

**Table S3: Single-peptide-based protein identification**

Table reporting the identification parameters of proteins identified with one single peptide, according to the Molecular and Cellular Proteomics guidelines.

The first two columns display protein accession and gene name retrieved from the UniProtKB-SwissProt database. The next columns give the mass/charge ratio of the selected precursor (m/z), the difference between the detected and the theoretic precursor m/z (error [Da]), the selected precursor charge (z) and the peptide sequence. The last three columns report the score (Hyperscore and Nextscore) and the expect values as calculated by the PeptideProphet algorithm (TPP, ISB, Seattle, USA).

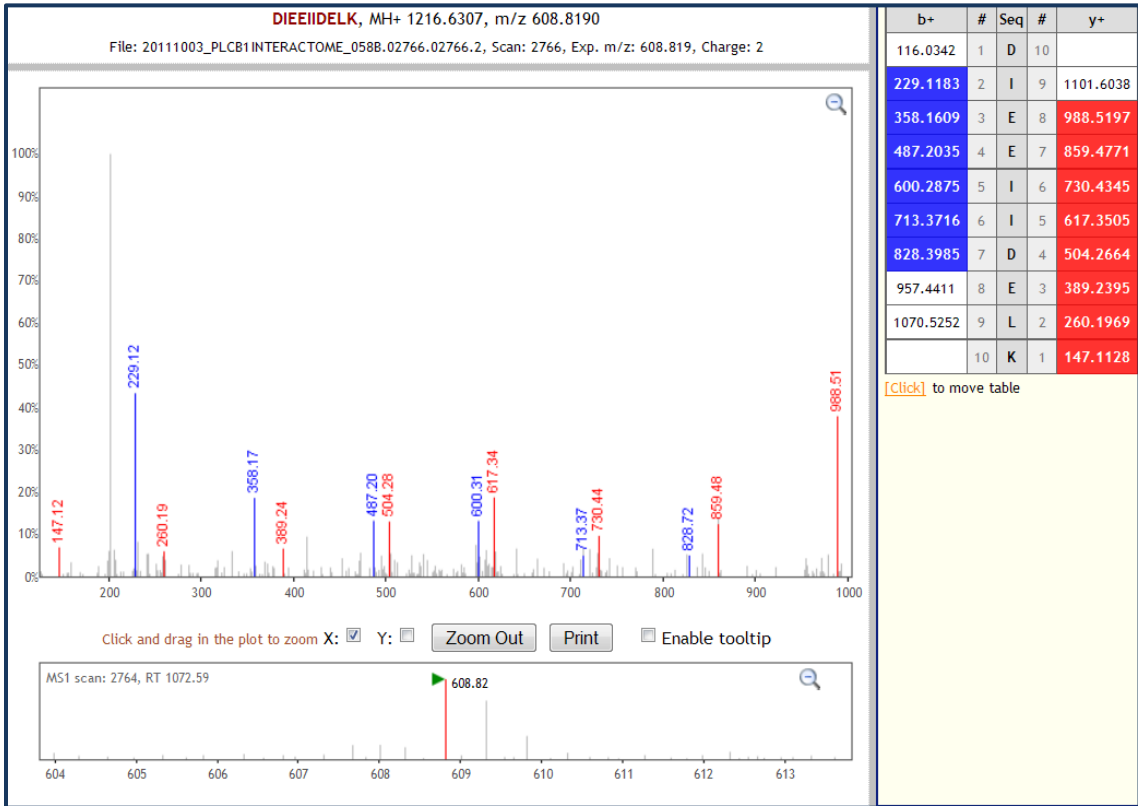
For protein name, MW, probability, % of coverage and number of spectra, refer to Table S2.

Acc. Nb.	Gene Name	m/z	Error [Da]	z	Peptide	Hyperscore	Nextscore	Expect
Q9D6J6	Ndufv2	608.819	0	2	DIEEIIDELK	551	502	2.7
Q8BK64	Ahsa1	805.7483	-0.0013	3	VFTTQELVQAFTHAPAALEADR	571	461	0.16
Q9D5T0	Atad1	953.5197	-0.0035	2	LQPSIIFIDEIDSFLR	487	395	0.81
Q9CQQ7	Atp5f1	614.3343	-0.0045	3	LGLIPEEFFQLYPK	638	479	0.094
P00920	Ca2	834.9878	-0.0088	2	AVQQPDGLAVLGIFLK	487	410	0.11
P60766	Cdc42	618.3279	-0.0039	3	NVFDEAILAALEPPEPK	573	468	0.32
Q6NVF9	Cpsf6	818.0988	-0.003	3	AVSDASAGDYGSAIETLVTAISLIK	639	506	0.043
Q99LI7	Cstf3	869.4747	-0.0055	2	FLAFESNIGDLASILK	486	357	0.11
O35343	Kpna4	604.3473	-0.0064	3	DAQVVQVVDGLSNILK	666	538	0.29
Q08288	Lyar	815.4334	0.0015	2	ELLQQISAFDNVPR	513	390	0.063
Q9DBD5	Pelp1	776.4771	0.0012	2	LLLLESISGLLQPR	419	348	0.28
O08709	Prdx6	763.9286	-0.0034	2	DLAILLGMLDPVEK	515	425	0.66
P46061	Rangap1	630.847	0.0003	2	TAVLDAIDALMK	462	373	1.3
P32067	Ssb	735.3854	-0.0019	2	GSIFAVFDSIQSAK	487	374	0.07
P63028	Tpt1	565.6139	-0.0027	3	DLISHDELFSDIYK	536	417	0.21
P62960	Ybx1	898.4153	-0.0047	2	SVGDGETVEFDVVEGEK	573	385	0.0018

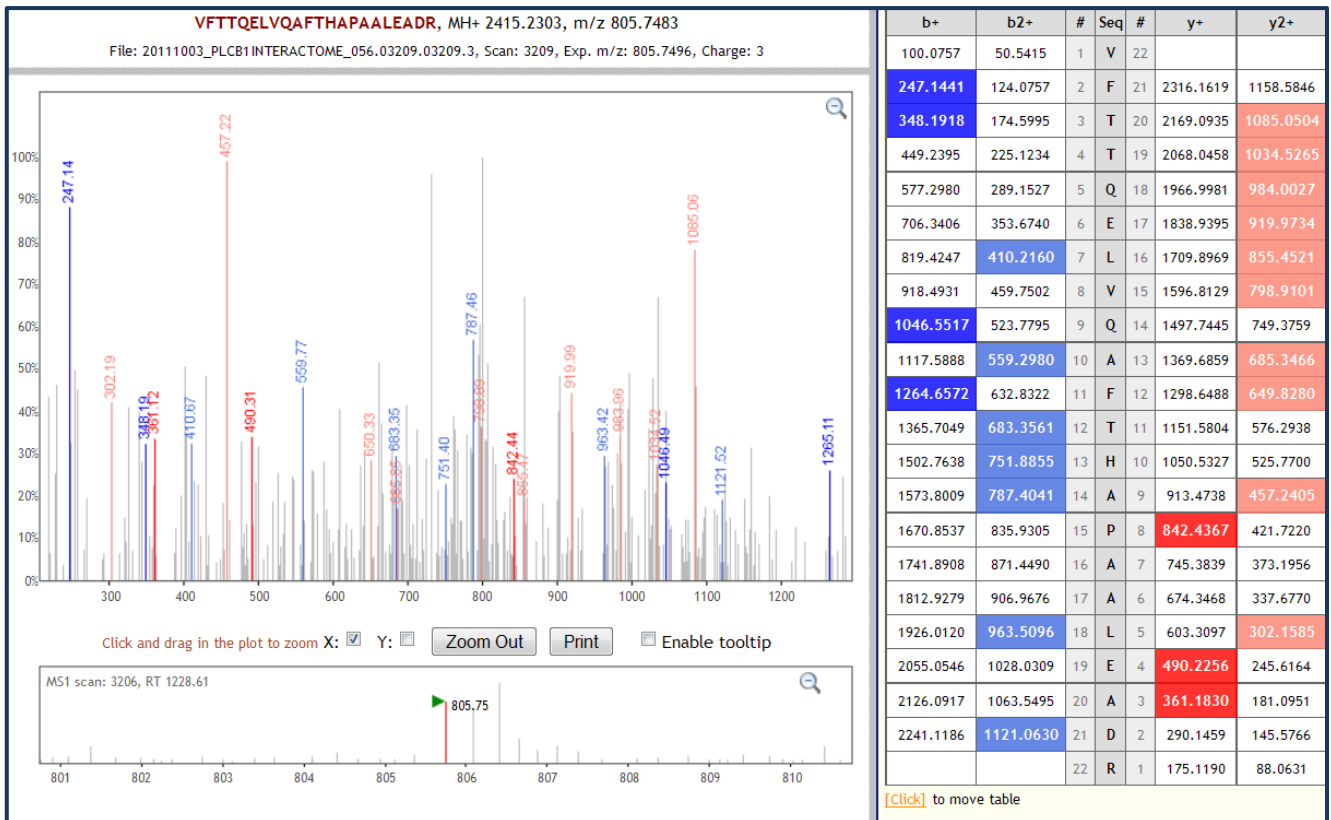
### Figure S1: Spectra of single-peptide-based protein identification

MS/MS spectra for each peptide listed in Table S3 are reported. Captions originated from the Lorikeet spectrum viewer integrated within the Trans Proteomic Pipeline v.4.6.2 (ISB, Seattle, USA). Spectra are labeled with the detected masses and a Table of the theoretical fragment assignments is provided on the right side.

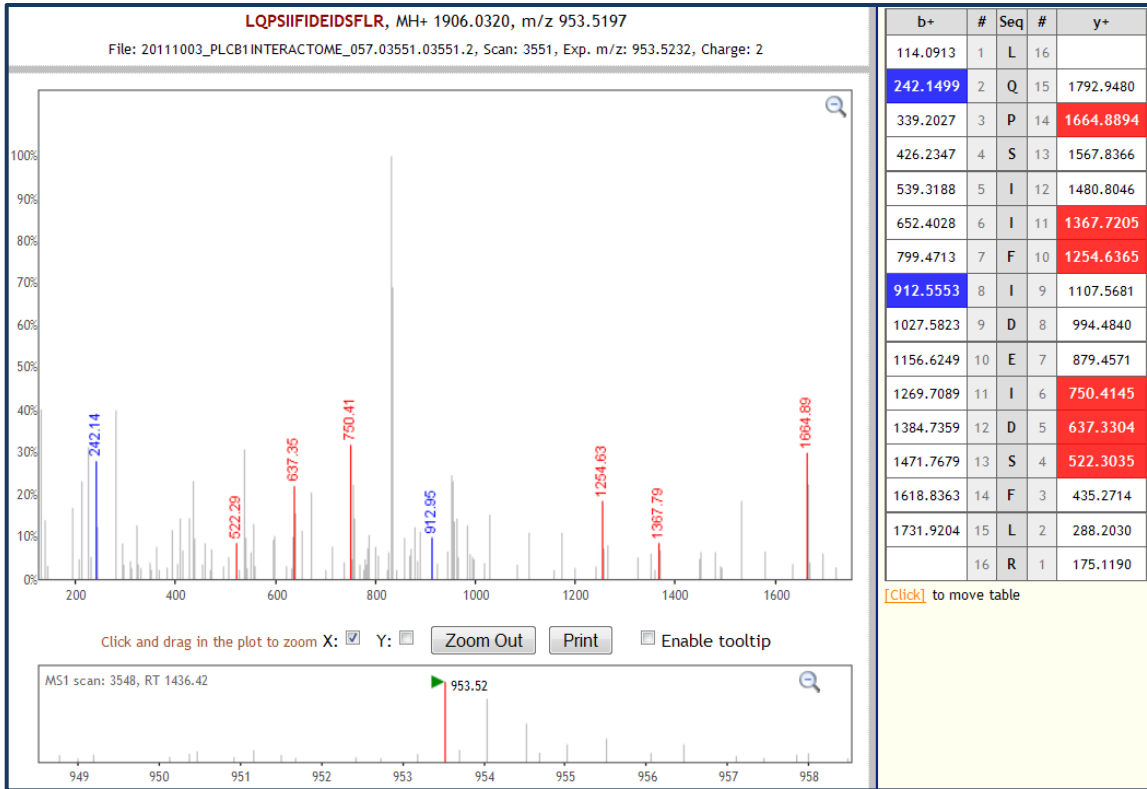
#### Q9D6J6\_Ndufv2\_NADH dehydrogenase [ubiquinone] flavoprotein 2, isoform 2



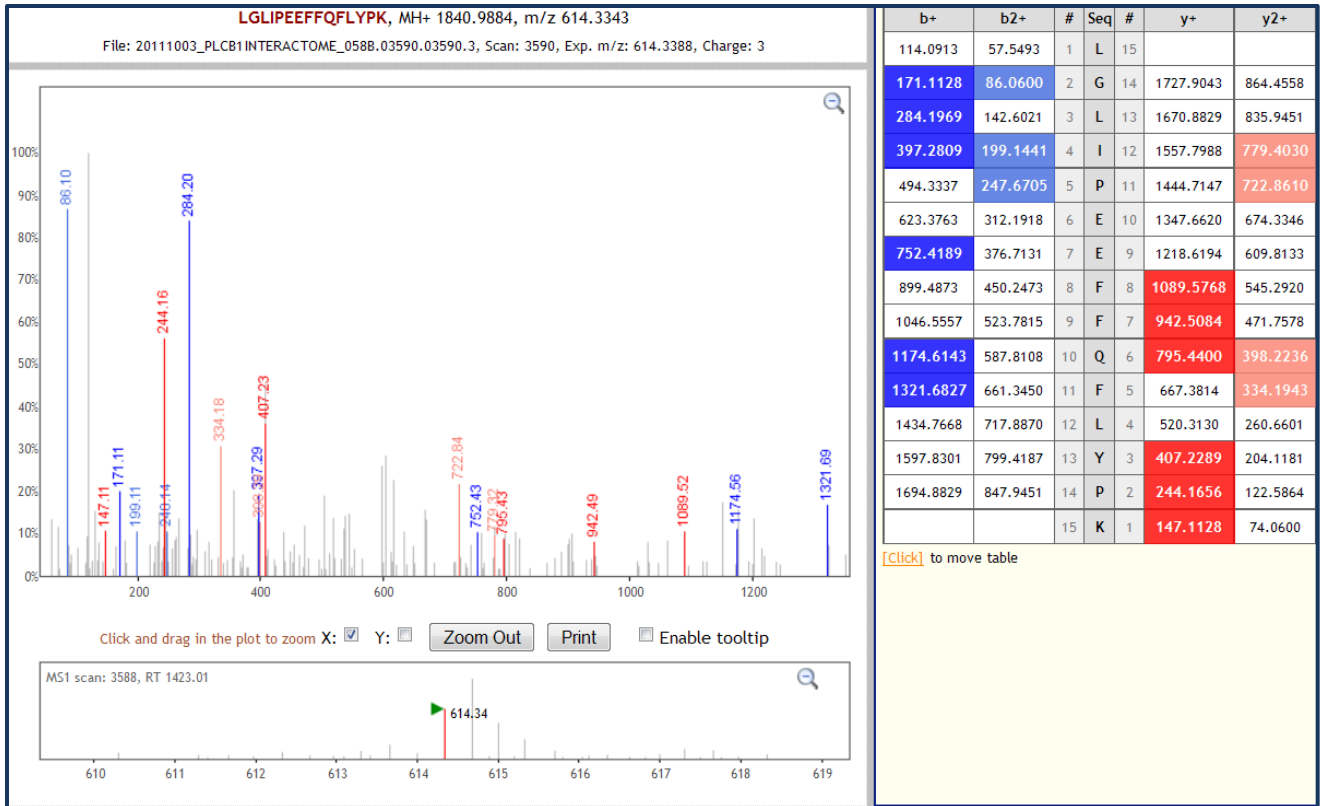
#### Q8BK64\_Ahsa1\_Activator of 90 kDa heat shock protein ATPase homolog 1



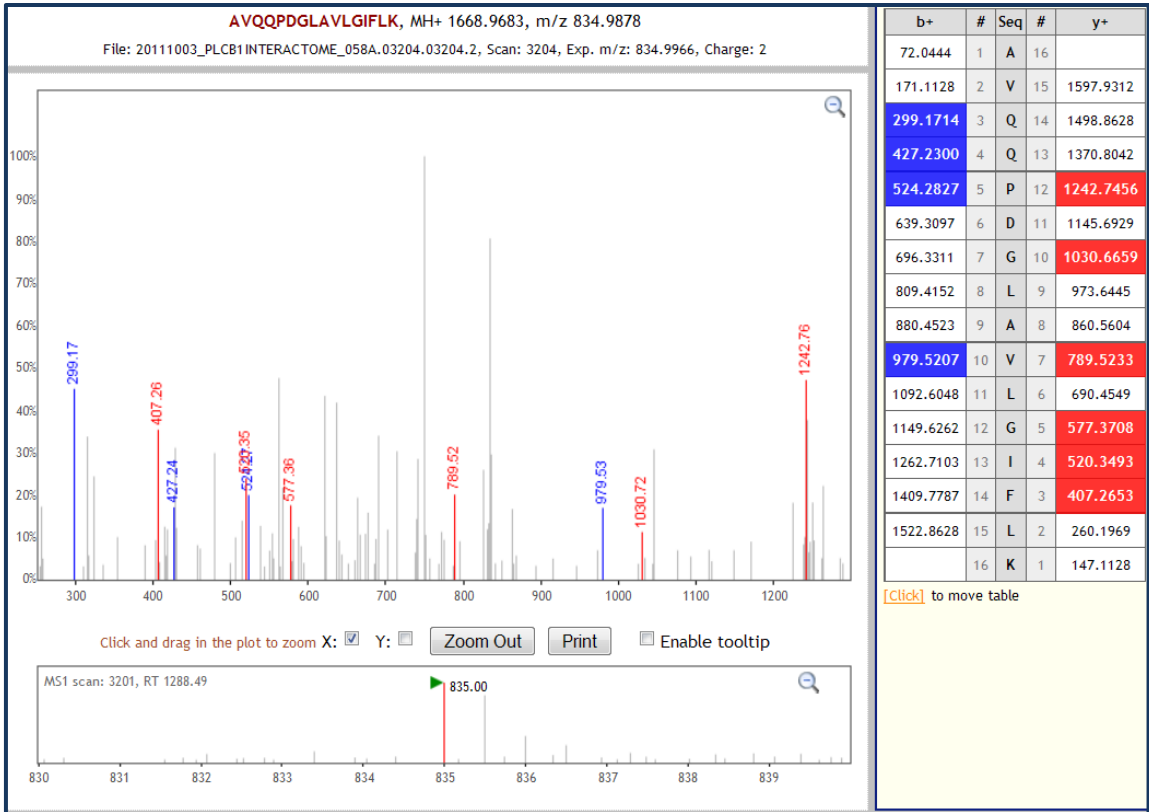
## Q9D5T0\_Atad1\_ATPase family AAA domain-containing protein 1



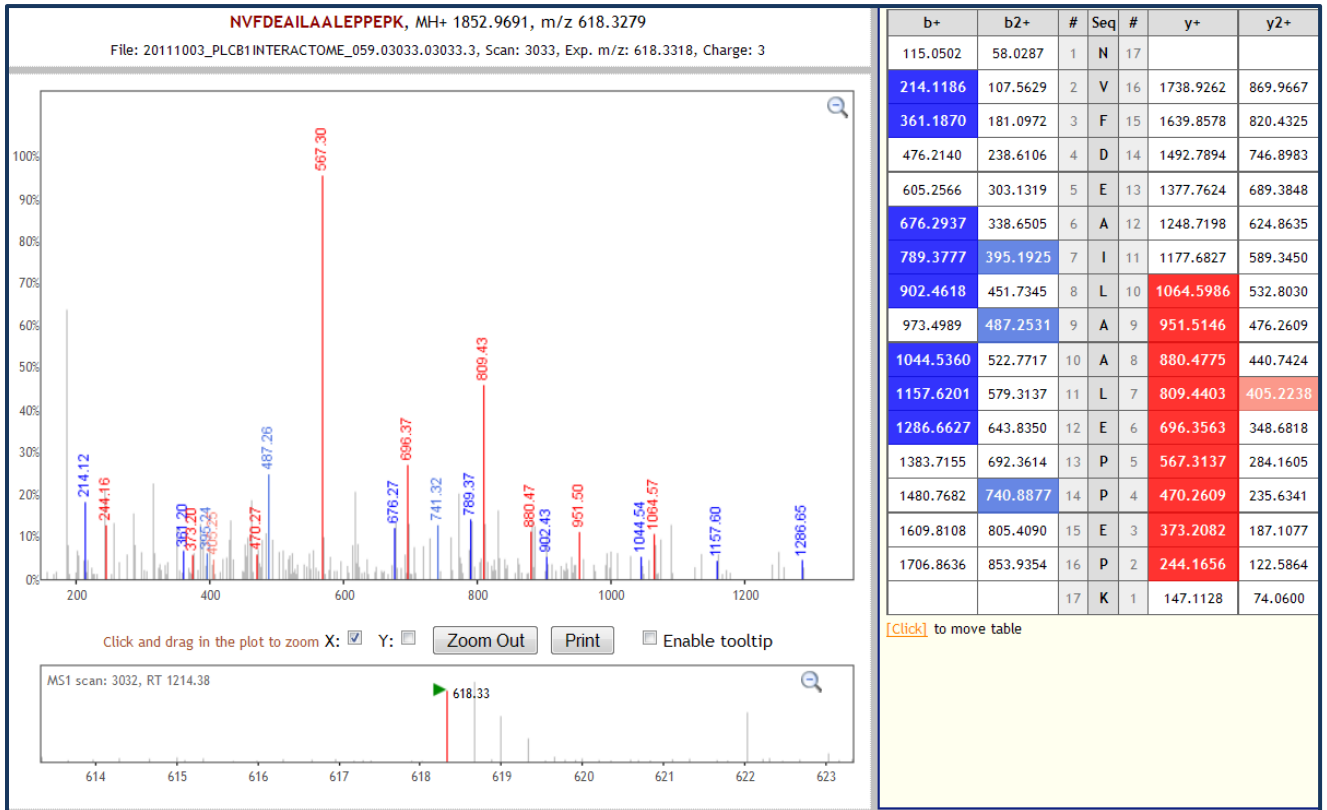
## Q9CQQ7\_Atp5f1\_ATP synthase subunit b



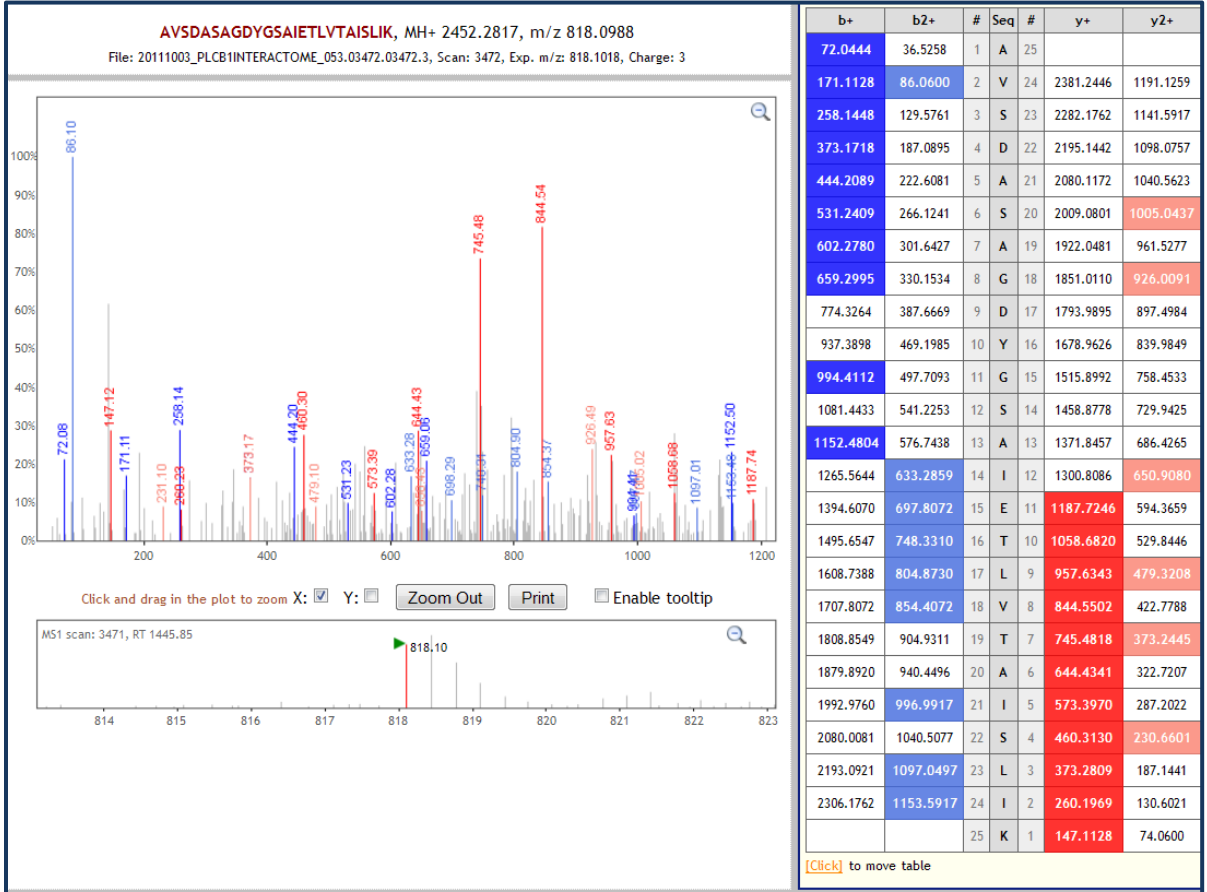
## P00920\_Ca2\_Carbonic anhydrase 2



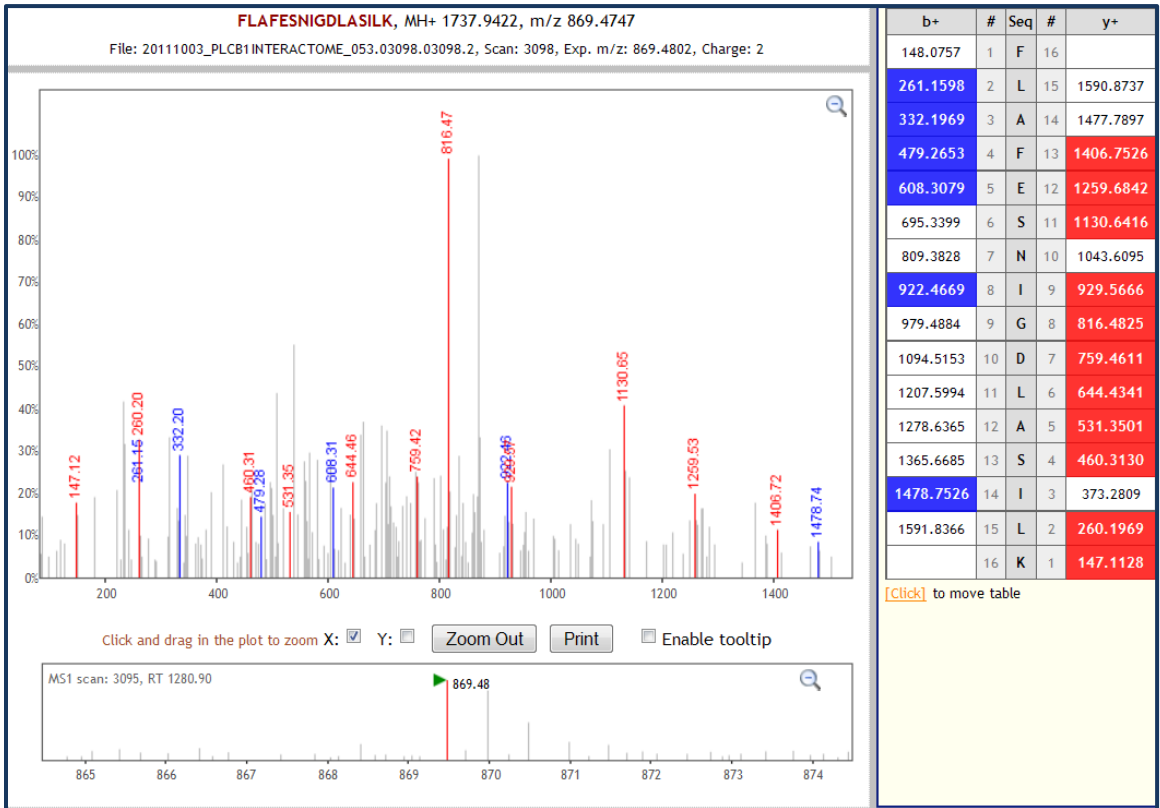
## P60766\_Cdc42\_Cell division control protein 42 homolog



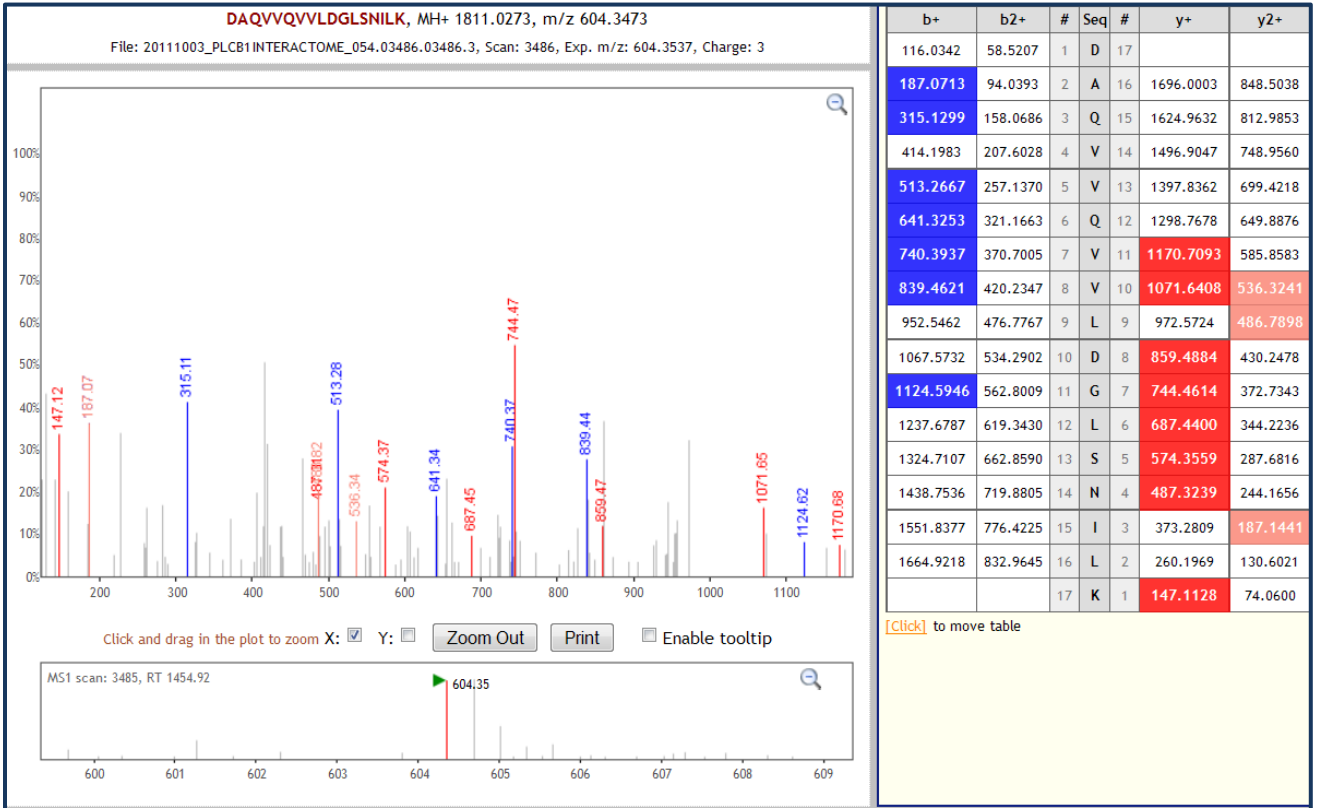
## Q6NVF9\_Cpsf6\_Cleavage and polyadenylation specificity factor subunit 6



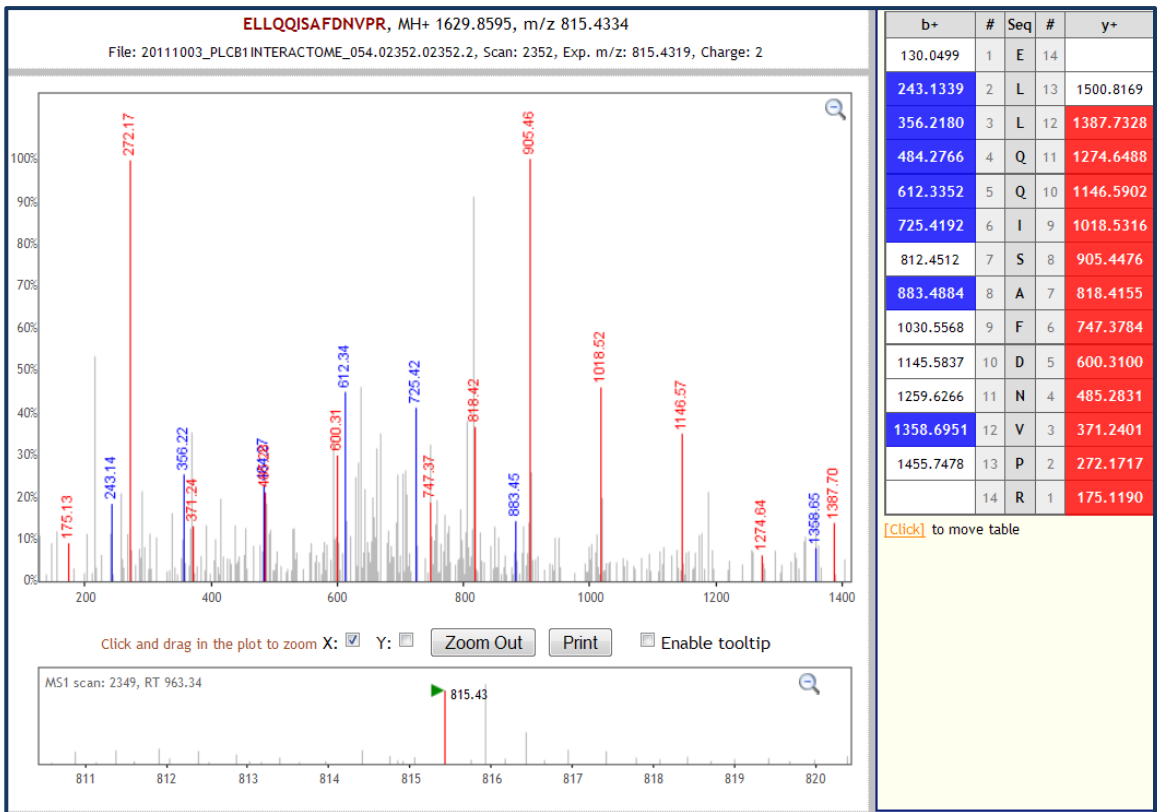
## Q99LI7\_Cstf3\_Cleavage stimulation factor subunit 3



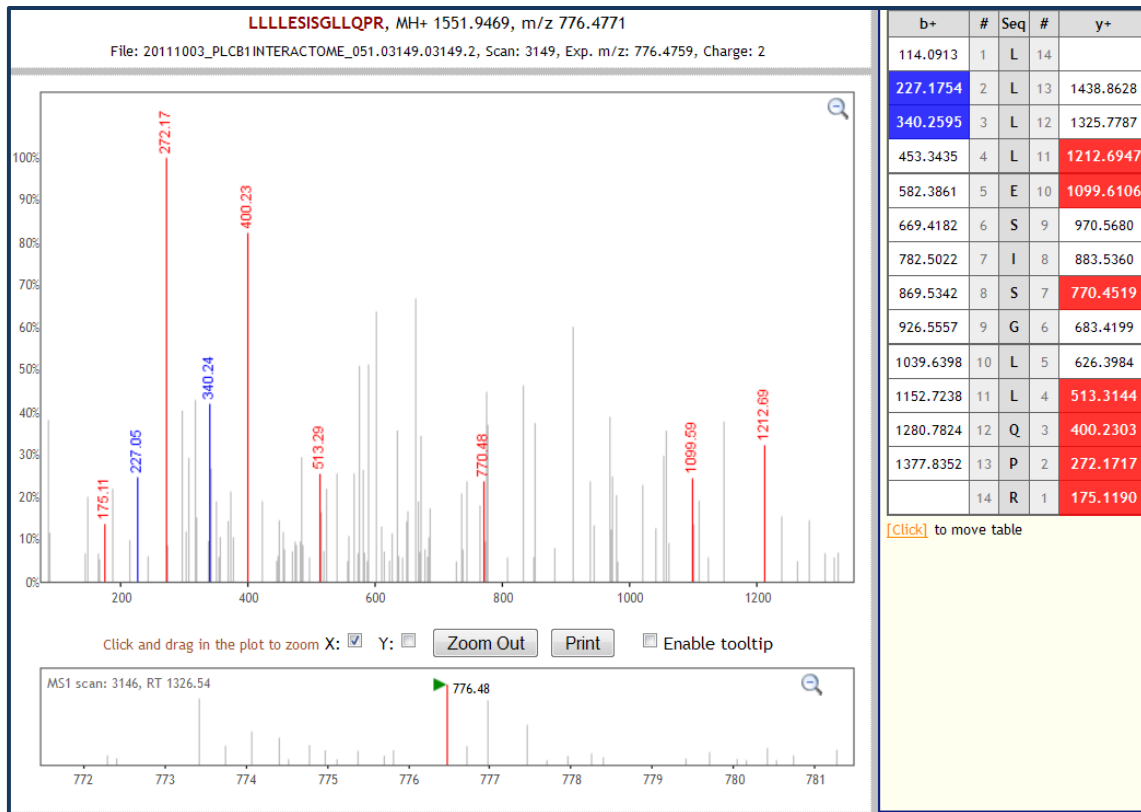
### Q05343\_Kpna4\_Importin subunit alpha-4



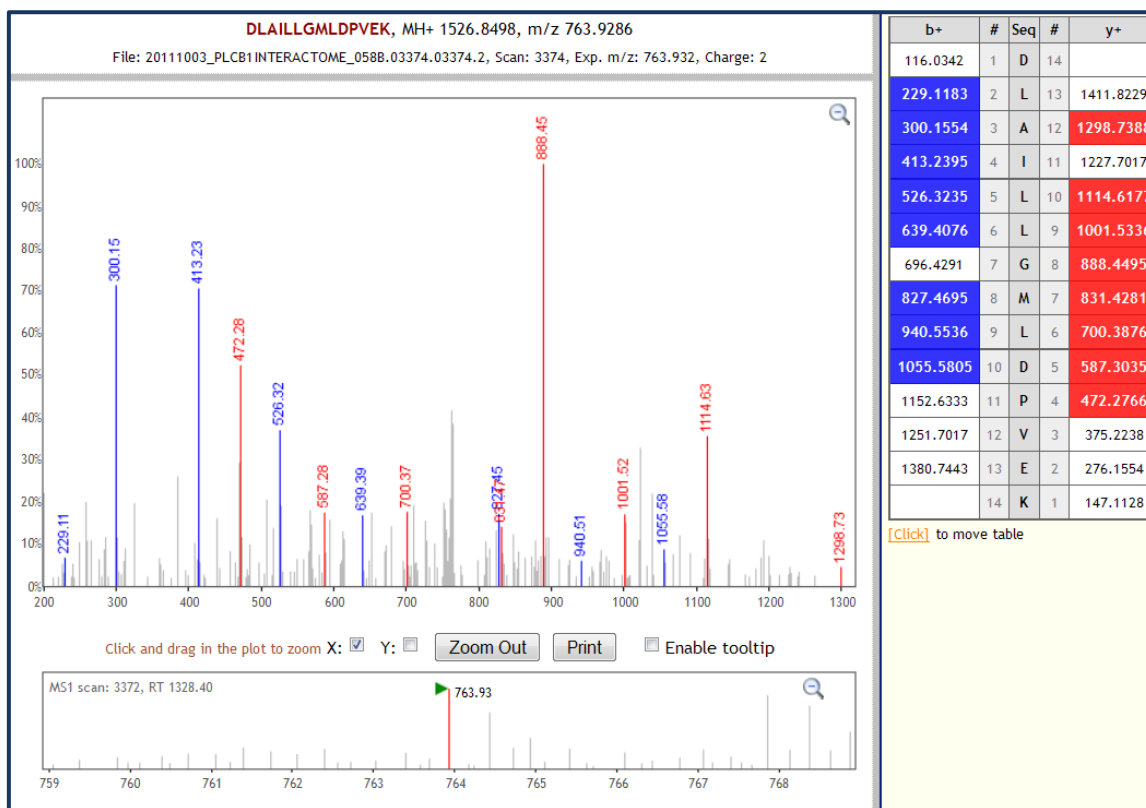
### Q08288\_Lyar\_Cell growth-regulating nucleolar protein



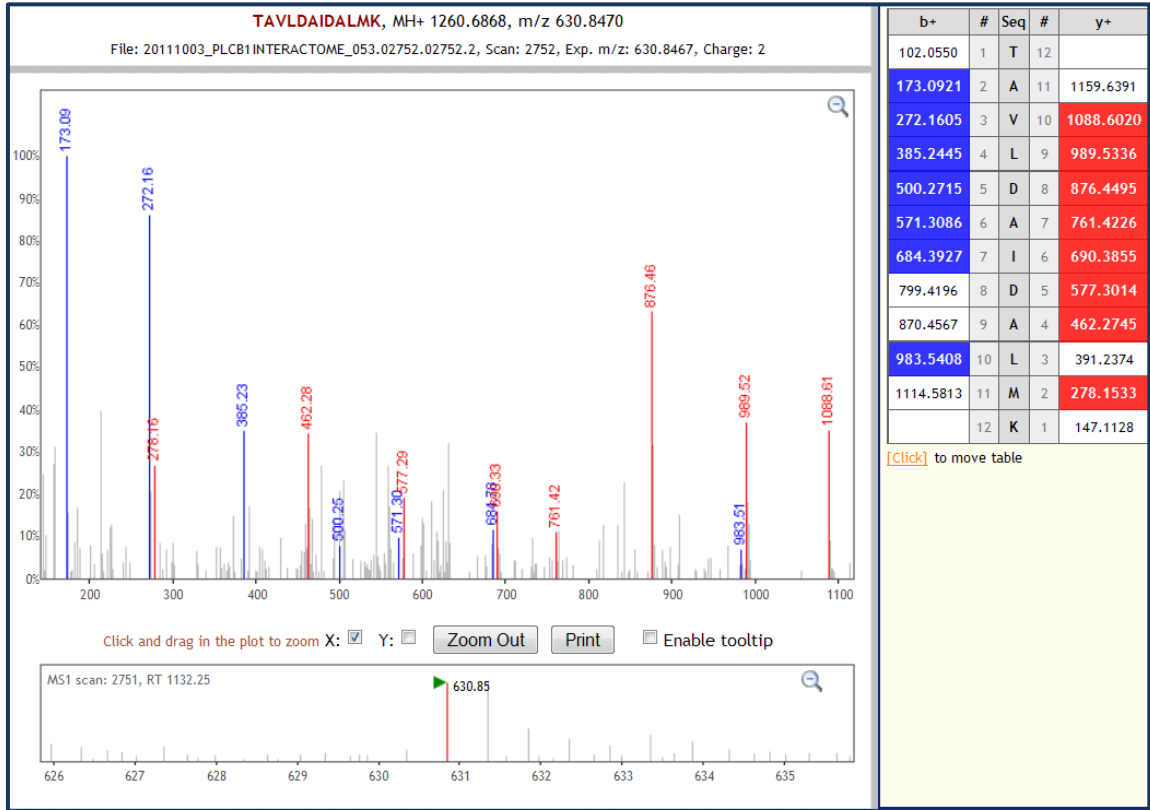
## Q9DBD5\_Pelp1\_Proline-, glutamic acid- and leucine-rich protein 1



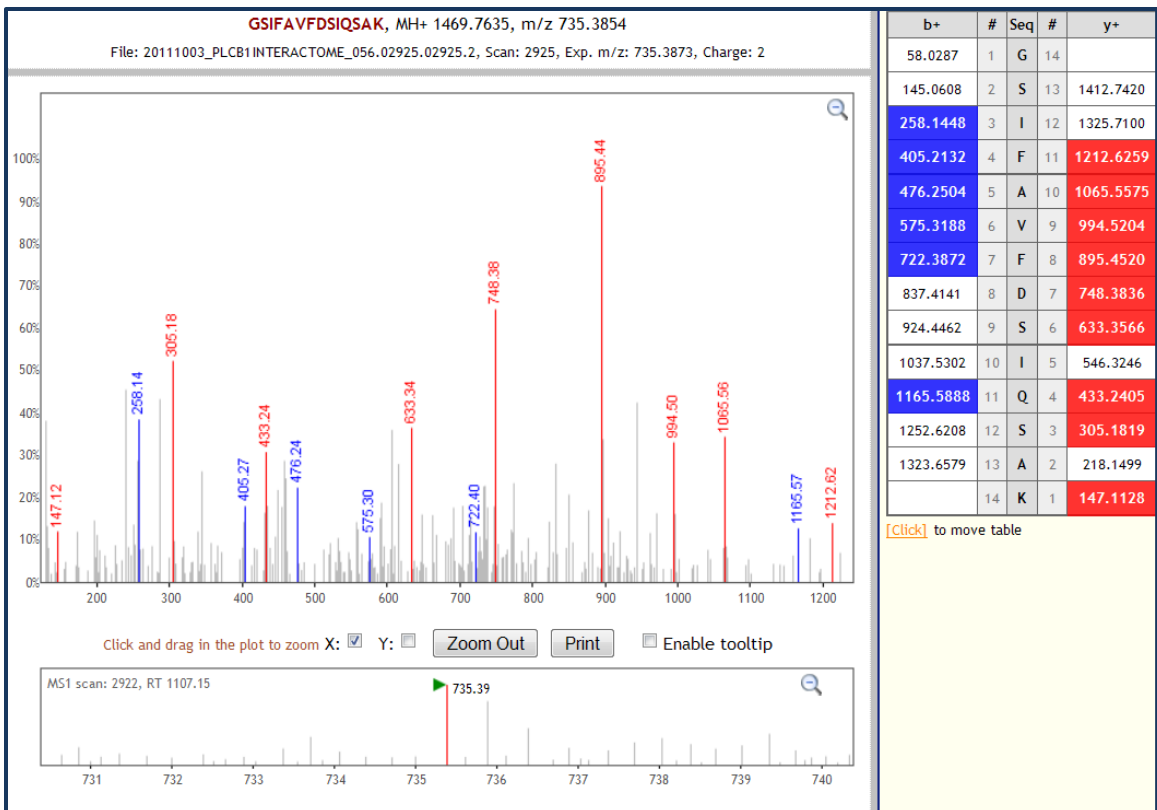
## O08709\_Prdx6\_Peroxiredoxin-6



## P46061\_Rangap1\_RanGTPase-activating protein 1

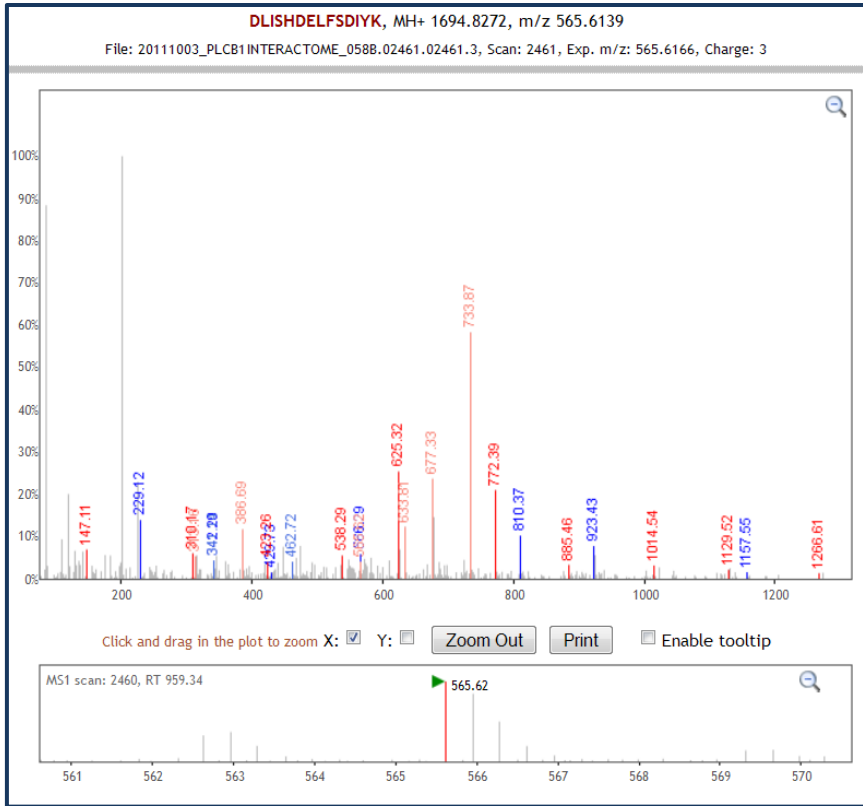


## P32067\_Ssb\_Lupus La protein homolog





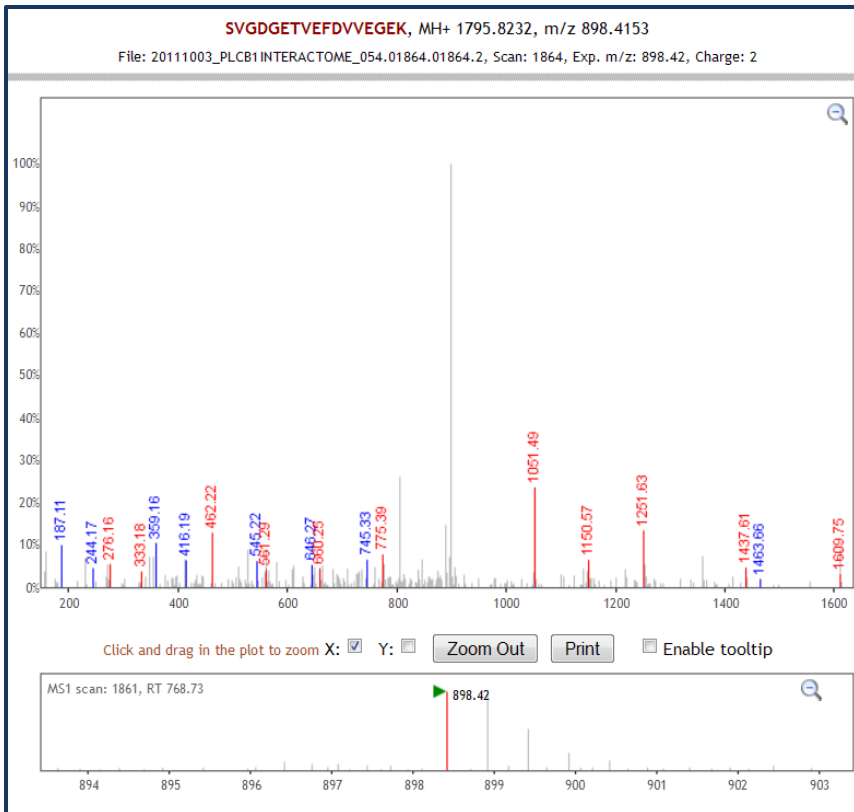
## P63028\_Tpt1\_Translationally-controlled tumor protein



b+	b2+	#	Seq #	y+	y2+
116.0342	58.5207	1	D 14		
229.1183	115.0628	2	L 13	1579.8003	790.4038
342.2023	171.6048	3	I 12	1466.7162	733.8617
429.2344	215.1208	4	S 11	1353.6321	677.3197
566.2933	283.6503	5	H 10	1266.6001	633.8037
681.3202	341.1638	6	D 9	1129.5412	565.2742
810.3628	405.6850	7	E 8	1014.5142	507.7608
923.4469	462.2271	8	L 7	885.4716	443.2395
1070.5153	535.7613	9	F 6	772.3876	386.6974
1157.5473	579.2773	10	S 5	625.3192	313.1632
1272.5743	636.7908	11	D 4	538.2871	269.6472
1385.6583	693.3328	12	I 3	423.2602	212.1337
1548.7217	774.8645	13	Y 2	310.1761	155.5917
		14	K 1	147.1128	74.0600

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## P62960\_Ybx1\_Nuclease-sensitive element-binding protein 1



b+	#	Seq #	y+
88.0393	1	S 17	
187.1077	2	V 16	1708.7912
244.1292	3	G 15	1609.7228
359.1561	4	D 14	1552.7013
416.1776	5	G 13	1437.6744
545.2202	6	E 12	1380.6529
646.2679	7	T 11	1251.6103
745.3363	8	V 10	1150.5626
874.3789	9	E 9	1051.4942
1021.4473	10	F 8	922.4516
1136.4742	11	D 7	775.3832
1235.5426	12	V 6	660.3563
1334.6111	13	V 5	561.2879
1463.6536	14	E 4	462.2195
1520.6751	15	G 3	333.1769
1649.7177	16	E 2	276.1554
	17	K 1	147.1128

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