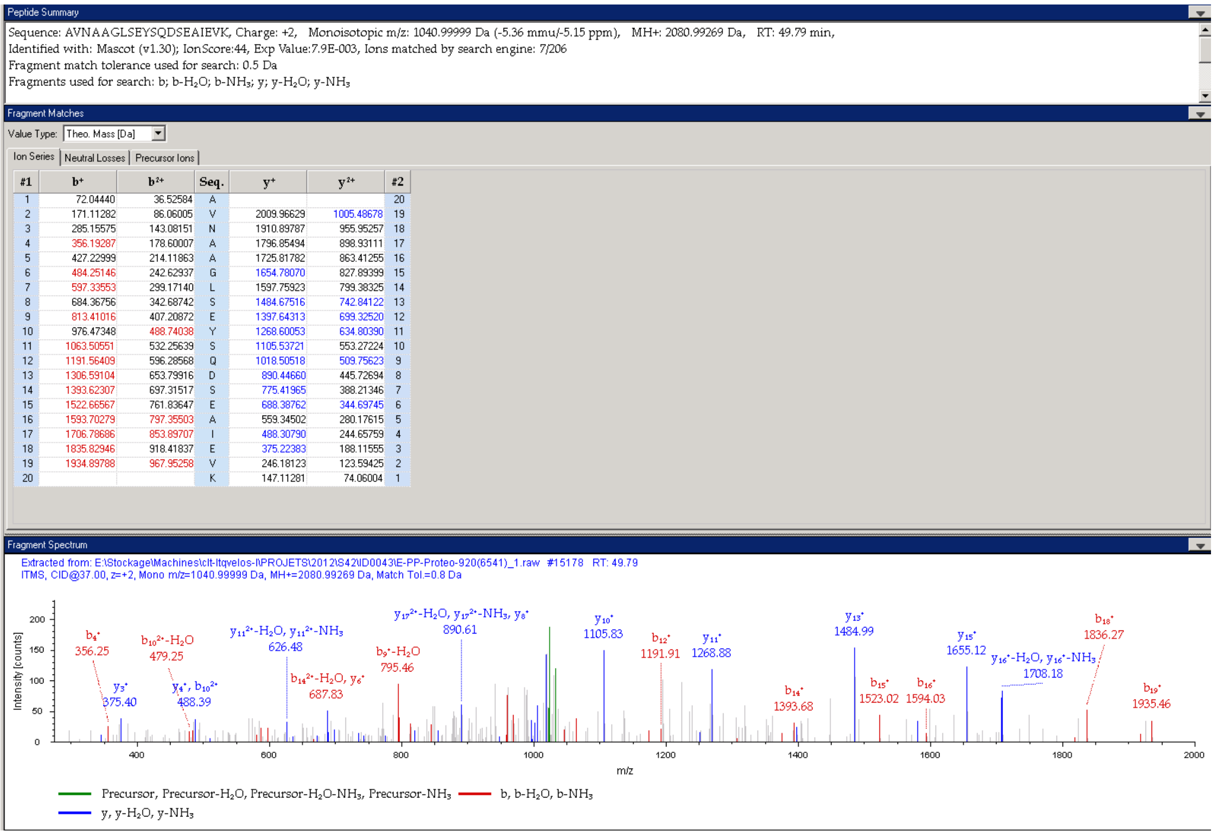
Sequence: ILVVNAAYFVGK, Charge: +2, Monoisotopic m/z: 647.43999 Da (+58.11 mmu/+89.75 ppm), MH+: 1293.87271 Da, RT: 63.56 min,
Identified with: Mascot (v1.30); IonScore:44, Exp Value:9.1E-003, Ions matched by search engine: 7/104
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-NH_3; y; y-NH_3

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			12
2	227.17542	114.09135	L	1180.67252	590.83990	11
3	326.24384	163.62556	V	1067.58845	534.29786	10
4	425.31226	213.15977	V	968.52003	484.76365	9
5	539.35519	270.18123	N	869.45161	435.22944	8
6	610.39231	305.69979	A	755.40868	378.20798	7
7	681.42943	341.21835	A	684.37156	342.68942	6
8	844.49275	422.75001	Y	613.33444	307.17086	5
9	991.56117	496.28422	F	450.27112	225.63920	4
10	1090.62959	545.81843	V	303.20270	152.10499	3
11	1147.65106	574.32917	G	204.13428	102.57078	2
12			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_1.raw #18925 RT: 63.56
ITMS, CID@37.00, z=+2, Mono m/z=647.43999 Da, MH+=1293.87271 Da, Match Tol.=0.8 Da

Protein references (1):
- Myomesin-1 OS=Homo sapiens GN=MYOM1 PE=1 SV=2 - [MYOM1_HUMAN]



Sequence: AVNAAGLSEYSQDSEAIEVK, Charge: +2, Monoisotopic m/z: 1040.99999 Da (-5.36 mmu/-5.15 ppm), MH+: 2080.99269 Da, RT: 49.79 min,
Identified with: Mascot (v1.30); IonScore:44, Exp Value:7.9E-003, Ions matched by search engine: 7/206
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

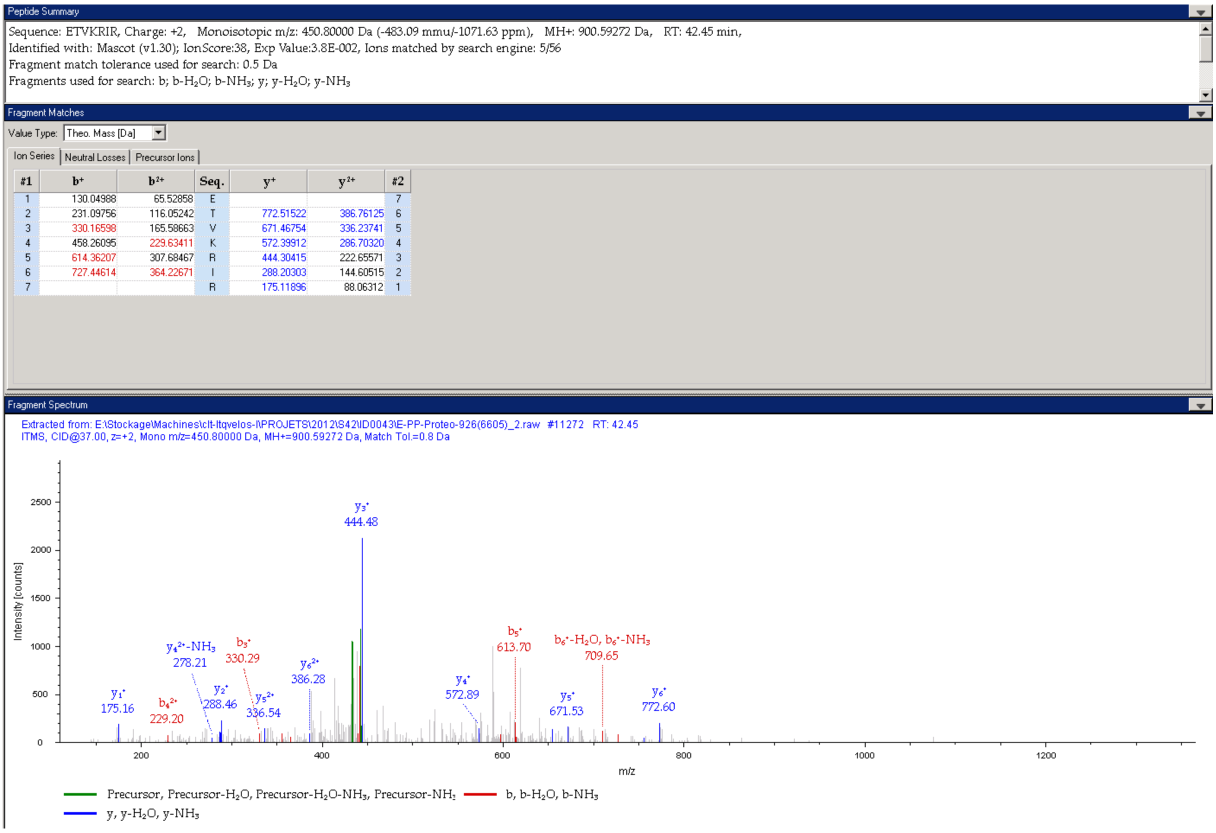
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			20
2	171.11282	86.06005	V	2009.96629	1005.48678	19
3	285.15575	143.08151	N	1910.89787	955.95257	18
4	356.19287	178.60007	A	1796.85494	898.93111	17
5	427.22999	214.11863	A	1725.81782	863.41255	16
6	484.25146	242.62937	G	1654.78070	827.89399	15
7	597.33553	299.17140	L	1597.75923	799.38325	14
8	684.36756	342.68742	S	1484.67516	742.84122	13
9	813.41016	407.20872	E	1397.64313	699.32520	12
10	976.47348	488.74038	Y	1268.60053	634.80390	11
11	1063.50551	532.25639	S	1105.53721	553.27224	10
12	1191.56409	596.28568	Q	1018.50518	509.75623	9
13	1306.59104	653.79916	D	890.44660	445.72694	8
14	1393.62307	697.31517	S	775.41965	388.21346	7
15	1522.66567	761.83647	E	688.38762	344.69745	6
16	1593.70279	797.35503	A	559.34502	280.17615	5
17	1706.78686	853.89707	I	488.30790	244.65759	4
18	1835.82946	918.41837	E	375.22383	188.11555	3
19	1934.89788	967.95258	V	246.18123	123.59425	2
20			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_1.raw #15178 RT: 49.79
ITMS, CID@37.00, z=+2, Mono m/z=1040.99999 Da, MH+=2080.99269 Da, Match Tol.=0.8 Da

Protein references (1):

- Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3 - [ATP7A_HUMAN]



Peptide Summary

Sequence: ETVKRIR, Charge: +2, Monoisotopic m/z: 450.80000 Da (-483.09 mmu/-1071.63 ppm), MH+: 900.59272 Da, RT: 42.45 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.8E-002, Ions matched by search engine: 5/56
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

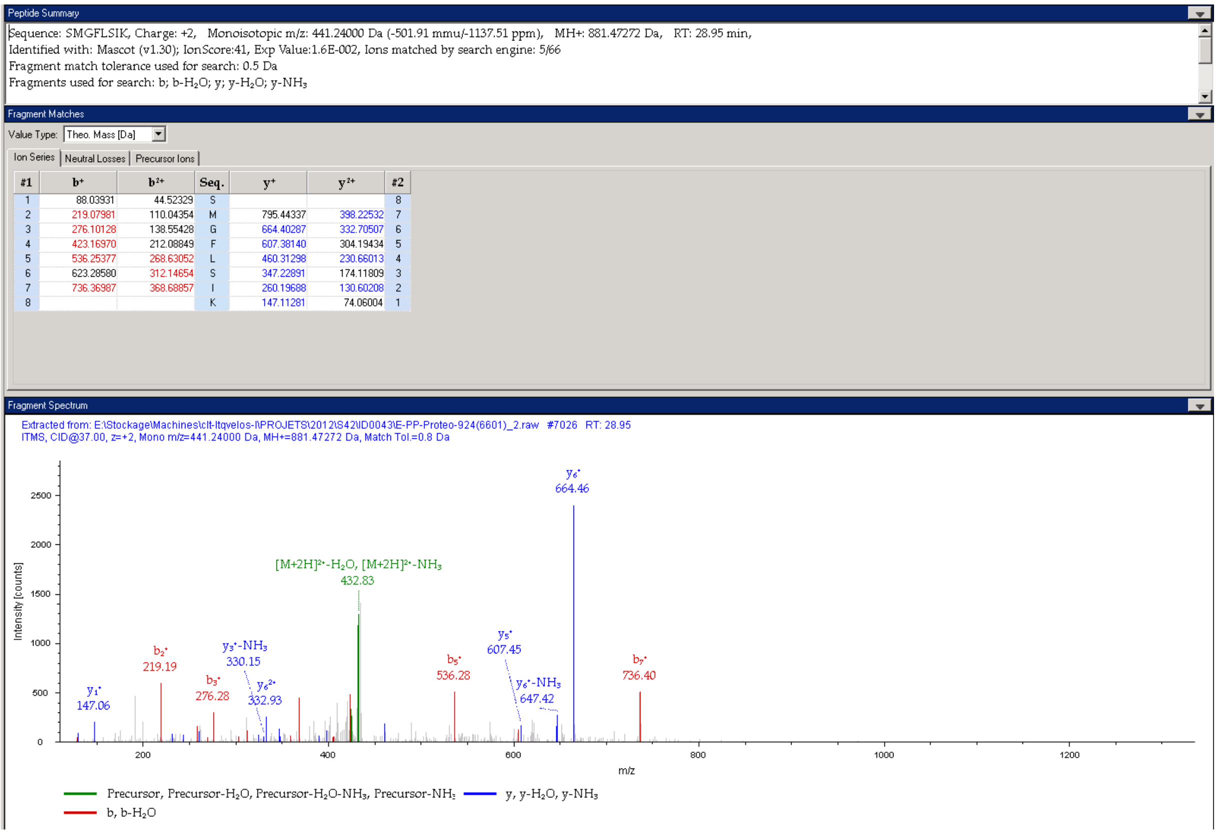
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			7
2	231.09756	116.05242	T	772.51522	386.76125	6
3	330.16598	165.58663	V	671.46754	336.23741	5
4	458.26095	229.63411	K	572.39912	286.70320	4
5	614.36207	307.68467	R	444.30415	222.65571	3
6	727.44614	364.22671	I	288.20303	144.60515	2
7			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_2.raw #11272 RT: 42.45
ITMS, CID@37.00, z=+2, Mono m/z=450.80000 Da, MH+=900.59272 Da, Match Tol.=0.8 Da

Protein references (1):
- Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 - [PTN13_HUMAN]



Peptide Summary

Sequence: SMGFLSIK, Charge: +2, Monoisotopic m/z: 441.24000 Da (-501.91 mmu/-1137.51 ppm), MH+: 881.47272 Da, RT: 28.95 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:1.6E-002, Ions matched by search engine: 5/66
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

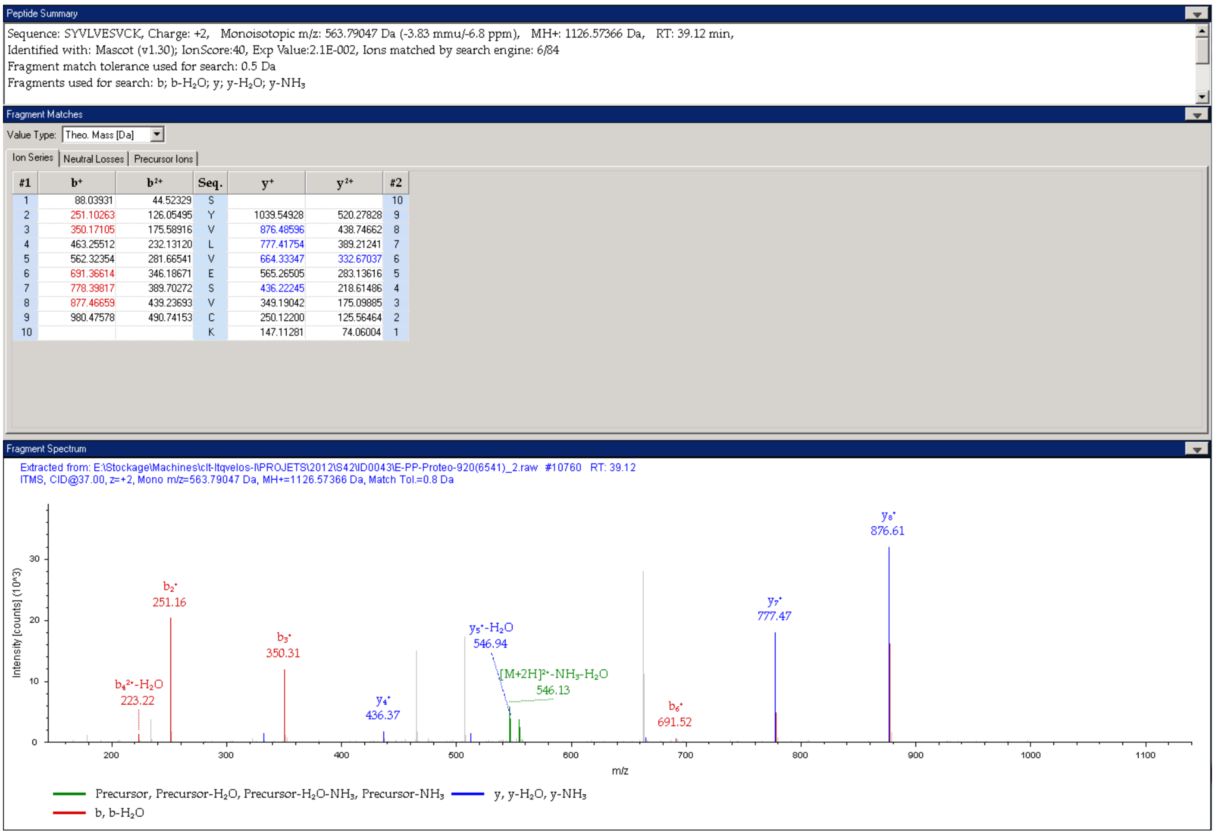
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			8
2	219.07981	110.04354	M	795.44337	398.22532	7
3	276.10128	138.55428	G	664.40287	332.70507	6
4	423.16970	212.08849	F	607.38140	304.19434	5
5	536.25377	268.63052	L	460.31298	230.66013	4
6	623.28580	312.14654	S	347.22891	174.11809	3
7	736.36987	368.68857	I	260.19688	130.60208	2
8			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #7026 RT: 28.95
ITMS, CID@37.00, z=+2, Mono m/z=441.24000 Da, MH+=881.47272 Da, Match Tol.=0.8 Da

Protein references (1):

- Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2 - [MDN1_HUMAN]



Peptide Summary

Sequence: SYVLVESVCK, Charge: +2, Monoisotopic m/z: 563.79047 Da (-3.83 mmu/-6.8 ppm), MH+: 1126.57366 Da, RT: 39.12 min,
Identified with: Mascot (v1.30); IonScore:40, Exp Value:2.1E-002, Ions matched by search engine: 6/84
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

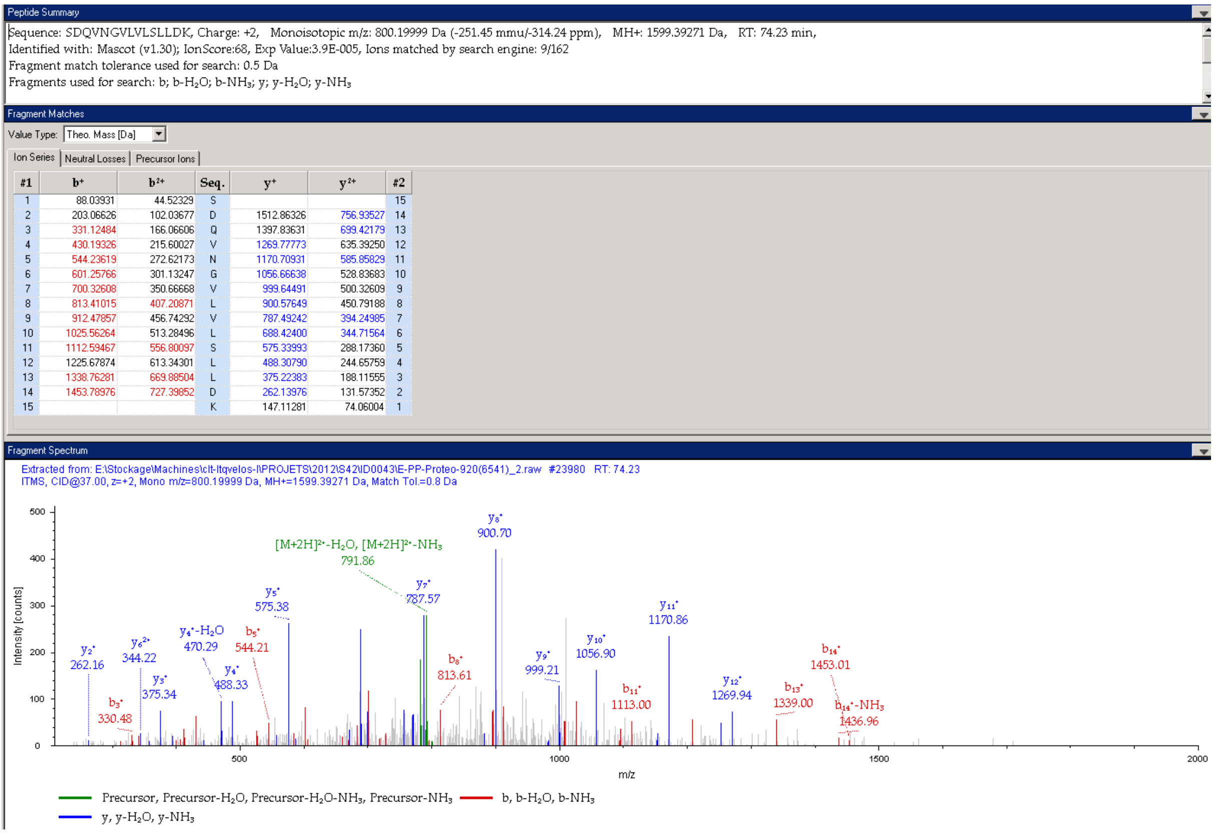
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			10
2	251.10263	126.05495	Y	1039.54928	520.27828	9
3	350.17105	175.58916	V	876.48596	438.74662	8
4	463.25512	232.13120	L	777.41754	389.21241	7
5	562.32354	281.66541	V	664.33347	332.67037	6
6	691.36614	346.18671	E	565.26505	283.13616	5
7	778.39817	389.70272	S	436.22245	218.61486	4
8	877.46659	439.23693	V	349.19042	175.09885	3
9	980.47578	490.74153	C	250.12200	125.56464	2
10			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #10760 RT: 39.12
ITMS, CID@37.00, z=+2, Mono m/z=563.79047 Da, MH+=1126.57366 Da, Match Tol.=0.8 Da

Protein references (1):

- Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]



Peptide Summary

Sequence: SDQVNGVLVLSLLDK, Charge: +2, Monoisotopic m/z: 800.19999 Da (-251.45 mmu/-314.24 ppm), MH+: 1599.39271 Da, RT: 74.23 min,
Identified with: Mascot (v1.30); IonScore:68, Exp Value:3.9E-005, Ions matched by search engine: 9/162
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

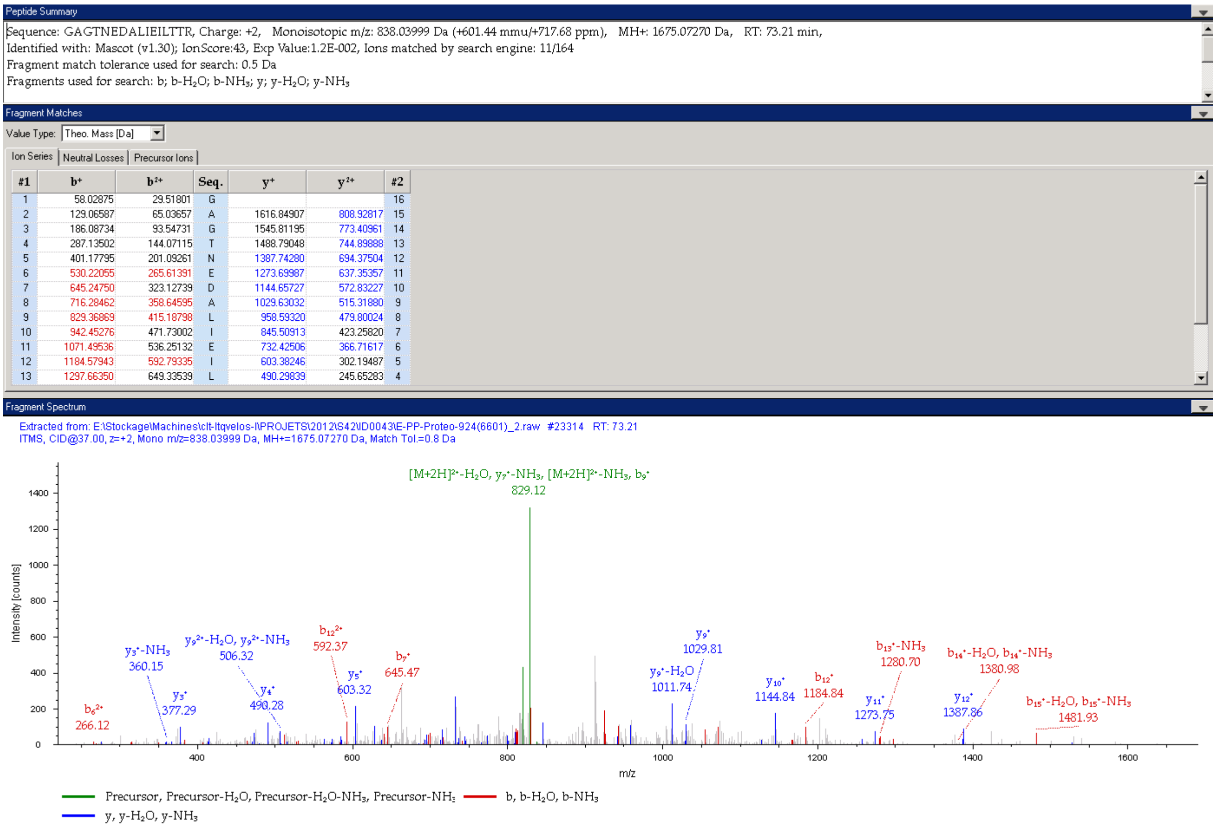
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			15
2	203.06626	102.03677	D	1512.86326	756.93527	14
3	331.12484	166.06606	Q	1397.83631	699.42179	13
4	430.19326	215.60027	V	1269.77773	635.39250	12
5	544.23619	272.62173	N	1170.70931	585.85829	11
6	601.25766	301.13247	G	1056.66638	528.83683	10
7	700.32608	350.66668	V	999.64491	500.32609	9
8	813.41015	407.20871	L	900.57649	450.79188	8
9	912.47857	456.74292	V	787.49242	394.24985	7
10	1025.56264	513.28496	L	688.42400	344.71564	6
11	1112.59467	556.80097	S	575.33993	288.17360	5
12	1225.67874	613.34301	L	488.30790	244.65759	4
13	1338.76281	669.88504	L	375.22383	188.11555	3
14	1453.78976	727.39852	D	262.13976	131.57352	2
15			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #23980 RT: 74.23
ITMS, CID@37.00, z=+2, Mono m/z=800.19999 Da, MH+=1599.39271 Da, Match Tol.=0.8 Da

Protein references (1):

- Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]



Peptide Summary

Sequence: GAGTNEDALIEILTTR, Charge: +2, Monoisotopic m/z: 838.03999 Da (+601.44 mmu/+717.68 ppm), MH+: 1675.07270 Da, RT: 73.21 min,
Identified with: Mascot (v1.30); IonScore:43, Exp Value:1.2E-002, Ions matched by search engine: 11/164
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

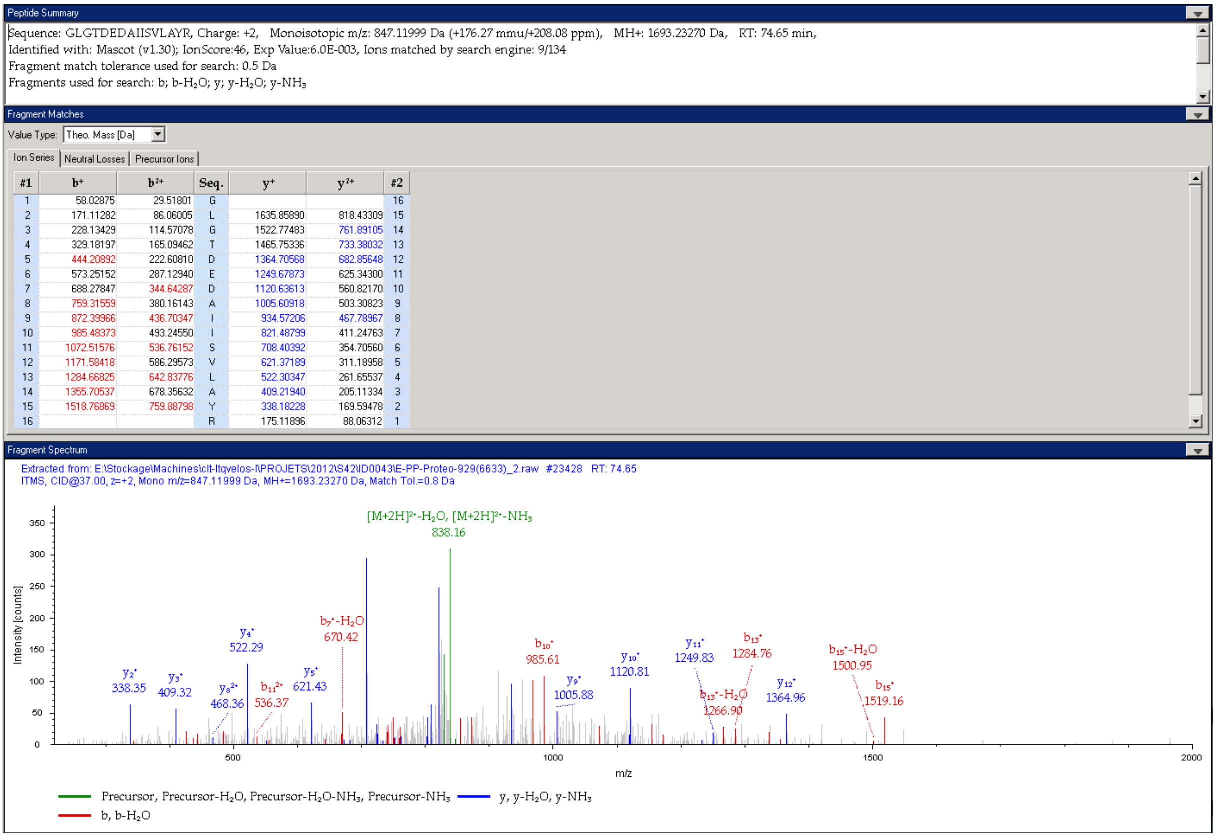
#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	58.02875	29.51801	G			16
2	129.06587	65.03657	A	1616.84907	808.92817	15
3	186.08734	93.54731	G	1545.81195	773.40961	14
4	287.13502	144.07115	T	1488.79048	744.89888	13
5	401.17795	201.09261	N	1387.74280	694.37504	12
6	530.22055	265.61391	E	1273.69987	637.35357	11
7	645.24750	323.12739	D	1144.65727	572.83227	10
8	716.28462	358.64595	A	1029.63032	515.31880	9
9	829.36869	415.18798	L	958.59320	479.80024	8
10	942.45276	471.73002	I	845.50913	423.25820	7
11	1071.49536	536.25132	E	732.42506	366.71617	6
12	1184.57943	592.79335	I	603.38246	302.19487	5
13	1297.66350	649.33539	L	490.29839	245.65283	4

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-924(6601)_2.raw #23314 RT: 73.21
ITMS, CID@37.00, z=+2, Mono m/z=838.03999 Da, MH+=1675.07270 Da, Match Tol.=0.8 Da

Protein references (1):

- Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]



Peptide Summary

Sequence: GLGTDEDAIISVLAYR, Charge: +2, Monoisotopic m/z: 847.11999 Da (+176.27 mmu/+208.08 ppm), MH+: 1693.23270 Da, RT: 74.65 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:6.0E-003, Ions matched by search engine: 9/134
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

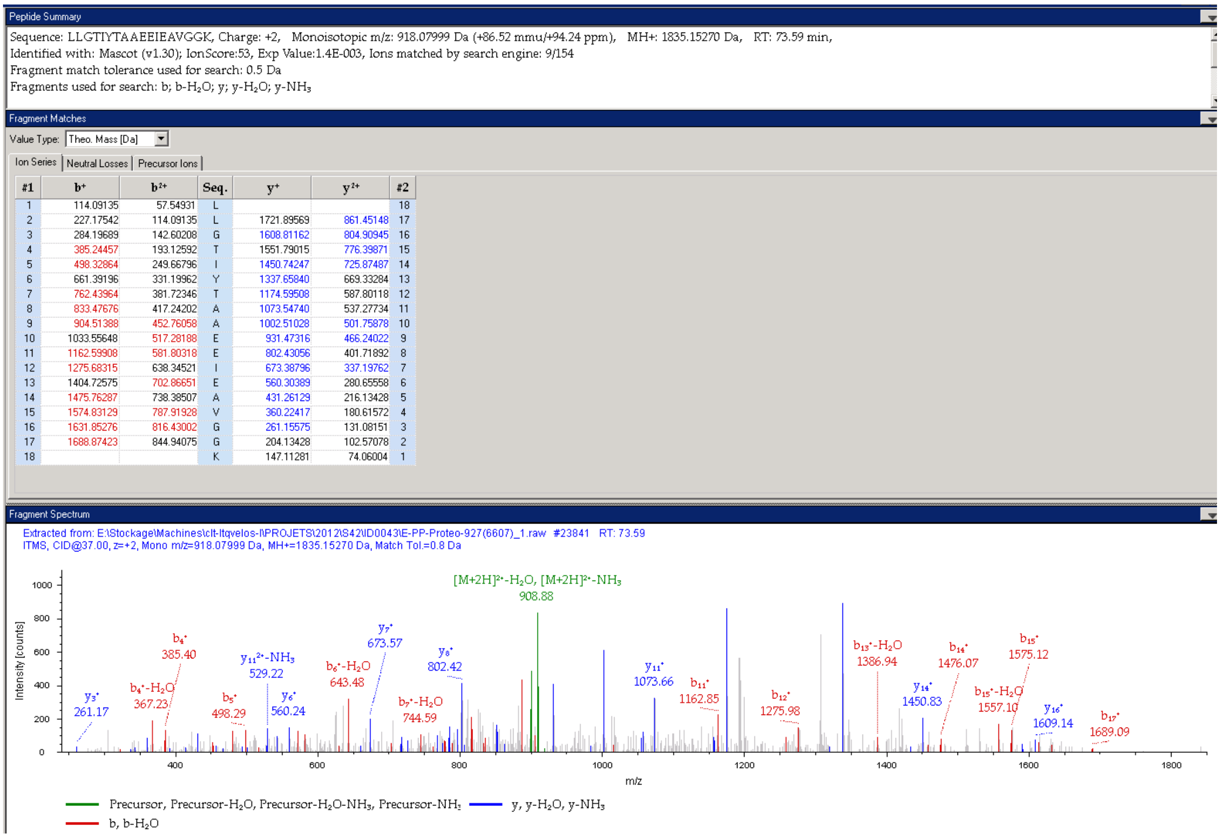
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			16
2	171.11282	86.06005	L	1635.85890	818.43309	15
3	228.13429	114.57078	G	1522.77483	761.89105	14
4	329.18197	165.09462	T	1465.75336	733.38032	13
5	444.20892	222.60810	D	1364.70568	682.85648	12
6	573.25152	287.12940	E	1249.67873	625.34300	11
7	688.27847	344.64287	D	1120.63613	560.82170	10
8	759.31559	380.16143	A	1005.60918	503.30823	9
9	872.39966	436.70347	I	934.57206	467.78967	8
10	985.48373	493.24550	I	821.48799	411.24763	7
11	1072.51576	536.76152	S	708.40392	354.70560	6
12	1171.58418	586.29573	V	621.37189	311.18958	5
13	1284.66825	642.83776	L	522.30347	261.65537	4
14	1355.70537	678.35632	A	409.21940	205.11334	3
15	1518.76869	759.88798	Y	338.18228	169.59478	2
16			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #23428 RT: 74.65
ITMS, CID@37.00, z=+2, Mono m/z=847.11999 Da, MH+=1693.23270 Da, Match Tol.=0.8 Da

Protein references (1):
- Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]



Peptide Summary

Sequence: LLGTIYTAAEEIEAVGGK, Charge: +2, Monoisotopic m/z: 918.07999 Da (+86.52 mmu/+94.24 ppm), MH+: 1835.15270 Da, RT: 73.59 min,
Identified with: Mascot (v1.30); IonScore:53, Exp Value:1.4E-003, Ions matched by search engine: 9/154
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

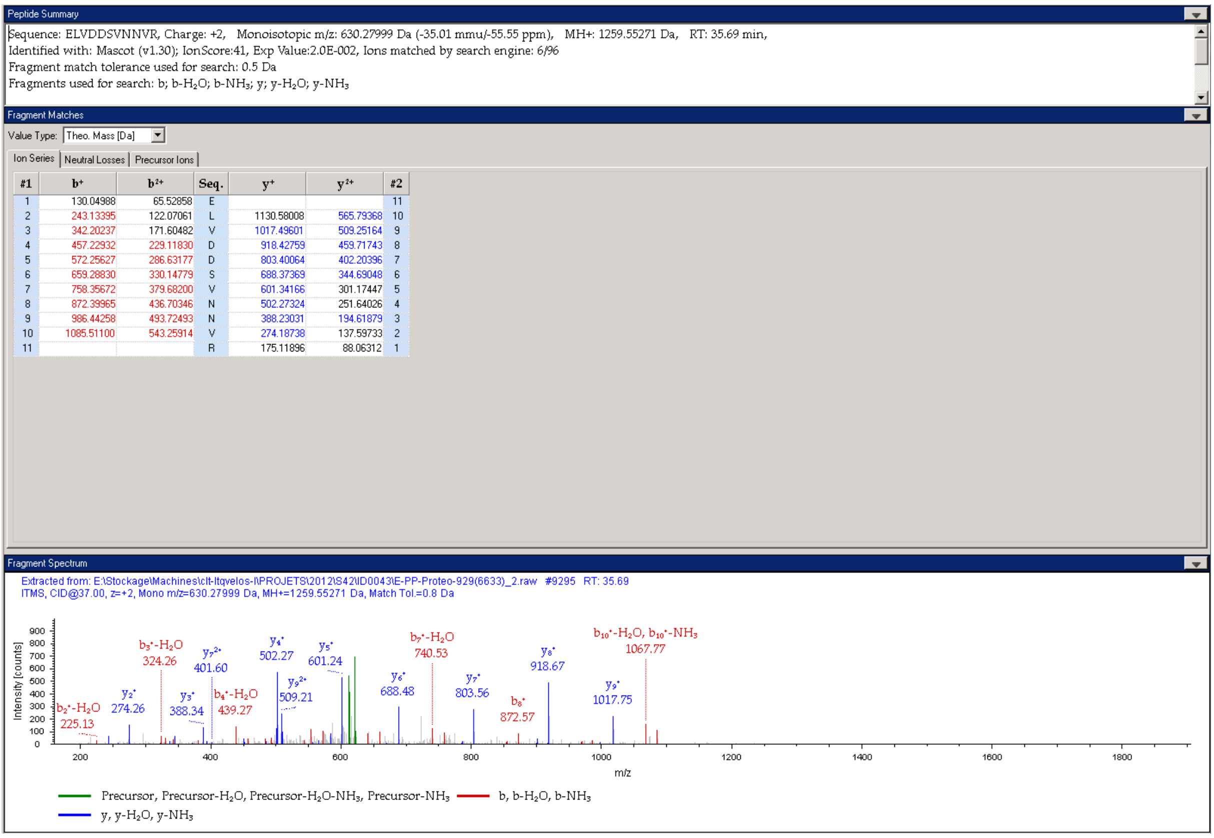
Ion Series | Neutral Losses | Precursor Ions

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			18
2	227.17542	114.09135	L	1721.89569	861.45148	17
3	284.19689	142.60208	G	1608.81162	804.90945	16
4	385.24457	193.12592	T	1551.79015	776.39871	15
5	498.32864	249.66796	I	1450.74247	725.87487	14
6	661.39196	331.19962	Y	1337.65840	669.33284	13
7	762.43964	381.72346	T	1174.59508	587.80118	12
8	833.47676	417.24202	A	1073.54740	537.27734	11
9	904.51388	452.76058	A	1002.51028	501.75878	10
10	1033.55648	517.28188	E	931.47316	466.24022	9
11	1162.59908	581.80318	E	802.43056	401.71892	8
12	1275.68315	638.34521	I	673.38796	337.19762	7
13	1404.72575	702.86651	E	560.30389	280.65558	6
14	1475.76287	738.38507	A	431.26129	216.13428	5
15	1574.83129	787.91928	V	360.22417	180.61572	4
16	1631.85276	816.43002	G	261.15575	131.08151	3
17	1688.87423	844.94075	G	204.13428	102.57078	2
18			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_1.raw #23841 RT: 73.59
ITMS, CID@37.00, z=+2, Mono m/z=918.07999 Da, MH+=1835.15270 Da, Match Tol.=0.8 Da

Protein references (1):
- Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PIMT_HUMAN]



Sequence: ELVDDSVNNVR, Charge: +2, Monoisotopic m/z: 630.27999 Da (-35.01 mmu/-55.55 ppm), MH+: 1259.55271 Da, RT: 35.69 min,
Identified with: Mascot (v1.30); IonScore:41, Exp Value:2.0E-002, Ions matched by search engine: 6/96
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

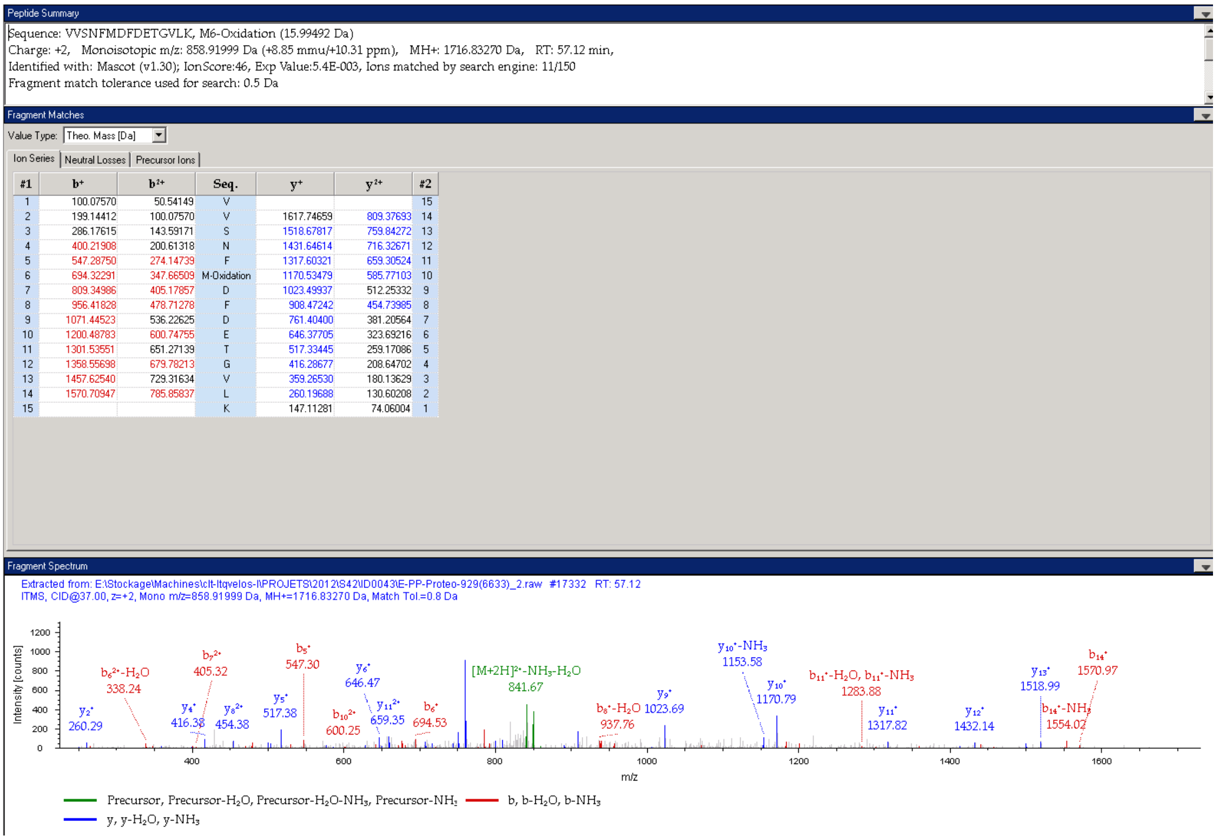
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			11
2	243.13395	122.07061	L	1130.58008	565.79368	10
3	342.20237	171.60482	V	1017.49601	509.25164	9
4	457.22932	229.11830	D	918.42759	459.71743	8
5	572.25627	286.63177	D	803.40064	402.20396	7
6	659.28830	330.14779	S	688.37369	344.69048	6
7	758.35672	379.68200	V	601.34166	301.17447	5
8	872.39965	436.70346	N	502.27324	251.64026	4
9	986.44258	493.72493	N	388.23031	194.61879	3
10	1085.51100	543.25914	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #9295 RT: 35.69
ITMS, CID@37.00, z=+2, Mono m/z=630.27999 Da, MH+=1259.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- Cytosolic 5'-nucleotidase 3 OS=Homo sapiens GN=NT5C3 PE=1 SV=3 - [5NT3_HUMAN]



Sequence: VVSNFMDFDETGVLK, M6-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 858.91999 Da (+8.85 mmu/+10.31 ppm), MH+: 1716.83270 Da, RT: 57.12 min,
Identified with: Mascot (v1.30); IonScore:46, Exp Value:5.4E-003, Ions matched by search engine: 11/150
Fragment match tolerance used for search: 0.5 Da

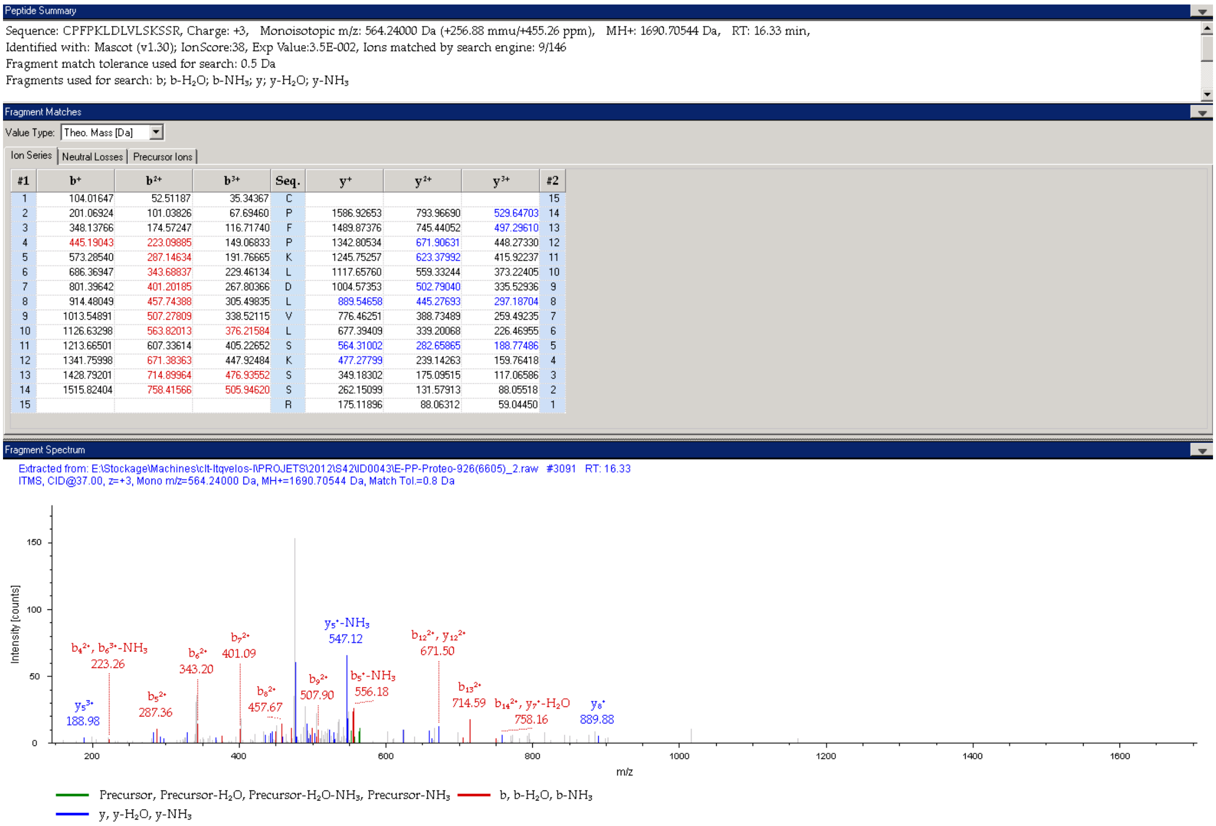
Value Type: Theo. Mass [Da]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	100.07570	50.54149	V			15
2	199.14412	100.07570	V	1617.74659	809.37693	14
3	286.17615	143.59171	S	1518.67817	759.84272	13
4	400.21908	200.61318	N	1431.64614	716.32671	12
5	547.28750	274.14739	F	1317.60321	659.30524	11
6	694.32291	347.66509	M-Oxidation	1170.53479	585.77103	10
7	809.34986	405.17857	D	1023.49937	512.25332	9
8	956.41828	478.71278	F	908.47242	454.73985	8
9	1071.44523	536.22625	D	761.40400	381.20564	7
10	1200.48783	600.74755	E	646.37705	323.69216	6
11	1301.53551	651.27139	T	517.33445	259.17086	5
12	1358.55698	679.78213	G	416.28677	208.64702	4
13	1457.62540	729.31634	V	359.26530	180.13629	3
14	1570.70947	785.85837	L	260.19688	130.60208	2
15			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-929(6633)_2.raw #17332 RT: 57.12
ITMS, CID@37.00, z=+2, Mono m/z=858.91999 Da, MH+=1716.83270 Da, Match Tol.=0.8 Da

Protein references (1):

- Uncharacterized protein C5orf42 OS=Homo sapiens GN=C5orf42 PE=1 SV=4 - [CE042_HUMAN]



Peptide Summary

Sequence: CPFPKLDLVLSKSSR, Charge: +3, Monoisotopic m/z: 564.24000 Da (+256.88 mmu/+455.26 ppm), MH+: 1690.70544 Da, RT: 16.33 min,
Identified with: Mascot (v1.30); IonScore:38, Exp Value:3.5E-002, Ions matched by search engine: 9/146
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

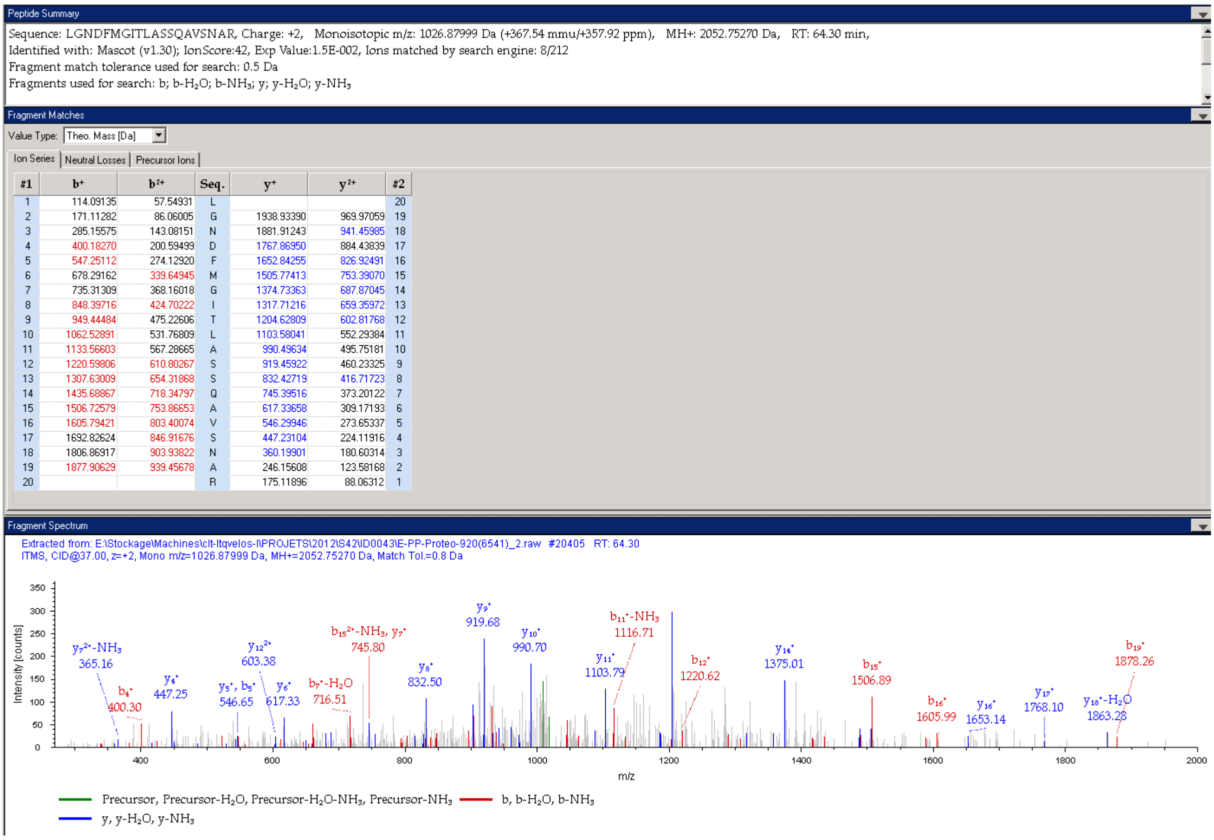
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	104.01647	52.51187	35.34367	C				15
2	201.06924	101.03826	67.69460	P	1586.92653	793.96690	529.64703	14
3	348.13766	174.57247	116.71740	F	1489.87376	745.44052	497.29610	13
4	445.19043	223.09885	149.06833	P	1342.80534	671.90631	448.27330	12
5	573.28540	287.14634	191.76665	K	1245.75257	623.37992	415.92237	11
6	686.36947	343.68837	229.46134	L	1117.65760	559.33244	373.22405	10
7	801.39642	401.20185	267.80366	D	1004.57353	502.79040	335.52936	9
8	914.48049	457.74388	305.49835	L	889.54658	445.27693	297.18704	8
9	1013.54891	507.27809	338.52115	V	776.46251	388.73489	259.49235	7
10	1126.63298	563.82013	376.21584	L	677.39409	339.20068	226.46955	6
11	1213.66501	607.33614	405.22652	S	564.31002	282.65865	188.77486	5
12	1341.75998	671.38363	447.92484	K	477.27799	239.14263	159.76418	4
13	1428.79201	714.89964	476.93552	S	349.18302	175.09515	117.06586	3
14	1515.82404	758.41566	505.94620	S	262.15099	131.57913	88.05518	2
15				R	175.11896	88.06312	59.04450	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_2.raw #3091 RT: 16.33
ITMS, CID@37.00, z=+3, Mono m/z=564.24000 Da, MH+=1690.70544 Da, Match Tol.=0.8 Da

Protein references (1):

- Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 - [GLOD4_HUMAN]



Sequence: LGNDFMGITLASSQAVSNAR, Charge: +2, Monoisotopic m/z: 1026.87999 Da (+367.54 mmu/+357.92 ppm), MH+: 2052.75270 Da, RT: 64.30 min,
Identified with: Mascot (v1.30); IonScore:42, Exp Value:1.5E-002, Ions matched by search engine: 8/212
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

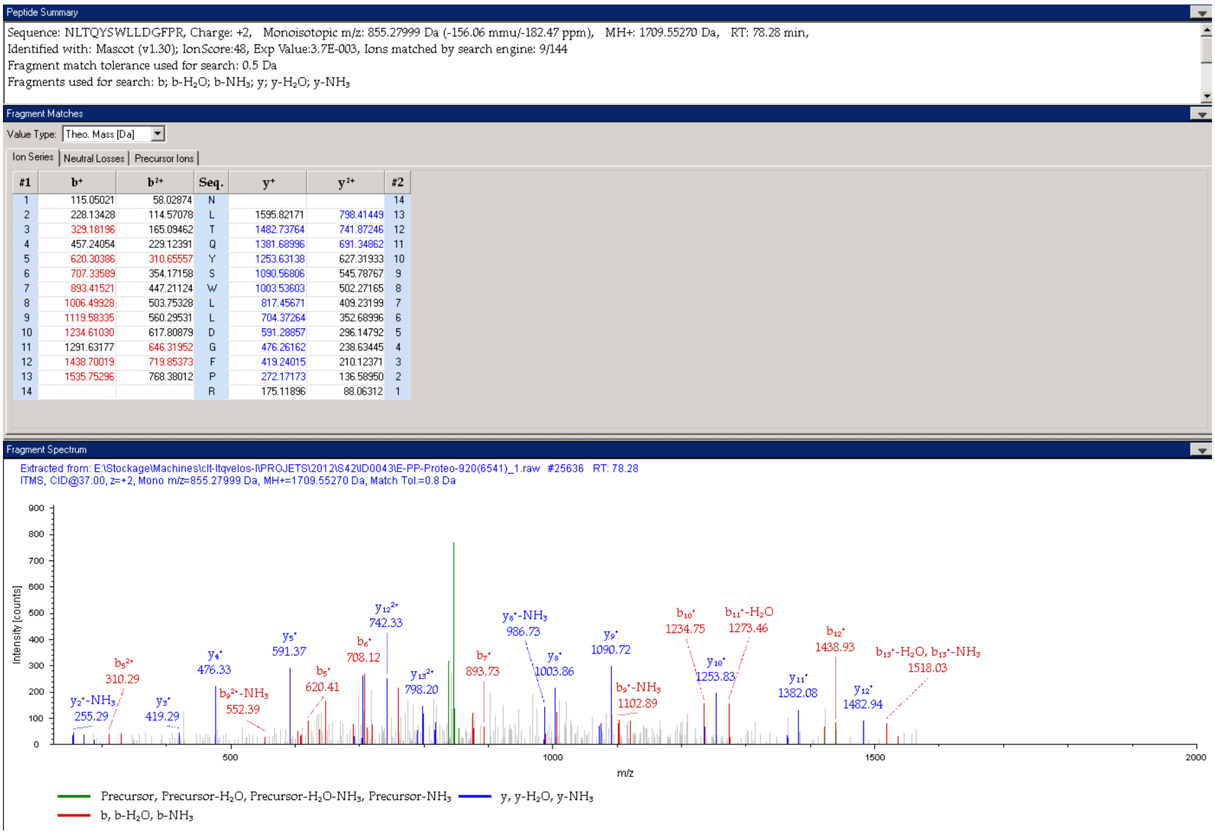
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			20
2	171.11282	86.06005	G	1938.93390	969.97059	19
3	285.15575	143.08151	N	1881.91243	941.45985	18
4	400.18270	200.59499	D	1767.86950	884.43839	17
5	547.25112	274.12920	F	1652.84255	826.92491	16
6	678.29162	339.64945	M	1505.77413	753.39070	15
7	735.31309	368.16018	G	1374.73363	687.87045	14
8	848.39716	424.70222	I	1317.71216	659.35972	13
9	949.44484	475.22606	T	1204.62809	602.81768	12
10	1062.52891	531.76809	L	1103.58041	552.29384	11
11	1133.56603	567.28665	A	990.49634	495.75181	10
12	1220.59806	610.80267	S	919.45922	460.23325	9
13	1307.63009	654.31868	S	832.42719	416.71723	8
14	1435.68867	718.34797	Q	745.39516	373.20122	7
15	1506.72579	753.86653	A	617.33658	309.17193	6
16	1605.79421	803.40074	V	546.29946	273.65337	5
17	1692.82624	846.91676	S	447.23104	224.11916	4
18	1806.86917	903.93822	N	360.19901	180.60314	3
19	1877.90629	939.45678	A	246.15608	123.58168	2
20			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_2.raw #20405 RT: 64.30
ITMS, CID@37.00, z=+2, Mono m/z=1026.87999 Da, MH+=2052.75270 Da, Match Tol.=0.8 Da

Protein references (1):

- GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]



Peptide Summary

Sequence: NLTQYSWLLDGFPR, Charge: +2, Monoisotopic m/z: 855.27999 Da (-156.06 mmu/-182.47 ppm), MH+: 1709.55270 Da, RT: 78.28 min,
Identified with: Mascot (v1.30); IonScore:48, Exp Value:3.7E-003, Ions matched by search engine: 9/144
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

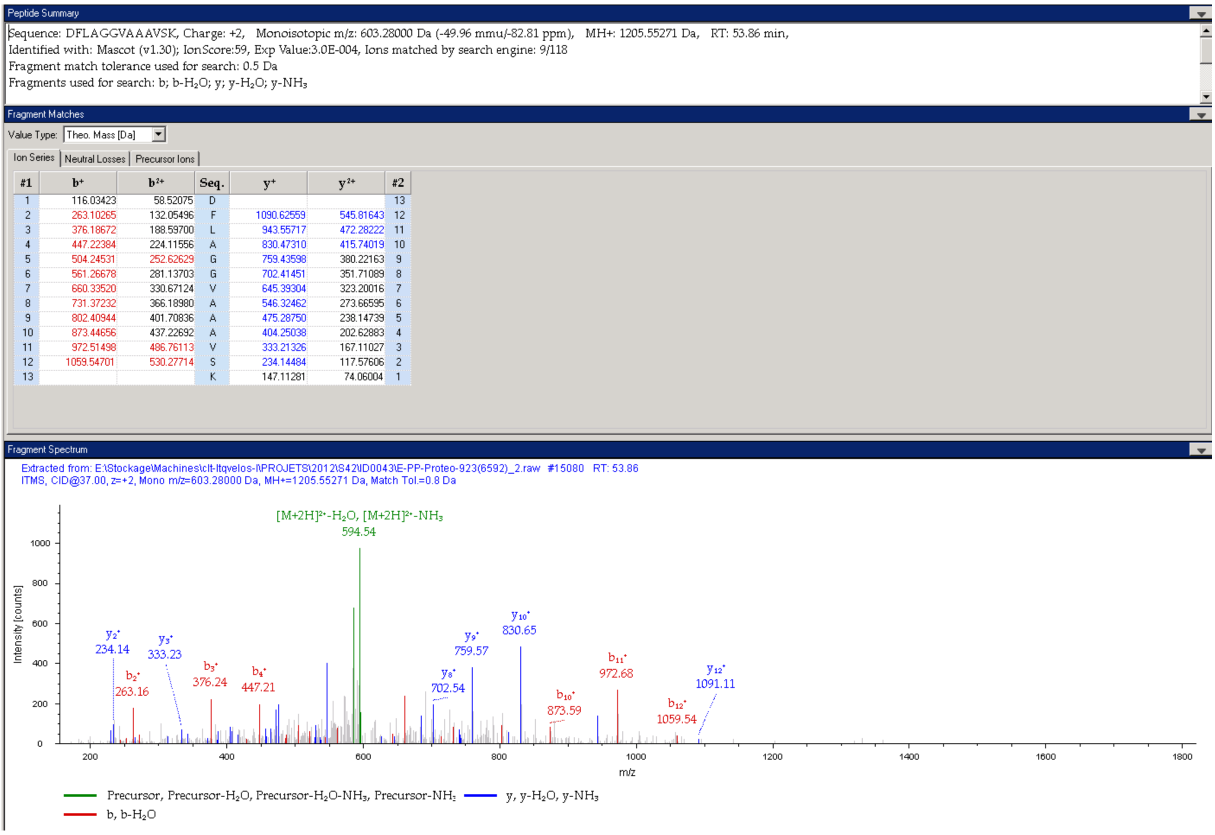
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			14
2	228.13428	114.57078	L	1595.82171	798.41449	13
3	329.18196	165.09462	T	1482.73764	741.87246	12
4	457.24054	229.12391	Q	1381.68996	691.34862	11
5	620.30386	310.65557	Y	1253.63138	627.31933	10
6	707.33589	354.17158	S	1090.56806	545.78767	9
7	893.41521	447.21124	W	1003.53603	502.27165	8
8	1006.49928	503.75328	L	817.45671	409.23199	7
9	1119.58335	560.29531	L	704.37264	352.68996	6
10	1234.61030	617.80879	D	591.28857	296.14792	5
11	1291.63177	646.31952	G	476.26162	238.63445	4
12	1438.70019	719.85373	F	419.24015	210.12371	3
13	1535.75296	768.38012	P	272.17173	136.58950	2
14			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-920(6541)_1.raw #25636 RT: 78.28
ITMS, CID@37.00, z=+2, Mono m/z=855.27999 Da, MH+=1709.55270 Da, Match Tol.=0.8 Da

Protein references (1):

- ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 - [ADT1_HUMAN]



Sequence: DFLAGGVAAAVSK, Charge: +2, Monoisotopic m/z: 603.28000 Da (-49.96 mmu/-82.81 ppm), MH+: 1205.55271 Da, RT: 53.86 min,
Identified with: Mascot (v1.30); IonScore:59, Exp Value:3.0E-004, Ions matched by search engine: 9/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

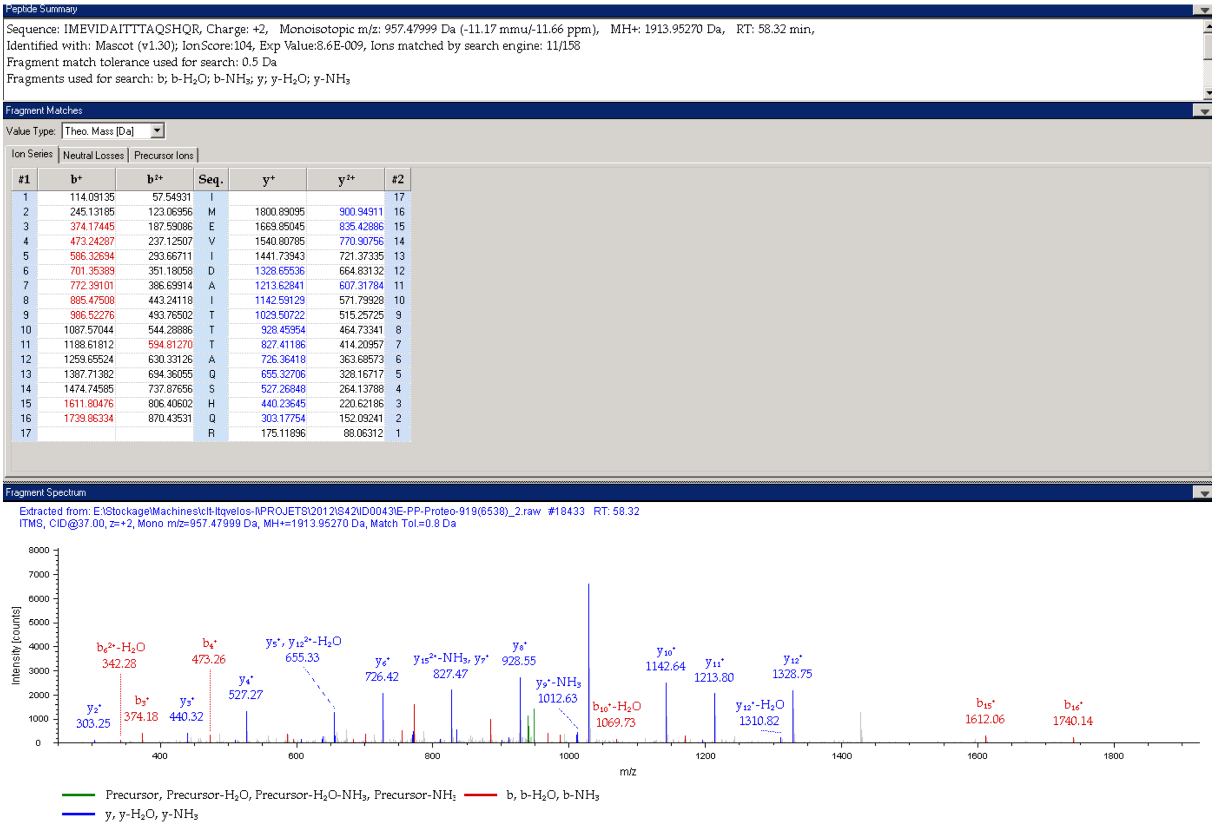
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			13
2	263.10265	132.05496	F	1090.62559	545.81643	12
3	376.18672	188.59700	L	943.55717	472.28222	11
4	447.22384	224.11556	A	830.47310	415.74019	10
5	504.24531	252.62629	G	759.43598	380.22163	9
6	561.26678	281.13703	G	702.41451	351.71089	8
7	660.33520	330.67124	V	645.39304	323.20016	7
8	731.37232	366.18980	A	546.32462	273.66595	6
9	802.40944	401.70836	A	475.28750	238.14739	5
10	873.44656	437.22692	A	404.25038	202.62883	4
11	972.51498	486.76113	V	333.21326	167.11027	3
12	1059.54701	530.27714	S	234.14484	117.57606	2
13			K	147.11281	74.06004	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-923(6592)_2.raw #15080 RT: 53.86
ITMS, CID@37.00, z=+2, Mono m/z=603.28000 Da, MH+=1205.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]



Sequence: IMEVIDAITTTAQSHQR, Charge: +2, Monoisotopic m/z: 957.47999 Da (-11.17 mmu/-11.66 ppm), MH+: 1913.95270 Da, RT: 58.32 min,

Identified with: Mascot (v1.30); IonScore:104, Exp Value:8.6E-009, Ions matched by search engine: 11/158

Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Value Type: Theo. Mass [Da]

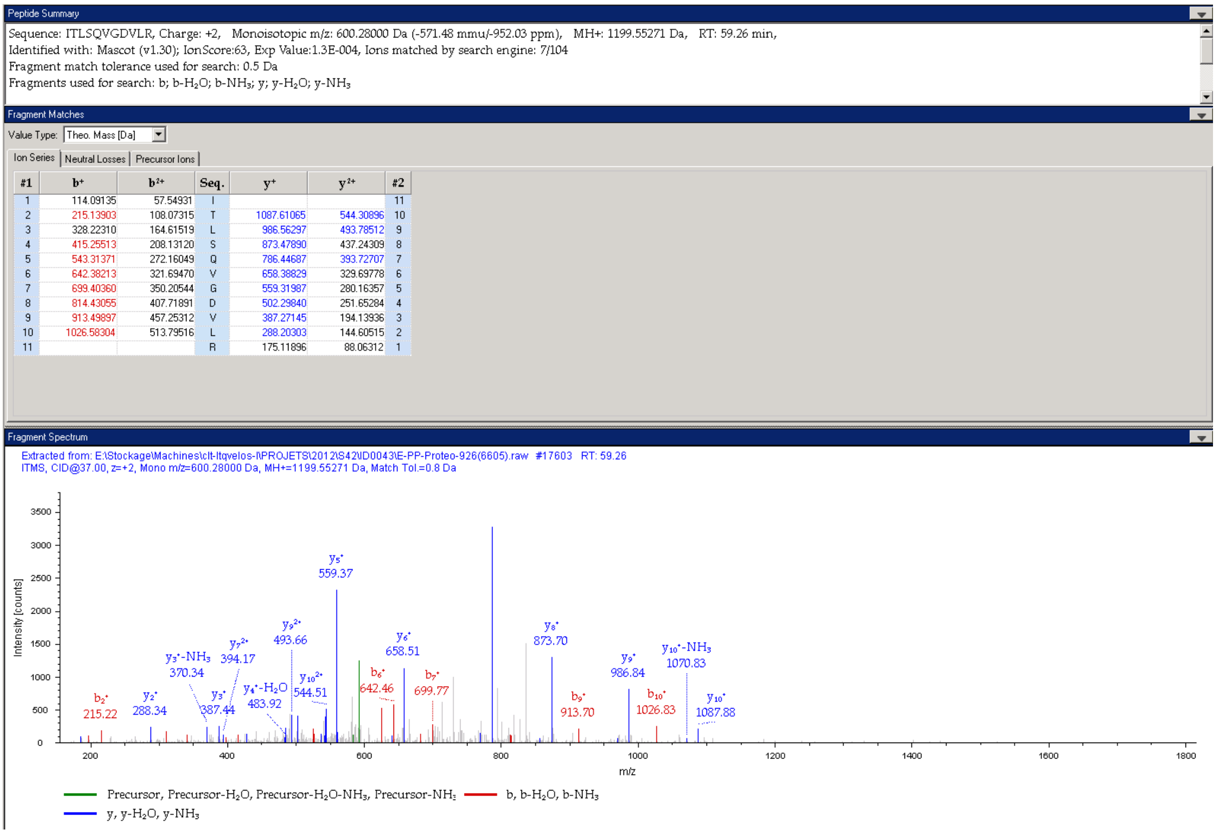
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			17
2	245.13185	123.06956	M	1800.89095	900.94911	16
3	374.17445	187.59086	E	1669.85045	835.42886	15
4	473.24287	237.12507	V	1540.80785	770.90756	14
5	586.32694	293.66711	I	1441.73943	721.37335	13
6	701.35389	351.18058	D	1328.65536	664.83132	12
7	772.39101	386.69914	A	1213.62841	607.31784	11
8	885.47508	443.24118	I	1142.59129	571.79928	10
9	986.52276	493.76502	T	1029.50722	515.25725	9
10	1087.57044	544.28886	T	928.45954	464.73341	8
11	1188.61812	594.81270	T	827.41186	414.20957	7
12	1259.65524	630.33126	A	726.36418	363.68573	6
13	1387.71382	694.36055	Q	655.32706	328.16717	5
14	1474.74585	737.87656	S	527.26848	264.13788	4
15	1611.80476	806.40602	H	440.23645	220.62186	3
16	1739.86334	870.43531	Q	303.17754	152.09241	2
17			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-919(6538)_2.raw #18433 RT: 58.32

ITMS, CID@37.00, z=+2, Mono m/z=957.47999 Da, MH+=1913.95270 Da, Match Tol.=0.8 Da

Protein references (1):

- Myosin light chain 1/3, skeletal muscle isoform OS=Homo sapiens GN=MYL1 PE=1 SV=3 - [MYL1_HUMAN]



Sequence: ITLSQVGDVLR, Charge: +2, Monoisotopic m/z: 600.28000 Da (-571.48 mmu/-952.03 ppm), MH+: 1199.55271 Da, RT: 59.26 min,
Identified with: Mascot (v1.30); IonScore:63, Exp Value:1.3E-004, Ions matched by search engine: 7/104
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

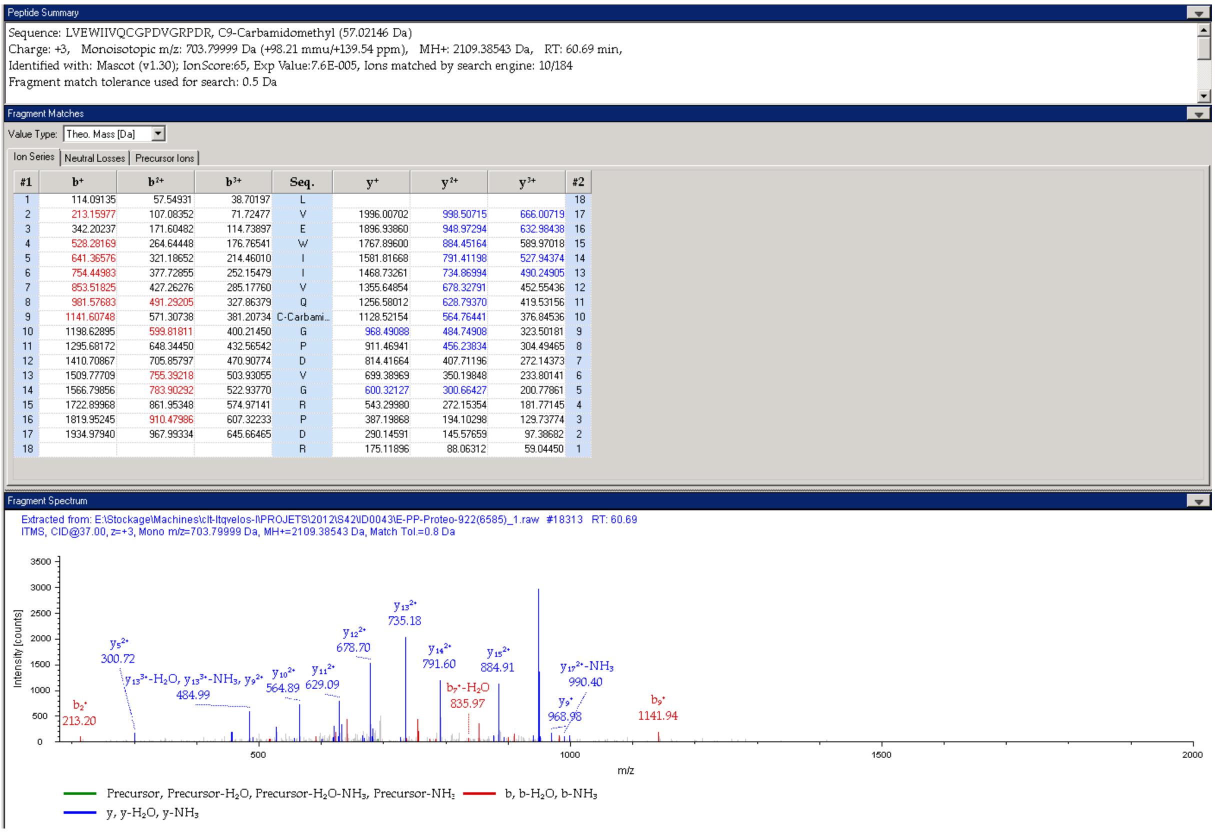
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			11
2	215.13903	108.07315	T	1087.61065	544.30896	10
3	328.22310	164.61519	L	986.56297	493.78512	9
4	415.25513	208.13120	S	873.47890	437.24309	8
5	543.31371	272.16049	Q	786.44687	393.72707	7
6	642.38213	321.69470	V	658.38829	329.69778	6
7	699.40360	350.20544	G	559.31987	280.16357	5
8	814.43055	407.71891	D	502.29840	251.65284	4
9	913.49897	457.25312	V	387.27145	194.13936	3
10	1026.58304	513.79516	L	288.20303	144.60515	2
11			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605).raw #17603 RT: 59.26
ITMS, CID@37.00, z=+2, Mono m/z=600.28000 Da, MH+=1199.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]



Peptide Summary

Sequence: LVEWIIVQCGPDVGRPDR, C9-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 703.79999 Da (+98.21 mmu/+139.54 ppm), MH+: 2109.38543 Da, RT: 60.69 min,
Identified with: Mascot (v1.30); IonScore:65, Exp Value:7.6E-005, Ions matched by search engine: 10/184
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

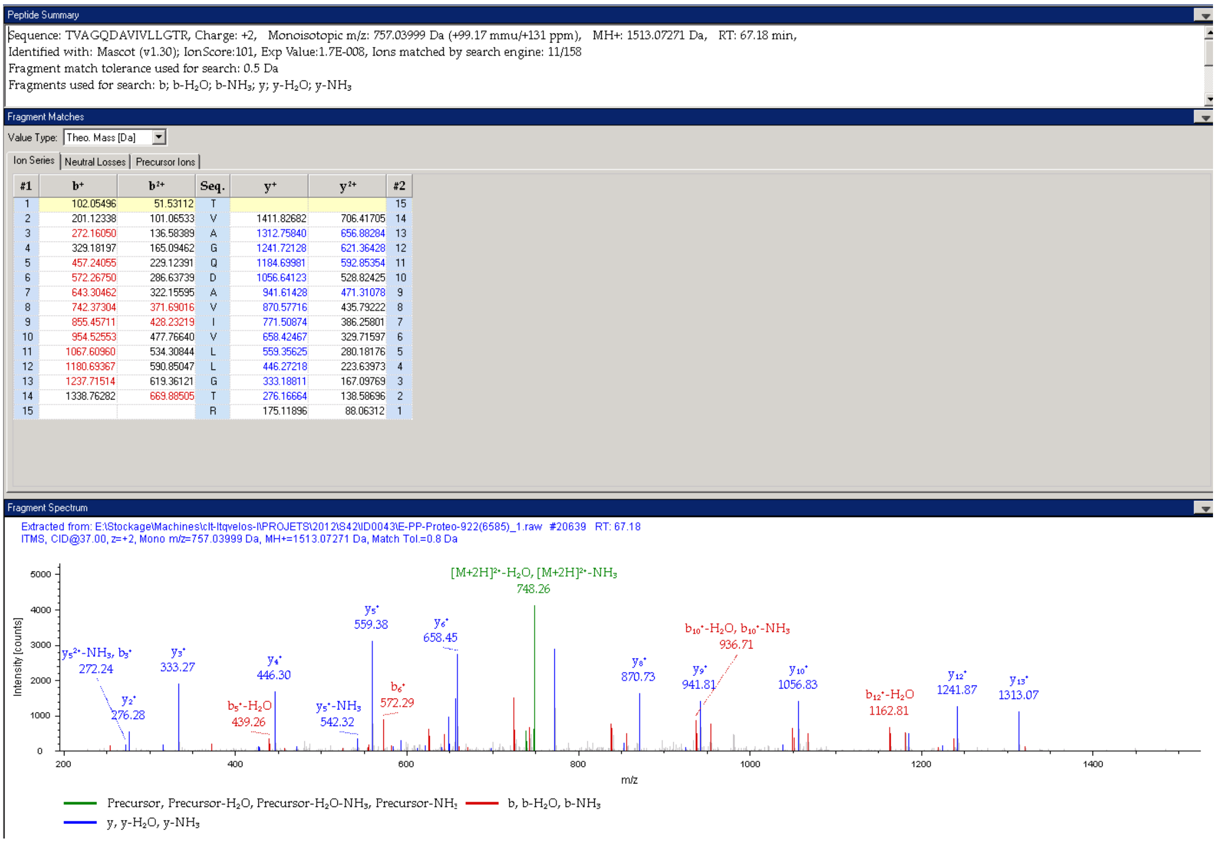
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				18
2	213.15977	107.08352	71.72477	V	1996.00702	998.50715	666.00719	17
3	342.20237	171.60482	114.73897	E	1896.93860	948.97294	632.98438	16
4	528.28169	264.64448	176.76541	W	1767.89600	884.45164	589.97018	15
5	641.36576	321.18652	214.46010	I	1581.81668	791.41198	527.94374	14
6	754.44983	377.72855	252.15479	I	1468.73261	734.86994	490.24905	13
7	853.51825	427.26276	285.17760	V	1355.64854	678.32791	452.55436	12
8	981.57683	491.29205	327.86379	Q	1256.58012	628.79370	419.53156	11
9	1141.60748	571.30738	381.20734	C-Carbami...	1128.52154	564.76441	376.84536	10
10	1198.62895	599.81811	400.21450	G	968.49088	484.74908	323.50181	9
11	1295.68172	648.34450	432.56542	P	911.46941	456.23834	304.49465	8
12	1410.70867	705.85797	470.90774	D	814.41664	407.71196	272.14373	7
13	1509.77709	755.39218	503.93055	V	699.38969	350.19848	233.80141	6
14	1566.79856	783.90292	522.93770	G	600.32127	300.66427	200.77861	5
15	1722.89968	861.95348	574.97141	R	543.29980	272.15354	181.77145	4
16	1819.95245	910.47986	607.32233	P	387.19868	194.10298	129.73774	3
17	1934.97940	967.99334	645.66465	D	290.14591	145.57659	97.38682	2
18				R	175.11896	88.06312	59.04450	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_1.raw #18313 RT: 60.69
ITMS, CID@37.00, z=+3, Mono m/z=703.79999 Da, MH+=2109.38543 Da, Match Tol.=0.8 Da

Protein references (1):
- Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]



Sequence: TVAGQDAVIVLLGTR, Charge: +2, Monoisotopic m/z: 757.03999 Da (+99.17 mmu/+131 ppm), MH+: 1513.07271 Da, RT: 67.18 min,
Identified with: Mascot (v1.30); IonScore:101, Exp Value:1.7E-008, Ions matched by search engine: 11/158
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

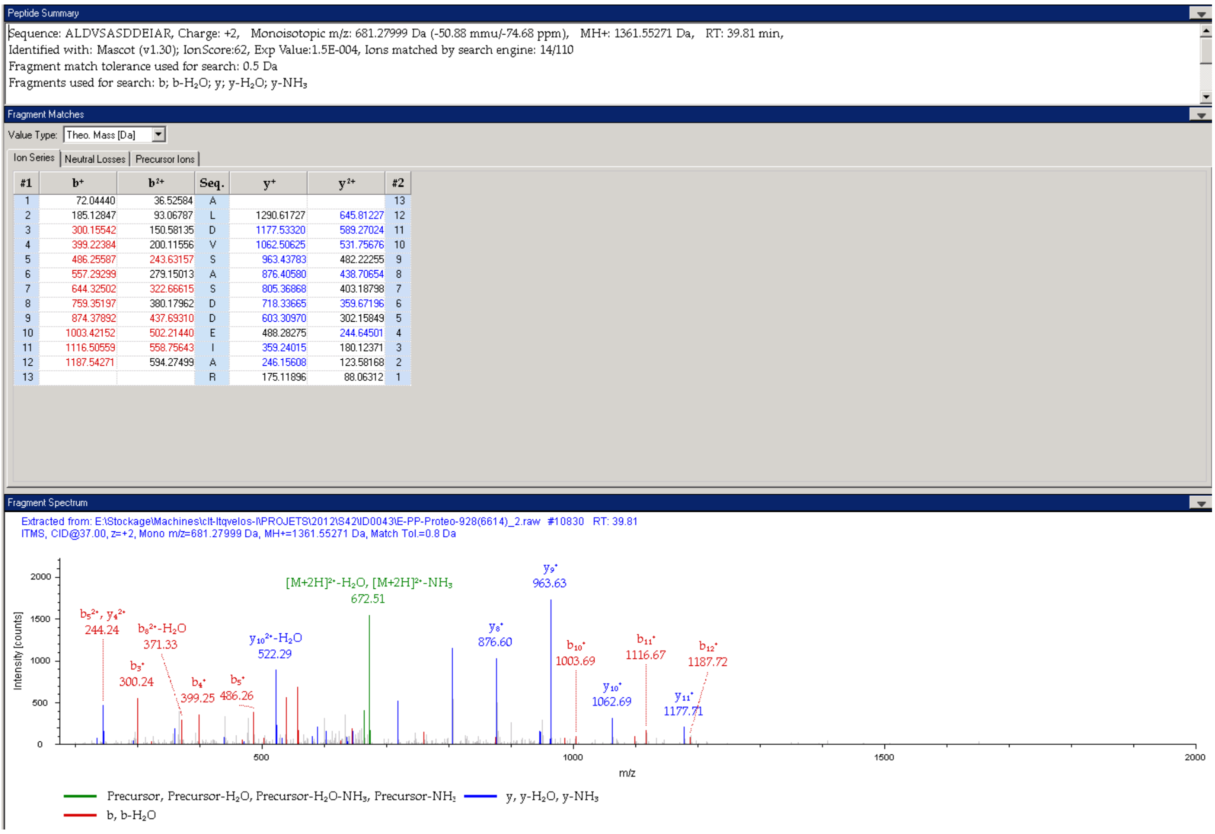
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			15
2	201.12338	101.06533	V	1411.82682	706.41705	14
3	272.16050	136.58389	A	1312.75840	656.88284	13
4	329.18197	165.09462	G	1241.72128	621.36428	12
5	457.24055	229.12391	Q	1184.69981	592.85354	11
6	572.26750	286.63739	D	1056.64123	528.82425	10
7	643.30462	322.15595	A	941.61428	471.31078	9
8	742.37304	371.69016	V	870.57716	435.79222	8
9	855.45711	428.23219	I	771.50874	386.25801	7
10	954.52553	477.76640	V	658.42467	329.71597	6
11	1067.60960	534.30844	L	559.35625	280.18176	5
12	1180.69367	590.85047	L	446.27218	223.63973	4
13	1237.71514	619.36121	G	333.18811	167.09769	3
14	1338.76282	669.88505	T	276.16664	138.58696	2
15			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-922(6585)_1.raw #20639 RT: 67.18
ITMS, CID@37.00, z=+2, Mono m/z=757.03999 Da, MH+=1513.07271 Da, Match Tol.=0.8 Da

Protein references (1):

- Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]



Peptide Summary

Sequence: ALDVSASDDEIAR, Charge: +2, Monoisotopic m/z: 681.27999 Da (-50.88 mmu/-74.68 ppm), MH+: 1361.55271 Da, RT: 39.81 min,
Identified with: Mascot (v1.30); IonScore:62, Exp Value:1.5E-004, Ions matched by search engine: 14/110
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series | Neutral Losses | Precursor Ions

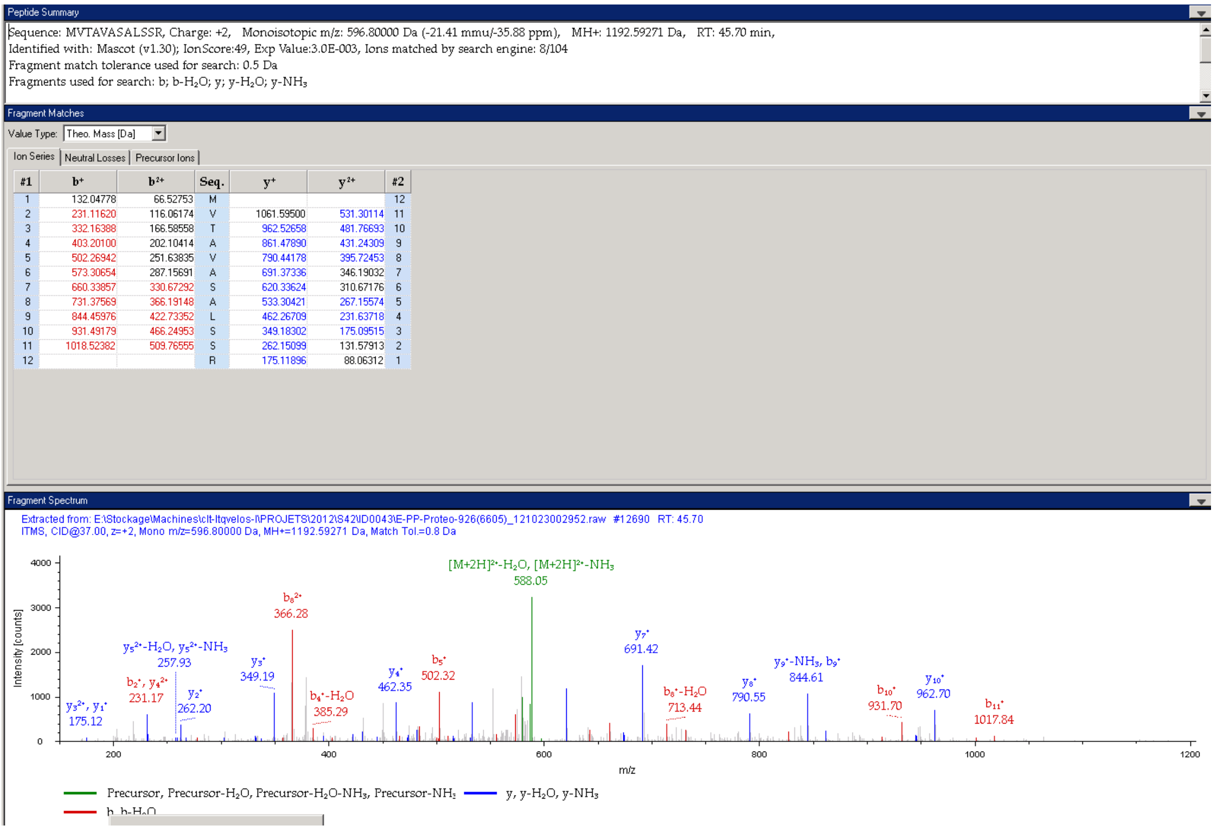
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	185.12847	93.06787	L	1290.61727	645.81227	12
3	300.15542	150.58135	D	1177.53320	589.27024	11
4	399.22384	200.11556	V	1062.50625	531.75676	10
5	486.25587	243.63157	S	963.43783	482.22255	9
6	557.29299	279.15013	A	876.40580	438.70654	8
7	644.32502	322.66615	S	805.36868	403.18798	7
8	759.35197	380.17962	D	718.33665	359.67196	6
9	874.37892	437.69310	D	603.30970	302.15849	5
10	1003.42152	502.21440	E	488.28275	244.64501	4
11	1116.50559	558.75643	I	359.24015	180.12371	3
12	1187.54271	594.27499	A	246.15608	123.58168	2
13			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\PROJETS\2012\S42\ID0043\E-PP-Proteo-928(6614)_2.raw #10830 RT: 39.81
ITMS, CID@37.00, z=+2, Mono m/z=681.27999 Da, MH+=1361.55271 Da, Match Tol.=0.8 Da

Protein references (1):

- Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 - [HBG1_HUMAN]



Peptide Summary

Sequence: MVTAVASALSSR, Charge: +2, Monoisotopic m/z: 596.80000 Da (-21.41 mmu/-35.88 ppm), MH+: 1192.59271 Da, RT: 45.70 min,
Identified with: Mascot (v1.30); IonScore:49, Exp Value:3.0E-003, Ions matched by search engine: 8/104
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

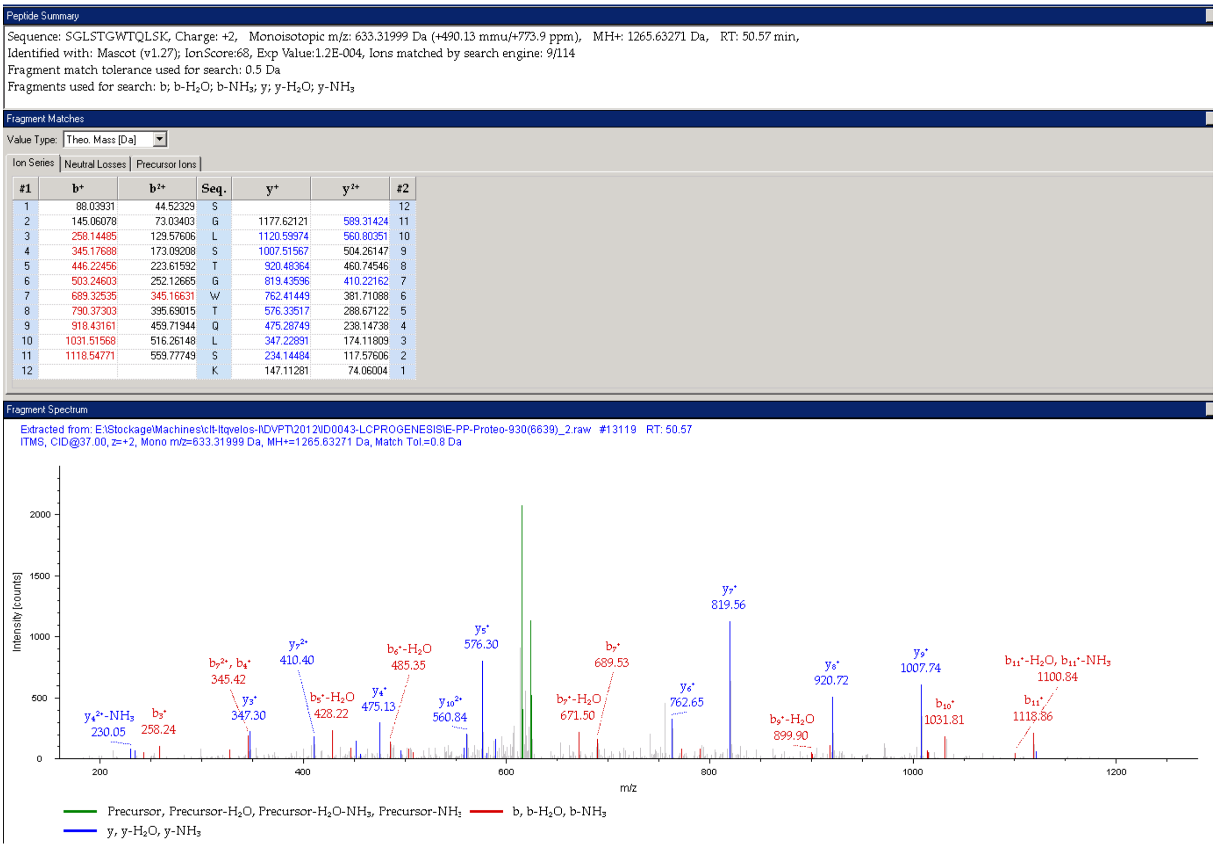
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	132.04778	66.52753	M			12
2	231.11620	116.06174	V	1061.59500	531.30114	11
3	332.16388	166.58558	T	962.52658	481.76693	10
4	403.20100	202.10414	A	861.47890	431.24309	9
5	502.26942	251.63835	V	790.44178	395.72453	8
6	573.30654	287.15691	A	691.37336	346.19032	7
7	660.33857	330.67292	S	620.33624	310.67176	6
8	731.37569	366.19148	A	533.30421	267.15574	5
9	844.45976	422.73352	L	462.26709	231.63718	4
10	931.49179	466.24953	S	349.18302	175.09515	3
11	1018.52382	509.76555	S	262.15099	131.57913	2
12			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-926(6605)_121023002952.raw #12690 RT: 45.70
ITMS, CID@37.00, z=+2, Mono m/z=596.80000 Da, MH+=1192.59271 Da, Match Tol.=0.8 Da

Protein references (1):

- Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]



Peptide Summary

Sequence: SGLSTGWTQLSK, Charge: +2, Monoisotopic m/z: 633.31999 Da (+490.13 mmu/+773.9 ppm), MH+: 1265.63271 Da, RT: 50.57 min,
Identified with: Mascot (v1.27); IonScore:68, Exp Value:1.2E-004, Ions matched by search engine: 9/114
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

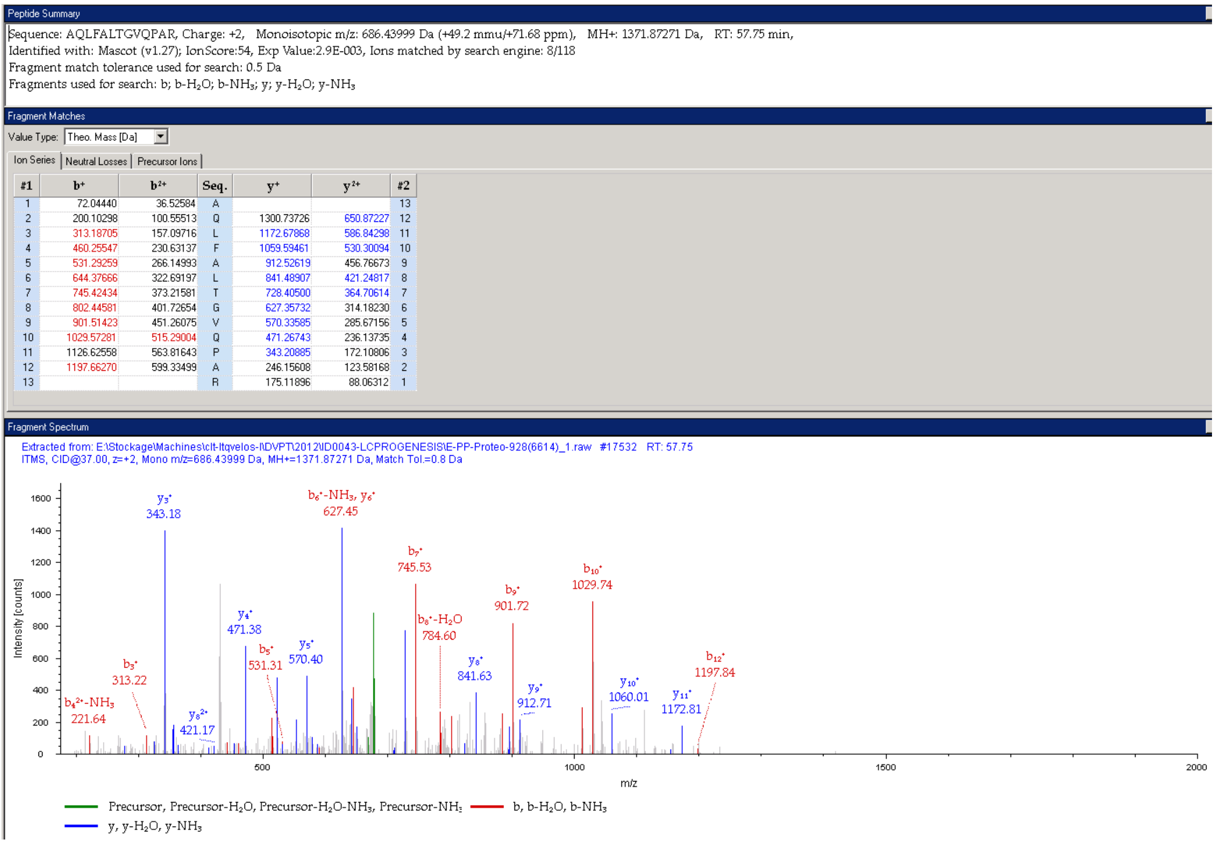
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			12
2	145.06078	73.03403	G	1177.62121	589.31424	11
3	258.14485	129.57606	L	1120.59974	560.80351	10
4	345.17688	173.09208	S	1007.51567	504.26147	9
5	446.22456	223.61592	T	920.48364	460.74546	8
6	503.24603	252.12665	G	819.43596	410.22162	7
7	689.32535	345.16631	W	762.41449	381.71088	6
8	790.37303	395.69015	T	576.33517	288.67122	5
9	918.43161	459.71944	Q	475.28749	238.14738	4
10	1031.51568	516.26148	L	347.22891	174.11809	3
11	1118.54771	559.77749	S	234.14484	117.57606	2
12			K	147.11281	74.06004	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #13119 RT: 50.57
ITMS, CID@37.00, z=+2, Mono m/z=633.31999 Da, MH+=1265.63271 Da, Match Tol.=0.8 Da

Protein references (6):

- Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3 - [UBP14_HUMAN]



Peptide Summary

Sequence: AQLFALTGVQPAR, Charge: +2, Monoisotopic m/z: 686.43999 Da (+49.2 mmu/+71.68 ppm), MH+: 1371.87271 Da, RT: 57.75 min,
Identified with: Mascot (v1.27); IonScore:54, Exp Value:2.9E-003, Ions matched by search engine: 8/118
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

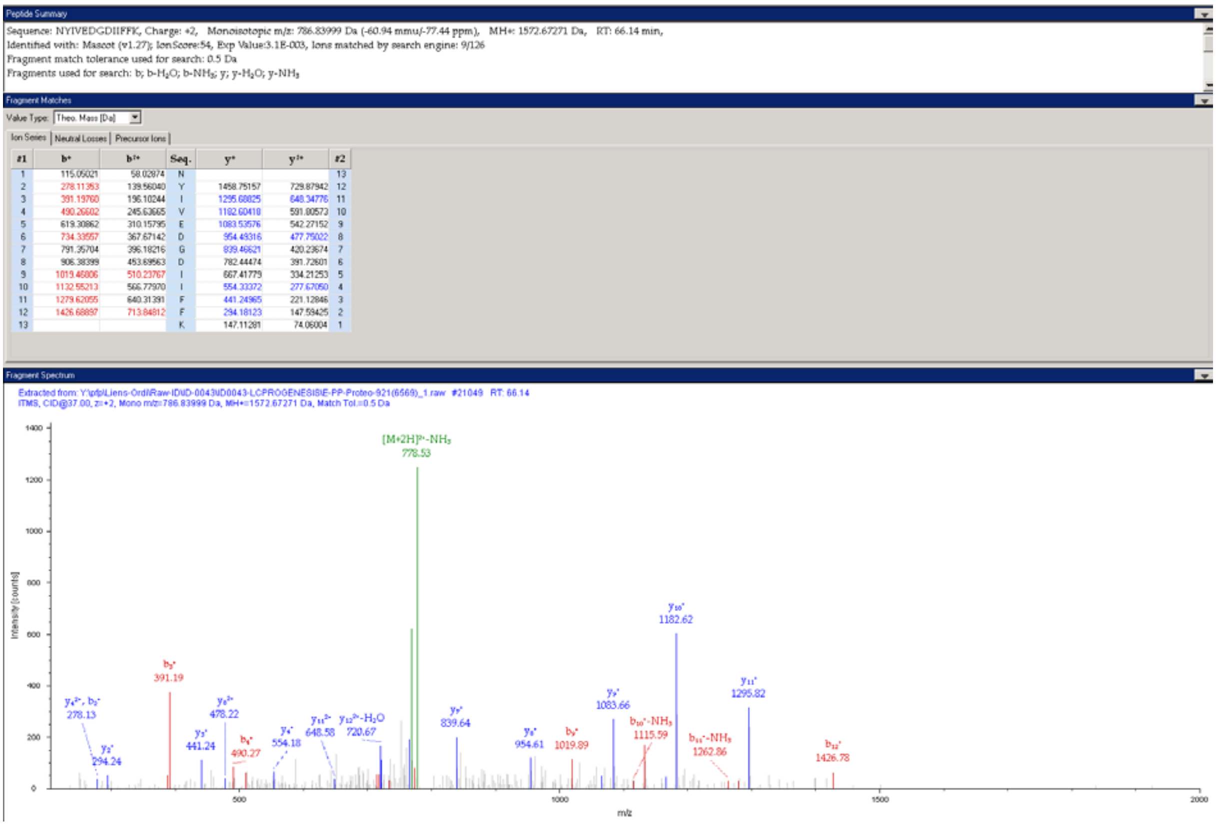
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	200.10298	100.55513	Q	1300.73726	650.87227	12
3	313.18705	157.09716	L	1172.67868	586.84298	11
4	460.25547	230.63137	F	1059.59461	530.30094	10
5	531.29259	266.14993	A	912.52619	456.76673	9
6	644.37666	322.69197	L	841.48907	421.24817	8
7	745.42434	373.21581	T	728.40500	364.70614	7
8	802.44581	401.72654	G	627.35732	314.18230	6
9	901.51423	451.26075	V	570.33585	285.67156	5
10	1029.57281	515.29004	Q	471.26743	236.13735	4
11	1126.62558	563.81643	P	343.20885	172.10806	3
12	1197.66270	599.33499	A	246.15608	123.58168	2
13			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-928(6614)_1.raw #17532 RT: 57.75
ITMS, CID@37.00, z=+2, Mono m/z=686.43999 Da, MH+=1371.87271 Da, Match Tol.=0.8 Da

Protein references (3):

- Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]



Sequence: NYIVEDGDIIFFK, Charge: +2, Monoisotopic m/z: 786.83999 Da (-60.94 mmu/-77.44 ppm), MH+: 1572.67271 Da, RT: 66.14 min,
Identified with: Mascot (v1.27); IonScore:54, Exp Value:3.1E-003, Ions matched by search engine: 9/126
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

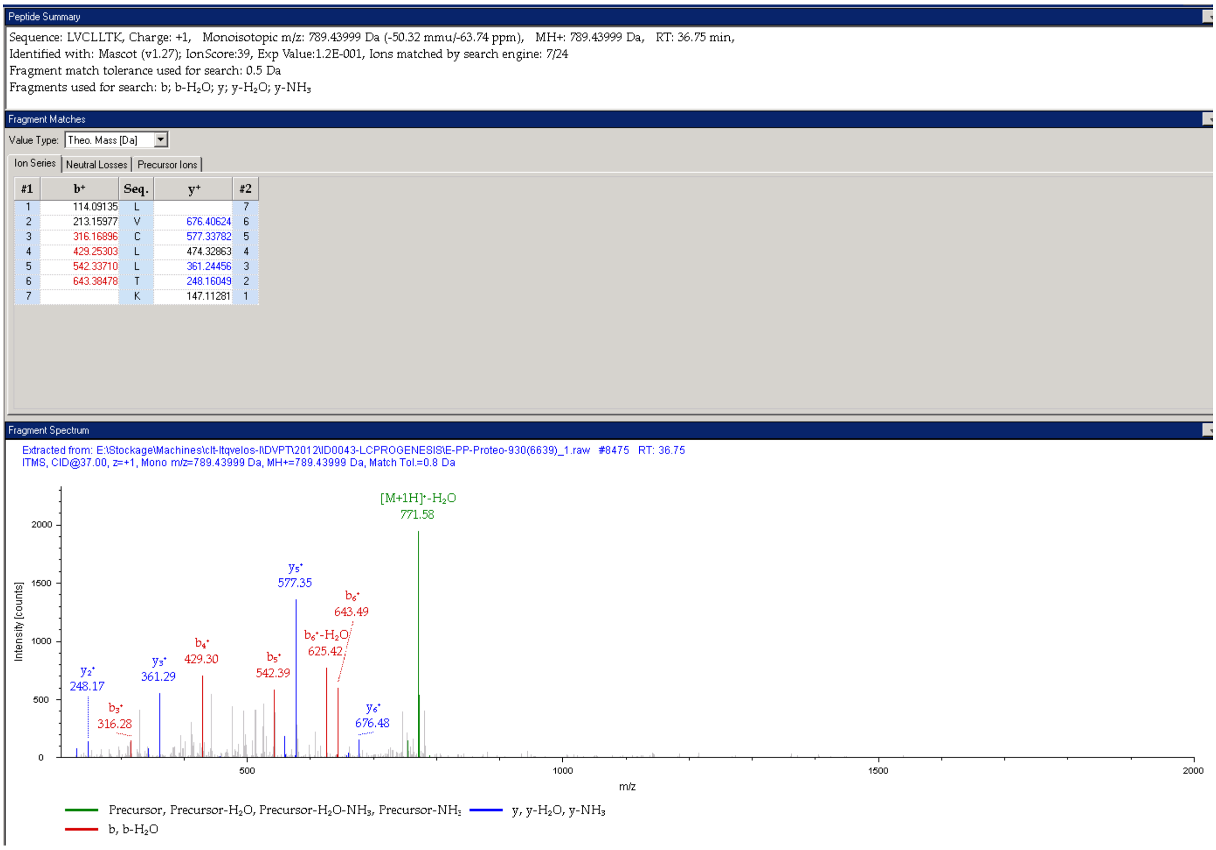
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			13
2	278.11353	139.56040	Y	1458.75157	729.87942	12
3	391.19760	196.10244	I	1295.68825	648.34776	11
4	490.26602	245.63665	V	1182.60418	591.80573	10
5	619.30862	310.15795	E	1083.53576	542.27152	9
6	734.33557	367.67142	D	954.49316	477.75022	8
7	791.35704	396.18216	G	839.46621	420.23674	7
8	906.38399	453.69563	D	782.44474	391.72601	6
9	1019.46806	510.23767	I	667.41779	334.21253	5
10	1132.55213	566.77970	I	554.33372	277.67050	4
11	1279.62055	640.31391	F	441.24965	221.12846	3
12	1426.68897	713.84812	F	294.18123	147.59425	2
13			K	147.11281	74.06004	1

Extracted from: Y:\pfp\Liens-Ordi\Raw-ID\ID-0043\ID0043-LCPROGENESIS\E-PP-Proteo-921(6569)_1.raw #21049 RT: 66.14
ITMS, CID@37.00, z=+2, Mono m/z=786.83999 Da, MH+=1572.67271 Da, Match Tol.=0.5 Da

Protein references (2):

- Protein TANC1 OS=Homo sapiens GN=TANC1 PE=1 SV=3 - [TANC1_HUMAN]



Peptide Summary

Sequence: LVCLLTK, Charge: +1,   Monoisotopic m/z: 789.43999 Da (-50.32 mmu/-63.74 ppm),   MH+: 789.43999 Da,   RT: 36.75 min,
Identified with: Mascot (v1.27); IonScore:39, Exp Value:1.2E-001, Ions matched by search engine: 7/24
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

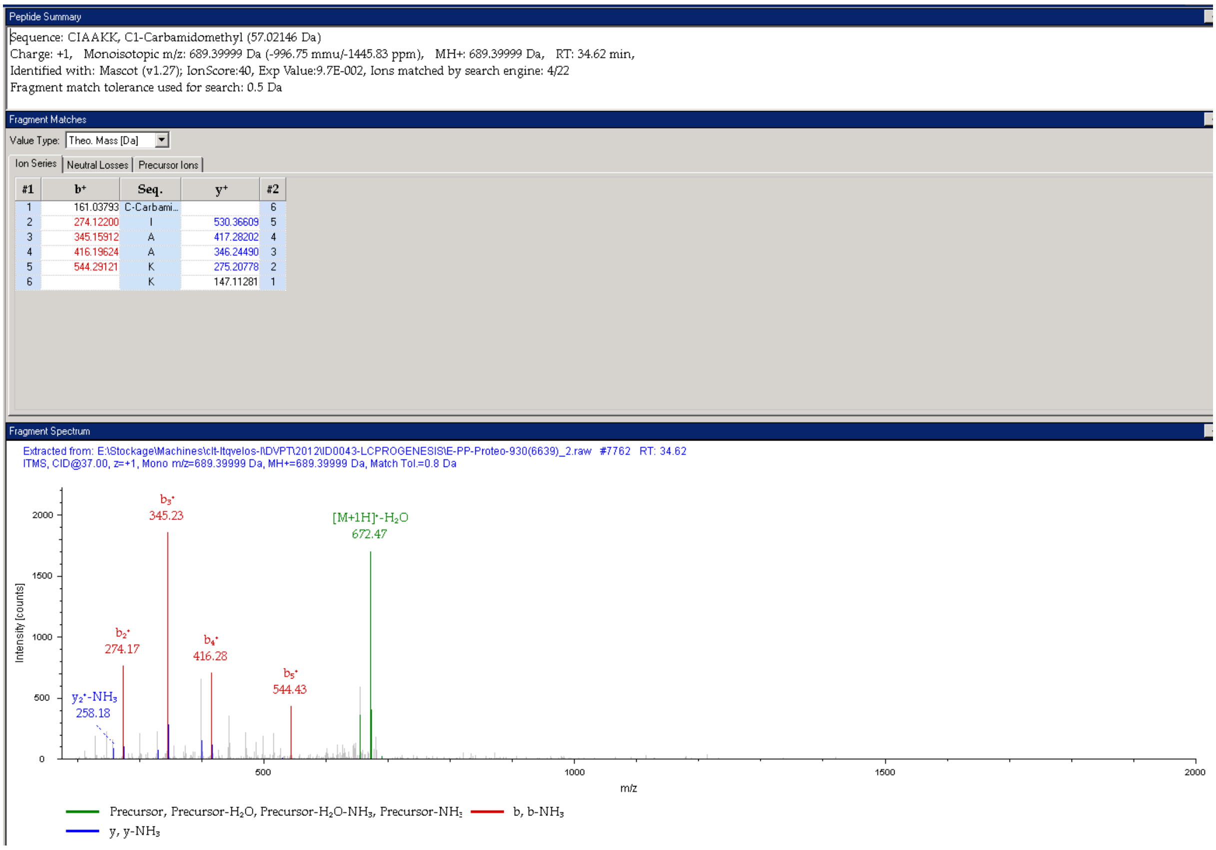
#1	b^+	Seq.	y^+	#2
1	114.09135	L		7
2	213.15977	V	676.40624	6
3	316.16896	C	577.33782	5
4	429.25303	L	474.32863	4
5	542.33710	L	361.24456	3
6	643.38478	T	248.16049	2
7		K	147.11281	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_1.raw   #8475   RT: 36.75
ITMS, CID@37.00, z=+1, Mono m/z=789.43999 Da, MH+=789.43999 Da, Match Tol.=0.8 Da

Protein references (2):

- Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 - [EXOSX_HUMAN]



Sequence: CIAAKK, C1-Carbamidomethyl (57.02146 Da)
Charge: +1, Monoisotopic m/z: 689.39999 Da (-996.75 mmu/-1445.83 ppm), MH+: 689.39999 Da, RT: 34.62 min,
Identified with: Mascot (v1.27); IonScore:40, Exp Value:9.7E-002, Ions matched by search engine: 4/22
Fragment match tolerance used for search: 0.5 Da

Value Type: Theo. Mass [Da]

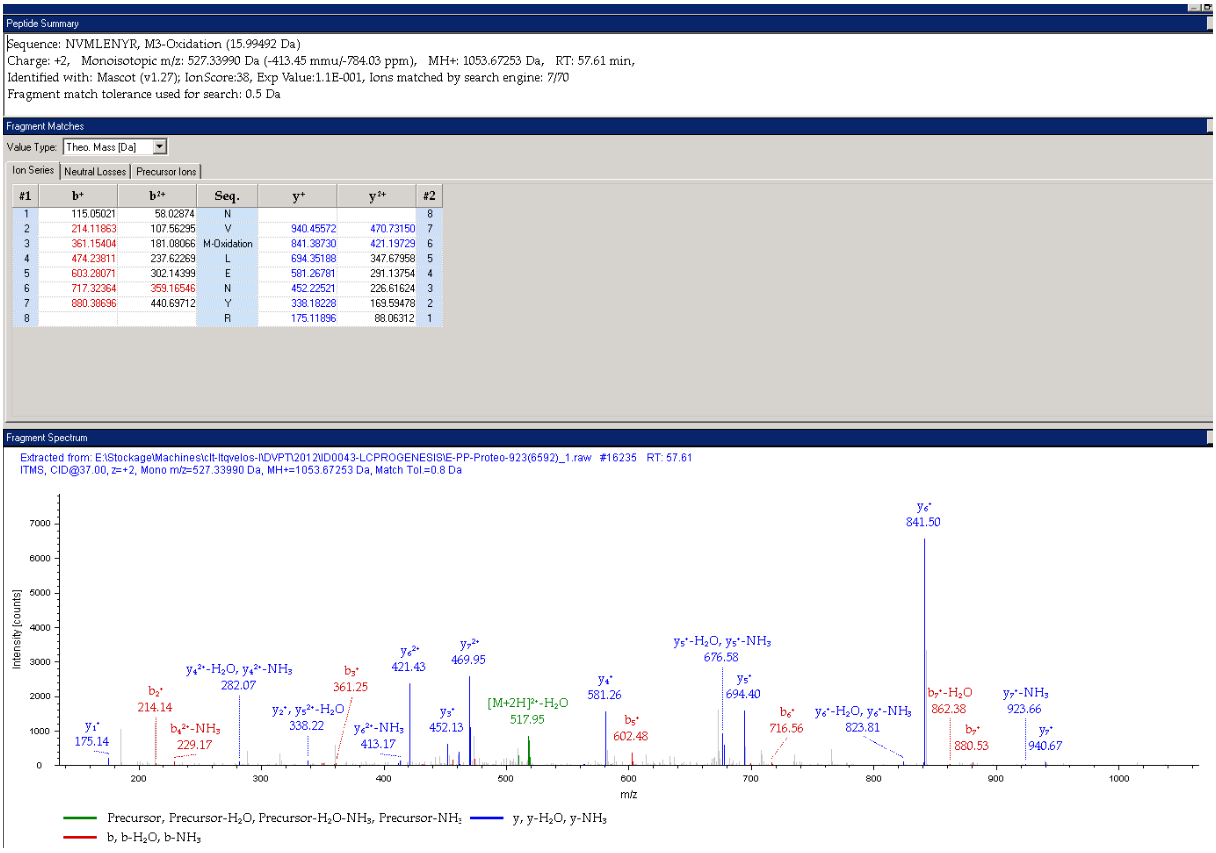
#1	b^+	Seq.	y^+	#2
1	161.03793	C-Carbami...		6
2	274.12200	I	530.36609	5
3	345.15912	A	417.28202	4
4	416.19624	A	346.24490	3
5	544.29121	K	275.20778	2
6		K	147.11281	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-930(6639)_2.raw #7762 RT: 34.62
ITMS, CID@37.00, z=+1, Mono m/z=689.39999 Da, MH+=689.39999 Da, Match Tol.=0.8 Da

Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
b, b-NH_3
y, y-NH_3

Protein references (24):

- Putative zinc finger protein LOC730110 OS=Homo sapiens PE=5 SV=3 - [YI017_HUMAN]



Peptide Summary

Sequence: NVMLENYR, M3-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 527.33990 Da (-413.45 mmu/-784.03 ppm), MH+: 1053.67253 Da, RT: 57.61 min,
Identified with: Mascot (v1.27); IonScore:38, Exp Value:1.1E-001, Ions matched by search engine: 7/70
Fragment match tolerance used for search: 0.5 Da

Fragment Matches

Value Type: Theo. Mass [Da]

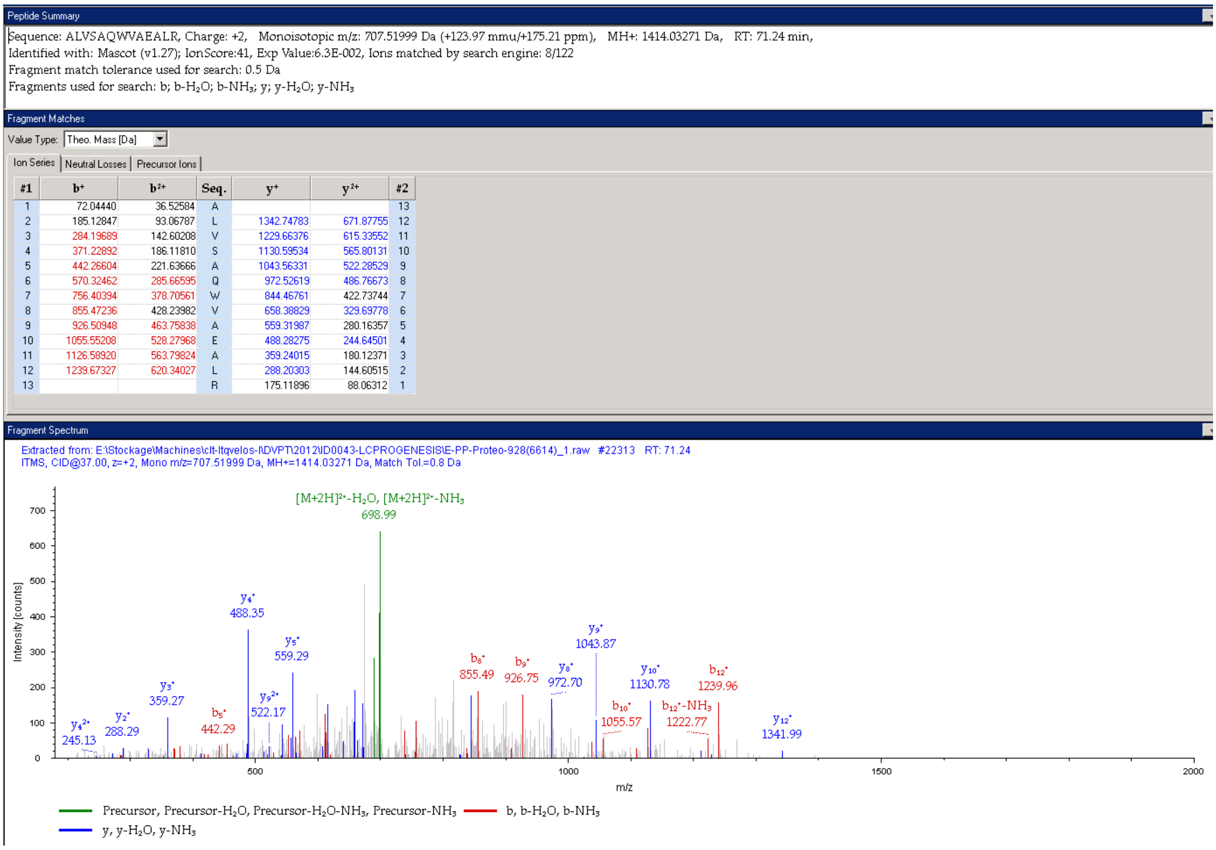
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			8
2	214.11863	107.56295	V	940.45572	470.73150	7
3	361.15404	181.08066	M-Oxidation	841.38730	421.19729	6
4	474.23811	237.62269	L	694.35188	347.67958	5
5	603.28071	302.14399	E	581.26781	291.13754	4
6	717.32364	359.16546	N	452.22521	226.61624	3
7	880.38696	440.69712	Y	338.18228	169.59478	2
8			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-923(6592)_1.raw #16235 RT: 57.61
ITMS, CID@37.00, z=+2, Mono m/z=527.33990 Da, MH+=1053.67253 Da, Match Tol.=0.8 Da

Protein references (3):

- 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]



Sequence: ALVSAQWVAEALR, Charge: +2, Monoisotopic m/z: 707.51999 Da (+123.97 mmu/+175.21 ppm), MH+: 1414.03271 Da, RT: 71.24 min,
Identified with: Mascot (v1.27); IonScore:41, Exp Value:6.3E-002, Ions matched by search engine: 8/122
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

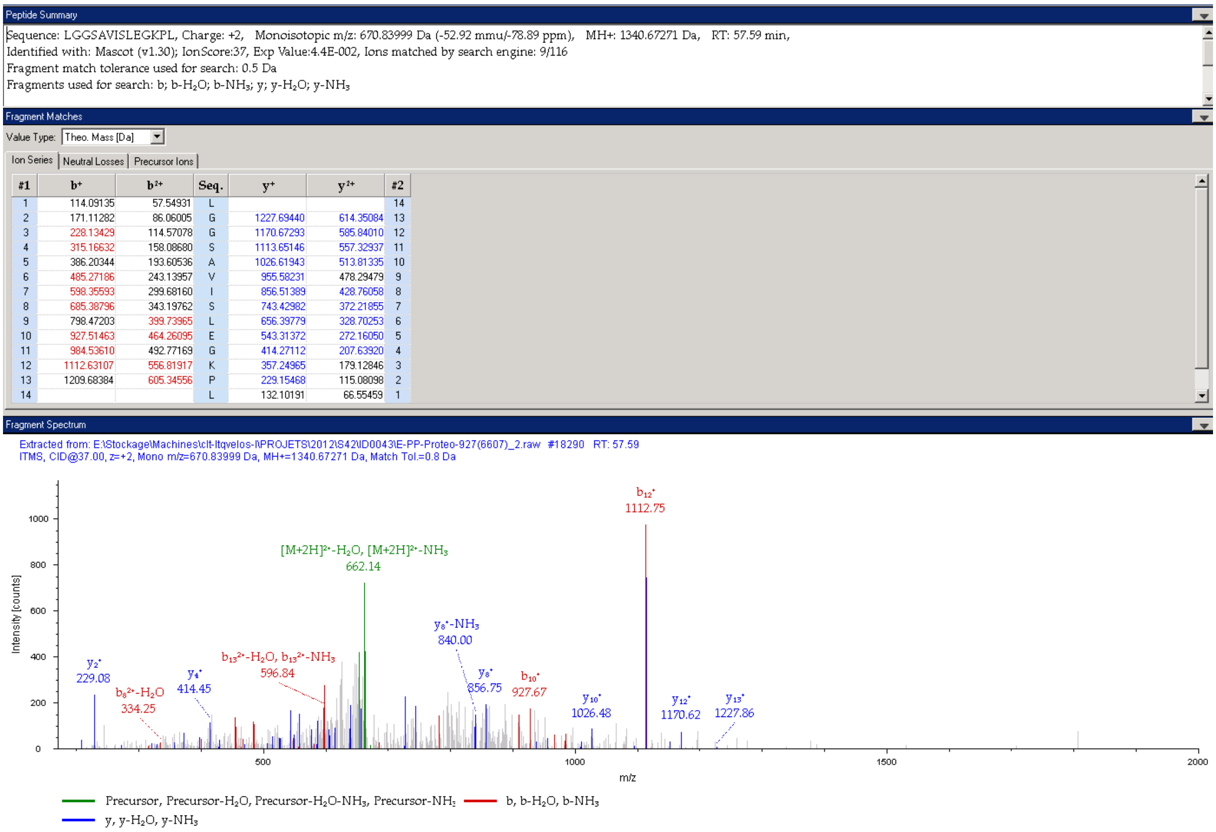
Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	185.12847	93.06787	L	1342.74783	671.87755	12
3	284.19689	142.60208	V	1229.66376	615.33552	11
4	371.22892	186.11810	S	1130.59534	565.80131	10
5	442.26604	221.63666	A	1043.56331	522.28529	9
6	570.32462	285.66595	Q	972.52619	486.76673	8
7	756.40394	378.70561	W	844.46761	422.73744	7
8	855.47236	428.23982	V	658.38829	329.69778	6
9	926.50948	463.75838	A	559.31987	280.16357	5
10	1055.55208	528.27968	E	488.28275	244.64501	4
11	1126.58920	563.79824	A	359.24015	180.12371	3
12	1239.67327	620.34027	L	288.20303	144.60515	2
13			R	175.11896	88.06312	1

Extracted from: E:\Stockage\Machines\clt-ltqvelos-l\DVPT\2012\ID0043-LCPROGENESIS\E-PP-Proteo-928(6614)_1.raw #22313 RT: 71.24
ITMS, CID@37.00, z=+2, Mono m/z=707.51999 Da, MH+=1414.03271 Da, Match Tol.=0.8 Da

Precursor, Precursor-H_2O, Precursor-H_2O-NH_3, Precursor-NH_3
b, b-H_2O, b-NH_3
y, y-H_2O, y-NH_3

Protein references (1):
- Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]



Peptide Summary

Sequence: LGGSAVISLEGKPL, Charge: +2, Monoisotopic m/z: 670.83999 Da (-52.92 mmu/-78.89 ppm), MH+: 1340.67271 Da, RT: 57.59 min,
Identified with: Mascot (v1.30); IonScore:37, Exp Value:4.4E-002, Ions matched by search engine: 9/116
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Fragment Matches

Value Type: Theo. Mass [Da]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			14
2	171.11282	86.06005	G	1227.69440	614.35084	13
3	228.13429	114.57078	G	1170.67293	585.84010	12
4	315.16632	158.08680	S	1113.65146	557.32937	11
5	386.20344	193.60536	A	1026.61943	513.81335	10
6	485.27186	243.13957	V	955.58231	478.29479	9
7	598.35593	299.68160	I	856.51389	428.76058	8
8	685.38796	343.19762	S	743.42982	372.21855	7
9	798.47203	399.73965	L	656.39779	328.70253	6
10	927.51463	464.26095	E	543.31372	272.16050	5
11	984.53610	492.77169	G	414.27112	207.63920	4
12	1112.63107	556.81917	K	357.24965	179.12846	3
13	1209.68384	605.34556	P	229.15468	115.08098	2
14			L	132.10191	66.55459	1

Fragment Spectrum

Extracted from: E:\Stockage\Machines\clt-ltqvelos-I\PROJETS\2012\S42\ID0043\E-PP-Proteo-927(6607)_2.raw #18290 RT: 57.59
ITMS, CID@37.00, z=+2, Mono m/z=670.83999 Da, MH+=1340.67271 Da, Match Tol.=0.8 Da